Summary

The summary file contains summary information for all the raw files processed with a single MaxQuant run. The summary information consists of some MaxQuant parameters, information of the raw file contents, and statistics on the peak detection. Based on this file a quick overview can be gathered on the quality of the data in the raw file.

The last row in this file contains the summary information for each column on each of the processed files.

Name	Separator	Description
Raw file		The raw file processed.
Experiment		Experiment name assigned to this LC-MS run in the experimental design.
Enzyme		The protease used to digest the protein sample.
Enzyme mode		The protease used to digest the protein sample.
Enzyme first search		The protease used for the first search.
Enzyme mode first search		The protease used for the first search.
Use enzyme first search		Marked with '+' when a different protease setup was used for the first search.
Variable modifications		The variable modification(s) used during the identification of peptides.
Variable modifications first search		The variable modification(s) used during the first search.
Use variable modifications first search		Marked with '+' when different variable modifications were used for the first search.
Multiplicity		The number of labels used.
Max. missed cleavages		The maximum allowed number of missed cleavages.
Max. labeled AAs		The maximum allowed of labeled amino acids in a peptide amino acid sequence.
Labels0		The labels used in the labeling experiment. Allowed values for X: 0=light; 1=medium; 2=heavy label partner.
Labels1		The labels used in the labeling experiment. Allowed values for X: 0=light; 1=medium; 2=heavy label partner.
Labels2		The labels used in the labeling experiment. Allowed values for X: 0=light; 1=medium; 2=heavy label partner.
LC-MS run type		The type of LC-MS run. Usually it will be 'Standard' which refers to a conventional shotgun proteomics run with data-dependent MS/MS.
Time-dependent recalibration		When marked with '+', time-dependent recalibration was applied to improve the data quality.
MS		The number of MS spectra recorded in this raw file.
MS/MS		The number of tandem MS spectra recorded in this raw file.
MS/MS Submitted		The number of tandem MS spectra submitted for analysis.
MS/MS Submitted (SIL)		The number of tandem MS spectra submitted for analysis, where the precursor ion was detected as part of a labeling cluster.
MS/MS Submitted (ISO)		The number of tandem MS spectra submitted for analysis, where the precursor ion was detected as an isotopic pattern.
MS/MS Submitted (PEAK)		The number of tandem MS spectra submitted for analysis, where the precursor ion was detected as a single peak.
MS/MS Identified		The total number of identified tandem MS spectra.
MS/MS Identified (SIL)		The total number of identified tandem MS spectra, where the precursor ion was detected as part of a labeling cluster.
MS/MS Identified (ISO)		The total number of identified tandem MS spectra, where the precursor ion was detected as an isotopic pattern.
MS/MS Identified (PEAK)		The total number of identified tandem MS spectra, where the precursor ion was detected as a single peak.
MS/MS Identified [%]		The percentage of identified tandem MS spectra.
MS/MS Identified (SIL) [%]		The percentage of identified tandem MS spectra, where the precursor ion was detected as part of a labeling cluster.
MS/MS Identified (ISO) [%]		The percentage of identified tandem MS spectra, where the precursor ion was detected as an isotopic pattern.
MS/MS Identified (PEAK) [%]		The percentage of identified tandem MS spectra, where the precursor ion was detected as a single peak.
Peptide Sequences Identified		The total number of unique peptide amino acid sequences identified from the recorded tandem mass spectra.
Peaks		The total number of peaks detected in the full scans.
Peaks Sequenced		The total number of peaks sequenced by tandem MS.

Peaks Sequenced [%]	The percentage of peaks sequenced by tandem MS.
Peaks Repeatedly Sequenced	The total number of peaks repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Peaks Repeatedly Sequenced [%]	The percentage of peaks repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Isotope Patterns	The total number of detected isotope patterns.
Isotope Patterns Sequenced	The total number of isotope patterns sequenced by tandem MS.
Isotope Patterns Sequenced (z>1)	The total number of isotope patterns sequenced by tandem MS with a charge state of 2 or more.
Isotope Patterns Sequenced [%]	The percentage of isotope patterns sequenced by tandem MS.
Isotope Patterns Sequenced (z>1) [%]	The percentage of isotope patterns sequenced by tandem MS with a charge state of 2 or more.
Isotope Patterns Repeatedly Sequenced	The total number of isotope patterns repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Isotope Patterns Repeatedly Sequenced [%]	The percentage of isotope patterns repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Multiplets	The total number of detected labeling triplets.
Multiplets z=1	The total number of detected labeling triplets with a charge state of 1.
Multiplets z=2	The total number of detected labeling triplets with a charge state of 2.
Multiplets z=3	The total number of detected labeling triplets with a charge state of 3.
Multiplets z=4	The total number of detected labeling triplets with a charge state of 4.
Multiplets z=5	The total number of detected labeling triplets with a charge state of 5.
Multiplets z=6	The total number of detected labeling triplets with a charge state of 6.
Multiplets z=7	The total number of detected labeling triplets with a charge state of 7.
Multiplets Sequenced	The total number of labeling triplets sequenced by tandem MS.
Multiplets Sequenced [%]	The percentage of labeling triplets sequenced by tandem MS.
Multiplets Repeatedly Sequenced	The total number of labeling triplets repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Multiplets Repeatedly Sequenced [%]	The percentage of labeling triplets repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Multiplets Identified	The total number of labeling triplets identified.
Multiplets Identified [%]	The percentage of labeling triplets identified.
Recalibrated	When marked with '+', the masses taken from the raw file were recalibrated.
Av. Absolute Mass Deviation [ppm]	The average absolute mass deviation found comparing to the identification mass in parts per million.
Mass Standard Deviation [ppm]	The standard deviation of the mass deviation found comparing to the identification mass in parts per million.
Av. Absolute Mass Deviation [mDa]	The average absolute mass deviation found comparing to the identification mass in milli-Dalton.
Mass Standard Deviation [mDa]	The standard deviation of the mass deviation found comparing to the identification mass in milli-Dalton.
Label free norm param	The normalization factor used to scale the intensity values in a label-free experiment.

Evidence

The evidence file combines all the information about the identified peptides and normally is the only file required for processing the results. Additional information about the peptides, modifications, proteins, etc. can be found in the other files by unique identifier linkage.

Name	Separator	Description
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column 'Sequence'.
K Count		The number of instances of K contained within the sequence. The value for this can reliably be determined in the case of labeling partners based on the distance between the partners. These counts are used to solidify the peptide identification process.
R Count		The number of instances of R contained within the sequence. The value for this can reliably be determined in the case of labeling partners based on the distance between the partners. These counts are used to solidify the peptide identification process.
Modifications		Post-translational modifications contained within the identified peptide sequence.
Modified sequence		Sequence representation including the post-translational modifications (abbreviation of the modification in brackets before the modified AA). The sequence is always surrounded by underscore characters ('_').
Oxidation (M) Probabilities		Sequence representation of the peptide including PTM positioning probabilities ([01], where 1 is best match) for 'Oxidation (M)'.
Oxidation (M) Score Diffs		Sequence representation for each of the possible PTM positions in each possible configuration, the difference is calculated between the identification score with the PTM added to that position and the best scoring identification where no PTM is added to that position. When this value is negative, it is unlikely that the particular modification is located at this position.
Acetyl (Protein N-term)		The number of occurrences of the modification 'Acetyl (Protein N-term)'.
Oxidation (M)		The number of occurrences of the modification 'Oxidation (M)'.
Missed cleavages		Number of missed enzymatic cleavages.
Proteins		The identifiers of the proteins this particular peptide is associated with.
Leading Proteins		The identifiers of the proteins in the proteinGroups file, with this protein as best match, this particular peptide is associated with. When multiple matches are found here, the best scoring protein can be found in the 'Leading Razor Protein' column.
Leading Razor Protein		The identifier of the best scoring protein, from the proteinGroups file this, this peptide is associated to.
Gene Names		Names of genes this peptide is associated with.
Protein Names		Names of proteins this peptide is associated with.
Туре		The type of MS/MS spectrum this sequence is derived from. MSMS – MS/MS for an unidentified peak. ISO-MSMS – MS/MS from an identified isotope cluster. MULTI-MSMS – MS/MS from an identified labeling cluster.
Labeling State		Labeling state of the precursor isotope pattern used to identify the peptide.
Raw file		The name of the RAW-file the mass spectral data was derived from.
Experiment		
MS/MS m/z		The m/z used for fragmentation (not necessarily the monoisotopic m/z).
Charge		The charge-state of the precursor ion.
m/z		The recalibrated mass-over-charge value of the precursor ion.
Mass		The predicted monoisotopic mass of the identified peptide sequence.
Resolution		The resolution of precursor ion measured in Full Width at Half Maximum (FWHM).
Uncalibrated - Calibrated m/z [ppm]		The difference between the uncalibrated and recalibrated mass-over-charge value of the precursor ion measured in parts-per-million. This gives an indication of the mass drift in the original data, which was automatically corrected by MaxQuant.

Uncalibrated - Calibrated m/z [Da]	The difference between the uncalibrated and recalibrated mass-over-charge value of the precursor ion measured in parts-per-million. This gives an indication of the mass drift in the original data, which was automatically corrected by MaxQuant.
Mass Error [ppm]	Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence in parts per million.
Mass Error [Da]	Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence in milli-Dalton.
Uncalibrated Mass Error [ppm]	Mass error of the uncalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence.
	Note: This column can contain missing values (denoted as NaN).
Uncalibrated Mass Error [Da]	Mass error of the uncalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence.
	Note: This column can contain missing values (denoted as NaN).
Max intensity m/z 0	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Max intensity m/z 1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Max intensity m/z 2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Retention time	The uncalibrated retention time in minutes in the elution profile of the precursor ion.
Retention length	The total retention time of the peak (last timepoint – first timepoint).
Calibrated retention time	The recalibrated retention time in minutes in the elution profile of the precursor ion.
Calibrated retention time start	The recalibrated retention start in minutes in the elution profile of the precursor ion.
Calibrated retention time finish	The recalibrated retention finish in minutes in the elution profile of the precursor ion.
Retention time calibration	The difference in minutes between the uncalibrated and recalibrated retention time. This gives an indication of the retention time drift in the original data, which was automatically corrected by MaxQuant.
Match time difference	Note: This column can contain missing values (NaN). When the option 'match between runs' is used in MaxQuant,
Water time directories	this value indicates the time difference between the feature from the raw file it was taken from and the feature from the raw file it was matched to.
Match m/z difference	When the option 'match between runs' is used in MaxQuant, this value indicates the m/z difference between the feature from the raw file it was taken from and the feature from the raw file it was matched to.
Match q-value	This is the q-value for features that have been identified by matching between runs'.
Match score	The andromeda score of the MS/MS identification that is the source of this identification by 'matching between runs'.
Number of data points	The number of data points (peak centroids) collected for this peptide feature.
Number of scans	The number of MS scans that the 3d peaks of this peptide feature are overlapping with.
Number of isotopic peaks	The number of isotopic peaks contained in this peptide feature.
PIF	Short for Parent Ion Fraction; indicates the fraction the target peak makes up of the total intensity in the inclusion window.
Fraction of total spectrum	The percentage the ion intensity makes up of the total intensity of the whole spectrum.
Base peak fraction	The percentage the parent ion intensity in comparison to the highest peak in the MS spectrum.
PEP	Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
MS/MS Count	The number of sequencing events for this sequence, which matches the number of identifiers stored in the column 'MS/MS IDs'. This number is independent of the times the AA sequence has been identified through (other) modifications (e.g. heavy label, oxidation, etc.), about which information can be found in the columns 'Labeling State' and 'Modification'.

MS/MS Scan Number	The RAW-file derived scan number of the MS/MS with the highest peptide identification score (the highest score is stored in the column 'Score').
Score	Andromeda score for the best associated MS/MS spectrum.
Delta score	Score difference to the second best identified peptide.
Combinatorics	Number of possible distributions of the modifications over the peptide sequence.
Ratio M/L	The ratio between two medium and light label partners.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L shift	
Ratio H/L	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L shift	
Ratio H/M	The ratio between two heavy and medium label partners.
Ratio H/M normalized	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M shift	
Intensity	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Reverse	When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.
Potential contaminant	When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
id	A unique (consecutive) identifier for each row in the evidence table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs	The identifier of the protein-group this redundant peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple id's can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Peptide ID	The identifier of the non-redundant peptide sequence.
Mod. peptide ID	Identifier of the associated modification summary stored in the file 'modificationSpecificPeptides.txt'.
MS/MS IDs	Identifier(s) of the associated MS/MS summary(s) stored in the file 'msms.txt'.
Best MS/MS	Identifier(s) of the best MS/MS associated spectrum stored in the file 'msms.txt'.
AIF MS/MS IDs	Identifier(s) of the associated All Ion Fragmentation MS/MS summary(s) stored in the file 'aifMsms.txt'.
Oxidation (M) site IDs	Identifier(s) of the modification summary stored in the file 'Oxidation (M)Sites.txt'.

Peptides

The peptides table contains information on the identified peptides in the processed raw-files.

Name	Separator	Description
Sequence		The amino acid sequence of the identified peptide.
N-term cleavage window		Sequence window from -8 to 8 around the N-terminal cleavage site of this peptide.
C-term cleavage window		Sequence window from -8 to 8 around the C-terminal cleavage site of this peptide.
Amino acid before		The amino acid in the protein sequence before the peptide.
First amino acid		The amino acid in the first position of the peptide sequence.
Second amino acid		The amino acid in the first position of the peptide sequence.
Second last amino acid		The amino acid in the last position of the peptide sequence.
Last amino acid		The amino acid in the last position of the peptide sequence.
Amino acid after		The amino acid in the protein sequence after the peptide.
A Count		The number of instances of the 'A' amino acid contained within the sequence.
R Count		The number of instances of the 'R' amino acid contained within the sequence.
N Count		The number of instances of the 'N' amino acid contained within the sequence.
D Count		The number of instances of the 'D' amino acid contained within the sequence.
C Count		The number of instances of the 'C' amino acid contained within the sequence.
Q Count		The number of instances of the 'Q' amino acid contained within the sequence.
E Count		The number of instances of the 'E' amino acid contained within the sequence.
G Count		The number of instances of the 'G' amino acid contained within the sequence.
H Count		The number of instances of the 'H' amino acid contained within the sequence.
I Count		The number of instances of the 'I' amino acid contained within the sequence.
L Count		The number of instances of the 'L' amino acid contained within the sequence.
K Count		The number of instances of the 'K' amino acid contained within the sequence.
M Count		The number of instances of the 'M' amino acid contained within the sequence.
F Count		The number of instances of the 'F' amino acid contained within the sequence.
P Count		The number of instances of the 'P' amino acid contained within the sequence.
S Count		The number of instances of the 'S' amino acid contained within the sequence.
T Count		The number of instances of the 'T' amino acid contained within the sequence.
W Count		The number of instances of the 'W' amino acid contained within the sequence.
Y Count		The number of instances of the 'Y' amino acid contained within the sequence.
V Count		The number of instances of the 'V' amino acid contained within the sequence.
U Count		The number of instances of the 'U' amino acid contained within the sequence.
Length		The length of the sequence stored in the column "Sequence".
Missed cleavages		Number of missed enzymatic cleavages.
Mass		Monoisotopic mass of the peptide.
Proteins		Identifiers of proteins this peptide is associated with.
Leading razor protein		Identifiers of the best scoring protein this peptide is associated with.
Start position		Position of the first amino acid of this peptide in the protein sequence. (one-based)
End position		Position of the last amino acid of this peptide in the protein sequence. (one-based)
Gene names		Names of genes this peptide is associated with.
Protein names		Names of proteins this peptide is associated with.

Unique (Groups)	When marked with '+', this particular peptide is unique to a single protein group in the proteinGroups file.
Unique (Proteins)	When marked with '+', this particular peptide is unique to a single protein sequence in the fasta file(s).
Charges	All charge states that have been observed.
PEP	Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
Score	Highest Andromeda score for the associated MS/MS spectra.
Experiment g1_GK1_Chromatin_AL	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_CPT	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_CR	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_HepHek	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_hilR	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_loIR	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_mH2A_1	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_mH2A_2	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_mH2A_3	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_TNFa_1	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_TNFa_2	Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_TNFa_3	Number of evidence entries for this 'Experiment'.
Experiment g1_KW10_110506	Number of evidence entries for this 'Experiment'.
Experiment g1_KW10_131126	Number of evidence entries for this 'Experiment'.
Experiment g1_KW10_140117	Number of evidence entries for this 'Experiment'.
Experiment g1_KW11_130125	Number of evidence entries for this 'Experiment'.
Experiment g1_KW11_140104_nE	Number of evidence entries for this 'Experiment'.
Experiment g1_KW11_140104_wE	Number of evidence entries for this 'Experiment'.
Experiment g1_KW12_130317	Number of evidence entries for this 'Experiment'.
Experiment g1_KW12_131223	Number of evidence entries for this 'Experiment'.
Experiment g1_KW13_130328	Number of evidence entries for this 'Experiment'.
Experiment g1_KW14_130317	Number of evidence entries for this 'Experiment'.
Experiment g1_KW15_130317	Number of evidence entries for this 'Experiment'.
Experiment g1_KW17_130319	Number of evidence entries for this 'Experiment'.
Experiment g1_KW8_120517	Number of evidence entries for this 'Experiment'.
Experiment g1_KW8_131126	Number of evidence entries for this 'Experiment'.
Experiment g1_KW8_140117	Number of evidence entries for this 'Experiment'.
Experiment g1_KW9_120425	Number of evidence entries for this 'Experiment'.
Experiment g1_KW9_120510	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H10	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H11	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H12	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H4	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H5	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H6	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H7	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H8	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H9	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa1_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa1_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa2_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa2_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa2_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa3_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa3_2	Number of evidence entries for this 'Experiment'.
	Number of evidence entries for this 'Experiment'.

Experiment g1_PX1194_PCa4_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa4_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa4_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa5_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa5_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa5_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa6_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa7_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18486	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18498	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18499	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18501	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18502	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18504	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18505	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18507	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18508	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18510	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18511	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18516	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18517	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18519	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18520	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18522	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18523	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18852	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18855	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18858	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18861	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18862	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18870	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18871	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18907	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18909	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18912	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18913	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18916	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19092	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19093	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19098	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19099	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19101	Number of evidence entries for this 'Experiment'.
Experiment g1_FX1406_GM19102	Number of evidence entries for this 'Experiment'.
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Experiment g1_PX1406_GM19108	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19114	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19116	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19119	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19127	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19128	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19130	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19131	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19137	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19138	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19140	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19143	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19144	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19147	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19152	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19153	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19160	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19172	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19192	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19193	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19200	Number of evidence entries for this 'Experiment'.
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Experiment g1_PX1406_GM19203	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19204	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19207	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19209	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19222	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19257	Number of evidence entries for this 'Experiment'.
Experiment g1_PX151_Rep1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX151_Rep2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX151_Rep3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1143-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1143-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1143-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1599-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1599-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1599-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1937-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1937-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1937-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC202-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC202-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC202-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC2218-1	Number of evidence entries for this 'Experiment'.
Experiment g1_FX309_HCC2218-2	Number of evidence entries for this 'Experiment'.
Experiment g1_FX309_HCC2218-3	Number of evidence entries for this 'Experiment'.
Experiment g1_FX309_HMEC1-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC1-2	Number of evidence entries for this 'Experiment'.
Experiment g1_FX309_HMEC1-3	Number of evidence entries for this 'Experiment'.
Experiment g1_FX309_HMEC2-1	Number of evidence entries for this 'Experiment'.
	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC2-2	
Experiment g1_PX309_HMEC2-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMTS1-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMTS1-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMTS1-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MCF10a-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MCF10a-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MCF10a-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MDAMB453-1	Number of evidence entries for this 'Experiment'.
Experiment	Number of evidence entries for this 'Experiment'.
g1_PX309_MDAMB453-2	
Experiment	Number of evidence entries for this 'Experiment'.
g1_PX309_MDAMB453-3	
Experiment g1_PX309_MFM223-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MFM223-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MFM223-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_0h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_0h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_0h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_BSA_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_BSA_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_BSA_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_FN_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_FN_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_FN_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_GFR_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_GFR_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_GFR_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_LAM_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_LAM_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_LAM_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 12h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 12h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 12h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 24h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 24h_2	Number of evidence entries for this 'Experiment'.

Experiment g1_PX359_Matr 24h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 30h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 30h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 30h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr dil_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr dil_2 Experiment g1_PX359_Matr dil_3	Number of evidence entries for this 'Experiment'. Number of evidence entries for this 'Experiment'.
Experiment g1_FX359_Matt dil_3 Experiment	Number of evidence entries for this 'Experiment'.
g1_PX419_human_18507 Experiment	Number of evidence entries for this 'Experiment'.
g1_PX419_human_18516	Number of evidence entires for this Experiment.
Experiment g1_PX419_human_19193	Number of evidence entries for this 'Experiment'.
Experiment g1_PX419_human_19204	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno092	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno441	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno561	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno691	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expA	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expB	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expC	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expD	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expE	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expF	Number of evidence entries for this 'Experiment'.
Experiment g2_PX089_Rep1	Number of evidence entries for this 'Experiment'.
Experiment g2_PX089_Rep2	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep1 20h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep1 6h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep2 20h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep2 6h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep3 20h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep3 6h	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_A_TSA_1	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_A_TSA_2	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_CC_1	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_CC_2	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_1	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_2	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_3	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_4	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_5	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_6	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_mH2A_4_5	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_ET	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_ET_2	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_nE	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_nE_2	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_rot_ET	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_wE	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_wE_2	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff3_Exp1	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff3_Exp2	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff4_Exp1	Number of evidence entries for this 'Experiment'.

Experiment g3_PX328_Diff4_Exp2 Experiment g3_PX328_Diff5_Exp1 Experiment g3_PX328_Diff5_Exp2 Experiment g3_PX597_A1_Spr	Number of evidence entries for this 'Experiment'. Number of evidence entries for this 'Experiment'. Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff5_Exp2	
-	Number of evidence entries for this 'Experiment'
Experiment at DV507 A1 Spr	
Experiment go_FA097_A1_opt	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_A2_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_A3_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_B1_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_B2_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_B3_Spr	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC_A	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC_B	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC_C	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-CPT_s1	Number of evidence entries for this 'Experiment'.
	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-CPT_s2	
Experiment g4_NCC-CPT_s3	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Ex1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Ex2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Ex3	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-rosco_s1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-rosco_s2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-rosco_s3	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-TSA_Exp1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-TSA_Exp2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-TSA_Exp3	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_A	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_B	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_C	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_D	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_E	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E1	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E2	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E3	Number of evidence entries for this 'Experiment'.
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Experiment g4_PX441_E4	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E5	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F1	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F2	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F3	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F4	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F5	Number of evidence entries for this 'Experiment'.
Ratio H/L	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	
Ratio H/L g1_GK1_Chromatin_AL	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_AL	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_AL	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_AL	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_AL	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_AL	
Ratio H/L g1_GK1_Chromatin_CPT	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_CPT	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_CPT	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 GK1 Chromatin CPT	quantities and quantities in the confidence quantity in the confidence quantities and the confidence quantities and the confidence quantities are confidence quantities are confidence quantities and the confidence quantities are
Ratio H/L g1_GK1_Chromatin_CR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_CR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_CR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_CR	
Ratio H/L g1_GK1_Chromatin_HepHek	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_HepHek	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_HepHek	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_HepHek	
Ratio H/L g1_GK1_Chromatin_hiIR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_hilR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_hilR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_hiIR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_hilR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_hiIR	
Ratio H/L g1_GK1_Chromatin_loIR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_loIR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_loIR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_loIR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_loIR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_loIR	
Ratio H/L g1_GK1_Chromatin_mH2A_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_1	
Ratio H/L g1_GK1_Chromatin_mH2A_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_2	Number of redundant peptides (MS1 features) used for quantitation.

Datia IIII inc. annuat	Number of reduced as the articles (MC4 feetures) used for
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_2	
Ratio H/L g1_GK1_Chromatin_mH2A_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_3	
Ratio H/L g1_GK1_Chromatin_TNFa_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_1	
Ratio H/L g1_GK1_Chromatin_TNFa_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_2	
Ratio H/L g1_GK1_Chromatin_TNFa_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_3	
Ratio H/L g1_KW10_110506	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_110506	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_110506	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_110506	
Ratio H/L g1_KW10_131126	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_131126	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1_KW10_131126	
Ratio H/L g1_KW10_140117	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_140117	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_140117	
Ratio H/L g1_KW11_130125 Ratio H/L normalized g1_KW11_130125	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_130125	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_130125	
Ratio H/L g1_KW11_140104_nE	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_140104_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_140104_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_nE	
Ratio H/L g1_KW11_140104_wE	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 KW11 140104 wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_140104_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_wE	
Ratio H/L g1_KW12_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW12_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_130317	
Ratio H/L g1_KW12_131223	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_131223	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW12_131223	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW12_131223	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW12_131223	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_131223	
Ratio H/L g1_KW13_130328	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW13_130328	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW13_130328	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_KW13_130328	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW13_130328	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW13_130328	
Ratio H/L g1_KW14_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW14_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW14_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW14_130317	
Ratio H/L g1_KW15_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW15_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW15_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW15_130317	
Ratio H/L g1_KW17_130319	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW17_130319	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW17_130319	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW17_130319	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW17_130319	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW17_130319	
Ratio H/L g1_KW8_120517	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_120517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW8_120517	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW8_120517	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_120517	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_120517	
Ratio H/L g1_KW8_131126	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW8_131126	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW8_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_131126	
Ratio H/L g1_KW8_140117	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW8_140117	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW8_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_140117	
Ratio H/L g1_KW9_120425	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_KW9_120425	I ne median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_KW9_120425	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW9_120425	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW9_120425	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW9_120425	
Ratio H/L g1_KW9_120510	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW9_120510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW9_120510	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW9_120510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW9_120510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW9_120510	
Ratio H/L q1 PX1194 H1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H1	
Ratio H/L g1_PX1194_H10	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H10	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H10	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H10	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H10	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H10	
Ratio H/L g1_PX1194_H11	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H11	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H11	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H11	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H11	
Ratio H/L g1_PX1194_H12	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H12	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H12	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H12	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H12	
Ratio H/L g1_PX1194_H2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H2	
Ratio H/L g1_PX1194_H3	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1194_H3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H3	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H3	
Ratio H/L g1_PX1194_H4	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_H4 Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g1_PX1194_H4	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H4	
Ratio H/L g1_PX1194_H5	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H5	
Ratio H/L g1_PX1194_H6	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H6	
Ratio H/L g1_PX1194_H7	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H7	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H7	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H7	
Ratio H/L g1_PX1194_H8	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H8	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H8	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H8	
Ratio H/L g1_PX1194_H9	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H9	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H9	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1_PX1194_H9	
Ratio H/L g1_PX1194_PCa1_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa1_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_1	
Ratio H/L g1_PX1194_PCa1_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa1_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_2	
Ratio H/L g1_PX1194_PCa2_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_1	
Ratio H/L g1_PX1194_PCa2_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_2	
Ratio H/L g1_PX1194_PCa2_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q1 PX1194 PCa2 3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_3	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX1194_PCa3_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa3_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count q1 PX1194 PCa3 1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
g1_PX1194_PCa3_1 Ratio H/L type g1_PX1194_PCa3_1	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX1194_PCa3_2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX1194_PCa3_2 Ratio H/L variability [%] g1_PX1194_PCa3_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa3_2	quantitation.

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa3_2	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_2	The section between two because of Political and con-
Ratio H/L g1_PX1194_PCa3_3 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa3_3	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_3	
Ratio H/L g1_PX1194_PCa4_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_1	
Ratio H/L g1_PX1194_PCa4_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_2	
Ratio H/L g1_PX1194_PCa4_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1 PX1194 PCa4 3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_3	
Ratio H/L g1_PX1194_PCa5_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_1	
Ratio H/L g1_PX1194_PCa5_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation
g1_PX1194_PCa5_2 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa5_2 Ratio H/L type g1_PX1194_PCa5_2	quantitation that are quantified with the re-quantify method.
Ratio H/L g1_PX1194_PCa5_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_3	quantitation that are quantined with the re-quantity method.
Ratio H/L g1_PX1194_PCa6_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa6_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa6_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa6_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa6_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa6_1	
Ratio H/L g1_PX1194_PCa7_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa7_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa7_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa7_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa7_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa7_1	
Ratio H/L g1_PX1406_GM18486	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18486	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18486	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18486	
Ratio H/L g1_PX1406_GM18498	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18498	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18498	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18498	
Ratio H/L g1_PX1406_GM18499	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18499	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18499	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18499	
Ratio H/L g1_PX1406_GM18501	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18501	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18501	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18501	
Ratio H/L g1_PX1406_GM18502	The ratio between two heavy and light label partners.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM18502 Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g1_PX1406_GM18502	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX1406 GM18502	
Ratio H/L g1 PX1406 GM18504	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18504	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18504	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18504	
Ratio H/L g1_PX1406_GM18505	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18505	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18505	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18505	
Ratio H/L g1_PX1406_GM18507	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18507	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18507	
Ratio H/L g1_PX1406_GM18508	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18508	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18508	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18508	
Ratio H/L g1_PX1406_GM18510	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18510	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18510	
Ratio H/L g1_PX1406_GM18511	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18511	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18511	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	quantitation that are quantitied with the re-quantity method.
g1_PX1406_GM18511 Ratio H/L g1_PX1406_GM18516	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18516	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18516	
Ratio H/L g1_PX1406_GM18517	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18517	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18517	
Ratio H/L g1_PX1406_GM18519	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18519	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18519	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18519	
Ratio H/L g1_PX1406_GM18520	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18520	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18520	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18520	
Ratio H/L g1_PX1406_GM18522	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18522	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18522	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18522	
Ratio H/L g1_PX1406_GM18523	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18523	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18523	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM18523 Ratio H/L g1_PX1406_GM18852	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX1406 GM18852	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18852	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX1406 GM18852	
Ratio H/L g1_PX1406_GM18855	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18855	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18855	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18855	
Ratio H/L g1_PX1406_GM18858	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18858	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18858	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18858	
Ratio H/L g1_PX1406_GM18861	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18861	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18861	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18861	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18861	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18861	
Ratio H/L g1_PX1406_GM18862	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18862	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18862	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18862	
Ratio H/L g1_PX1406_GM18870	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18870	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18870	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18870	
Ratio H/L g1_PX1406_GM18871	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM18871	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18871	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18871	
Ratio H/L g1_PX1406_GM18907	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18907	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18907	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18907	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18907	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18907	
Ratio H/L g1_PX1406_GM18909	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18909	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18909	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18909	
Ratio H/L g1_PX1406_GM18912	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18912	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18912	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18912	
Ratio H/L g1_PX1406_GM18913	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18913	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18913	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18913	
Ratio H/L g1_PX1406_GM18916	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18916	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18916	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18916	
Ratio H/L g1_PX1406_GM19092	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19092	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19092	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19092	
Ratio H/L g1_PX1406_GM19093	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19093	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19093	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19093	
Ratio H/L g1_PX1406_GM19098	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19098	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19098	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19098	
Ratio H/L g1_PX1406_GM19099	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19099	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19099	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19099	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19099	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19099	
Ratio H/L g1_PX1406_GM19101	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19101	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19101	
Ratio H/L g1_PX1406_GM19102	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19102	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19102	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19102	
Ratio H/L g1_PX1406_GM19108	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19108	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19108	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19108	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19108	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1 PX1406 GM19108	
Ratio H/L g1_PX1406_GM19114	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX1406 GM19114	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19114	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19114	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19114	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19114	
Ratio H/L g1_PX1406_GM19116	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19116	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19116	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19116	
Ratio H/L g1_PX1406_GM19119	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19119	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19119	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19119	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1 PX1406 GM19119	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19119	quantitude war are quantitude war are to quantity monitor.
Ratio H/L g1_PX1406_GM19127	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19127	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19127	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19127	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19127	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19127	
Ratio H/L g1_PX1406_GM19128	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19128	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19128	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19128	
Ratio H/L g1_PX1406_GM19130	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19130	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19130	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19130	
Ratio H/L g1_PX1406_GM19131	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM19131	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19131	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19131	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19131	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19131	
Ratio H/L g1_PX1406_GM19137	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19137	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19137	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19137	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19137	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19137	
Ratio H/L g1_PX1406_GM19138	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19138	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19138	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for guantitation that are guantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19138	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g1_PX1406_GM19140	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19140	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19140	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19140	
Ratio H/L g1_PX1406_GM19143	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19143	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19143	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19143	
Ratio H/L g1_PX1406_GM19144	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19144	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19144	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19144	
Ratio H/L g1_PX1406_GM19147	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19147	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19147	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
<u> </u>	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19147	
Ratio H/L g1_PX1406_GM19152	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19152	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19152	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19152	
Ratio H/L g1_PX1406_GM19153	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19153	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19153	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19153	
Ratio H/L g1_PX1406_GM19160	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19160	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19160	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19160	
Ratio H/L g1_PX1406_GM19172	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19172	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19172	
Ratio H/L g1_PX1406_GM19192	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19192	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19192	
Ratio H/L g1_PX1406_GM19193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19193	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM19193 Ratio H/L g1_PX1406_GM19200	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19200	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19200	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19200	
Ratio H/L g1_PX1406_GM19203	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19203	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19203	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19203	
Ratio H/L g1_PX1406_GM19204	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19204	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19204	
Ratio H/L g1_PX1406_GM19207	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19207	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19207	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19207	
Ratio H/L g1_PX1406_GM19209	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19209	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19209	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19209	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19209	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19209	
Ratio H/L g1_PX1406_GM19222	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19222	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19222	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19222	
Ratio H/L g1_PX1406_GM19257	The ratio between two heavy and light label partners.

Ratio H.L. Quarbellity [95] gray 1, 1406, GM19257 Ratio H.L. Quantified the peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H.L. Quantified the peptides (MS1 features) used for quantifiation. Number of redundant peptides (MS1 features) used for quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantified of quantifiation that are quantifie	Ratio H/L normalized g1_PX1406_GM19257	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
naturally logarithmized ratios times 100. Ratio HJL count of 1, PX1406_GM19257 Ratio HJL count of 1, PX1406_GM19257 Ratio HJL count of 1, PX1406_GM19257 Ratio HJL preserved the state of the state	Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX151_Rep1 Again HL iso-count g1_PX151_Rep2 Again HL iso-count g1_PX151_Rep3 Again HL iso-coun		naturally logarithmized ratios times 100.
guentitation that are quantified with the re-quantity method. Ratio H.U. ppc gl. PX151 Rep1 The ratio between two heavy and light label partners. Ratio H.U. q. PX151 Rep1 Ratio H.U. arisability [%] gl. pX151 Rep1 Ratio H.U. varisability [%] gl. pX151 Rep1 Ratio H.U. varisability [%] gl. pX151 Rep1 Ratio H.U. varisability [%] gl. pX151 Rep1 Ratio H.U. count gl. pX151_Rep1 Ratio H.U. count gl. pX151_Rep1 Ratio H.U. count gl. pX151_Rep1 Ratio H.U. arisability [%] gl. pX151 Rep1 Ratio H.U. arisability [%] gl. pX151 Rep2 Ratio H.U. gl. pX151 Rep2 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151 Rep2 The ratio between two medium and light label partners. Ratio H.U. arisability [%] gl. pX151 Rep2 The ratio between two medium and light label partners. Ratio H.U. arisability [%] gl. pX151 Rep2 Ratio H.U. arisability [%] gl. pX151 Rep2 Ratio H.U. count gl. pX151_Rep2 Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. count gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. count gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. count gl. pX151_Rep3 Ratio H.U. arisab		
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Ratio H/L q1 PX151 Rep1 Ratio H/L q1 PX151 Rep1 Ratio H/L q1 normalized g1/PX151 Rep1 Ratio H/L variability (%) g1/PX151 Rep1 Ratio H/L variability (%) g1/PX151 Rep1 Ratio H/L count g1 PX151 Rep1 Ratio H/L count g1 PX151 Rep1 Ratio H/L q1 PX151 Rep2 Ratio H/L q1 PX151 Rep3 Ratio H/L q1 PX151 R	Ratio H/L type	
The median of the total ratio population was shirted to 1. Ratio H/L variability (%) g1_PX151_Rep1 Ratio H/L solid to 1. Ratio H/L sol	3 =	The ratio between two heavy and light label partners.
peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX151_Rep1 Ratio H/L iso-count g1_PX151_Rep1 Ratio H/L nype g1_PX151_Rep1 Ratio H/L nype g1_PX151_Rep2 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX151_Rep2 The median of the total ratio population was shifted to 1. Ratio H/L so-count g1_PX151_Rep2 Ratio H/L count g1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L g1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L count g1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L count g1_PX151_Rep3 R	· · · · · · · · · · · · · · · · · ·	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Ratio H/L count g1_PX309_HCC1143-2 Ratio H/L iso-count g1_PX309_HCC1143-2 Ratio H/L type g1_PX309_HCC1143-2 Ratio H/L type g1_PX309_HCC1143-2 Ratio H/L g1_PX309_HCC1143-3 Ratio H/L normalized g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L count Number of redundant peptides (MS1 features) used for		peptides. It is calculated as the standard deviation of the
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Ratio H/L variability [%] g1_PX309_HCC1143-3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count Number of redundant peptides (MS1 features) used for	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
Ratio H/L count Number of redundant peptides (MS1 features) used for	Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
IUI PASUS ITUUTT43-3 I IUUANTITATION.	Ratio H/L count g1_PX309_HCC1143-3	

Ratio H/L iso-count g1_PX309_HCC1143-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-3	
Ratio H/L g1_PX309_HCC1599-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1599-1	
Ratio H/L g1_PX309_HCC1599-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX309 HCC1599-2	
Ratio H/L g1_PX309_HCC1599-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX309 HCC1599-3	
Ratio H/L g1_PX309_HCC1937-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-1	
Ratio H/L g1_PX309_HCC1937-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-2	
Ratio H/L g1_PX309_HCC1937-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-3	

Ratio H/L g1_PX309_HCC202-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-1	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_HCC202-1	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC202-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC202-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC2218-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-1	
Ratio H/L g1_PX309_HCC2218-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-2	
Ratio H/L g1_PX309_HCC2218-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-3	
Ratio H/L g1_PX309_HMEC1-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Ratio H/L variability [%] g1_PX309_HMEC1-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX309_HMEC1-1	quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC1-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC1-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC2-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	quarintation and quarintou wan are to quarinty mounds.
Ratio H/L g1_PX309_HMEC2-2	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 HMEC2-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_HMEC2-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	quantity morror.
Ratio H/L g1_PX309_HMEC2-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	gammy manage
Ratio H/L g1_PX309_HMTS1-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
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Ratio H/L iso-count g1_PX309_HMTS1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-1	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX309_HMTS1-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-2	
Ratio H/L g1_PX309_HMTS1-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-3	
Ratio H/L g1_PX309_MCF10a-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MCF10a-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MCF10a-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a-3	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 MCF10a-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-3	
Ratio H/L g1_PX309_MDAMB453-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g1_PX309_MDAMB453-2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_MDAMB453-2	The median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_PX309_MDAMB453-2	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-2	
Ratio H/L g1_PX309_MDAMB453-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-3	
Ratio H/L g1_PX309_MFM223-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX359_0h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_1	
Ratio H/L g1_PX359_0h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_2	Number of redundant peptides (MS1 features) used for quantitation.

	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g1_PX359_0h_2	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_2	
Ratio H/L g1_PX359_0h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_3	
Ratio H/L g1_PX359_BSA_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_1	
Ratio H/L g1_PX359_BSA_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_2	
Ratio H/L g1_PX359_BSA_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_3	
Ratio H/L g1_PX359_FN_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_1	
Ratio H/L g1_PX359_FN_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_2	
Ratio H/L g1_PX359_FN_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_3	quarintainen inat are quarintee mir ine te quarinty menteur
Ratio H/L g1_PX359_GFR_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_1	
Ratio H/L g1_PX359_GFR_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_2	
Ratio H/L g1_PX359_GFR_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_3	
Ratio H/L g1_PX359_LAM_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_1	
Ratio H/L g1_PX359_LAM_2 Ratio H/L normalized	The ratio between two heavy and light label partners.
g1_PX359_LAM_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_2	
Ratio H/L g1_PX359_LAM_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_3	
Ratio H/L g1_PX359_Matr 12h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_PX359_Matr 12h_1	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_1	
Ratio H/L g1_PX359_Matr 12h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_2	
Ratio H/L g1_PX359_Matr 12h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_3	
Ratio H/L g1_PX359_Matr 24h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 24h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_1	
Ratio H/L g1_PX359_Matr 24h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 24h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 24h 2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_2	
Ratio H/L g1_PX359_Matr 24h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 24h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 24h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_3	
Ratio H/L g1_PX359_Matr 30h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 30h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 30h_1	Number of redundant peptides (MS1 features) used for quantitation.
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Ratio H/L iso-count g1_PX359_Matr 30h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_1	
Ratio H/L g1_PX359_Matr 30h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 30h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 30h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 30h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_2	
Ratio H/L g1_PX359_Matr 30h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 30h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 30h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 30h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_3	
Ratio H/L g1_PX359_Matr dil_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_1	
Ratio H/L g1_PX359_Matr dil_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_2	
Ratio H/L g1_PX359_Matr dil_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_3	
Ratio H/L g1_PX419_human_18507	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_18507	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18507	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_18507	

Ratio H/L g1_PX419_human_18516	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_18516	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX419 human 18516	quantition in a series of the
Ratio H/L g1_PX419_human_19193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_19193	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_19193	
Ratio H/L g1_PX419_human_19204	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_19204	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_19204	
Ratio H/L g1_PX438_Xeno092	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno092	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno092	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno092	
Ratio H/L g1_PX438_Xeno441 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno441	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno441	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno441	
Ratio H/L g1_PX438_Xeno561	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno561	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno561	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno561	
Ratio H/L g1_PX438_Xeno691	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno691	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno691	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX438_Xeno691 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX438_Xeno691	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno691	The ratio between two beauty and light label partners
Ratio H/L g2_PX058_expA Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expA	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expA	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expA	
Ratio H/L g2_PX058_expB	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expB	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expB	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expB	The watis hadroness to be a second light label and second
Ratio H/L g2_PX058_expC Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expC	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expC	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expC	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expC	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expC	The watis hadrones to be a second light label and second
Ratio H/L g2_PX058_expD Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expD	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expD	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expD	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expD	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expD	The water hadron or true hadron and light label and some
Ratio H/L g2_PX058_expE Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expE	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expE	
Ratio H/L g2_PX058_expF	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expF	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expF	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expF	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expF	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expF	
Ratio H/L g2_PX089_Rep1	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX089_Rep1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g2_PX089_Rep1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX089_Rep1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX089_Rep1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX089_Rep1	
Ratio H/L g2_PX089_Rep2	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX089_Rep2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX089_Rep2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX089_Rep2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g2_PX089_Rep2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX089_Rep2	quantitation that are quantified with the re-quantity method.
Ratio H/L g2_PX537_exp14 rep1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g2_PX537_exp14 rep1 20h Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g2_PX537_exp14 rep1 20h	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep1 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep1 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 20h	
Ratio H/L g2_PX537_exp14 rep1 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep1 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep1 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q2 PX537 exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 6h	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g2_PX537_exp14 rep2	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep2 20h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 20h	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g2_PX537_exp14 rep2 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep2 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g2_PX537_exp14 rep2 6h	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 6h	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 6h	quantity monod.
Ratio H/L g2_PX537_exp14 rep3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep3 20h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
92_11/0001_exp 14 1epo 2011	naturally logarithmized ratios times 100.

Ratio H/L count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g2_PX537_exp14 rep3 20h Ratio H/L type g2_PX537_exp14	quantitation that are quantified with the re-quantify method.
rep3 20h Ratio H/L g2_PX537_exp14 rep3 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep3 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 6h	
Ratio M/L g3_GK1_Chromatin_A_TSA_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_1	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_1	
Ratio H/L g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_A_TSA_1	
Ratio H/M g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_A_TSA_1	
Ratio M/L g3_GK1_Chromatin_A_TSA_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_2	
Ratio H/L g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_A_TSA_2	quantitation that are quantified with the re-quantity method.
Ratio H/M g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3 GK1 Chromatin A TSA 2	
Ratio M/L g3_GK1_Chromatin_CC_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_CC_1	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_CC_1	
Ratio H/L g3_GK1_Chromatin_CC_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_CC_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_1	
Ratio H/M g3_GK1_Chromatin_CC_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_CC_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_1	
Ratio M/L g3_GK1_Chromatin_CC_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_CC_2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_CC_2	
Ratio H/L g3_GK1_Chromatin_CC_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_2	
Ratio H/M g3_GK1_Chromatin_CC_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_2	
Ratio M/L g3_GK1_Chromatin_EHT_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_1	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_1	
Ratio H/L g3_GK1_Chromatin_EHT_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3 GK1 Chromatin EHT 1	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_1	
Ratio H/M g3 GK1 Chromatin EHT 1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_1	
Ratio M/L g3_GK1_Chromatin_EHT_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_2	
Ratio H/L g3_GK1_Chromatin_EHT_2	The ratio between two heavy and light label partners.

Ratio H/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_2	
Ratio H/M g3_GK1_Chromatin_EHT_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count q3 GK1 Chromatin EHT 2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_2	
Ratio M/L g3_GK1_Chromatin_EHT_3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_3	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_3	
Ratio H/L g3_GK1_Chromatin_EHT_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_3	
Ratio H/M g3_GK1_Chromatin_EHT_3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_3	
Ratio M/L g3_GK1_Chromatin_EHT_4	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_4	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_4	

Ratio H/L g3_GK1_Chromatin_EHT_4	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_4	
Ratio H/M g3_GK1_Chromatin_EHT_4	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_4	
Ratio M/L g3_GK1_Chromatin_EHT_5	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_5	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_5	
Ratio H/L g3_GK1_Chromatin_EHT_5	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_5	
Ratio H/M g3_GK1_Chromatin_EHT_5	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_5	
Ratio M/L g3_GK1_Chromatin_EHT_6	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_6	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio M/L type	
g3_GK1_Chromatin_EHT_6	
Ratio H/L g3_GK1_Chromatin_EHT_6	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_6	
Ratio H/M g3_GK1_Chromatin_EHT_6	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_6	
Ratio M/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_mH2A_4_5	
Ratio H/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_mH2A_4_5	
Ratio H/M g3_GK1_Chromatin_mH2A_4_5	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L g3_KW35_ET	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio M/L type g3_KW35_ET	
Ratio H/L g3_KW35_ET	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_ET	
Ratio H/M g3_KW35_ET	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET	
Ratio M/L g3_KW35_ET_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET_2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_ET_2	
Ratio H/L g3_KW35_ET_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_ET_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_ET_2	
Ratio H/M g3_KW35_ET_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET_2	
Ratio M/L g3_KW35_nE	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_nE	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_nE	
Ratio H/L g3_KW35_nE	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

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Ratio H/L count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE	
Ratio H/M g3_KW35_nE	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_nE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE	
Ratio M/L g3_KW35_nE_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_nE_2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_nE_2	
Ratio H/L g3_KW35_nE_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_nE_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE_2	
Ratio H/M g3_KW35_nE_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_nE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE_2	
Ratio M/L g3_KW35_rot_ET	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_rot_ET	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_rot_ET	
Ratio H/L g3_KW35_rot_ET	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_rot_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_rot_ET	
Ratio H/M g3_KW35_rot_ET	The ratio between two heavy and medium label partners.

Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_KW35_rot_ET	partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_rot_ET	
Ratio M/L g3_KW35_wE	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE	
Ratio H/L g3_KW35_wE	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE	
Ratio H/M g3_KW35_wE	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE	
Ratio M/L g3_KW35_wE_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE_2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE_2	
Ratio H/L g3_KW35_wE_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE_2	
Ratio H/M g3_KW35_wE_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/M iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE_2	quantities and quantities that the re-quantity modifies.
Ratio M/L g3_PX328_Diff3_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp1	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff3_Exp1	
Ratio H/L g3_PX328_Diff3_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp1	
Ratio H/M g3_PX328_Diff3_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp1	
Ratio M/L g3_PX328_Diff3_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff3_Exp2	
Ratio H/L g3_PX328_Diff3_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp2	
Ratio H/M g3_PX328_Diff3_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp2	

Ratio M/L g3_PX328_Diff4_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp1	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff4_Exp1	
Ratio H/L g3_PX328_Diff4_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff4_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff4_Exp1	
Ratio H/M g3_PX328_Diff4_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff4_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff4_Exp1	
Ratio M/L g3_PX328_Diff4_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp2	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff4_Exp2	
Ratio H/L g3_PX328_Diff4_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff4_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff4_Exp2	
Ratio H/M g3_PX328_Diff4_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff4_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff4_Exp2	
Ratio M/L g3_PX328_Diff5_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized	The ratio between two medium and light label partners.

1. Ratio H/M variability [%] g3_PX328_Diff5_Exp1 Ratio H/M count g3_PX328_Diff5_Exp1 Ratio H/M iso-count g3_PX328_Diff5_Exp1 Ratio M/L iso-count g3_PX328_Diff5_Exp2 Ratio M/L normalized g3_PX328_Diff5_Exp2 Ratio M/L variability [%] g3_PX328_Diff5_Exp2 Ratio M/L count g3_PX328_Diff5_Exp2 Ratio M/L iso-count g3_PX328_Diff5_Exp2 Ratio H/L normalized g3_PX328_Diff5_Exp2 Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized g3_PX328_Diff5_Exp2 Ratio H/L count g3_PX328_Diff5_Exp2 Ratio H/L cou		
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Ratio M/L type g3_PX597_A3_Spr	Ratio M/L iso-count g3_PX597_A3_Spr	
	Ratio M/L type g3_PX597_A3_Spr	

Ratio H/L normalized g3_PX597_A3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A3_Spr	
Ratio H/M g3_PX597_A3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A3_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A3_Spr	
Ratio M/L g3_PX597_B1_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B1_Spr	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B1_Spr	
Ratio H/L g3_PX597_B1_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B1_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B1_Spr	
Ratio H/M g3_PX597_B1_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B1_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B1_Spr	
Ratio M/L g3_PX597_B2_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B2_Spr	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B2_Spr	
Ratio H/L g3_PX597_B2_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B2_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B2_Spr	
Ratio H/M g3_PX597_B2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_PX597_B2_Spr	partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B2_Spr	
Ratio M/L g3_PX597_B3_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B3_Spr	The ratio between two medium and light label partners.
Ratio M/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B3_Spr	
Ratio H/L g3_PX597_B3_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B3_Spr	
Ratio H/M g3_PX597_B3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B3_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B3_Spr	
Ratio H/L g4_NCC_A	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_A	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC_A	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_A	
Ratio H/L g4_NCC_B	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_B	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC_B	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_B	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count g4_NCC_B Ratio H/L iso-count g4_NCC_B	
0 = -	quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g4_NCC_B	quantitation. Number of redundant peptides (MS1 features) used for

Ratio H/L variability [%] g4_NCC_C	Coefficient of variability over all redundant quantifiable
	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_C	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_C	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_C	
Ratio H/L g4_NCC-CPT_s1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT_s1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- CPT_s1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s1	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g4_NCC- CPT_s1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s1	
Ratio H/L g4_NCC-CPT_s2	The ratio between two heavy and light label partners.
	, , , , , , , , , , , , , , , , , , ,
Ratio H/L normalized g4_NCC- CPT_s2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-CPT_s2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- CPT_s2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s2	
Ratio H/L g4_NCC-CPT_s3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT s3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-CPT_s3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s3	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g4_NCC- CPT_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s3	
Ratio H/L g4_NCC-HU_Ex1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU_Ex1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- HU_Ex1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-HU_Ex1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex1	
Ratio H/L g4_NCC-HU_Ex2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU Ex2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- HU_Ex2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g4_NCC-HU_Ex2	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU Ex2	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex2	The second secon
Ratio H/L g4_NCC-HU_Ex3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-HU_Ex3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-HU_Ex3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-HU_Ex3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex3	
Ratio H/L g4_NCC-rosco_s1	The ratio between two heavy and light label partners.

Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
rosco_s1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-rosco_s1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-rosco_s1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s1	
Ratio H/L g4_NCC-rosco_s2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- rosco s2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-rosco_s2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-rosco_s2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s2	
Ratio H/L g4_NCC-rosco_s3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-rosco_s3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-rosco_s3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s3	
Ratio H/L g4_NCC-TSA_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- TSA_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- TSA_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp1	
Ratio H/L g4_NCC-TSA_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-TSA_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-TSA_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp2	
Ratio H/L g4_NCC-TSA_Exp3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- TSA_Exp3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-TSA_Exp3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp3	
Ratio H/L g4_PX183_A	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_A	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_A	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H.V. and p.Y.183_B Ratio H.V. and p.Y.183_C Ratio H.V. and p.V. and p.V	Ratio H/L type g4_PX183_A	
Ratio H/L normalized g4_PX183_B Ratio H/L variability (%) get px183_B Ratio H/L variability (%) get px183_B Ratio H/L count g4_PX183_B Ratio H/L count g4_PX183_B Ratio H/L so-count g4_PX183_C Ratio H/L variability (%) get px183_C Ratio H/L count g4_PX183_C Ratio H/L variability (%) get px183_C Ratio H/L variability (%) get px183_C Ratio H/L count g4_PX183_C Ratio H/L variability (%) get px183_C Ratio H/L variability (%) get px183_C Ratio H/L count g4_PX183_C Ratio H/L so-count g4_PX183_D Ratio H/L so-count g4_PX183_E Ratio H/L so-count g4		The ratio between two heavy and light label partners.
peptides, it is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX183_B Ratio H/L count g4_PX183_B Ratio H/L count g4_PX183_B Ratio H/L variability (%) peptides, H/S count g4_PX183_C Ratio H/L variability (%) Ratio H/L variability (%) peptides, H/S count g4_PX183_C Ratio H/L yariability (%) pertides (MS1 features) used for quantitation that are quantified with the re-quantity method. Ratio H/L variability (%) peptides, H/S count g4_PX183_C Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) peptides. H/S calculated as the standard deviation of the naturally forgarithmized ratio between two medium and light label partners. Ratio H/L variability (MS1) peptides. H/S calculated as the standard deviation of the naturally forgarithmized ratio between two medium and light label partners. Ratio H/L variability (MS1) peptides. H/S calculated as the standard deviation of the naturally forgarithmized ratio between two medium and light label partners. Ratio H/L so-count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L so-count g4_PX183_E Ratio H/L so-count g4_PX441_E1 Ratio H/L so-count g4_PX441_E1 R	<u> </u>	Normalized ratio between two medium and light label partners.
Ratio H/L Iso-count g4_PX183_B Ratio H/L Iso-count g4_PX183_B Ratio H/L Iyop g4_PX183_B Ratio H/L Iyop g4_PX183_B Ratio H/L Iyop g4_PX183_C Ratio H/L p4_PX183_C Ratio H/L service in the service i		peptides. It is calculated as the standard deviation of the
Ratio H/L type g4_PX183_B Ratio H/L type g4_PX183_C Ratio H/L normalized g4_PX183_C Ratio H/L variability [%] g4_PX183_C Ratio H/L so-count g4_PX183_C Ratio H/L type g4_PX183_D The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L type g4_PX183_D The ratio between two heavy and light label partners. Ratio H/L variability (%) g4_PX183_D Ratio H/L so-count g4_PX183_E Ratio H/L variability (%) g4_PX183_E The ratio between two heavy and light label partners. Ratio H/L variability (%) g4_PX183_E Ratio H/L variability	Ratio H/L count g4_PX183_B	
Ratio H/L pd_PX183_C Ratio H/L variability [%] Ratio H/L count g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L so-count g4_PX183_D Ratio H/L variability [%] Ratio H/L variability [%] Ratio H/L variability [%] Ratio H/L count g4_PX183_D Ratio H/L so-count g4_PX183_D Ratio H/L variability (%) Ratio H/L varia	Ratio H/L iso-count g4_PX183_B	
Ratio H/L normalized g4_PX183_C Ratio H/L variability [%] g4_PX183_C Ratio H/L variability [%] g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L variability [%] g4_PX183_D Ratio H/L sio-count g4_PX183_D Ratio H/L variability [%] g4_PX183_B Ratio H/L variability [%] g4_PX183_E Ratio H/L variability [%] g4_PX184_E1 Ratio H/L variability [%] g4_PX184_E2 Ratio H/L variability [%] g4_PX184_E2 Ratio H/L variability	Ratio H/L type g4_PX183_B	
The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g/4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L sise-count g4_PX183_C Ratio H/L sise-count g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_D Ratio H/L sise-count g4_PX183_D Ratio H/L variability [%] g/4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L sise-count g4_PX183_D Ra	Ratio H/L g4_PX183_C	The ratio between two heavy and light label partners.
peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX183_C Ratio H/L iso-count g4_PX183_C Ratio H/L ype g4_PX183_C Ratio H/L ype g4_PX183_C Ratio H/L variability [%] g4_PX183_D Ratio H/L variability [%] g4_PX183_D Ratio H/L variability [%] g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L so-count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L ype g4_PX183_E Ratio H/L variability [%] g4_PX183_E Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E3 Ratio H/L count g4_PX184_E3 Ratio H/L count g4_PX184_E3 Ratio H/L count g4_PX184_E3 Ratio	Ratio H/L normalized g4_PX183_C	
quantitation. Ratio H/L iso-count g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L variability [%] g4_PX183_D Ratio H/L variability (%] g4_PX183_E Ratio H/L variability (%) g4_PX184_E2 Ratio H/L variability (%) g4_PX184_E2 Ratio H		peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method. Ratio H/L pd_PX183_D Ratio H/L pd_PX183_D Ratio H/L pd_PX183_D Ratio H/L variability [%] gd_PX183_D Ratio H/L variability [%] gain this period of the total ratio population was shifted to the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation that are quantified as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L type g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L variability [%] g4_PX183_E Ratio H/L variability [%] g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L riso-count g4_PX183_E Ratio H/L peg g4_PX183_E Ratio H/L peg g4_PX183_E Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L peg g4_PX183_E Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L peg g4_PX183_E Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L peg g4_PX183_E Ratio H/L variability [%] g4_PX441_E1 Ratio H/L variability [%] g4_PX441_E1 Ratio H/L variability [%] g4_PX441_E1 Ratio H/L variability [%] g4_PX441_E2 Ratio H/L peg g4_PX441_E1 Ratio H/L peg g4_PX441_E1 Ratio H/L peg g4_PX441_E2 Ratio H/L peg g4_PX441_E2 Ratio H/L peg g4_PX441_E3 Ratio H/L count g4_PX4	Ratio H/L count g4_PX183_C	
Ratio H/L g4_PX183_D Ratio H/L normalized g4_PX183_D Ratio H/L normalized g4_PX183_D Ratio H/L normalized g4_PX183_D Ratio H/L variability [%] g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L siso-count g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L variability [%] g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L type g4_PX183_D Ratio H/L count g4_PX441_E1 Ratio H/L count g4_PX441_E2 Ratio H/L count g4_PX441_E3 Rati	Ratio H/L iso-count g4_PX183_C	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
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g4_PX441_E2 peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L type g4_PX441_E2 Ratio H/L g4_PX441_E3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L normalized g4_PX441_E2	
Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L g4_PX441_E3 Ratio H/L normalized g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Normalized ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method. Ratio H/L type g4_PX441_E2 Ratio H/L q4_PX441_E3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L count g4_PX441_E2	Number of redundant peptides (MS1 features) used for
Ratio H/L g4_PX441_E3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L iso-count g4_PX441_E2	
Ratio H/L normalized g4_PX441_E3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L type g4_PX441_E2	
Ratio H/L normalized g4_PX441_E3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		The ratio between two heavy and light label partners.
Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		Normalized ratio between two medium and light label partners.
Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		peptides. It is calculated as the standard deviation of the
	Ratio H/L count g4_PX441_E3	Number of redundant peptides (MS1 features) used for

Ratio H/L iso-count g4_PX441_E3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E3	quantitation that are quantitied with the re-quantity mentur.
Ratio H/L g4_PX441_E4	The ratio between two heavy and light label partners.
Ratio H/L g4_FX441_E4 Ratio H/L normalized g4_PX441_E4	Normalized ratio between two medium and light label partners.
Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g4_PX441_E4	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E4	
Ratio H/L g4_PX441_E5	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E5	
Ratio H/L g4_PX441_F1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F1	
Ratio H/L g4_PX441_F2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F2	
Ratio H/L g4_PX441_F3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F3	
Ratio H/L g4_PX441_F4	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F4	
Ratio H/L g4_PX441_F5	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F5	quantitation that are quantities in quantity meanes.
Intensity	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_CPT	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

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Intensity g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_110506	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_110506	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_131126	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_131126	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_140117	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_140117	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_130125	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_130125	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_130125	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_140104_nE	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_nE	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_nE	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_140104_wE	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_wE	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
	linked to the heavy label partner.

Intensity g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
intensity g1_KW12_130317	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_120517	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_131126	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_140117	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW9_120425	Summed to the heavy laber partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1194_H7	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H9	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
 	Summed up eXtracted Ion Current (XIC) of the isotopic cluster

Intensity g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_2	Summed up extracted lon Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa6_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa7_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa7_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18502	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18504	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18505	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18507	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18508	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18510	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18510	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18511	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18520	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18855	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18855	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18855	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18858	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18858	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18861	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19093	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
; I	mined to the light label partilel.

Intensity g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19138	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19143	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19144	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19147	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19147	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19152	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19152	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19152	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19153	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19153	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity L g1_PX1406_GM19160 Intensity H g1_PX1406_GM19160 Intensity g1_PX1406_GM19172 Intensity L g1_PX1406_GM19172 Intensity H g1_PX1406_GM19172 Intensity g1_PX1406_GM19192 Intensity H g1_PX1406_GM19192 Intensity H g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193 Intensity H g1_PX1406_GM19193	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster labeled experiment this is the total intensity of all the isotopic cluster associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic clusters are the label cluster.
Intensity g1_PX1406_GM19172 Intensity L g1_PX1406_GM19172 Intensity H g1_PX1406_GM19172 Intensity g1_PX1406_GM19192 Intensity L g1_PX1406_GM19192 Intensity H g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity L g1_PX1406_GM19172 Intensity H g1_PX1406_GM19172 Intensity g1_PX1406_GM19192 Intensity L g1_PX1406_GM19192 Intensity H g1_PX1406_GM19192 Intensity g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19172 Intensity g1_PX1406_GM19192 Intensity L g1_PX1406_GM19192 Intensity H g1_PX1406_GM19192 Intensity g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity g1_PX1406_GM19192 Intensity L g1_PX1406_GM19192 Intensity H g1_PX1406_GM19192 Intensity g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity L g1_PX1406_GM19192 Intensity H g1_PX1406_GM19192 Intensity g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19192 Intensity g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19193 Intensity L g1_PX1406_GM19193	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity L g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
, , , ,	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity H g1_PX1406_GM19193	linked to the heavy label partner.
i .	
Intensity g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19200	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19209	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19222	Summed by the rieary laber partier. Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster

Intensity g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX309_HCC1937-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
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Intensity g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX359_Matr 30h_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno092	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno441	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

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Intensity H Summed up eXtracted Ion Current (XIC) of the isotopic cluster	Intensity M	Summed up eXtracted Ion Current (XIC) of the isotopic cluster

Intensity g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_mH2A_4_5	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
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Intensity g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_ET_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_ET_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_nE	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_nE_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_rot_ET	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_rot_ET	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_wE	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_wE_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff3_Exp1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
illerisity go_i Aozo_Dillo_LApz	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff5_Exp1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff5_Exp2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A1_Spr	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A2_Spr	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A3_Spr	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g3_PX597_B1_Spr Intensity L g3_PX597_B1_Spr Intensity H g3_PX597_B1_Spr Intensity H g3_PX597_B2_Spr Intensity L g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity G3_PX597_B3_Spr Intensity H g4_NCC_A Intensity H g4_NCC_A Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity G4_NCC_C	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted lon Current (XIC) of all isotopic cluster labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted lon Current (XIC) of the isotopic cluster labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the laght label partner. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the label cluster. Summed up extracted lon Current (XIC) of the isotopic cluster linked to the label cluster.
Intensity M g3_PX597_B1_Spr Intensity H g3_PX597_B2_Spr Intensity L g3_PX597_B2_Spr Intensity M g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity H g3_PX597_B3_Spr Intensity L g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity G4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity L g4_NCC_C Intensity L g4_NCC_C	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity H g3_PX597_B1_Spr Intensity g3_PX597_B2_Spr Intensity M g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity H g3_PX597_B3_Spr Intensity L g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g4_NCC_A Intensity H g4_NCC_A Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity H g4_NCC_C Intensity H g4_NCC_C Intensity H g4_NCC_C	linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B2_Spr Intensity L g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity L g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity g4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity G4_NCC_C Intensity L g4_NCC_C Intensity H g4_NCC_C	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity L g3_PX597_B2_Spr Intensity M g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity g3_PX597_B3_Spr Intensity L g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity G4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_A Intensity G4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity L g4_NCC_C	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity M g3_PX597_B2_Spr Intensity H g3_PX597_B2_Spr Intensity g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity g4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity H g4_NCC_C Intensity H g4_NCC_C	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner.
Intensity H g3_PX597_B3_Spr Intensity L g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity L g4_NCC_A Intensity H g4_NCC_A Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity L g4_NCC_C	linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B3_Spr Intensity L g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity L g4_NCC_A Intensity H g4_NCC_A Intensity H g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity H g4_NCC_C	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner.
Intensity L g3_PX597_B3_Spr Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity g4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity H g4_NCC_C	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner.
Intensity M g3_PX597_B3_Spr Intensity H g3_PX597_B3_Spr Intensity g4_NCC_A Intensity H g4_NCC_A Intensity H g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity H g4_NCC_C	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner.
Intensity H g3_PX597_B3_Spr Intensity g4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_A Intensity g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity J g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_A Intensity L g4_NCC_A Intensity H g4_NCC_A Intensity g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity H g4_NCC_C Intensity g4_NCC_C	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g4_NCC_A Intensity H g4_NCC_A Intensity g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity G4_NCC_C Intensity L g4_NCC_C	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity H g4_NCC_A Intensity g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity g4_NCC_C Intensity L g4_NCC_C	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity g4_NCC_B Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity g4_NCC_C Intensity L g4_NCC_C	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g4_NCC_B Intensity H g4_NCC_B Intensity g4_NCC_C Intensity L g4_NCC_C Intensity H g4_NCC_C	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity H g4_NCC_B Intensity g4_NCC_C Intensity L g4_NCC_C Intensity H g4_NCC_C	
Intensity g4_NCC_C Intensity L g4_NCC_C Intensity H g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity L g4_NCC_C Intensity H g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity H g4_NCC_C	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
, 0 = =	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a
Intensity L g4_NCC-CPT_s3	labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity H g4_NCC-CPT_s3	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g4_PX183_B	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_C	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_D	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_E	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E4	Summed up eXtracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E5	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Reverse	When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.
Potential contaminant	When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
id	A unique (consecutive) identifier for each row in the peptides table, which is used to cross-link the information in this table with the information stored in the other tables.
Protein group IDs	The identifiers of the protein groups this peptide was linked to, referenced against the proteinGroups table.
Mod. peptide IDs	Identifier(s) for peptide sequence(s), associated with the peptide, referenced against the corresponding modified peptides table.
Evidence IDs	Identifier(s) for analyzed peptide evidence associated with the protein group referenced against the evidences table.
MS/MS IDs	The identifiers of the MS/MS scans identifying this peptide, referenced against the msms table.
Best MS/MS	The identifier of the best (in terms of quality) MS/MS scan identifying this peptide, referenced against the msms table.
Oxidation (M) site IDs	Identifier(s) for site(s) associated with the protein group, which show(s) evidence of the modification, referenced against the appropriate modification site file.
MS/MS Count	

Modification-specific peptides

Name	Separator	Description
Sequence		The identified AA sequence of the peptide.
K Count		The number of instances of the 'K' AA contained within the sequence. The value for this can reliably be determined in the case of SILAC partners based on the distance between the partners. These counts are used to solidify the peptide identification process.
R Count		The number of instances of the 'R' AA contained within the sequence. The value for this can reliably be determined in the case of SILAC partners based on the distance between the partners. These counts are used to solidify the peptide identification process.
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to 'unmodified'.
Mass		Charge corrected mass of the precursor ion.
Mass Fractional Part		The values after the decimal point (ie value - floor(value)).
Protein Groups		IDs of the protein groups to whoch this peptide belongs.
Proteins		The identifiers of the proteins this particular peptide is associated with.
Gene Names		Names of genes this peptide is associated with.
Protein Names		Names of proteins this peptide is associated with.
Unique (Groups)		When marked with '+', this particular peptide is unique to a single protein group in the proteinGroups file.
Unique (Proteins)		When marked with '+', this particular peptide is unique to a single protein sequence in the fasta file(s).
Acetyl (Protein N-term)		Number of Acetyl (Protein N-term) on this peptide.
Oxidation (M)		Number of Oxidation (M) on this peptide.
Missed cleavages		Number of missed enzymatic cleavages.
Experiment g1_GK1_Chromatin_AL		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_CPT		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_CR		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_HepHek		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_hilR		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_loIR		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_mH2A_1		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_mH2A_2		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_mH2A_3		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_TNFa_1		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_TNFa_2		Number of evidence entries for this 'Experiment'.
Experiment g1_GK1_Chromatin_TNFa_3		Number of evidence entries for this 'Experiment'.
Experiment g1_KW10_110506		Number of evidence entries for this 'Experiment'.
Experiment g1_KW10_131126		Number of evidence entries for this 'Experiment'.
Experiment g1_KW10_140117		Number of evidence entries for this 'Experiment'.
Experiment g1_KW11_130125		Number of evidence entries for this 'Experiment'.
Experiment g1_KW11_140104_nE		Number of evidence entries for this 'Experiment'.
Experiment g1_KW11_140104_wE		Number of evidence entries for this 'Experiment'.
Experiment g1_KW12_130317		Number of evidence entries for this 'Experiment'.
Experiment g1_KW12_131223		Number of evidence entries for this 'Experiment'.
Experiment g1_KW13_130328		Number of evidence entries for this 'Experiment'.
Experiment g1_KW14_130317		Number of evidence entries for this 'Experiment'.
Experiment g1_KW15_130317		Number of evidence entries for this 'Experiment'.
Experiment g1_KW17_130319		Number of evidence entries for this 'Experiment'.
Experiment g1_KW8_120517		Number of evidence entries for this 'Experiment'.
Experiment g1_KW8_131126	1	Number of evidence entries for this 'Experiment'.
Experiment g1_KW8_140117		Number of evidence entries for this 'Experiment'.

Experiment g1_KW9_120425	Number of evidence entries for this 'Experiment'.
Experiment g1_KW9_120510	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H10	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H11	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H12	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H4	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H5	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H6	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H7	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H8	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_H9 Experiment g1_PX1194_PCa1_1	Number of evidence entries for this 'Experiment'. Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa1_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa2_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa2_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa2_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa3_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa3_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa3_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa4_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa4_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa4_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa5_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa5_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa5_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa6_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1194_PCa7_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18486	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18498	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18499	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18501	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18502	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18504	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18505	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18507	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18508	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18510	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18511	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18516 Experiment g1_PX1406_GM18517	Number of evidence entries for this 'Experiment'. Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18519	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18520	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18522	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18523	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18852	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18855	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18858	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18861	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18862	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18870	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18871	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18907	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18909	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18912	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18913	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM18916	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19092	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19093	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19098	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19099 Experiment g1_PX1406_GM19101	Number of evidence entries for this 'Experiment'.
	Number of evidence entries for this 'Experiment'.

Experiment g1_PX1406_GM19102	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19108	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19114	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19116	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19119	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19127	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19128	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19130	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19131	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19137	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19138	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19140	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19143	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19144	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19147	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19152	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19153	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19160	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19172	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19192	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19193	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19200	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19203	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19204	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19207	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19209	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19222	Number of evidence entries for this 'Experiment'.
Experiment g1_PX1406_GM19257	Number of evidence entries for this 'Experiment'.
Experiment g1_PX151_Rep1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX151_Rep2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX151_Rep3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1143-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1143-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1143-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1599-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1599-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1599-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1937-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1937-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC1937-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC202-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC202-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC202-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC2218-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC2218-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HCC2218-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC1-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC1-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC1-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC2-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC2-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMEC2-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMTS1-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMTS1-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_HMTS1-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MCF10a-1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MCF10a-2	Number of evidence entries for this 'Experiment'. Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MCF10a-3	·
Experiment g1_PX309_MDAMB453-1	Number of evidence entries for this 'Experiment'.
Experiment	Number of evidence entries for this 'Experiment'.
g1_PX309_MDAMB453-2	
Experiment	Number of evidence entries for this 'Experiment'.
g1_PX309_MDAMB453-3	
Experiment g1_PX309_MFM223-1	Number of evidence entries for this 'Experiment'.

Experiment g1_PX309_MFM223-2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX309_MFM223-3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_0h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_0h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_0h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_BSA_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_BSA_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_BSA_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_FN_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_FN_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_FN_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_GFR_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_GFR_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_GFR_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_LAM_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_LAM_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_LAM_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 12h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 12h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 12h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 24h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 24h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 24h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 30h_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 30h_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr 30h_3	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr dil_1	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr dil_2	Number of evidence entries for this 'Experiment'.
Experiment g1_PX359_Matr dil_3	Number of evidence entries for this 'Experiment'.
Experiment	Number of evidence entries for this 'Experiment'.
g1_PX419_human_18507	·
Experiment g1_PX419_human_18516	Number of evidence entries for this 'Experiment'.
Experiment g1_PX419_human_19193	Number of evidence entries for this 'Experiment'.
Experiment g1_PX419_human_19204	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno092	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno441	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno561	Number of evidence entries for this 'Experiment'.
Experiment g1_PX438_Xeno691	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expA	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expB	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expC	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expD	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expE	Number of evidence entries for this 'Experiment'.
Experiment g2_PX058_expF	Number of evidence entries for this 'Experiment'.
Experiment g2_PX089_Rep1	Number of evidence entries for this 'Experiment'.
Experiment g2_PX089_Rep2	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep1 20h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep1 6h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep2 20h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep2 6h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep3 20h	Number of evidence entries for this 'Experiment'.
Experiment g2_PX537_exp14 rep3 6h	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_A_TSA_1	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_A_TSA_2	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_CC_1	Number of evidence entries for this 'Experiment'.

Experiment g3_GK1_Chromatin_CC_2	Number of evidence entries for this 'Experiment'.
Experiment	Number of evidence entries for this 'Experiment'.
g3_GK1_Chromatin_EHT_1 Experiment	Number of evidence entries for this 'Experiment'.
g3_GK1_Chromatin_EHT_2	Number of evidence entires for this Experiment.
Experiment g3_GK1_Chromatin_EHT_3	Number of evidence entries for this 'Experiment'.
Experiment g3_GK1_Chromatin_EHT_4	Number of evidence entries for this 'Experiment'.
Experiment	Number of evidence entries for this 'Experiment'.
g3_GK1_Chromatin_EHT_5 Experiment	Number of evidence entries for this 'Experiment'.
g3_GK1_Chromatin_EHT_6	Number of evidence entries for this Experiment.
Experiment g3_GK1_Chromatin_mH2A_4_5	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_ET	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_ET_2	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_nE	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_nE_2	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_rot_ET	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_wE	Number of evidence entries for this 'Experiment'.
Experiment g3_KW35_wE_2	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff3_Exp1	Number of evidence entries for this 'Experiment'.
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Experiment g3_PX328_Diff3_Exp2	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff4_Exp1	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff4_Exp2	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff5_Exp1	Number of evidence entries for this 'Experiment'.
Experiment g3_PX328_Diff5_Exp2	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_A1_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_A2_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_A3_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_B1_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_B2_Spr	Number of evidence entries for this 'Experiment'.
Experiment g3_PX597_B3_Spr	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC_A	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC_B	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC_C	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-CPT_s1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-CPT_s2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-CPT_s3	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Ex1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Ex2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Ex3	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-rosco_s1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-rosco_s2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-rosco_s3	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-TSA_Exp1	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-TSA_Exp2	Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-TSA_Exp3	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_A	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_B	Number of evidence entries for this 'Experiment'.
Experiment g4_PX183_C	Number of evidence entries for this 'Experiment'.
Experiment g4_F X103_C Experiment g4_PX183_D	Number of evidence entries for this 'Experiment'.
Experiment g4_FX183_E	Number of evidence entries for this 'Experiment'.
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Experiment g4_PX441_E1	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E2	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E3	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E4	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_E5	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F1	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F2	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F3	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F4	Number of evidence entries for this 'Experiment'.
Experiment g4_PX441_F5	Number of evidence entries for this 'Experiment'.
Retention time	Retention time in minutes averaged over the evidence entries
	belonging to this modification-specific peptide.

Calibrated retention time	Calibrated retention time averaged over the evidence entries belonging to this modification-specific peptide. Obviously this only makes sense if retention time recalibration has been performed which is the case when matching between run is selected.
Charges	All charge states that have been observed.
PEP	Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
MS/MS scan number	The RAW-file derived scan number of the MS/MS with the highest peptide identification score (the highest score is stored in the column 'Score').
Raw file	The name of the RAW-file the mass spectral data was derived from.
Score	Andromeda score for the best identified among the associated MS/MS spectra.
Delta score	Score difference to the second best identified peptide.
Ratio H/L	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners The median of the total ratio population was shifted to 1.
Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	
Ratio H/L g1_GK1_Chromatin_AL	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_AL	Normalized ratio between two medium and light label partners The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_AL	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_AL	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_AL	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_AL	
Ratio H/L g1_GK1_Chromatin_CPT	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_CPT	Normalized ratio between two medium and light label partners The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_CPT	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_CPT	
Ratio H/L g1_GK1_Chromatin_CR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_CR	Normalized ratio between two medium and light label partners The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_CR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_CR	
Ratio H/L g1_GK1_Chromatin_HepHek	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_HepHek	Normalized ratio between two medium and light label partners The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_HepHek	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_HepHek	

Ratio H/L g1_GK1_Chromatin_hilR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_hilR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_hilR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_hilR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_hilR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	
Ratio H/L g1_GK1_Chromatin_loIR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_loIR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_loIR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_loIR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_loIR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_loIR	
Ratio H/L g1_GK1_Chromatin_mH2A_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_1	
Ratio H/L g1_GK1_Chromatin_mH2A_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_2	
Ratio H/L g1_GK1_Chromatin_mH2A_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_3	
Ratio H/L g1_GK1_Chromatin_TNFa_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_1	

Ratio H/L g1_GK1_Chromatin_TNFa_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_GK1_Chromatin_TNFa_2	quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_2	
Ratio H/L g1_GK1_Chromatin_TNFa_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_3	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g1_KW10_110506	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_110506	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_110506	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_110506	
Ratio H/L g1_KW10_131126	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_131126	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_131126	
Ratio H/L g1_KW10_140117	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_140117	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_140117	
Ratio H/L g1_KW11_130125	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_130125	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_130125	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_130125	
Ratio H/L g1_KW11_140104_nE	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_140104_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_140104_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_KW11_140104_nE Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_KW11_140104_nE Ratio H/L g1_KW11_140104_wE	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_140104_wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_140104_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_wE	
Ratio H/L g1_KW12_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW12_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_130317	
Ratio H/L g1_KW12_131223	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_131223	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW12_131223	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW12_131223	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW12_131223	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_131223	
Ratio H/L g1_KW13_130328 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_KW13_130328	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW13_130328	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW13_130328	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW13_130328	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW13_130328	
Ratio H/L g1_KW14_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW14_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW14_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW14_130317	
Ratio H/L g1_KW15_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW15_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW15_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW15_130317	
Ratio H/L g1_KW17_130319	The ratio between two heavy and light label partners.

Ratio H.M. carability [%] Ratio H.M. count g1_KW17_130319 Ratio H.M. population of the naturally logarithmized ratios times 100. Ratio H.M. population of the naturally logarithmized ratios times 100. Ratio H.M. population of the naturally logarithmized ratios times 100. Ratio H.M. pop g1_KW17_130319 Ratio H.M. g1_KW8_120517 The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H.M. g1_KW8_120517 The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H.M. count g1_KW8_120517 Ratio H.M. g1_KW8_120517 Ratio H.M. g1_KW8_120517 Ratio H.M. g1_KW8_120517 Ratio H.M. count g1_KW8_120517 Ratio H.M. g1_KW8_130158 Ratio H.M. g1_KW8_13128 The ratio between two heavy and light label partners. Nationally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quartitation. That are quartified with the re-quartify method. Ratio H.M. g1_KW8_13128 Ratio H.M. carability [%] g1_KW8_13128 The ratio between two heavy and light label partners. Normalized g1_KW8_131128 Ratio H.M. variability [%] g1_KW8_131128 Ratio H.M. variability [%] g1_KW8_131128 Ratio H.M. g1_KW8	Ratio H/L normalized g1_KW17_130319	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L count g1_KW17_130319 Ratio H/L iso-count Ratio H/L spe g1_KW17_130319 Ratio H/L g1_KW8 120817 Ratio H/L count g1_KW8_120517 Ratio H/L g1_KW8_131126 Ratio H/L count g1_KW8_131126 Ratio H/L count g1_KW8_131126 Ratio H/L count g1_KW8_131126 Ratio H/L count g1_KW8_131126 Ratio H/L g1_KW8_131126 Ratio H/L count g1_KW8_130117 Ratio H/L count g1_KW8_130117 Ratio H/L count g1_KW8_130117 Ratio H/L count g1_KW8_130117 Ratio H/L cou	Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
guantitation that are quantified with the re-quantify method. Ratio HLV, per J. KW18, 120517 Ratio HLV, new J. State S	Ratio H/L count g1_KW17_130319	Number of redundant peptides (MS1 features) used for
Ratio HL, Dat KWB, 120517 Ratio HL, Dat KWB, 120517 Ratio HL, Date Wash (120517) Ratio HL, Date Wash (120517) Ratio HL, Date Wash (120517) Ratio HL, Variability (%) Ratio HL, Count g1 KWB, 120517 Ratio HL, Count g1 KWB, 120517 Ratio HL, Leo-count g1 KWB, 120517 Ratio HL, Leo-count g1 KWB, 120517 Ratio HL, Leo-count g1 KWB, 120517 Ratio HL, Sey Count g1 KWB, 131126 Ratio HL, Sey Count g1 KWB, 140117 The ratio between two heavy and light label partners. Ratio HL, Lyng g1 KWB, 140117 The ratio between two heavy and light label partners. Ratio HL, Sey Count g1 KWB, 140117 Ratio HL, Variability (%) g1 KWB, 140117 Ratio HL, Sey Count g1		
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Ratio H/L iso-count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H5	
Ratio H/L g1_PX1194_H6	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H6	
Ratio H/L g1_PX1194_H7	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H7	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H7	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H7	
Ratio H/L g1_PX1194_H8	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H8	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H8	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H8	
Ratio H/L g1_PX1194_H9	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H9	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H9	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H9	
Ratio H/L g1_PX1194_PCa1_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa1_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_1	
Ratio H/L g1_PX1194_PCa1_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa1_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_2	
Ratio H/L g1_PX1194_PCa2_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa2_1	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_1 Ratio H/L g1_PX1194_PCa2_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1 PX1194 PCa2 2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_2	
Ratio H/L g1_PX1194_PCa2_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_3	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1194_PCa2_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_3	The spatial behavior to the second Policy I. I. I.
Ratio H/L g1_PX1194_PCa3_1 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa3_1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa3_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa3_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_1	
Ratio H/L g1_PX1194_PCa3_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa3_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa3_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa3_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_2	
Ratio H/L g1_PX1194_PCa3_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa3_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_3	
Ratio H/L g1_PX1194_PCa4_1 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa4_1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
	augnitation that are acceptified with the re-
g1_PX1194_PCa4_1	quantitation that are quantified with the re-quantify method.
	quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners.

Ratio H/L variability [%] g1_PX1194_PCa4_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g1 PX1194 PCa4 2	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_2	
Ratio H/L g1_PX1194_PCa4_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa4_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_3	
Ratio H/L g1_PX1194_PCa5_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_1	
Ratio H/L g1_PX1194_PCa5_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa5_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_2	
Ratio H/L g1_PX1194_PCa5_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_3	
Ratio H/L g1_PX1194_PCa6_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa6_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa6_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa6_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa6_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa6_1	The retic between two because and limit to be a second
Ratio H/L g1_PX1194_PCa7_1 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa7_1 Ratio H/L variability [%] g1_PX1194_PCa7_1	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa7_1 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa7_1 Ratio H/L type g1_PX1194_PCa7_1	quantitation that are quantified with the re-quantify method.
Ratio H/L g1_PX1406_GM18486	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM18486	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18486	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18486	
Ratio H/L g1_PX1406_GM18498	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18498	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18498	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18498	
Ratio H/L g1_PX1406_GM18499	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18499	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18499	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18499	
Ratio H/L g1_PX1406_GM18501	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18501	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18501	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18501	
Ratio H/L g1_PX1406_GM18502	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18502	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18502	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18502	
Ratio H/L g1_PX1406_GM18504	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18504	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18504	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18504	
Ratio H/L g1_PX1406_GM18505	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18505	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18505	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18505	
Ratio H/L g1_PX1406_GM18507	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18507	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18507	
Ratio H/L g1_PX1406_GM18508	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18508	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18508	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18508	
Ratio H/L g1_PX1406_GM18510	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18510	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18510	
Ratio H/L g1_PX1406_GM18511	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18511	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18511	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18511	
Ratio H/L g1_PX1406_GM18516	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18516	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18516	
Ratio H/L g1_PX1406_GM18517	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18517	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM18517 Ratio H/L g1_PX1406_GM18519	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18519	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18519	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18519	
Ratio H/L g1_PX1406_GM18520	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18520	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18520	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18520	
Ratio H/L g1_PX1406_GM18522	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18522	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18522	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18522	
Ratio H/L g1_PX1406_GM18523	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18523	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18523	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18523	
Ratio H/L g1_PX1406_GM18852	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18852	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18852	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18852	
Ratio H/L g1_PX1406_GM18855	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18855	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18855	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18855	
Ratio H/L g1_PX1406_GM18858	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM18858	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18858	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18858	
Ratio H/L g1_PX1406_GM18861	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18861	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18861	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18861	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18861	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18861	
Ratio H/L g1_PX1406_GM18862	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18862	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18862	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18862	
Ratio H/L g1_PX1406_GM18870	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18870	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18870	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18870	
Ratio H/L g1_PX1406_GM18871	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18871	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18871	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18871	
Ratio H/L g1_PX1406_GM18907	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18907	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18907	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18907	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18907	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18907	,
Ratio H/L g1_PX1406_GM18909	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18909	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18909	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
<u> </u>	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18909	
Ratio H/L g1_PX1406_GM18912	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18912	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18912	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18912	
Ratio H/L g1_PX1406_GM18913	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18913	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18913	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18913	
Ratio H/L g1_PX1406_GM18916	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18916	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18916	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18916	
Ratio H/L g1_PX1406_GM19092	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19092	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19092	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19092	
Ratio H/L g1_PX1406_GM19093	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19093	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19093	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19093	
Ratio H/L g1_PX1406_GM19098	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19098	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19098	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM19098 Ratio H/L g1_PX1406_GM19099	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19099	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19099	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19099	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19099	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19099	
Ratio H/L g1_PX1406_GM19101	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19101	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19101	
Ratio H/L g1_PX1406_GM19102	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19102	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19102	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19102	
Ratio H/L g1_PX1406_GM19108	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19108	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19108	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19108	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19108	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19108	
Ratio H/L g1_PX1406_GM19114	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19114	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19114	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19114	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19114	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19114	
Ratio H/L g1_PX1406_GM19116	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19116	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19116	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19116	
Ratio H/L g1_PX1406_GM19119	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM19119	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19119	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19119	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19119	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19119	
Ratio H/L g1_PX1406_GM19127	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19127	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19127	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19127	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19127	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19127	
Ratio H/L g1_PX1406_GM19128	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19128	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19128	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19128	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g1_PX1406_GM19130	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19130	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19130	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19130	
Ratio H/L g1_PX1406_GM19131	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19131	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19131	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19131	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19131	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19131	
Ratio H/L g1_PX1406_GM19137	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19137	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19137	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19137	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q1 PX1406 GM19137	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19137	
Ratio H/L g1_PX1406_GM19138	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19138	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19138	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
_	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19138 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX1406_GM19138 Ratio H/L g1_PX1406_GM19140	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19140	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19140	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19140	
Ratio H/L g1_PX1406_GM19143	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19143	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19143	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX1406 GM19143	
Ratio H/L g1_PX1406_GM19144	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19144	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19144	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19144	
Ratio H/L g1_PX1406_GM19147	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19147	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19147	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19147	
Ratio H/L g1_PX1406_GM19152	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19152	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19152	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19152	
Ratio H/L g1_PX1406_GM19153	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19153	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19153	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1 PX1406 GM19153	
Ratio H/L g1_PX1406_GM19160	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX1406 GM19160	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19160	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19160	
Ratio H/L g1_PX1406_GM19172	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19172	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19172	
Ratio H/L g1_PX1406_GM19192	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19192	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19192	
Ratio H/L g1_PX1406_GM19193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19193	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19193	
Ratio H/L g1_PX1406_GM19200	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19200	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19200	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19200	
Ratio H/L g1_PX1406_GM19203	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19203	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19203	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19203	
Ratio H/L g1_PX1406_GM19204	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19204	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX1406 GM19204	
Ratio H/L g1_PX1406_GM19207	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19207	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19207	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19207	
Ratio H/L g1_PX1406_GM19209	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19209	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19209	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19209	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19209	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19209	
Ratio H/L g1_PX1406_GM19222	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19222	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19222	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19222	
Ratio H/L g1_PX1406_GM19257	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19257	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19257	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19257	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19257	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19257	
Ratio H/L g1_PX151_Rep1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX151_Rep1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX151_Rep1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX151_Rep1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX151_Rep1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX151_Rep1	
Ratio H/L g1_PX151_Rep2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX151_Rep2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX151_Rep2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX151_Rep2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX151_Rep2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX151_Rep2	
Ratio H/L g1_PX151_Rep3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX151_Rep3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX151_Rep3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX151_Rep3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX151_Rep3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX151_Rep3	
Ratio H/L g1_PX309_HCC1143-1	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 HCC1143-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1143-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count q1 PX309 HCC1143-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1 PX309 HCC1143-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-1	
Ratio H/L g1_PX309_HCC1143-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1143-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1143-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1143-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1143-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-2	
Ratio H/L g1_PX309_HCC1143-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1143-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1143-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1143-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1143-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-3	
Ratio H/L g1_PX309_HCC1599-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1599-1	
Ratio H/L g1_PX309_HCC1599-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1599-2	

Patio H/I at PY300 HCC1500 3	The ratio between two beauty and light label partners
Ratio H/L g1_PX309_HCC1599-3 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX309_HCC1599-3	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
Ratio H/L variability [%] g1_PX309_HCC1599-3	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1599-3	
Ratio H/L g1_PX309_HCC1937-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-1	
Ratio H/L g1_PX309_HCC1937-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX309 HCC1937-2	
Ratio H/L g1_PX309_HCC1937-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-3	
Ratio H/L g1_PX309_HCC202-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
g1_PX309_HCC202-1 Ratio H/L type g1_PX309_HCC202-	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX309_HCC202-2	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 HCC202-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
g1_PX309_HCC202-2 Ratio H/L type g1_PX309_HCC202-	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX309_HCC202-3	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_HCC202-3	The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g1_PX309_HCC202-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q1 PX309 HCC202-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202- 3	quantitation that are quantified with the re quantity method.
Ratio H/L g1_PX309_HCC2218-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-1	
Ratio H/L g1_PX309_HCC2218-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-2	
Ratio H/L g1_PX309_HCC2218-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count a1 PX309 HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-3	
Ratio H/L g1_PX309_HMEC1-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count q1 PX309 HMEC1-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC1-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC1-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX309_HMEC1-3	quantitation.

Ratio H/L iso-count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	quantitation that are quantified with the re-quantity method.
Ratio H/L g1_PX309_HMEC2-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	
Ratio H/L g1_PX309_HMEC2-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	
Ratio H/L g1_PX309_HMEC2-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	
Ratio H/L g1_PX309_HMTS1-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-1	
Ratio H/L g1_PX309_HMTS1-2 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX309_HMTS1-2	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-2	
Ratio H/L g1_PX309_HMTS1-3 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX309_HMTS1-3	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-3 Ratio H/L g1_PX309_MCF10a-1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_MCF10a-1	The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g1_PX309_MCF10a-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX309_MCF10a-1 Ratio H/L iso-count	quantitation.
g1_PX309_MCF10a-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MCF10a-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MCF10a-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-3	
Ratio H/L g1_PX309_MDAMB453-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX309 MDAMB453-1	
Ratio H/L g1_PX309_MDAMB453-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX309 MDAMB453-2	
Ratio H/L g1_PX309_MDAMB453-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX309 MDAMB453-3	
Ratio H/L g1_PX309_MFM223-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation.
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Ratio H/L iso-count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	quantitation that are quantified with the re quantity method.
Ratio H/L g1_PX309_MFM223-2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_MFM223-2	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-3	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 MFM223-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count q1 PX309 MFM223-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX309_MFM223-3 Ratio H/L type g1_PX309_MFM223-	quantitation that are quantified with the re-quantify method.
3	
Ratio H/L g1_PX359_0h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_1	
Ratio H/L g1_PX359_0h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_2	
Ratio H/L g1_PX359_0h_3 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX359_0h_3	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_3	
Ratio H/L g1_PX359_BSA_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_1	
Ratio H/L g1_PX359_BSA_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g1_PX359_BSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_2	
Ratio H/L g1_PX359_BSA_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_3	
Ratio H/L g1_PX359_FN_1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_FN_1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_1	
Ratio H/L g1_PX359_FN_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_2	
Ratio H/L g1_PX359_FN_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_3	
Ratio H/L g1_PX359_GFR_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g1_PX359_GFR_1	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX359_GFR_1 Ratio H/L type g1_PX359_GFR_1	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_2	
Ratio H/L g1_PX359_GFR_3	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX359_GFR_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_3	
Ratio H/L g1_PX359_LAM_1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_LAM_1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_1	
Ratio H/L g1_PX359_LAM_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_2	
Ratio H/L g1_PX359_LAM_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_PX359_LAM_3	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_3	
Ratio H/L g1_PX359_Matr 12h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_1	
Ratio H/L g1_PX359_Matr 12h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_2	
Ratio H/L g1_PX359_Matr 12h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_Matr 12h_3	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H.U. por g1_PX359_Matr 24h_1 Ratio H.U. p1_PX359_Matr 24h_1 Ratio H.I. ornibratized g1_PX359_Matr 24h_1 Ratio H.I. ornibratized g1_PX359_Matr 24h_1 Ratio H.I. ornibratized g1_PX359_Matr 24h_1 Ratio H.U. count g1_PX359_Matr g2h_1 Ratio H.U. por g1_PX359_Matr g2h_1 Ratio H.U. count g1_PX359_Matr g2h_1 Ratio H.U. count g1_PX359_Matr g2h_1 Ratio H.U. count g1_PX359_Matr g2h_2 Ratio H.U. count g1_PX359_Matr g2h_1 Ratio H.U. count g1_PX359_Matr g2h_1 Ratio H.U. count g1_PX359_Matr g2h_2 Ratio H.U. pre g1_PX359_Matr g2h_2 Ratio H.U. pre g1_PX359_Matr g2h_2 Ratio H.U. serbasily (%) g1_PX359_Matr g2h_3 Ratio H.U. count g1_PX359_Matr g2h_2 Ratio H.U. count g1_PX359_Matr g2h_2 Ratio H.U. serbasily (%) g1_PX359_Matr g2h_3 Ratio H.U. count g1_PX359_Matr g2h_2 Ratio H.U. serbasily (%) g1_PX359_Matr g2h_3 Ratio H.U. count g1_PX359_Matr g2h_2 Ratio H.U. serbasily (%) g1_PX359_Matr g2h_3 Ratio H.U. count g1_PX359	Ratio H/L iso-count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio HL, ornalized All Count of the Count o		
Agaio HAL vasibility (%) expensibility (%) expen		The ratio between two heavy and light label partners.
gl_PX359_Matr 24h_1 Ratio H/L count gl_PX359_Matr 24h_1 Ratio H/L count gl_PX359_Matr 24h_1 Ratio H/L iso-count gl_PX359_Matr 24h_1 Ratio H/L iso-count gl_PX359_Matr 24h_1 Ratio H/L type gl_PX359_Matr 24h_1 Ratio H/L type gl_PX359_Matr 24h_2 Ratio H/L type gl_PX359_Matr 24h_2 Ratio H/L pgl_PX359_Matr 24h_2 Ratio H/L owneralized gl_PX359_Matr 24h_2 Ratio H/L count gl_PX359_Matr 24h_2 Ratio H/L so-count gl_PX359_Matr 24h_3 Ratio H/L so-count gl_PX359_Matr 24h_3 Ratio H/L so-count gl_PX359_Matr 24h_3 Ratio H/L pgl_PX359_Matr 24h_3 Ratio H/L so-count gl_PX359_Matr 24h_3 Ratio H/L pgl_PX359_Matr 24h_3 Rat	Ratio H/L normalized g1_PX359_Matr 24h_1	
Quantitation. Ratio HJL iso-count g1_PX359_Matr Quantitation that are quantified with the re-quantify method. Ratio HJL iso-count g1_PX359_Matr PX359_Matr PX359_M	Ratio H/L variability [%] g1_PX359_Matr 24h_1	peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method. Ratio H/L nype g1_PX359_Matr 24h_2 Ratio H/L normalized 1_PX359_Matr 24h_2 Ratio H/L normalized 2_PX359_Matr 24h_2 Ratio H/L count g1_PX359_Matr 24h_2 Ratio H/L count g1_PX359_Matr 24h_2 Ratio H/L count g1_PX359_Matr 24h_2 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 2		
24h_1		
Ratio H/L cormalized g1 PX359 Matr 24h .2 Ratio H/L variability [%] g1 PX359 Matr 24h .2 Ratio H/L count g1 PX359 Matr 24h .2 Ratio H/L count g1 PX359 Matr 24h .2 Ratio H/L count g1 PX359 Matr 24h .2 Ratio H/L so-count g1 PX359 Matr 24h .2 Ratio H/L type g1 PX359 Matr 24h .2 Ratio H/L type g1 PX359 Matr 24h .3 Ratio H/L count g1 PX359 Matr 24h .3 Ratio H/L count g1 PX359 Matr 24h .3 Ratio H/L variability [%] g1 PX359 Matr 24h .3 Ratio H/L variability (%) g1 PX359 Matr 24h .3 Ratio H/L count g1 PX359 Matr 24h .3 Ratio H/L so-count g1 PX		
g1_PX359_Matr 24h_2 The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g1_PX359_Matr 24h_2 Ratio H/L count g1_PX359_Matr 24h_2 Ratio H/L count g1_PX359_Matr 24h_2 Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L iso-count g1_PX359_Matr 24h_2 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantity method. Ratio H/L g1_PX359_Matr 24h_3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio betw	Ratio H/L g1_PX359_Matr 24h_2	The ratio between two heavy and light label partners.
g1_PX359_Matr 24h_2 Ratio H/L count g1_PX359_Matr 24h_3 Ratio H/L rount g1_PX359_Matr 30h_1 Ratio H/L rount g1_PX359_Matr 30h_2 Ratio H/L rount g1_PX359_Matr 30h_3 Ratio H/L rount g1_PX359_Ma	Ratio H/L normalized g1_PX359_Matr 24h_2	
quantitation. Ratio H/L iso-count g1_PX359_Matr 24h_2	Ratio H/L variability [%] g1_PX359_Matr 24h_2	peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method.		
24h 2 "The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX359_Matr 24h_3 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX359_Matr 24h_3 The median of the total ratio population was shifted to 1. Ratio H/L variability (%) g1_PX359_Matr 24h_3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX359_Matr 24h_3 Normalized normalized g1_PX359_Matr 24h_3 Normalized ratio between two heavy and light label partners. Ratio H/L rount g1_PX359_Matr 30h_1 The ratio between two heavy and light label partners. Ratio H/L variability [%] g1_PX359_Matr 30h_1 The ratio between two heavy and light label partners. Ratio H/L count g1_PX359_Matr 30h_1 The ratio between two heavy and light label partners. Ratio H/L count g1_PX359_Matr 30h_1 The ratio between two heavy and light label partners. Ratio H/L count g1_PX359_Matr 30h_1 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX359_Matr 30h_1 Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L iso-count g1_PX359_Matr 30h_2 The ratio between two heavy and light label partners. Ratio H/L normalized 1 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L normalized 1 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L normalized 2 Normalized 2 Normalized ratio between two heavy and light label partners. Ratio H/L count g1_PX359_Matr 30h_2 Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L count g1_PX359_Matr 30h_2 Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L count g1_PX359_Matr 30h_3 The ratio between two heavy and light label part		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L normalized g1_PX359_Matr 24h_3 Ratio H/L variability [%] g1_PX359_Matr 24h_3 Ratio H/L variability [%] g1_PX359_Matr 24h_3 Ratio H/L count g1_PX359_Matr 24h_3 Ratio H/L count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L g1_PX359_Matr 24h_3 Ratio H/L g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L normalized g1_PX359_Matr 30h_1 Ratio H/L normalized g1_PX359_Matr 30h_1 Ratio H/L variability [%] g1_PX359_Matr 30h_1 Ratio H/L so-count g1_PX359_Matr 30h_2 Ratio H/L so-count g1_PX359_Matr 30h_3 Rat		
State Stat	Ratio H/L g1_PX359_Matr 24h_3	The ratio between two heavy and light label partners.
peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX359_Matr 24h_3 Ratio H/L iso-count g1_PX359_Matr 24h_3 Ratio H/L so-count g1_PX359_Matr 24h_3 Ratio H/L type g1_PX359_Matr 24h_3 Ratio H/L g1_PX359_Matr 30h_1 Ratio H/L q1_PX359_Matr 30h_1 Ratio H/L count g1_PX359_Matr 30h_1 Ratio H/L count g1_PX359_Matr 30h_1 Ratio H/L q1_PX359_Matr 30h_2 Ratio H/L q1_PX359_Matr 30h_3 Ratio H/L	Ratio H/L normalized g1_PX359_Matr 24h_3	
Quantitation.	Ratio H/L variability [%] g1_PX359_Matr 24h_3	peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method. Ratio H/L type g1_PX359_Matr 30h_1 Ratio H/L normalized g1_PX359_Matr 30h_1 Ratio H/L variability [%] g1_PX359_Matr 30h_1 Ratio H/L variability [%] p2_PX359_Matr 30h_1 Ratio H/L variability [%] p2_PX359_Matr 30h_1 Ratio H/L count g1_PX359_Matr 30h_1 Ratio H/L count g1_PX359_Matr 30h_1 Ratio H/L count g1_PX359_Matr 30h_1 Ratio H/L iso-count g1_PX359_Matr 30h_2 Ratio H/L normalized g1_PX359_Matr 30h_2 Ratio H/L normalized g1_PX359_Matr 30h_2 Ratio H/L count g1_PX359_Matr 30h_2 Ratio H/L so-count g1_PX359_Matr 30h_3 Ratio H/L on-malized g1_PX359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L normalized m1 count g1 p2 p359_Matr 30h_2 Ratio H/L so-count g1_PX359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L normalized m1 count g1 p2 p359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L on-malized m1 count g1 p2 p359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L on-malized m1 count g1 p2 p359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L count g1_PX359_Matr 30h_3 Ratio H		
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Ratio H/L so-count g1_PX359_Matr 30h_1 Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L variability [%] g1_PX359_Matr 30h_2 Ratio H/L count g1_PX359_Matr 30h_2 Ratio H/L count g1_PX359_Matr 30h_2 Ratio H/L mormalized g1_PX359_Matr 30h_2 Ratio H/L variability [%] g1_PX359_Matr 30h_2 Ratio H/L variability [%] g1_PX359_Matr 30h_2 Ratio H/L count g1_PX359_Matr 30h_2 Ratio H/L count g1_PX359_Matr 30h_2 Ratio H/L iso-count g1_PX359_Matr 30h_2 Ratio H/L iso-count g1_PX359_Matr 30h_2 Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L variability [%] g1_PX359_Matr 30h_3	Ratio H/L variability [%] g1_PX359_Matr 30h_1	peptides. It is calculated as the standard deviation of the
auantitation that are quantified with the re-quantify method. Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L g1_PX359_Matr 30h_2 Ratio H/L variability [%] g1_PX359_Matr 30h_2 Ratio H/L count g1_PX359_Matr 30h_2 Ratio H/L iso-count g1_PX359_Matr 30h_2 Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L variability [%] g1_PX359_Matr 30h_2 Ratio H/L iso-count g1_PX359_Matr 30h_2 Ratio H/L iso-count g1_PX359_Matr 30h_2 Ratio H/L type g1_PX359_Matr 30h_3 Ratio H/L type g1_PX359_Matr 30h_3 Ratio H/L variability [%] g1_PX359_Matr 30h_3 Ratio H/L variability [%] g1_PX359_Matr 30h_3 Ratio H/L variability [%] Coefficient of variability over all redundant quantificable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L type g1_PX359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L variability [%] Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX359_Matr 30h_3 Number of redundant peptides (MS1 features) used for quantitation.		
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30h_2 quantitation that are quantified with the re-quantify method. Ratio H/L type g1_PX359_Matr 30h_2 Ratio H/L g1_PX359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX359_Matr 30h_3 The median of the total ratio population was shifted to 1. Ratio H/L variability [%] Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX359_Matr 30h_3 Number of redundant peptides (MS1 features) used for quantitation.		
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Ratio H/L g1_PX359_Matr 30h_3 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX359_Matr 30h_3 Ratio H/L variability [%] g1_PX359_Matr 30h_3 Ratio H/L count g1_PX359_Matr Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX359_Matr Number of redundant peptides (MS1 features) used for quantitation.		
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30h_3 quantitation.		peptides. It is calculated as the standard deviation of the
		Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g1_PX359_Matr Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.	Ratio H/L iso-count g1_PX359_Matr	Number of redundant peptides (MS1 features) used for
Ratio H/L type g1_PX359_Matr 30h_3		

Ratio H/L g1_PX359_Matr dil_1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr	
Ratio H/L g1_PX359_Matr dil_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_2	
Ratio H/L g1_PX359_Matr dil_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_3	
Ratio H/L g1_PX419_human_18507	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_18507	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18507	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_18507	
Ratio H/L g1_PX419_human_18516	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_18516	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_18516	
Ratio H/L g1_PX419_human_19193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_19193	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_19193	
Ratio H/L g1_PX419_human_19204	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Detical Manager Program	Out the standard control of th
Ratio H/L variability [%] g1_PX419_human_19204	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX419_human_19204 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX419_human_19204	The matic hature on true has any and light label manter on
Ratio H/L g1_PX438_Xeno092 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno092	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno092	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno092	
Ratio H/L g1_PX438_Xeno441	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno441	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno441	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno441	
Ratio H/L g1_PX438_Xeno561	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno561	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno561	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno561	
Ratio H/L g1_PX438_Xeno691	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno691	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno691	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno691	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX438_Xeno691 Ratio H/L type g1_PX438_Xeno691	quantitation that are quantified with the re-quantify method.
Ratio H/L g2_PX058_expA	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expA	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expA	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g2_PX058_expA	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expA	
Ratio H/L g2_PX058_expB	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expB	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expB	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	<u> </u>
g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio HL, Grandbilly (%) g2-PX058_expC Ratio HL, oranbellity (%) g2-PX058_expC Ratio HL, g2-PX058_expC Ratio HL, g2-PX058_expC Ratio HL, g2-PX058_expD Ratio HL, g3-PX058_expD Ratio HL, g3-PX058_expD Ratio HL, g3-PX058_expD Ratio HL, g3-PX058_expD Ratio HL, count g2-PX058_expD Ratio HL, count g3-PX058_expD Ratio HL, g4-PX058_expD Ratio HL, g4-PX058_expB Ra	D. J. J. W. C. D. (2000)	
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		Number of redundant peptides (MS1 features) used for

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g2_PX537_exp14 rep1 20h Ratio H/L type g2 PX537 exp14	quantitation that are quantified with the re-quantify method.
rep1 20h	The ratio between two began and light lobel partners
Ratio H/L g2_PX537_exp14 rep1 6h Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX537_exp14 rep1 6h	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep1 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 6h	
Ratio H/L g2_PX537_exp14 rep2 20h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep2 20h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 20h	
Ratio H/L g2_PX537_exp14 rep2 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep2 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep2 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 6h	
Ratio H/L g2_PX537_exp14 rep3 20h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep3 20h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 20h	
Ratio H/L g2_PX537_exp14 rep3 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2 PX537 exp14 rep3 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep3 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 6h	
Ratio M/L g3_GK1_Chromatin_A_TSA_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio M/L type	
g3_GK1_Chromatin_A_TSA_1 Ratio H/L	The ratio between two heavy and light label partners.
g3_GK1_Chromatin_A_TSA_1 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_GK1_Chromatin_A_TSA_1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_A_TSA_1	
Ratio H/M g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_A_TSA_1	
Ratio M/L g3_GK1_Chromatin_A_TSA_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_2	
Ratio H/L g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_2 Ratio H/L type	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
g3_GK1_Chromatin_A_TSA_2	
Ratio H/M g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_A_TSA_2	
Ratio M/L g3_GK1_Chromatin_CC_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_CC_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.

Ratio M/L iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type	quantitation that are quantities with the re quantity method.
g3_GK1_Chromatin_CC_1 Ratio H/L g3_GK1_Chromatin_CC_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_CC_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_1	
Ratio H/M g3_GK1_Chromatin_CC_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_CC_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_1	
Ratio M/L g3_GK1_Chromatin_CC_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_CC_2	
Ratio H/L g3_GK1_Chromatin_CC_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_2	
Ratio H/M g3_GK1_Chromatin_CC_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_2	
Ratio M/L g3_GK1_Chromatin_EHT_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio M/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_1	quantitation that are quantified with the re-quantity method.
Ratio H/L g3_GK1_Chromatin_EHT_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_1	
Ratio H/M g3_GK1_Chromatin_EHT_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_1	
Ratio M/L g3_GK1_Chromatin_EHT_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_2	
Ratio H/L g3_GK1_Chromatin_EHT_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_2	
Ratio H/M g3_GK1_Chromatin_EHT_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_2	
Ratio M/L g3_GK1_Chromatin_EHT_3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.

Ratio M/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3 GK1 Chromatin EHT 3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_3	
Ratio H/L g3_GK1_Chromatin_EHT_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_3	
Ratio H/M g3_GK1_Chromatin_EHT_3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_3	
Ratio M/L g3_GK1_Chromatin_EHT_4	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_4	
Ratio H/L g3_GK1_Chromatin_EHT_4	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_4	
Ratio H/M g3_GK1_Chromatin_EHT_4	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_4	
Ratio M/L g3_GK1_Chromatin_EHT_5	The ratio between two medium and light label partners.

Ratio M/L normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_5	quantitation that are quantition with the re-quantity motion.
Ratio H/L g3 GK1 Chromatin EHT 5	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_5	
Ratio H/M g3_GK1_Chromatin_EHT_5	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_5	
Ratio M/L g3_GK1_Chromatin_EHT_6	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_6	
Ratio H/L g3_GK1_Chromatin_EHT_6	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_6	
Ratio H/M g3_GK1_Chromatin_EHT_6	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_6	

Ratio M/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_mH2A_4_5	
Ratio H/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_mH2A_4_5	
Ratio H/M g3_GK1_Chromatin_mH2A_4_5	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L g3_KW35_ET	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_ET	
Ratio H/L g3_KW35_ET	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_ET	
Ratio H/M g3_KW35_ET	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET	
Ratio M/L g3_KW35_ET_2	The ratio between two medium and light label partners.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
g3_KW35_ET_2	The median of the total ratio population was shifted to 1.

Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two heavy and light label partners.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two heavy and medium label partners.
Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two medium and light label partners.
Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two heavy and light label partners.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two heavy and medium label partners.
Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two medium and light label partners.
Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L g3_KW35_nE_2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_KW35_nE_2 Ratio H/L variability [%] g3_KW35_nE_2	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g3_KW35_nE_2	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g3_KW35_nE_2	quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE_2	quantitation that are quantitied with the re-quantity method.
Ratio H/M g3_KW35_nE_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_KW35_nE_2	partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE_2	
Ratio M/L g3_KW35_rot_ET	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_rot_ET	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_rot_ET	
Ratio H/L g3_KW35_rot_ET	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_rot_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_rot_ET	
Ratio H/M g3_KW35_rot_ET	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_rot_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_rot_ET	
Ratio M/L g3_KW35_wE	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE	
Ratio H/L g3_KW35_wE	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_KW35_wE	quantitation that are quantified with the re-quantify method.
Ratio H/M g3_KW35_wE	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE	
Ratio M/L g3_KW35_wE_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE_2	
Ratio H/L g3_KW35_wE_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE_2	
Ratio H/M g3_KW35_wE_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE_2	
Ratio M/L g3_PX328_Diff3_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff3_Exp1	
Ratio H/L g3_PX328_Diff3_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp1	
Ratio H/M g3_PX328_Diff3_Exp1	The ratio between two heavy and medium label partners.

Ratio H/M normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp1	
Ratio M/L g3_PX328_Diff3_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type	quantition in the quantition of quantity mention
g3_PX328_Diff3_Exp2 Ratio H/L g3_PX328_Diff3_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_PX328_Diff3_Exp2 Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g3_PX328_Diff3_Éxp2	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp2	
Ratio H/M g3_PX328_Diff3_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp2	
Ratio M/L g3_PX328_Diff4_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff4_Exp1	gasanasan mar are quantinos mar are re quantiny meditor.
Ratio H/L g3_PX328_Diff4_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_PX328_Diff4_Exp1 Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g3_PX328_Diff4_Éxp1	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff4_Exp1	
Ratio H/M g3_PX328_Diff4_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_PX328_Diff4_Exp1	partners. The median of the total ratio population was shifted to 1.

Ratio HM variability (%) gogether. Expt peoples. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio HM count Number of redundant peptides (MT leadures) used for naturally logarithmized ratios times 100. Ratio HM so count Q		
ga PX328 DIFIA Expt quantitation from the count of ga PX328 DIFIA Expt quantitation that are quantified with the re-quantify method. gas PX328 DIFIA Expt Ratio HM (spc) Again (Am) Ga PX328 DIFIA Expt The ratio between two medium and light label partners. Ratio ML (and FX282 DIFIA Expt) The ratio between two medium and light label partners. Ratio ML (normalized ap PX328 DIFIA Expt) Normalized and to between two heavy and light label partners. Ratio ML variability (%) Coofficient of variability operal in redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratioe times 100. Ratio ML count (applied Expt) Normalized and count of the calculation of the calculat		peptides. It is calculated as the standard deviation of the
gal PX328_Diff4_Exp1 gal brill type g3_PX328_Diff4_Exp1 gal brill type g3_PX328_Diff4_Exp1 Ratio MU_ga_PX328_Diff4_Exp2 Ratio MU_ga_PX328_Diff6_Exp1 Ratio MU_ga_		
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Ratio ML, Dan PX328 Diff4 Exp2 Ratio ML, Daniella Exp2 Ratio ML, Variability (%) G3_PX328 Diff4_Exp2 Ratio ML, Variability (%) G3_PX328 Diff4_Exp2 Ratio ML, Second Ratio ML, Variability (%) G3_PX328 Diff4_Exp2 Ratio ML, Second Ratio ML, Second Ratio ML, Second Ratio ML, Variability (%) G3_PX328 Diff4_Exp2 Ratio ML, Second Ratio ML, Rat	Ratio H/M type	
Ratio M.L. normalized go P.Y328 Diff4 Exp2 Ratio M.L. variability (%) go P.Y328 Diff4 Exp2 Ratio M.L. variability (%) go P.Y328 Diff4 Exp2 Ratio M.L. count go P.Y328 Diff4 Exp2 Ratio M.L. so-count go P.Y328 Diff4 Exp2 Ratio M.R. so-count go P.Y328 Diff5 Exp1 Ratio M.R. so-count go P.Y328 Diff5 Exp1 Ratio M.R. so-count go P.Y328 Dif		The ratio between two medium and light label partners
Ratio ML variability [96] ag. PX328_Diff4_Exp2 Ratio ML variability [86] ag. PX328_Diff4_Exp2 The ratio between two heavy and light label partners. Ratio ML variability [86] ag. PX328_Diff4_Exp2 Ratio HL variability [86] ag. PX328_Diff4_Exp2 The ratio between two heavy and medium label partners. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio HM variability [86] ag. PX328_Diff4_Exp2 The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. Normalized ratio between two heavy and light label partners. Normalized ratio between two heavy and light label partners. Ratio HM variability [86] ag. PX328_Diff4_Exp2 Ratio HM variability [86] ag. PX328_Diff4_Exp2 Ratio HM variability [86] ag. PX328_Diff4_Exp1 Ratio HM variability [86] ag. PX328_Diff6_Exp1 Ratio HM variability [86] ag. PX328_Diff6_Exp1 Ratio HM variability [86] ag	Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
Ratio ML court 32 PX32B Diff4 Exp2 Ratio ML general Section of the	Ratio M/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio ML iso-count guarantization that are quantified with the re-quantify method. guarantization that are quantified with the re-quantify method. ga PX328 Diff4 Exp2 Ratio HL ga PX328 Diff4 Exp2 Ratio HL ga PX328 Diff4 Exp2 Ratio HL garantization that are quantified with the re-quantify method. garantization of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. garantization. garantization. garantization that are quantified with the re-quantify method. garantization with the re-quantify method. garantization with the re-quantify m		Number of redundant peptides (MS1 features) used for
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		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the

Ratio H/M count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff5_Exp1	
Ratio M/L g3_PX328_Diff5_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff5_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff5_Exp2	
Ratio H/L g3_PX328_Diff5_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff5_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff5_Exp2	
Ratio H/M g3_PX328_Diff5_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff5_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff5_Exp2	
Ratio M/L g3_PX597_A1_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A1_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A1_Spr	
Ratio H/L g3_PX597_A1_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A1_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A1_Spr	
Ratio H/M g3_PX597_A1_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A1_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/M type g3_PX597_A1_Spr	
Ratio M/L g3_PX597_A2_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A2_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A2_Spr	
Ratio H/L g3_PX597_A2_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A2_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A2_Spr	
Ratio H/M g3_PX597_A2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A2_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A2_Spr	
Ratio M/L g3_PX597_A3_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A3_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A3_Spr	
Ratio H/L g3_PX597_A3_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A3_Spr	
Ratio H/M g3_PX597_A3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A3_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/M iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A3_Spr	
Ratio M/L g3_PX597_B1_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B1_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio M/L count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for
Detic M/I inc. count	quantitation.
Ratio M/L iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B1_Spr	
Ratio H/L g3_PX597_B1_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B1_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B1_Spr	
Ratio H/M g3_PX597_B1_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B1_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B1_Spr	
Ratio M/L g3_PX597_B2_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B2_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B2_Spr	
Ratio H/L g3_PX597_B2_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B2_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B2_Spr	
Ratio H/M g3_PX597_B2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B2_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B2_Spr	
Ratio M/L g3_PX597_B3_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B3_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B3_Spr	
Ratio H/L g3_PX597_B3_Spr	The ratio between two heavy and light label partners.

Ratio H/L normalized g3_PX597_B3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B3_Spr	
Ratio H/M g3_PX597_B3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B3_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B3_Spr	
Ratio H/L g4_NCC_A	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_A	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC_A	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_A	
Ratio H/L g4_NCC_B	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_B	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC_B	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_B	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_B	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_B	
Ratio H/L g4_NCC_C	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_C	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC_C	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_C	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_C	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_C	
Ratio H/L g4_NCC-CPT_s1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT_s1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- CPT_s1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- CPT_s1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s1	
Ratio H/L g4_NCC-CPT_s2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT_s2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-CPT_s2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s2	Number of redundant peptides (MS1 features) used for
	quantitation.

Ratio HU, D.4 NCC-CPT_33 The ratio between two neavy and light label partners. Ratio HVL normalized g4_NCC- CPT_35. Ratio HVL count g4_NCC-CPT_33 Ratio HVL pxpe g4_NCC-WCC-CPT_33 Ratio HVL pxpe g4_NCC-WCC-CPT_34 Ratio HVL pxpe g4_NCC-WCC-CPT_34 Ratio HVL pxpe g4_NCC-WCC-CPT_34 Ratio HVL carability (%) g4_NCC-WCC-WCC-WCC-WCC-WCC-WCC-WCC-WCC-WCC-	Ratio H/L type g4_NCC-CPT_s2	
CPT_83	7. 5 = -	The ratio between two heavy and light label partners.
CPT_s3 apoptides, It is calculated as the standard deviation of the naturally logarithmized ratios times 1:00. Ratio H/L count g4_NCC-CPT_s3 Ratio H/L type g4_NCC-H_Ex1 Ratio H/L count g4_NCC-H_Ex1 Ratio H/L carability (%) g4_NCC-type peptides. It is calculated as the standard deviation of the naturally logarithmized ratio between two medium and light label partners. Ratio H/L count g4_NCC-H_Ex1 Ratio H/L count g4_NCC-HU_Ex1 Ratio H/L type g4_NCC-type g4_NC		Normalized ratio between two medium and light label partners.
Ratio H/L Iso-count g4_NCC- CPT_s3 Ratio H/L Iso-count g4_NCC- CPT_s3 Ratio H/L yep g4_NCC-CPT_s3 Ratio H/L yep g4_NCC-H/L Ex1 The ratio between two heavy and light label partners. Ratio H/L normalized g4_NCC- H/L Ex1 The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable periods. It is calculated as the standard deviation of the naturally logarithmized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L count g4_NCC-H/L Ex1 Ratio H/L count g4_NCC-H/L Ex1 Ratio H/L so-count g4_NCC-H/L Ex1 Ratio H/L Normalized g4_NCC-H/L Ex1 Ratio H/L yep g4_NCC-H/L Ex1 Ratio H/L yep g4_NCC-H/L Ex1 Ratio H/L variability (%) g4_NCC- H/L Ex2 The ratio between two heavy and light label partners. Ratio H/L variability (%) g4_NCC- H/L Ex2 The ratio between two heavy and light label partners. Ratio H/L variability (%) g4_NCC- H/L Ex2 The ratio between two medium and light label partners. Ratio H/L count g4_NCC-H/L Ex2 Ratio H/L variability (%) g4_NCC- H/L Ex2 The ratio between two medium and light label partners. Ratio H/L count g4_NCC-H/L Ex2 Ratio H/L count g4_NCC-H/L Ex2 Ratio H/L count g4_NCC-H/L Ex2 Ratio H/L count g4_NCC-H/L Ex3 Ratio H/L count g4_NCC-H/L Ex3 Ratio H/L normalized g4_NCC-H/L Ex3 Ratio H/L q4_NCC-H/L Ex3 Ratio H/L q4_NCC-H/L Ex3 The ratio between two medium and light label partners. Ratio H/L q4_NCC-H/L Ex3 The ratio between two medium and light label partners. Ratio H/L q4_NCC-H/L Ex3 The ratio between two medium and light label partners. Ratio H/L q4_NCC-H/L Ex3 The ratio between two medium and light label partners. Ratio H/L q4_NCC-H/L Ex3 The ratio between two medium and light label partners. Ratio H/L q4_NCC-H/L Ex3 The ratio between two medium and light label partners. Ratio H/L variability (%) g4_NCC- H/L Ex3 The ratio between two medium and light label partners. Ratio H/L variability (%) g4_NCC- H/L Ex3 The ratio between tw		peptides. It is calculated as the standard deviation of the
CPT_S3 quantitation that are quantified with the re-quantify method. Ratio H/L pg q4, NCC-H/L Ex1 Ratio H/L pg q4, NCC-H/L Ex1 Ratio H/L variability [%] g4, NCC-H/L Ex1 Ratio H/L so-count g4, NCC-H/L Ex2 The ratio between two period in the total ratio population was shifted to 1. Ratio H/L so-count g4, NCC-H/L Ex2 The ratio between two heavy and light label partners. Ratio H/L sarbality [%] g4, NCC-H/L Ex2 The ratio between two medium and light label partners. Ratio H/L variability [%] g4, NCC-H/L Ex2 Ratio H/L variability [%] g4, NCC-H/L Ex2 Ratio H/L count g4, NCC-H/L Ex2 Ratio H/L count g4, NCC-H/L Ex2 Ratio H/L so-count g4, NCC-H/L Ex3 Ratio H/L so-count g4, NCC-H/L Ex3 The ratio between two heavy and light label partners. Ratio H/L so-count g4, NCC-H/L Ex3 The ratio between two heavy and light label partners. Ratio H/L so-count g4, NCC-H/L Ex3 The ratio between two heavy and light label partners. Ratio H/L variability (%) g4, NCC-H/L Ex3 The ratio between two heavy and light label partners. Ratio H/L variability (%) g4, NCC-H/L Ex3 Ratio H/L by g4, NCC-H/L Ex3 R	Ratio H/L count g4_NCC-CPT_s3	Number of redundant peptides (MS1 features) used for
Ratio H/L g4 NCC-HU Ex1 Ratio H/L normalized g4 NCC- HU_Ex1 Ratio H/L variability [%] g4_NCC- HU_Ex1 Ratio H/L so-count g4_NCC- Ratio H/L so-count g4_NCC- HU_Ex1 Ratio H/L so-count g4_NCC- Ratio H/L so-count g4_NCC- HU_Ex1 Ratio H/L g4_NCC-HU_Ex1 Ratio H/L g4_NCC-HU_Ex2 Ratio H/L g4_NCC-HU_Ex2 Ratio H/L g4_NCC-HU_Ex2 Ratio H/L count g4_NCC- HU_Ex1 Ratio H/L g4_NCC-HU_Ex2 Ratio H/L count g4_NCC- HU_Ex2 Ratio H/L so-count g4_NCC- HU_Ex2 Ratio H/L so-count g4_NCC- HU_Ex3 Ratio H/L loo-count g4_NCC- HU_Ex3 Ratio H/L variability (%) g4_NCC- HU_Ex3 Ratio H/L loo-count g4_NCC- HU_Ex3 Ratio H/L variability (%) g4_NCC- HU_Ex3 Ratio H/L loo-count g4_NCC- Ratio H/L loo-count g4_NCC- Ratio H/L loo-count g4_NCC- Ratio H/L loo-count g4_NCC- Ratio		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L normalized 94_NCC-HU_Ex1 Ratio H/L variability [%] 94_NCC-HU_Ex1 Ratio H/L count g4_NCC-HU_Ex1 Ratio H/L so-count g4_NCC-HU_Ex2 Ratio H/L variability [%] g4_NCC-HU_Ex2 Ratio H/L so-count g4_NCC-HU_Ex3 Ratio H/L variability [%] g4_NCC-HU_Ex3 Ratio H/L so-count g4_NCC-HU_Ex3 Ratio H/L so-	Ratio H/L type g4_NCC-CPT_s3	
The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_NCC- H/L Ext Ratio H/L count g4_NCC-HU_Ext Ratio H/L count g4_NCC-HU_Ext Ratio H/L so-count g4_NCC-HU_Ext Ratio H/L so-count g4_NCC-HU_Ext Ratio H/L so-count g4_NCC-HU_Ext Ratio H/L so-count g4_NCC-HU_Ext Ratio H/L type g4_NCC-HU_Ext Ratio H/L so-count g4_NCC- HU_Ex2 The ratio between two heavy and light label partners. Ratio H/L sariability [%] g4_NCC- HU_Ex2 Ratio H/L count g4_NCC-HU_Ex2 Ratio H/L count g4_NCC-HU_Ex2 Ratio H/L so-count g4_NCC- HU_Ex2 Ratio H/L so-count g4_NCC- HU_Ex2 Ratio H/L so-count g4_NCC- HU_Ex2 Ratio H/L so-count g4_NCC-HU_Ex2 Ratio H/L so-count g4_NCC-HU_Ex3 Ratio H/L so-count g4_	Ratio H/L g4_NCC-HU_Ex1	The ratio between two heavy and light label partners.
PhU_EX1 Ratio H/L count g4_NCC-HU_Ex1 Ratio H/L iso-count g4_NCC-HU_Ex1 Ratio H/L iso-count g4_NCC-HU_Ex1 Ratio H/L iso-count g4_NCC-HU_Ex1 Ratio H/L iso-count g4_NCC-HU_Ex1 Ratio H/L ype g4_NCC-HU_Ex2 Ratio H/L normalized g4_NCC-HU_Ex2 Ratio H/L avaiability [%] g4_NCC-HU_Ex2 Ratio H/L count g4_NCC-HU_Ex2 Ratio H/L count g4_NCC-HU_Ex2 Ratio H/L count g4_NCC-HU_Ex2 Ratio H/L iso-count g4_NCC-HU_Ex2 Ratio H/L iso-count g4_NCC-HU_Ex2 Ratio H/L count g4_NCC-HU_Ex2 Ratio H/L iso-count g4_NCC-HU_Ex3 Ratio H/L variability [%] g4_NCC-HU_Ex2 Ratio H/L variability [%] g4_NCC-HU_Ex3 Ratio H/L variability [%] g4_NCC-HU_Ex3 Ratio H/L iso-count g4_NCC-HU_Ex3 Ratio H/L variability [%] g4_NCC-HU_Ex3 Ratio H/L count g4_NCC-HU_Ex3 Ratio H/L count g4_NCC-HU_Ex3 Ratio H/L count g4_NCC-HU_Ex3 Ratio H/L variability over all redundant applies (MS1 features) used for quantitation that are quantitied with the re-quantity method. Ratio H/L variability [%] g4_NCC-NC-NC-NC-NC-NC-NC-NC-NC-NC-NC-NC-NC-		The median of the total ratio population was shifted to 1.
quantitation. Ratio H/L iso-count g4_NCC-HU_Ex1 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L g4_NCC-HU_Ex2 The ratio between two heavy and light label partners. Ratio H/L variability [%] g4_NCC-HU_Ex2 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to was shifted to the naturally logarithmized ratio between two medium and light label partners. The median of the total ratio population was shifted to the naturally logarithmized ratio population was shifted to the naturally logarithmized ratios times 100. Ratio H/L variability [%] g4_NCC-HU_Ex2 Section of the naturally logarithmized ratios times 100. Ratio H/L iso-count g4_NCC-HU_Ex2 Section of the naturally logarithmized ratios times 100. Ratio H/L type g4_NCC-HU_Ex3 The ratio between two heavy and light label partners. Ratio H/L variability [%] g4_NCC-HU_Ex3 The ratio between two medium and light label partners. The median of the total ratio population was shifted to the naturally logarithmized ratios times 100. Ratio H/L count g4_NCC-HU_Ex3 The ratio between two medium and light label partners. The median of the total ratio population was shifted to the naturally logarithmized ratios times 100. Ratio H/L count g4_NCC-HU_Ex3 Section 100 to the naturally logarithmized ratios times 100. Ratio H/L so-count g4_NCC-HU_Ex3 Section 100 to the naturally logarithmized ratios times 100. Ratio H/L type g4_NCC-HU_Ex3 Section 100 to the naturally logarithmized ratios times 100. Ratio H/L variability [%] g4_NCC-Tosco s1 Section 100 to the naturally logarithmized ratios times 100. Ratio H/L variability [%] g4_NCC-Tosco s1 Section 100 to the naturally logarithmized ratio between two medium and light label partners. The median of the total ratio population was shifted to the naturally logarithmized ratio between two medium and light label partners. The median of the total ratio p		peptides. It is calculated as the standard deviation of the
HU_EX1 quantitation that are quantified with the re-quantify method.	Ratio H/L count g4_NCC-HU_Ex1	
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Ratio H/L g4_NCC-rosco_s3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_NCC-rosco_s3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_NCC-rosco_s3 Number of redundant peptides (MS1 features) used for		
Ratio H/L normalized g4_NCC- rosco_s3 Ratio H/L variability [%] g4_NCC- rosco_s3 Ratio H/L variability [%] g4_NCC- rosco_s3 Ratio H/L variability [%] g4_NCC- rosco_s3 Ratio H/L count g4_NCC-rosco_s3 Number of redundant peptides (MS1 features) used for	Ratio H/L type g4_NCC-rosco_s2	
Ratio H/L normalized g4_NCC- rosco_s3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_NCC- rosco_s3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_NCC-rosco_s3 Number of redundant peptides (MS1 features) used for	Ratio H/L g4_NCC-rosco_s3	The ratio between two heavy and light label partners.
Ratio H/L variability [%] g4_NCC- rosco_s3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_NCC-rosco_s3 Number of redundant peptides (MS1 features) used for	Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
Ratio H/L count g4_NCC-rosco_s3 Number of redundant peptides (MS1 features) used for	Ratio H/L variability [%] g4_NCC-	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
	Ratio H/L count g4_NCC-rosco_s3	, ,

Ratio H/L iso-count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s3	quantitation that are quantition with the re-quantity method.
Ratio H/L g4_NCC-TSA_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized q4 NCC-	Normalized ratio between two medium and light label partners.
TSA_Exp1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- TSA_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp1	
Ratio H/L g4_NCC-TSA_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- TSA_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-TSA_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp2	
Ratio H/L g4_NCC-TSA_Exp3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-TSA_Exp3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-TSA_Exp3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp3	
Ratio H/L g4_PX183_A	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_A	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_A	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_A	
Ratio H/L g4_PX183_B	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_B	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_B	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX183_B	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_B	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_B	
Ratio H/L g4_PX183_C	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_C	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_C	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX183_C	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_C	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_C	
Ratio H/L g4_PX183_D	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_D	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_D	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g4_PX183_D	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g4_PX183_D	quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the requestion method.
Datio II/I type at DV192 D	quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_D	The resign between two began and light lebel negtrons
Ratio H/L g4_PX183_E	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_E	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_E	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX183_E	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_E	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_E	
Ratio H/L g4_PX441_E1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E1	
Ratio H/L g4_PX441_E2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E2	
Ratio H/L g4_PX441_E3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E3	
Ratio H/L g4_PX441_E4	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E4	
Ratio H/L g4_PX441_E5	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E5	
Ratio H/L g4_PX441_F1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g4_PX441_F1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F1	
Ratio H/L g4_PX441_F2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F2	
Ratio H/L g4_PX441_F3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F3	
Ratio H/L g4_PX441_F4	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F4	
Ratio H/L g4_PX441_F5	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F5	
Intensity	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_GK1_Chromatin_CR	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_loIR	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_1	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_2	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_1	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
g00a1.11 u_0	annou to the heavy label partitor.

Intensity g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_110506	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_131126	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_140117	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_130125	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_130125	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_140104_nE	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_nE	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_140104_wE	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_130317	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW12_131223	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW13_130328	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW14_130317	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
	annous to the light labor partition.

Intensity g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_131126	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H10	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H5	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H9	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa1_1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
	Summed up extracted Ion Current (XIC) of the isotopic cluster

Intensity g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18502	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18517	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18519	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18520	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
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Intensity g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18855	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18855	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18855	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18862	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18871	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18871	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18871	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18907	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18907	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19099	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
	linked to the light label partner.

Intensity g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19119	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19127	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19128	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19130	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19131	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19137	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19137	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19138	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM19140	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19147	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19172	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19192	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19192	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19192	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
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Intensity g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a
	labeled experiment this is the total intensity of all the isotopic
Intensity L g1_PX309_HCC202-1	labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity L g1_PX309_HCC202-2 Intensity H g1_PX309_HCC202-2 Intensity g1_PX309_HCC202-3 Intensity L g1_PX309_HCC202-3 Intensity H g1_PX309_HCC202-3 Intensity g1_PX309_HCC2218-1 Intensity L g1_PX309_HCC2218-1	patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity g1_PX309_HCC202-3 Intensity L g1_PX309_HCC202-3 Intensity H g1_PX309_HCC202-3 Intensity g1_PX309_HCC2218-1	linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic cluster linked to the heavy label partner. Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g1_PX309_HCC202-3 Intensity H g1_PX309_HCC202-3 Intensity g1_PX309_HCC2218-1	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity H g1_PX309_HCC202-3 Intensity g1_PX309_HCC2218-1	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity g1_PX309_HCC2218-1	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g1_PX309_HCC2218-1	patterno in the labor elabor.
	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
3	linked to the heavy label partner.

Intensity L g1_PX309_MFM223-1 Intensity H g1_PX309_MFM223-2 Intensity L g1_PX309_MFM223-2 Intensity H g1_PX309_MFM223-2 Intensity H g1_PX309_MFM223-3 Intensity L g1_PX309_MFM223-3	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity g1_PX309_MFM223-2 Intensity L g1_PX309_MFM223-2 Intensity H g1_PX309_MFM223-2 Intensity g1_PX309_MFM223-3	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity L g1_PX309_MFM223-2 Intensity H g1_PX309_MFM223-2 Intensity g1_PX309_MFM223-3	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity H g1_PX309_MFM223-2 Intensity g1_PX309_MFM223-3	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity g1_PX309_MFM223-3	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
,,,,	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity L a1 PX309 MFM223-3	
	3 1
Intensity H g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g1_PX419_human_18507	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18507	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18507	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_19204	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno092	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno441	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno561	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno561	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno561	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expA	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expB	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep2 20h	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
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Intensity g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic actions in the label cluster.
Intensity L g2_PX537_exp14 rep3 20h	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
g3_GK1_Chromatin_EHT_3	linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3 GK1 Chromatin EHT 5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_nE	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_nE_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
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Intensity L g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity M g3_KW35_nE_2	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity H g3_KW35_nE_2	linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity g3_KW35_rot_ET	linked to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_rot_ET	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_wE	Summed to the street of the street (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff5_Exp2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g4_NCC_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_B	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_C	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L gd NCC rosco 52	Summed up attracted for Current (VIC) of the instance cluster
Intensity L g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp1	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_A	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_B	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_C	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_C	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_D	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_E	Summed to the heavy label partner. Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_E	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

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Intensity L g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F5	Summed up extracted fon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Reverse	When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.

Potential contaminant	When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
id	A unique (consecutive) identifier for each row in the peptides table, which is used to cross-link the information in this table with the information stored in the other tables.
Protein group IDs	The identifiers of the protein groups this peptide was linked to, referenced against the proteinGroups table.
Peptide ID	Identifier of the associated peptide sequence summary, which can be found in the file 'peptides.txt'.
Evidence IDs	Identifier(s) for analyzed peptide evidence associated with the protein group referenced against the evidences table.
MS/MS IDs	The identifiers of the MS/MS scans identifying this peptide, referenced against the msms table.
Best MS/MS	The identifier of the best (in terms of quality) MS/MS scan identifying this peptide, referenced against the msms table.
Oxidation (M) site IDs	Identifier(s) for site(s) associated with this peptide, which show(s) evidence of the modification, referenced against the appropriate modification site file.
MS/MS Count	

Oxidation (M)Sites

Name	Separator	Description
Proteins		Identifiers of proteins this site is associated with.
Positions within proteins		For each protein identifier in the 'Proteins' column you find here the psoition of the site in the respective protein sequence. The index of the first amino acid in the sequence is 1.
Leading proteins		
Protein		Identifier of the protein this peptide is associated with.
Protein names		Names of proteins this peptide is associated with.
Gene names		Names of genes this peptide is associated with.
Fasta headers		Descriptions of proteins this peptide is associated with.
Localization prob		
Score diff		
PEP		The posterior error probability (PEP) of the best identified modified peptide containing this site.
Score		The Andromeda score of the best identified modified peptide containing this site.
Delta score		The Andromeda delta score of the best identified modified peptide containing this site.
Score for localization		The Andromeda score of the MS/MS spectrum used for calculating the localization score for this site.
Localization prob g1_GK1_Chromatin_AL		
Score diff g1_GK1_Chromatin_AL		
PEP g1_GK1_Chromatin_AL		
Score g1_GK1_Chromatin_AL		
Localization prob g1_GK1_Chromatin_CPT		
Score diff g1_GK1_Chromatin_CPT		
PEP g1_GK1_Chromatin_CPT		
Score g1_GK1_Chromatin_CPT		
Localization prob g1_GK1_Chromatin_CR		
Score diff g1_GK1_Chromatin_CR		
PEP g1_GK1_Chromatin_CR		
Score g1_GK1_Chromatin_CR		
Localization prob g1_GK1_Chromatin_HepHek		
Score diff g1_GK1_Chromatin_HepHek		
PEP g1_GK1_Chromatin_HepHek		
Score g1_GK1_Chromatin_HepHek		
Localization prob g1 GK1 Chromatin hilR		
Score diff g1_GK1_Chromatin_hilR		
PEP g1_GK1_Chromatin_hilR		
Score g1_GK1_Chromatin_hilR		
Localization prob g1_GK1_Chromatin_loIR		
Score diff g1_GK1_Chromatin_loIR		
PEP g1_GK1_Chromatin_loIR		
Score g1_GK1_Chromatin_loIR		
Localization prob g1_GK1_Chromatin_mH2A_1		
Score diff g1_GK1_Chromatin_mH2A_1		
PEP g1_GK1_Chromatin_mH2A_1		
Score g1_GK1_Chromatin_mH2A_1		
Localization prob g1_GK1_Chromatin_mH2A_2		
Score diff g1_GK1_Chromatin_mH2A_2		
PEP g1_GK1_Chromatin_mH2A_2 Score		
g1_GK1_Chromatin_mH2A_2		

Localization prob g1_GK1_Chromatin_mH2A_3	
Score diff	
g1_GK1_Chromatin_mH2A_3 PEP g1_GK1_Chromatin_mH2A_3	
Score	
g1_GK1_Chromatin_mH2A_3	
Localization prob g1_GK1_Chromatin_TNFa_1	
Score diff g1_GK1_Chromatin_TNFa_1	
PEP g1_GK1_Chromatin_TNFa_1	
Score g1_GK1_Chromatin_TNFa_1	
Localization prob g1_GK1_Chromatin_TNFa_2	
Score diff	
g1_GK1_Chromatin_TNFa_2	
PEP g1_GK1_Chromatin_TNFa_2 Score g1_GK1_Chromatin_TNFa_2	
Localization prob	
g1_GK1_Chromatin_TNFa_3	
Score diff g1_GK1_Chromatin_TNFa_3	
PEP g1_GK1_Chromatin_TNFa_3	
Score g1_GK1_Chromatin_TNFa_3	
Localization prob g1_KW10_110506	
Score diff g1_KW10_110506 PEP g1_KW10_110506	
Score g1_KW10_110506	
Localization prob g1_KW10_131126	
Score diff g1_KW10_131126	
PEP g1_KW10_131126	
Score g1_KW10_131126	
Localization prob g1_KW10_140117	
Score diff g1_KW10_140117 PEP g1_KW10_140117	
Score g1_KW10_140117	
Localization prob g1_KW11_130125	
Score diff g1_KW11_130125	
PEP g1_KW11_130125	
Score g1_KW11_130125 Localization prob	
g1_KW11_140104_nE	
Score diff g1_KW11_140104_nE	
PEP g1_KW11_140104_nE	
Score g1_KW11_140104_nE Localization prob	
g1_KW11_140104_wE	
Score diff g1_KW11_140104_wE	
PEP g1_KW11_140104_wE	
Score g1_KW11_140104_wE Localization prob g1_KW12_130317	
Score diff g1_KW12_130317	
PEP g1_KW12_130317	
Score g1_KW12_130317	
Localization prob g1_KW12_131223	
Score diff g1_KW12_131223	
PEP g1_KW12_131223 Score g1_KW12_131223	
Localization prob g1_KW13_130328	
Score diff g1_KW13_130328	
PEP g1_KW13_130328	
Score g1_KW13_130328	
Localization prob g1_KW14_130317	
Score diff g1_KW14_130317 PEP g1_KW14_130317	
Score g1_KW14_130317	

Localization prob g1_KW15_130317	
Score diff g1_KW15_130317	
PEP g1_KW15_130317	
Score g1_KW15_130317	
Localization prob g1_KW17_130319	
Score diff g1_KW17_130319	
PEP g1_KW17_130319	
Score g1_KW17_130319	
Localization prob g1_KW8_120517	
Score diff g1_KW8_120517	
PEP g1_KW8_120517	
Score g1_KW8_120517	
Localization prob g1_KW8_131126	
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Localization prob g1_KW8_140117	
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Localization prob g1_KW9_120425	
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Localization prob g1_KW9_120510	
Score diff g1_KW9_120510	
PEP g1_KW9_120510	
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Localization prob g1_PX1194_H1	
Score diff g1_PX1194_H1	
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Localization prob g1_PX1194_H10	
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Localization prob g1_PX1194_H11	
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Localization prob g1_PX1194_H12	
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Localization prob g1_PX1194_H2	
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Localization prob g1_PX1194_PCa1_1		
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Localization prob g1_PX1406_GM19140	
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PEP g1_PX1406_GM19140	
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Localization prob g1_PX1406_GM19143	
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Localization prob g1_PX1406_GM19200		
Score diff g1_PX1406_GM19200		
PEP g1_PX1406_GM19200		
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Localization prob g1_PX1406_GM19203		
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Localization prob g1_PX1406_GM19207		
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Localization prob g1_PX1406_GM19209		
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Localization prob g1_PX1406_GM19222		
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Localization prob g1_PX1406_GM19257		
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Localization prob g1_PX151_Rep2	
Score diff g1_PX151_Rep2	
PEP g1_PX151_Rep2	
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Localization prob g1_PX151_Rep3	
Score diff g1_PX151_Rep3	
PEP g1_PX151_Rep3	
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Localization prob	
g1_PX309_HCC1143-2	
Score diff g1_PX309_HCC1143-2	
PEP g1_PX309_HCC1143-2	
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Localization prob g1_PX309_HCC1143-3	
Score diff g1_PX309_HCC1143-3	
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g1_PX309_HCC1599-2	
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Localization prob	
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Score diff g1_PX309_HCC1937-1	
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PEP g1_PX309_HCC1937-2	
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Localization prob	
g1_PX309_HCC1937-3	
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PEP g1_PX309_HCC1937-3	
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g1_PX309_HCC202-1	
Score diff g1_PX309_HCC202-1	
PEP g1_PX309_HCC202-1	
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Localization prob g1_PX309_HCC202-2	
Score diff g1_PX309_HCC202-2	
PEP g1_PX309_HCC202-2	
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Localization prob	
g1_PX309_HCC202-3	
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g1_PX309_HCC2218-2		
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Score diff g1_PX309_MFM223-3		
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Localization prob g1_PX359_0h_1		
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Localization prob g1_PX359_0h_3		
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Localization prob g1_PX359_FN_3	
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PEP g1_PX359_FN_3	
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Localization prob g1_PX359_LAM_2	
Score diff g1_PX359_LAM_2	
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Localization prob g1_PX359_LAM_3	
Score diff g1_PX359_LAM_3	
PEP g1_PX359_LAM_3	
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Localization prob g1_PX359_Matr 12h_1	
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PEP g1_PX359_Matr 12h_1	
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Localization prob g1_PX359_Matr	
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Localization prob g1_PX359_Matr	
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Localization prob g1_PX359_Matr		
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Score diff g1_PX359_Matr dil_1		
PEP g1_PX359_Matr dil_1		
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Localization prob g1_PX359_Matr dil 2		
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PEP g1_PX359_Matr dil_2		
Score g1_PX359_Matr dil_2		
Localization prob g1_PX359_Matr dil_3		
Score diff g1_PX359_Matr dil_3		
PEP g1_PX359_Matr dil_3		
Score g1_PX359_Matr dil_3		
Localization prob g1_PX419_human_18507		
Score diff g1_PX419_human_18507		
PEP g1_PX419_human_18507		
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g1_PX419_human_18516		
Score diff g1_PX419_human_18516		
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Localization prob g1_PX419_human_19193		
Score diff g1_PX419_human_19193		
PEP g1_PX419_human_19193		
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Localization prob		
g1_PX419_human_19204		
Score diff g1_PX419_human_19204		
PEP g1_PX419_human_19204		
Score g1_PX419_human_19204		
Localization prob g1_PX438_Xeno092		
Score diff g1_PX438_Xeno092		
PEP g1_PX438_Xeno092		
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Localization prob		
g1_PX438_Xeno441		
Score diff g1_PX438_Xeno441		
PEP g1_PX438_Xeno441		
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Localization prob g1_PX438_Xeno561		
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Score diff g2_PX058_expA	
PEP g2_PX058_expA	
Score g2_PX058_expA	
Localization prob g2_PX058_expB	
Score diff g2_PX058_expB	
PEP g2_PX058_expB	
Score g2_PX058_expB	
Localization prob g2_PX058_expC	
Score diff g2_PX058_expC	
PEP g2_PX058_expC	
Score g2_PX058_expC	
Localization prob g2_PX058_expD	
Score diff g2_PX058_expD	
PEP g2_PX058_expD	
Score g2_PX058_expD	
Localization prob g2_PX058_expE	
Score diff g2_PX058_expE	
PEP g2_PX058_expE	
Score g2_PX058_expE	
Localization prob g2_PX058_expF	
Score diff g2_PX058_expF PEP g2_PX058_expF	
Score g2_PX058_expF	
Localization prob g2_PX089_Rep1	
Score diff g2_PX089_Rep1	
PEP g2_PX089_Rep1	
Score g2_PX089_Rep1	
Localization prob g2_PX089_Rep2	
Score diff g2_PX089_Rep2	
PEP g2_PX089_Rep2	
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Localization prob g2_PX537_exp14	
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Localization prob g2_PX537_exp14	
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Localization prob g2_PX537_exp14	
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Localization prob g3_GK1_Chromatin_A_TSA_1	
Score diff g3_GK1_Chromatin_A_TSA_1	
PEP g3_GK1_Chromatin_A_TSA_1	
Score g3_GK1_Chromatin_A_TSA_1	
Localization prob g3_GK1_Chromatin_A_TSA_2	
Score diff g3_GK1_Chromatin_A_TSA_2	
PEP g3_GK1_Chromatin_A_TSA_2	
Score g3_GK1_Chromatin_A_TSA_2	
Localization prob g3_GK1_Chromatin_CC_1	
Score diff g3 GK1 Chromatin CC 1	
PEP g3_GK1_Chromatin_CC_1	
Score g3_GK1_Chromatin_CC_1	
Localization prob g3_GK1_Chromatin_CC_2	
Score diff	
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Score diff g3_GK1_Chromatin_EHT_1	
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Localization prob g3_GK1_Chromatin_EHT_2	
Score diff g3_GK1_Chromatin_EHT_2	
PEP g3_GK1_Chromatin_EHT_2	
Score g3_GK1_Chromatin_EHT_2	
Localization prob g3_GK1_Chromatin_EHT_3	
Score diff g3_GK1_Chromatin_EHT_3	
PEP g3_GK1_Chromatin_EHT_3	
Score g3_GK1_Chromatin_EHT_3	
Localization prob g3_GK1_Chromatin_EHT_4	
Score diff g3_GK1_Chromatin_EHT_4	
PEP g3_GK1_Chromatin_EHT_4	
Score g3_GK1_Chromatin_EHT_4	
Localization prob g3_GK1_Chromatin_EHT_5	
Score diff g3_GK1_Chromatin_EHT_5	
PEP g3_GK1_Chromatin_EHT_5	
Score g3_GK1_Chromatin_EHT_5	
Localization prob g3_GK1_Chromatin_EHT_6	
Score diff g3_GK1_Chromatin_EHT_6	
PEP g3_GK1_Chromatin_EHT_6	
Score g3_GK1_Chromatin_EHT_6	
Localization prob g3_GK1_Chromatin_mH2A_4_5	
Score diff g3_GK1_Chromatin_mH2A_4_5	
PEP g3_GK1_Chromatin_mH2A_4_5	
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Score g3_GK1_Chromatin_mH2A_4_5	
Localization prob g3_KW35_ET	
Score diff g3_KW35_ET	
PEP g3_KW35_ET	
Score g3_KW35_ET	
Localization prob g3_KW35_ET_2	
Score diff g3_KW35_ET_2	
PEP g3_KW35_ET_2	
Score g3_KW35_ET_2	
Localization prob g3_KW35_nE	
Score diff g3_KW35_nE	
PEP g3_KW35_nE	
Score g3_KW35_nE	
Localization prob g3_KW35_nE_2	
Score diff g3_KW35_nE_2 PEP g3_KW35_nE_2	
Score g3_KW35_nE_2	
Localization prob g3_KW35_rot_ET	
Score diff g3_KW35_rot_ET	
PEP g3_KW35_rot_ET	
Score g3_KW35_rot_ET	
Localization prob g3_KW35_wE	
Score diff g3_KW35_wE	
PEP g3_KW35_wE	
Score g3_KW35_wE	
Localization prob g3_KW35_wE_2	
Score diff g3_KW35_wE_2	
PEP g3_KW35_wE_2	
Score g3_KW35_wE_2 Localization prob	
g3_PX328_Diff3_Exp1	
Score diff g3_PX328_Diff3_Exp1	
PEP g3_PX328_Diff3_Exp1	
Score g3_PX328_Diff3_Exp1	
Localization prob g3_PX328_Diff3_Exp2	
Score diff g3_PX328_Diff3_Exp2	
PEP g3_PX328_Diff3_Exp2	
Score g3_PX328_Diff3_Exp2	
Localization prob g3_PX328_Diff4_Exp1	
Score diff g3_PX328_Diff4_Exp1	
PEP g3_PX328_Diff4_Exp1	
Score g3_PX328_Diff4_Exp1	
Localization prob g3_PX328_Diff4_Exp2	
Score diff g3_PX328_Diff4_Exp2	
PEP g3_PX328_Diff4_Exp2	
Score g3_PX328_Diff4_Exp2	
Localization prob g3_PX328_Diff5_Exp1	
Score diff g3_PX328_Diff5_Exp1	
PEP g3_PX328_Diff5_Exp1	
Score g3_PX328_Diff5_Exp1	
Localization prob g3_PX328_Diff5_Exp2	
Score diff g3_PX328_Diff5_Exp2	
PEP g3_PX328_Diff5_Exp2	
Score g3_PX328_Diff5_Exp2	
Localization prob g3_PX597_A1_Spr	
Score diff g3_PX597_A1_Spr	
PEP g3_PX597_A1_Spr	
Score g3_PX597_A1_Spr	
Localization prob g3_PX597_A2_Spr	

Score diff g3_PX597_A2_Spr	
PEP g3_PX597_A2_Spr	
Score g3_PX597_A2_Spr	
Localization prob	
g3_PX597_A3_Spr	
Score diff g3_PX597_A3_Spr	
PEP g3_PX597_A3_Spr	
Score g3_PX597_A3_Spr	
Localization prob g3_PX597_B1_Spr	
Score diff g3_PX597_B1_Spr	
PEP g3_PX597_B1_Spr	
Score g3_PX597_B1_Spr	
Localization prob	
g3_PX597_B2_Spr	
Score diff g3_PX597_B2_Spr	
PEP g3_PX597_B2_Spr	
Score g3_PX597_B2_Spr	
Localization prob	
g3_PX597_B3_Spr Score diff g3_PX597_B3_Spr	
PEP g3_PX597_B3_Spr	
Score g3_PX597_B3_Spr	
Localization prob g4_NCC_A	
Score diff g4_NCC_A	
PEP g4_NCC_A	
Score g4_NCC_A	
Localization prob g4_NCC_B	
Score diff g4_NCC_B	
PEP g4_NCC_B	
Score g4_NCC_B	
Localization prob g4_NCC_C	
Score diff g4_NCC_C	
PEP g4_NCC_C	
Score g4_NCC_C	
Localization prob g4_NCC-CPT_s1	
Score diff g4_NCC-CPT_s1	
PEP g4_NCC-CPT_s1	
Score g4_NCC-CPT_s1	
Localization prob g4_NCC-CPT_s2	
Score diff g4_NCC-CPT_s2	
PEP g4_NCC-CPT_s2	
Score g4_NCC-CPT_s2	
Localization prob g4_NCC-CPT_s3	
Score diff g4_NCC-CPT_s3	
PEP g4_NCC-CPT_s3	
Score g4_NCC-CPT_s3	
Localization prob g4_NCC-HU_Ex1	
Score diff g4_NCC-HU_Ex1	
PEP g4_NCC-HU_Ex1	
Score g4_NCC-HU_Ex1	
Localization prob g4_NCC-HU_Ex2	
Score diff g4_NCC-HU_Ex2	
PEP g4_NCC-HU_Ex2	
Score g4_NCC-HU_Ex2	
Localization prob g4_NCC-HU_Ex3	
Score diff g4_NCC-HU_Ex3	
PEP g4_NCC-HU_Ex3	
Score g4_NCC-HU_Ex3	
Localization prob g4_NCC-rosco_s1	
Score diff g4_NCC-rosco_s1 PEP g4_NCC-rosco_s1	
Score g4_NCC-rosco_s1	
Localization prob g4_NCC-rosco_s2	
Score diff g4_NCC-rosco_s2	
00010 dili 9+_1400-10000_52	

PEP g4_NCC-rosco_s2	
Score g4_NCC-rosco_s2	
Localization prob g4_NCC-rosco_s3	
Score diff g4_NCC-rosco_s3	
PEP g4_NCC-rosco_s3	
Score g4_NCC-rosco_s3	
Localization prob g4_NCC-	
TSA_Exp1	
Score diff g4_NCC-TSA_Exp1	
PEP g4_NCC-TSA_Exp1	
Score g4_NCC-TSA_Exp1	
Localization prob q4 NCC-	
TSA_Exp2	
Score diff g4_NCC-TSA_Exp2	
PEP g4_NCC-TSA_Exp2	
Score g4_NCC-TSA_Exp2	
Localization prob g4_NCC- TSA_Exp3	
Score diff g4_NCC-TSA_Exp3	
PEP g4_NCC-TSA_Exp3	
Score g4_NCC-TSA_Exp3	
Localization prob g4_PX183_A	
Score diff g4_PX183_A	
PEP g4_PX183_A	
Score g4_PX183_A	
Localization prob g4_PX183_B	
Score diff g4_PX183_B	
PEP g4_PX183_B	
Score g4_PX183_B	
Localization prob g4_PX183_C	
Score diff g4_PX183_C	
PEP g4_PX183_C	
Score g4_PX183_C	
Localization prob g4_PX183_D	
Score diff g4_PX183_D	
PEP g4_PX183_D	
Score g4_PX183_D	
Localization prob g4_PX183_E	
Score diff g4_PX183_E	
PEP g4_PX183_E	
Score g4_PX183_E	
Localization prob g4_PX441_E1	
Score diff g4_PX441_E1	
PEP g4_PX441_E1	
Score g4_PX441_E1	
Localization prob g4_PX441_E2	
Score diff g4_PX441_E2	
PEP g4_PX441_E2	
Score g4_PX441_E2	
Localization prob g4_PX441_E3	
Score diff g4_PX441_E3	
PEP g4_PX441_E3	
Score g4_PX441_E3	
Localization prob g4_PX441_E4	
Score diff g4_PX441_E4	
PEP g4_PX441_E4	
Score g4_PX441_E4	
Localization prob g4_PX441_E5	
Score diff g4_PX441_E5	
PEP g4_PX441_E5	
Score g4_PX441_E5	
Localization prob g4_PX441_F1	
Score diff g4_PX441_F1	
PEP g4_PX441_F1	
Score g4_PX441_F1	

Localization prob g4_PX441_F2	
Score diff g4_PX441_F2	
PEP g4_PX441_F2	
Score g4_PX441_F2	
Localization prob g4_PX441_F3	
Score diff g4_PX441_F3	
PEP g4_PX441_F3	
Score g4_PX441_F3	
Localization prob g4_PX441_F4	
Score diff g4_PX441_F4	
PEP g4_PX441_F4	
Score g4_PX441_F4	
Localization prob g4_PX441_F5	
Score diff g4_PX441_F5	
PEP g4_PX441_F5	
Score g4_PX441_F5	
Diagnostic peak	Different countries of Ocidenties (M) as a soft-less that this either
Number of Oxidation (M)	Different numbers of Oxidation (M) on peptides that this site is involved in.
Amino acid	
Sequence window	
Modification window	
Peptide window coverage	
Oxidation (M) Probabilities	
Oxidation (M) Score diffs	
Position in peptide	
Charge	Charge state of the precursor ion.
Mass error [ppm]	Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence.
Ratio H/L	The ratio between two heavy and light label partners.
Ratio H/L1	The ratio between two heavy and light label partners.
Ratio H/L2	The ratio between two heavy and light label partners.
Ratio H/L3	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	
Ratio H/L localized	
Ratio H/L nmods	
Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	
Occupancy L	
Occupancy H	
Ratio H/L g1_GK1_Chromatin_AL	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_AL1	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_AL2	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_AL3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_AL	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_AL1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_AL2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_AL3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L unmod. pep.	
g1_GK1_Chromatin_AL Ratio H/L localized	
g1_GK1_Chromatin_AL	
Ratio H/L nmods g1_GK1_Chromatin_AL	
Ratio H/L variability [%] g1_GK1_Chromatin_AL	
Ratio H/L count g1_GK1_Chromatin_AL	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_AL	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	quantitation that are quantified with the re quantify method.
g1_GK1_Chromatin_AL Occupancy L	
g1_GK1_Chromatin_AL Occupancy H	
g1_GK1_Ćhromatin_AL Ratio H/L g1_GK1_Chromatin_CPT	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_GK1_Chromatin_CPT1 Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_CPT2 Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_CPT3	, , ,
Ratio H/L normalized g1_GK1_Chromatin_CPT	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_CPT1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_CPT2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_CPT3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	
Ratio H/L localized g1_GK1_Chromatin_CPT	
Ratio H/L nmods g1_GK1_Chromatin_CPT	
Ratio H/L variability [%] g1_GK1_Chromatin_CPT	
Ratio H/L count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 GK1 Chromatin CPT	
Occupancy L	
g1_GK1_Chromatin_CPT Occupancy H	
g1_GK1_Ćhromatin_CPT Ratio H/L g1_GK1_Chromatin_CR	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CR1	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CR2	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CR3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 GK1 Chromatin CR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_CR1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_GK1_Chromatin_CR2 Ratio H/L normalized g1_GK1_Chromatin_CR3	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_CR	The median of the total ratio population was stilled to 1.
Ratio H/L localized g1_GK1_Chromatin_CR	
Ratio H/L nmods	
g1_GK1_Chromatin_CR Ratio H/L variability [%] g1_GK1_Chromatin_CR	
g1_GK1_Chromatin_CR Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_GK1_Chromatin_CR	quantitation.

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Ratio H/L iso-count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_CR	
Occupancy L g1_GK1_Chromatin_CR	
Occupancy H g1_GK1_Chromatin_CR	
Ratio H/L g1_GK1_Chromatin_HepHek	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_HepHek1	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_HepHek2	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_HepHek3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_HepHek	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_HepHek1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 GK1 Chromatin HepHek 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_HepHek3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_HepHek	
Ratio H/L localized g1_GK1_Chromatin_HepHek	
Ratio H/L nmods g1_GK1_Chromatin_HepHek	
Ratio H/L variability [%] g1_GK1_Chromatin_HepHek	
Ratio H/L count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
g1_GK1_Chromatin_HepHek Ratio H/L type	quantitation that are quantined with the re-quantity method.
g1_GK1_Chromatin_HepHek Occupancy L	
g1_GK1_Chromatin_HepHek Occupancy H	
g1_GK1_Chromatin_HepHek Ratio H/L g1_GK1_Chromatin_hilR	The ratio between two beauty and light label partners
Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_GK1_Chromatin_hilR1 Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_hiIR2 Ratio H/L	, , ,
g1_GK1_Chromatin_hilR3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_hilR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_hilR1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_hilR2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_hilR3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_hilR	
Ratio H/L localized g1_GK1_Chromatin_hilR	
Ratio H/L nmods g1_GK1_Chromatin_hiIR	
Ratio H/L variability [%] g1_GK1_Chromatin_hilR	
Ratio H/L count g1_GK1_Chromatin_hilR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_hiIR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_hiIR	
Occupancy L g1_GK1_Chromatin_hiIR	
Occupancy H g1_GK1_Chromatin_hilR	
Ratio H/L g1_GK1_Chromatin_loIR	The ratio between two heavy and light label partners.

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Ratio H/L g1_GK1_Chromatin_loIR1	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_loIR2	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_loIR3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_loIR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_loIR1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_loIR3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_loIR	The median of the tetal raine population need of the
Ratio H/L localized g1_GK1_Chromatin_loIR	
Ratio H/L nmods g1_GK1_Chromatin_loIR	
Ratio H/L variability [%] g1_GK1_Chromatin_lolR	
Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_GK1_Chromatin_loIR Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_GK1_Chromatin_loIR Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_GK1_Chromatin_loIR Occupancy L	
g1_GK1_Chromatin_loIR Occupancy H	
g1_GK1_Chromatin_loIR Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_mH2A_1 Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_mH2A_11 Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_mH2A_12 Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_mH2A_13	Normalized ratio between two medium and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_1	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_mH2A_1	
Ratio H/L localized g1_GK1_Chromatin_mH2A_1	
Ratio H/L nmods g1_GK1_Chromatin_mH2A_1	
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_1	
Ratio H/L count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_1	
Occupancy L g1_GK1_Chromatin_mH2A_1	
Occupancy H g1_GK1_Chromatin_mH2A_1	
Ratio H/L g1_GK1_Chromatin_mH2A_2	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_21	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_22	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_23	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_GK1_Chromatin_mH2A_2	The median of the total ratio population was shifted to 1.

g1 GKI, Chromatin, mH2A, 2, 1 Ratio HL, normalized g1_GKI, Chromatin, mH2A, 2, 2 Ratio HL, normalized g1_GKI, Chromatin, mH2A, 3, 2 Ratio HL, normalized g1_GKI, Chromatin, mH2A, 3, 3 Ratio HL, normalized g1_GKI, Chromatin, mH2A, 3, 3 Ratio HL, normalized g1_GKI, Chromatin, mH2A, 3, 3 Ratio HL, normalized g1_GKI, nor	Ratio H/L normalized	Namediand satis between two modium and light label neglects
g1_GK1_Chromatin_mt2A_2 2 The median of the total ratio population was shifted to 1. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. The median of the total ratio population was shifted to 1. The median of the total ratio population was shifted to 1. The median of the total ratio population was shifted to 1. The ratio between two he		•
The median of the total ratio population was shifted to 1.		The median of the total ratio population was shifted to 1.
g1_GK1_Chromatin_mH2A_2 Ratio HU localized g1_GK1_Chromatin_mH2A_2 Ratio HU localized g1_GK1_Chromatin_mH2A_2 Ratio HU months g1_GK1_Chromatin_mH2A_2 Ratio HU months g1_GK1_Chromatin_mH2A_2 Ratio HU months g1_GK1_Chromatin_mH2A_2 Ratio HU conton g1_GK1_Chromatin_mH2A_3 g1_GK1_Chromatin		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_GK1_Chromatin_mH2A_2 Ratio HL variability [%] g1_GK1_Chromatin_mH2A_2 Ratio HL variability [%] g1_GK1_Chromatin_mH2A_2 Ratio HL variability [%] g1_GK1_Chromatin_mH2A_2 Ratio HL count g1_GK1_Chromatin_mH2A_3 Ratio HL	Ratio H/L unmod. pep. g1_GK1_Chromatin_mH2A_2	
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Comparing methods Comp		The ratio between two heavy and light label partners.
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GK1_Chromatin_mH2A_3		The ratio between two heavy and light label partners.
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GK1 Chromatin mH2A 3 The median of the total ratio population was shifted to 1.		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Ratio H/L nmods g1_GK1_Chromatin_mH2A_3 Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3 Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3 Ratio H/L count g1_GK1_Chromatin_mH2A_3 Ratio H/L iso-count g1_GK1_Chromatin_mH2A_3 Ratio H/L type g1_GK1_Chromatin_mH2A_3 Occupancy L g1_GK1_Chromatin_mH2A_3 Occupancy L g1_GK1_Chromatin_mH2A_3 The ratio between two heavy and light label partners. g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1_1 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L unmod. pep. g1_GK1_Chromatin_mH2A_3	
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3 Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3 Ratio H/L count g1_GK1_Chromatin_mH2A_3 Ratio H/L iso-count g1_GK1_Chromatin_mH2A_3 Ratio H/L type g1_GK1_Chromatin_mH2A_3 Occupancy L g1_GK1_Chromatin_mH2A_3 Occupancy H g1_GK1_Chromatin_mH2A_3 Ratio H/L g1_GK1_Chromatin_mH2A_3 The ratio between two heavy and light label partners. Ratio H/L g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
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g1_GK1_Chromatin_mH2A_3 Ratio H/L type g1_GK1_Chromatin_mH2A_3 Occupancy L g1_GK1_Chromatin_mH2A_3 Occupancy H g1_GK1_Chromatin_mH2A_3 Ratio H/L g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_1_1 Ratio H/L g1_GK1_Chromatin_TNFa_1_2 Ratio H/L g1_GK1_Chromatin_TNFa_1_3 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1_3 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1_1 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rotio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rotio H/L normalized Normalized ratio between two medium and light label partners.		
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g1_GK1_Chromatin_mH2A_3 Occupancy H g1_GK1_Chromatin_mH2A_3 Ratio H/L g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
Ratio H/L g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.		
g1_GK1_Chromatin_TNFa_1 Ratio H/L g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.		
g1_GK1_Chromatin_TNFa_11 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized Normalized ratio between two heavy and light label partners. Normalized ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_12 Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1 Ratio H/L normalized Normalized ratio between two heavy and light label partners. Normalized ratio between two heavy and light label partners. Normalized ratio between two heavy and light label partners.	Ratio H/L	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_13 Ratio H/L normalized g1_GK1_Chromatin_TNFa_1	Ratio H/L	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_1	Ratio H/L	The ratio between two heavy and light label partners.
g1_GK1_Chromatin_TNFa_11		
		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
y - GN - G	Ratio H/L normalized g1_GK1_Chromatin_TNFa_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_13 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.		
Ratio H/L unmod. pep. g1_GK1_Chromatin_TNFa_1		

Ratio H/L localized	
g1_GK1_Chromatin_TNFa_1	
Ratio H/L nmods g1_GK1_Chromatin_TNFa_1	
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_1	
Ratio H/L count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_1	
Occupancy L g1_GK1_Chromatin_TNFa_1	
Occupancy H g1_GK1_Chromatin_TNFa_1	
Ratio H/L g1_GK1_Chromatin_TNFa_2	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_21	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_22	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_TNFa_2	
Ratio H/L localized g1_GK1_Chromatin_TNFa_2	
Ratio H/L nmods g1_GK1_Chromatin_TNFa_2	
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_2	
Ratio H/L count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_2	
Occupancy L g1_GK1_Chromatin_TNFa_2	
Occupancy H g1_GK1_Chromatin_TNFa_2	
Ratio H/L g1_GK1_Chromatin_TNFa_3	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_31	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_32	The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_GK1_Chromatin_TNFa_3	
Ratio H/L localized g1_GK1_Chromatin_TNFa_3	
Ratio H/L nmods g1_GK1_Chromatin_TNFa_3	
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_3	
Ratio H/L count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_3	
Occupancy L g1_GK1_Chromatin_TNFa_3	
Occupancy H g1_GK1_Chromatin_TNFa_3	
Ratio H/L g1_KW10_110506	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1105061	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1105062	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1105063	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_110506	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1105061	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1105062	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1105063	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW10_110506	
Ratio H/L localized g1_KW10_110506	
Ratio H/L nmods g1_KW10_110506	
Ratio H/L variability [%] g1_KW10_110506	
Ratio H/L count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_110506	
Occupancy L g1_KW10_110506	
Occupancy H g1_KW10_110506	
Ratio H/L g1_KW10_131126	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1311261	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1311262	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1311263	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1311261	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1311262	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1311263	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW10_131126	
Ratio H/L localized g1_KW10_131126	
Ratio H/L nmods g1_KW10_131126	
Ratio H/L variability [%] g1_KW10_131126	
Ratio H/L count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_131126	
Occupancy L g1_KW10_131126	
Occupancy H g1_KW10_131126	
Ratio H/L g1_KW10_140117	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1401171	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1401172	The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_1401173	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1401171	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1401172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW10_1401173	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

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Ratio H/L unmod. pep. g1_KW10_140117	
Ratio H/L localized g1 KW10 140117	
Ratio H/L nmods g1_KW10_140117	
Ratio H/L variability [%] g1_KW10_140117	
Ratio H/L count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_140117	
Occupancy L g1_KW10_140117	
Occupancy H g1_KW10_140117 Ratio H/L g1_KW11_130125	The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_1301251	The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_1301252	The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_1301253	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_130125	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_1301251	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_1301252	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_1301253	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW11_130125	
Ratio H/L localized g1_KW11_130125	
Ratio H/L nmods g1_KW11_130125	
Ratio H/L variability [%] g1_KW11_130125	
Ratio H/L count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_130125	
Occupancy L g1_KW11_130125	
Occupancy H g1_KW11_130125	The ratio between two because and light label partners
Ratio H/L g1_KW11_140104_nE Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_KW11_140104_nE1	, , ,
Ratio H/L g1_KW11_140104_nE2	The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_140104_nE3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_140104_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_140104_nE1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_140104_nE2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_140104_nE3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW11_140104_nE	
Ratio H/L localized g1_KW11_140104_nE	
Ratio H/L nmods g1_KW11_140104_nE	
Ratio H/L variability [%] g1_KW11_140104_nE	
Ratio H/L count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_nE	
Occupancy L g1_KW11_140104_nE	
Occupancy H g1_KW11_140104_nE	
Ratio H/L g1_KW11_140104_wE	The ratio between two heavy and light label partners.

Ratio H/L	The ratio between two heavy and light label partners.
g1_KW11_140104_wE1 Ratio H/L	The ratio between two heavy and light label partners.
g1_KW11_140104_wE2	, , ,
Ratio H/L g1_KW11_140104_wE3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_140104_wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_140104_wE1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 KW11 140104 wE 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW11_140104_wE3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW11_140104_wE	The model of the total ratio population was stilled to 1.
Ratio H/L localized	
g1_KW11_140104_wE Ratio H/L nmods	
g1_KW11_140104_wE Ratio H/L variability [%]	
g1_KW11_140104_wE	
Ratio H/L count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_wE	
Occupancy L g1_KW11_140104_wE	
Occupancy H g1_KW11_140104_wE	
Ratio H/L g1_KW12_130317	The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_1303171	The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_1303172	The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_1303173	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW12_1303171	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q1 KW12 130317 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW12_1303173	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW12_130317	The model of the total ratio population has similar to the
Ratio H/L localized	
g1_KW12_130317 Ratio H/L nmods g1_KW12_130317	
5 =	
Ratio H/L variability [%] g1_KW12_130317	
Ratio H/L count g1_KW12_130317	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_130317	quantity motion.
Occupancy L g1_KW12_130317	
Occupancy H g1_KW12_130317	
Ratio H/L g1_KW12_131223	The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_1312231	The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_1312232	The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_1312233	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_131223	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW12_1312231	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW12_1312232	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_KW12_1312233 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_KW12_131223 Ratio H/L localized	
g1_KW12_131223	

Ratio H/L nmods g1_KW12_131223	
Ratio H/L variability [%]	
g1_KW12_131223	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_KW12_131223 Ratio H/L type g1_KW12_131223	quantitation that are quantified with the re-quantify method.
Occupancy L g1_KW12_131223	
Occupancy H g1_KW12_131223	
Ratio H/L g1_KW13_130328	The ratio between two heavy and light label partners.
Ratio H/L g1_KW13_1303281	The ratio between two heavy and light label partners.
Ratio H/L g1_KW13_1303282	The ratio between two heavy and light label partners.
Ratio H/L g1_KW13_1303283	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW13_130328	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW13_1303281	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW13_1303282	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW13_1303283	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW13_130328	
Ratio H/L localized g1_KW13_130328	
Ratio H/L nmods g1_KW13_130328 Ratio H/L variability [%]	
g1_KW13_130328	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_KW13_130328 Ratio H/L type g1_KW13_130328	quantitation that are quantified with the re-quantify method.
Occupancy L g1_KW13_130328	
Occupancy H g1_KW13_130328	
Ratio H/L g1_KW14_130317	The ratio between two heavy and light label partners.
Ratio H/L g1_KW14_1303171	The ratio between two heavy and light label partners.
Ratio H/L g1_KW14_1303172	The ratio between two heavy and light label partners.
Ratio H/L g1_KW14_1303173	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW14_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW14_1303171	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW14_1303172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW14_1303173	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW14_130317	
Ratio H/L localized g1_KW14_130317	
Ratio H/L nmods g1_KW14_130317	
Ratio H/L variability [%] g1_KW14_130317	
Ratio H/L count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW14_130317	
Occupancy L g1_KW14_130317	
Occupancy H g1_KW14_130317	
Ratio H/L g1_KW15_130317	The ratio between two heavy and light label partners.
Ratio H/L g1_KW15_1303171	The ratio between two heavy and light label partners.
Ratio H/L g1_KW15_1303172	The ratio between two heavy and light label partners.
Ratio H/L g1_KW15_1303173 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_KW15_130317	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW15_1303171	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW15_1303172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_KW15_1303173 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_KW15_130317	
Ratio H/L localized g1_KW15_130317	
Ratio H/L nmods g1_KW15_130317	
Ratio H/L variability [%] g1_KW15_130317	
Ratio H/L count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q1 KW15 130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW15_130317	quantitation that are quantitied with the re-quantity method.
Occupancy L g1_KW15_130317	
Occupancy H g1_KW15_130317	
Ratio H/L g1_KW17_130319	The ratio between two heavy and light label partners.
Ratio H/L g1_KW17_1303191	The ratio between two heavy and light label partners.
Ratio H/L g1_KW17_1303192	The ratio between two heavy and light label partners.
Ratio H/L g1_KW17_1303193 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_KW17_130319	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW17_1303191	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW17_1303192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW17_1303193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW17_130319	
Ratio H/L localized g1_KW17_130319	
Ratio H/L nmods g1_KW17_130319	
Ratio H/L variability [%] g1_KW17_130319	
Ratio H/L count g1_KW17_130319	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW17_130319	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW17_130319	
Occupancy L g1_KW17_130319	
Occupancy H g1_KW17_130319	The contradiction of the second of the secon
Ratio H/L g1_KW8_120517	The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1205171 Ratio H/L g1_KW8_1205172	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1205172 Ratio H/L g1_KW8_1205173	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_120517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1205172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1205173	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW8_120517	The median of the total ratio population was stilled to 1.
Ratio H/L localized g1_KW8_120517	
Ratio H/L nmods g1_KW8_120517	
Ratio H/L variability [%] g1_KW8_120517	
Ratio H/L count g1_KW8_120517	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_KW8_120517	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-guantify method.
Ratio H/L type g1_KW8_120517	, , , , , , , , , , , , , , , , , , , ,
Occupancy L g1_KW8_120517	
Occupancy H g1_KW8_120517	
Ratio H/L g1_KW8_131126	The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1311261	The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1311262	The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1311263	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_KW8_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1311261	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1311262	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1311263	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW8_131126	
Ratio H/L localized q1 KW8 131126	
Ratio H/L nmods g1_KW8_131126	
Ratio H/L variability [%] g1_KW8_131126	
Ratio H/L count g1_KW8_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_131126	
Occupancy L g1_KW8_131126	
Occupancy H g1_KW8_131126	The ratio between two beauty and light label partners
Ratio H/L g1_KW8_140117 Ratio H/L g1_KW8_1401171	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1401172	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_1401173	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1401171	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1401172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW8_1401173	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW8_140117	
Ratio H/L localized g1_KW8_140117	
Ratio H/L nmods g1_KW8_140117	
Ratio H/L variability [%] g1_KW8_140117	
Ratio H/L count g1_KW8_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count a1 KW8 140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_140117	quantitation that are quantities that the requarity methods
Occupancy L g1_KW8_140117	
Occupancy H g1_KW8_140117	
Ratio H/L g1_KW9_120425	The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_1204251	The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_1204252 Ratio H/L g1_KW9_1204253	The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_1204253 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_KW9_120425 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_KW9_1204251 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_KW9_1204252	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW9_1204253	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW9_120425	
Ratio H/L localized g1_KW9_120425	
Ratio H/L nmods g1_KW9_120425 Ratio H/L variability [%]	
g1_KW9_120425	Number of redundant and the (MOCC)
Ratio H/L count g1_KW9_120425	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW9_120425	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW9_120425	

Occupancy H g1_KW9_120425	
Ratio H/L g1_KW9_120510	The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_1205101	The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_1205102	The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_1205103	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW9_120510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW9_1205101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW9_1205102	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_KW9_1205103	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_KW9_120510	
Ratio H/L localized g1_KW9_120510	
Ratio H/L nmods g1_KW9_120510	
Ratio H/L variability [%] g1_KW9_120510	
Ratio H/L count g1_KW9_120510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW9_120510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW9_120510	
Occupancy L g1_KW9_120510	
Occupancy H g1_KW9_120510	
Ratio H/L g1_PX1194_H1 Ratio H/L g1_PX1194_H11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H12	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H13	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_H1 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1194_H11	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H1	
Ratio H/L localized g1_PX1194_H1	
Ratio H/L nmods g1_PX1194_H1	
Ratio H/L variability [%] g1_PX1194_H1	
Ratio H/L count g1_PX1194_H1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H1	
Occupancy L g1_PX1194_H1	
Occupancy H g1_PX1194_H1	
Ratio H/L g1_PX1194_H10	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H101 Ratio H/L g1_PX1194_H102	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H102 Ratio H/L g1_PX1194_H103	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H10	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q1 PX1194 H10 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H103	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H10	The median of the letter ratio population was stilled to 1.
Ratio H/L localized q1 PX1194 H10	
Ratio H/L nmods g1_PX1194_H10	
Ratio H/L variability [%]	
91_1-110	

Ratio H/L count g1_PX1194_H10	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H10	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H10	The same of the same plants and the same plants are same plants.
Occupancy L g1_PX1194_H10	
Occupancy H g1_PX1194_H10	
Ratio H/L g1_PX1194_H11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H111	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H112	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H113	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H111	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H112	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H113	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H11	
Ratio H/L localized g1_PX1194_H11	
Ratio H/L nmods g1_PX1194_H11	
Ratio H/L variability [%] g1_PX1194_H11	
Ratio H/L count g1_PX1194_H11	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H11	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H11	
Occupancy L g1_PX1194_H11	
Occupancy H g1_PX1194_H11	
Ratio H/L g1_PX1194_H12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H121	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H122	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H123	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H121	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H122	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H123	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H12	
Ratio H/L localized g1_PX1194_H12	
Ratio H/L nmods g1_PX1194_H12	
Ratio H/L variability [%] g1_PX1194_H12	
Ratio H/L count g1_PX1194_H12	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H12	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H12	
Occupancy L g1_PX1194_H12	
Occupancy H g1_PX1194_H12	
Ratio H/L g1_PX1194_H2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Datio III/I unmod non	
Ratio H/L unmod. pep. g1_PX1194_H2	
Ratio H/L localized g1_PX1194_H2	
Ratio H/L nmods g1_PX1194_H2	
Ratio H/L variability [%] g1_PX1194_H2	
Ratio H/L count g1_PX1194_H2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H2	quantitation that are quantitied with the re-quantity method.
Occupancy L g1_PX1194_H2	
Occupancy H g1_PX1194_H2	
Ratio H/L g1_PX1194_H3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H3	
Ratio H/L localized g1_PX1194_H3	
Ratio H/L nmods g1_PX1194_H3	
Ratio H/L variability [%] g1_PX1194_H3	
Ratio H/L count g1_PX1194_H3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H3	
Occupancy L g1_PX1194_H3	
Occupancy H g1_PX1194_H3 Ratio H/L g1 PX1194 H4	The ratio between two began and light label portners
Ratio H/L g1_PX1194_H41	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H42	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H43	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H41	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H42	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H43	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H4	
Ratio H/L localized g1_PX1194_H4	
Ratio H/L nmods g1_PX1194_H4	
Ratio H/L variability [%] g1_PX1194_H4	
Ratio H/L count g1_PX1194_H4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H4	
Occupancy L g1_PX1194_H4	
Occupancy H g1_PX1194_H4	The ratio hetures the beautiful light light light and
Ratio H/L g1_PX1194_H5 Ratio H/L g1_PX1194_H5 1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H51 Ratio H/L g1_PX1194_H52	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H53	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Y1_1^1134_1131	The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_H52 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1194_H53 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1194_H5	
Ratio H/L localized g1_PX1194_H5	
Ratio H/L nmods g1_PX1194_H5	
Ratio H/L variability [%] g1_PX1194_H5	
Ratio H/L count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H5	
Occupancy L g1_PX1194_H5	
Occupancy H g1_PX1194_H5	
Ratio H/L g1_PX1194_H6	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H61	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H62	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H63	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H61	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H62	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H63	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H6	
Ratio H/L localized g1_PX1194_H6	
Ratio H/L nmods g1_PX1194_H6	
Ratio H/L variability [%] g1_PX1194_H6	
Ratio H/L count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H6	
Occupancy L g1_PX1194_H6	
Occupancy H g1_PX1194_H6	
Ratio H/L g1_PX1194_H7	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H71	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H72	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H73	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H7	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H71	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H72	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H73	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H7	
Ratio H/L localized g1_PX1194_H7	
Ratio H/L nmods g1_PX1194_H7	
Ratio H/L variability [%] g1_PX1194_H7	
Ratio H/L count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H7	
Occupancy L g1_PX1194_H7	
Occupancy H g1_PX1194_H7	
Ratio H/L g1_PX1194_H8	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H81	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H82	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H83	The ratio between two heavy and light label partners.

Ratio H/L normalized q1 PX1194 H8	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_H81 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1194_H82 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1194_H83 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1194_H8	
Ratio H/L localized g1_PX1194_H8 Ratio H/L nmods g1_PX1194_H8	
Ratio H/L variability [%]	
Ratio H/L count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H8	
Occupancy L g1_PX1194_H8 Occupancy H g1_PX1194_H8	
Ratio H/L g1_PX1194_H9	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H91	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H92	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H93	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H9	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H91	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H92	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_H93	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_H9	
Ratio H/L localized g1_PX1194_H9	
Ratio H/L nmods g1_PX1194_H9 Ratio H/L variability [%]	
g1_PX1194_H9 Ratio H/L count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g1_PX1194_H9	quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L type g1_PX1194_H9	quantitation that are quantified with the re-quantify method.
Occupancy L g1_PX1194_H9	
Occupancy H g1_PX1194_H9	
Ratio H/L g1_PX1194_PCa1_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa1_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa1_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa1_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa1_1	
Ratio H/L localized g1_PX1194_PCa1_1	
Ratio H/L nmods g1_PX1194_PCa1_1	
Ratio H/L variability [%] g1_PX1194_PCa1_1	
Ratio H/L count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_1	
Occupancy L g1_PX1194_PCa1_1	

Occupancy H g1_PX1194_PCa1_1	
Ratio H/L g1_PX1194_PCa1_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa1_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa1_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa1_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa1_2	
Ratio H/L localized g1_PX1194_PCa1_2	
Ratio H/L nmods g1_PX1194_PCa1_2	
Ratio H/L variability [%] g1_PX1194_PCa1_2	
Ratio H/L count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_2	
Occupancy L g1_PX1194_PCa1_2	
Occupancy H g1_PX1194_PCa1_2 Ratio H/L g1_PX1194_PCa2_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa2_1	
Ratio H/L localized g1_PX1194_PCa2_1	
Ratio H/L nmods g1_PX1194_PCa2_1	
Ratio H/L variability [%] g1_PX1194_PCa2_1	
Ratio H/L count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_1	
Occupancy L g1_PX1194_PCa2_1	
Occupancy H g1_PX1194_PCa2_1	
Ratio H/L g1_PX1194_PCa2_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_22 Ratio H/L g1_PX1194_PCa2_23	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_23 Ratio H/L normalized g1_PX1194_PCa2_2	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total fatto population was stilled to 1.
g1_PX1194_PCa2_2 Ratio H/L localized g1_PX1194_PCa2_2	
Ratio H/L nmods	
g1_PX1194_PCa2_2	

Ratio H/L variability [%]	
g1_PX1194_PCa2_2 Ratio H/L count	Number of redundant partides (MC1 features) used for
g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_2	
Occupancy L g1_PX1194_PCa2_2	
Occupancy H g1_PX1194_PCa2_2	
Ratio H/L g1_PX1194_PCa2_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_33 Ratio H/L normalized	The ratio between two heavy and light label partners.
g1_PX1194_PCa2_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa2_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa2_3	
Ratio H/L localized g1_PX1194_PCa2_3	
Ratio H/L nmods g1_PX1194_PCa2_3	
Ratio H/L variability [%] g1_PX1194_PCa2_3	
Ratio H/L count g1_PX1194_PCa2_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_3	
Occupancy L g1_PX1194_PCa2_3	
Occupancy H g1_PX1194_PCa2_3	
Ratio H/L g1_PX1194_PCa3_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa3_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa3_1	
Ratio H/L localized g1_PX1194_PCa3_1	
Ratio H/L nmods g1_PX1194_PCa3_1	
Ratio H/L variability [%] g1_PX1194_PCa3_1	
Ratio H/L count g1_PX1194_PCa3_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa3_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_1	
Occupancy L g1_PX1194_PCa3_1	
Occupancy H g1_PX1194_PCa3_1	
Ratio H/L g1_PX1194_PCa3_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa3_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners
g1_PX1194_PCa3_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa3_2	
Ratio H/L localized g1_PX1194_PCa3_2	
Ratio H/L nmods g1_PX1194_PCa3_2	
Ratio H/L variability [%]	
Ratio H/L count g1_PX1194_PCa3_2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1194_PCa3_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_2	, , , , , , , , , , , , , , , , , , ,
Occupancy L g1_PX1194_PCa3_2	
Occupancy H g1_PX1194_PCa3_2	The vestion best were the server and limbs label to enter any
Ratio H/L g1_PX1194_PCa3_3 Ratio H/L g1_PX1194_PCa3_31	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_33	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_PCa3_3 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa3_31	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa3_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa3_3	
Ratio H/L localized g1_PX1194_PCa3_3	
Ratio H/L nmods g1_PX1194_PCa3_3	
Ratio H/L variability [%] g1_PX1194_PCa3_3	
Ratio H/L count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_3	
Occupancy L g1_PX1194_PCa3_3	
Occupancy H g1_PX1194_PCa3_3	
Ratio H/L g1_PX1194_PCa4_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_12 Ratio H/L g1_PX1194_PCa4_13	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_13 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa4_1	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa4_1	
Ratio H/L localized g1_PX1194_PCa4_1	
Ratio H/L nmods g1_PX1194_PCa4_1	
Ratio H/L variability [%] g1_PX1194_PCa4_1	
Ratio H/L count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_1	quantition and are quantition with the re-quantity method.
Occupancy L g1_PX1194_PCa4_1	
Occupancy H g1_PX1194_PCa4_1	

Potio H/I, c1, DV1104, DCc4, 2	The ratio between two began and light label partners
Ratio H/L g1_PX1194_PCa4_2 Ratio H/L g1_PX1194_PCa4_21	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_23	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_PCa4_2	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa4_2	
Ratio H/L localized g1_PX1194_PCa4_2	
Ratio H/L nmods g1_PX1194_PCa4_2	
Ratio H/L variability [%] g1_PX1194_PCa4_2	
Ratio H/L count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_2	
Occupancy L g1_PX1194_PCa4_2	
Occupancy H g1_PX1194_PCa4_2	
Ratio H/L g1_PX1194_PCa4_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_32 Ratio H/L g1_PX1194_PCa4_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_33 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa4_3	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa4_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa4_3	
Ratio H/L localized g1_PX1194_PCa4_3	
Ratio H/L nmods g1_PX1194_PCa4_3	
Ratio H/L variability [%] g1_PX1194_PCa4_3	
Ratio H/L count g1_PX1194_PCa4_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_3	
Occupancy L g1_PX1194_PCa4_3	
Occupancy H g1_PX1194_PCa4_3	
Ratio H/L g1_PX1194_PCa5_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_12 Ratio H/L g1_PX1194_PCa5_13	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners
Ratio H/L g1_PX1194_PCa5_13 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa5_1	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa5_1	
Ratio H/L localized g1_PX1194_PCa5_1	
Ratio H/L nmods g1_PX1194_PCa5_1	

Ratio H/L variability [%]	
g1_PX1194_PCa5_1 Ratio H/L count	Number of redundant postides (MS1 feetures) used for
g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_1	
Occupancy L g1_PX1194_PCa5_1	
Occupancy H g1_PX1194_PCa5_1	
Ratio H/L g1_PX1194_PCa5_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa5_2	
Ratio H/L localized g1_PX1194_PCa5_2	
Ratio H/L nmods g1_PX1194_PCa5_2	
Ratio H/L variability [%] g1_PX1194_PCa5_2	
Ratio H/L count g1_PX1194_PCa5_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_2	
Occupancy L g1_PX1194_PCa5_2	
Occupancy H g1_PX1194_PCa5_2	
Ratio H/L g1_PX1194_PCa5_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_33 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa5_3	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa5_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa5_3	
Ratio H/L localized g1_PX1194_PCa5_3	
Ratio H/L nmods g1_PX1194_PCa5_3	
Ratio H/L variability [%] g1_PX1194_PCa5_3	
Ratio H/L count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_3	
Occupancy L g1_PX1194_PCa5_3	
Occupancy H g1_PX1194_PCa5_3	
Ratio H/L g1_PX1194_PCa6_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa6_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa6_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa6_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa6_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa6_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized g1_PX1194_PCa6_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa6_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the telah rane paparanen mas similar to m
Ratio H/L localized g1_PX1194_PCa6_1	
Ratio H/L nmods	
g1_PX1194_PCa6_1 Ratio H/L variability [%]	
g1_PX1194_PCa6_1 Ratio H/L count g1 PX1194 PCa6_1	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa6_1 Ratio H/L type g1_PX1194_PCa6_1	quantitation that are quantified with the re-quantify method.
Occupancy L g1_PX1194_PCa6_1	
Occupancy H g1_PX1194_PCa6_1	
Ratio H/L g1_PX1194_PCa7_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa7_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa7_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa7_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX1194 PCa7 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1194 PCa7 1 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa7_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1194_PCa7_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1194_PCa7_1	
Ratio H/L localized g1_PX1194_PCa7_1	
Ratio H/L nmods g1_PX1194_PCa7_1	
Ratio H/L variability [%] g1_PX1194_PCa7_1	
Ratio H/L count g1_PX1194_PCa7_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa7_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa7_1	
Occupancy L g1_PX1194_PCa7_1	
Occupancy H g1_PX1194_PCa7_1	
Ratio H/L g1_PX1406_GM18486	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184861	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184862	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184863	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18486	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184861	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184862	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184863	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18486	
Ratio H/L localized g1_PX1406_GM18486	
Ratio H/L nmods g1_PX1406_GM18486	
Ratio H/L variability [%] g1_PX1406_GM18486	
Ratio H/L count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406'_GM18486 Occupancy L	
g1_PX1406_GM18486	
Occupancy H g1_PX1406_GM18486	
Ratio H/L g1_PX1406_GM18498 Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX1406_GM184981	, , ,
Ratio H/L g1_PX1406_GM184982	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184983	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18498	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184981	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184982	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184983	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18498	
Ratio H/L localized g1_PX1406_GM18498	
Ratio H/L nmods g1_PX1406_GM18498	
Ratio H/L variability [%] g1_PX1406_GM18498	
Ratio H/L count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18498	
Occupancy L g1_PX1406_GM18498	
Occupancy H g1_PX1406_GM18498	
Ratio H/L g1_PX1406_GM18499	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184991	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184992	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM184993	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18499	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184991	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184992	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM184993	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18499	
Ratio H/L localized g1_PX1406_GM18499	
Ratio H/L nmods g1_PX1406_GM18499	
Ratio H/L variability [%] g1_PX1406_GM18499	
Ratio H/L count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18499	
Occupancy L g1_PX1406_GM18499	
Occupancy H g1_PX1406_GM18499	
Ratio H/L g1_PX1406_GM18501	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185011	The ratio between two heavy and light label partners.

Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM185012 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM185013 Ratio H/L normalized g1_PX1406_GM18501	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM185011 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM185012 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM185013 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18501	
Ratio H/L localized g1_PX1406_GM18501	
Ratio H/L nmods g1_PX1406_GM18501	
Ratio H/L variability [%] g1_PX1406_GM18501	
Ratio H/L count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18501	
Occupancy L g1_PX1406_GM18501	
Occupancy H g1_PX1406_GM18501	
Ratio H/L g1_PX1406_GM18502	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185021	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185022	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185023	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18502	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185021	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185022	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185023	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18502	
Ratio H/L localized g1_PX1406_GM18502	
Ratio H/L nmods g1_PX1406_GM18502	
Ratio H/L variability [%] g1_PX1406_GM18502	
Ratio H/L count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18502	
Occupancy L g1_PX1406_GM18502	
Occupancy H g1_PX1406_GM18502	
Ratio H/L g1_PX1406_GM18504	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185041	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185042	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185043	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18504	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185041	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185042	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM185043 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18504	
Ratio H/L localized g1_PX1406_GM18504	
Ratio H/L nmods g1_PX1406_GM18504	
Ratio H/L variability [%] g1_PX1406_GM18504	
Ratio H/L count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18504	
Occupancy L g1_PX1406_GM18504	
Occupancy H g1_PX1406_GM18504	
Ratio H/L g1_PX1406_GM18505	The ratio between two heavy and light label partners.
Ratio H/L g1 PX1406 GM18505 1	The ratio between two heavy and light label partners.
Ratio H/L g1 PX1406 GM18505 2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185053	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18505	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185051	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185052	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185053	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18505	
Ratio H/L localized g1_PX1406_GM18505	
Ratio H/L nmods g1_PX1406_GM18505	
Ratio H/L variability [%] g1_PX1406_GM18505	
Ratio H/L count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18505	
Occupancy L g1_PX1406_GM18505	
Occupancy H g1_PX1406_GM18505	
Ratio H/L g1_PX1406_GM18507	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185071	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185072	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185073	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185071	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185072	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185073	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18507	
Ratio H/L localized g1_PX1406_GM18507	
Ratio H/L nmods g1_PX1406_GM18507	
Ratio H/L variability [%] g1_PX1406_GM18507	

Ratio H/L count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18507	quantification that are quantified with the re-quantify method.
Occupancy L g1_PX1406_GM18507	
Occupancy H	
g1_PX1406_GM18507 Ratio H/L g1_PX1406_GM18508	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM185081 Ratio H/L g1_PX1406_GM185082	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185083	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18508	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185081	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM18508 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185083	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18508	
Ratio H/L localized g1_PX1406_GM18508	
Ratio H/L nmods g1_PX1406_GM18508	
Ratio H/L variability [%] g1_PX1406_GM18508	
Ratio H/L count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18508	
Occupancy L g1_PX1406_GM18508	
Occupancy H g1_PX1406_GM18508	
Ratio H/L g1_PX1406_GM18510	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185101	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185102	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185103	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185102	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185103	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18510	
Ratio H/L localized g1_PX1406_GM18510	
Ratio H/L nmods g1_PX1406_GM18510	
Ratio H/L variability [%] g1_PX1406_GM18510	
Ratio H/L count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18510	
Occupancy L g1_PX1406_GM18510	
Occupancy H g1_PX1406_GM18510	

Ratio H/L g1_PX1406_GM18511	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185111	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185112	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185113	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18511	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185111	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185112	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185113	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18511	
Ratio H/L localized g1_PX1406_GM18511	
Ratio H/L nmods g1_PX1406_GM18511	
Ratio H/L variability [%] g1_PX1406_GM18511	
Ratio H/L count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18511	
Occupancy L g1_PX1406_GM18511	
Occupancy H g1_PX1406_GM18511	
Ratio H/L g1_PX1406_GM18516 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM185161	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185162	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185163	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185161	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185162	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185163	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18516	
Ratio H/L localized g1_PX1406_GM18516	
Ratio H/L nmods g1_PX1406_GM18516	
Ratio H/L variability [%] g1_PX1406_GM18516	
Ratio H/L count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18516	
Occupancy L g1_PX1406_GM18516	
Occupancy H g1_PX1406_GM18516	
Ratio H/L g1_PX1406_GM18517	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185171	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185172	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185173	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM185171 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM185172 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM185173 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18517 Ratio H/L localized	
g1_PX1406_GM18517	
Ratio H/L nmods g1_PX1406_GM18517	
Ratio H/L variability [%] g1_PX1406_GM18517	
Ratio H/L count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18517	
Occupancy L g1_PX1406_GM18517	
Occupancy H g1_PX1406_GM18517	
Ratio H/L g1_PX1406_GM18519	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185191	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185192	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18519	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185191	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18519	
Ratio H/L localized g1_PX1406_GM18519	
Ratio H/L nmods g1_PX1406_GM18519	
Ratio H/L variability [%] g1_PX1406_GM18519	
Ratio H/L count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18519	
Occupancy L g1_PX1406_GM18519	
Occupancy H g1_PX1406_GM18519	
Ratio H/L g1_PX1406_GM18520	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185201	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185202	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185203	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18520	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185201	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185202	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185203	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18520	
Ratio H/L localized g1_PX1406_GM18520	

Ratio H/L nmods	
g1_PX1406_GM18520 Ratio H/L variability [%]	
g1_PX1406_GM18520	Number of contract of the (ACC) (contract)
Ratio H/L count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18520	
Occupancy L g1_PX1406_GM18520	
Occupancy H g1_PX1406_GM18520	
Ratio H/L g1_PX1406_GM18522	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185221	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185222	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185223	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18522	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185221	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185222	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185223	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18522	
Ratio H/L localized g1_PX1406_GM18522	
Ratio H/L nmods g1_PX1406_GM18522	
Ratio H/L variability [%] g1_PX1406_GM18522	
Ratio H/L count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18522	
Occupancy L g1_PX1406_GM18522	
Occupancy H g1_PX1406_GM18522	
Ratio H/L g1_PX1406_GM18523	The ratio between two heavy and light label partners.
g1_PX1406_GM185231	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185232	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM185233	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18523	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185231	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185232	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM185233	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18523	
Ratio H/L localized g1_PX1406_GM18523	
Ratio H/L nmods g1_PX1406_GM18523	
Ratio H/L variability [%] g1_PX1406_GM18523	
Ratio H/L count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18523	

Occupancy L g1_PX1406_GM18523	
Occupancy H	
g1_PX1406_GM18523 Ratio H/L g1_PX1406_GM18852	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188521	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188522	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188523	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX1406 GM18852	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188521	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188522	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM188523 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18852 Ratio H/L localized	
g1_PX1406_GM18852 Ratio H/L nmods	
g1_PX1406_GM18852 Ratio H/L variability [%]	
g1_PX1406_GM18852	Number of and and a service (MOA (set use)) and (se
Ratio H/L count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18852	
Occupancy L g1_PX1406_GM18852	
Occupancy H g1_PX1406_GM18852	
Ratio H/L g1_PX1406_GM18855	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188551	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188552	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188553	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18855	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188551	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188552	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188553	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18855	
Ratio H/L localized g1_PX1406_GM18855	
Ratio H/L nmods g1_PX1406_GM18855	
Ratio H/L variability [%]	
Ratio H/L count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18855	gastination that are quantities with the re-quantity method.
Occupancy L g1_PX1406_GM18855	
Occupancy H	
g1_PX1406_GM18855 Ratio H/L g1_PX1406_GM18858	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188581	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188582	The ratio between two heavy and light label partners.
Y1_F1400_0 10000Z	

Ratio H/L g1_PX1406_GM188583	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18858	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM18858 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188582	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX1406_GM188583 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18858 Ratio H/L localized	
g1_PX1406_GM18858 Ratio H/L nmods	
g1_PX1406_GM18858 Ratio H/L variability [%]	
g1_PX1406_GM18858	
Ratio H/L count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18858	
Occupancy L g1_PX1406_GM18858	
Occupancy H g1 PX1406 GM18858	
Ratio H/L g1_PX1406_GM18861	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM188611 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM188612 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM188613 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM18861 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM188611	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188612	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188613	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18861	
Ratio H/L localized g1_PX1406_GM18861	
Ratio H/L nmods g1_PX1406_GM18861	
Ratio H/L variability [%] g1_PX1406_GM18861	
Ratio H/L count	Number of redundant peptides (MS1 features) used for quantitation.
g1_PX1406_GM18861 Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM18861 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX1406_GM18861 Occupancy L	
g1_PX1406_GM18861 Occupancy H	
g1_PX1406_GM18861	
Ratio H/L g1_PX1406_GM18862	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188621	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188622	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188623	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18862	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM188622 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM188623	The median of the total ratio population was shifted to 1.

Ratio H/L unmod. pep.	
g1_PX1406_GM18862	
Ratio H/L localized g1_PX1406_GM18862	
Ratio H/L nmods g1_PX1406_GM18862	
Ratio H/L variability [%] g1_PX1406_GM18862	
Ratio H/L count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18862	
Occupancy L g1_PX1406_GM18862	
Occupancy H g1_PX1406_GM18862	
Ratio H/L g1_PX1406_GM18870	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188701	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188702	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188703	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18870	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188701	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188702	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188703	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18870	
Ratio H/L localized g1_PX1406_GM18870	
Ratio H/L nmods g1_PX1406_GM18870	
Ratio H/L variability [%] g1_PX1406_GM18870	
Ratio H/L count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18870	
Occupancy L g1_PX1406_GM18870	
Occupancy H g1_PX1406_GM18870	
Ratio H/L g1_PX1406_GM18871	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188711	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188712	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM188713	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18871	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188711	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188712	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM188713	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18871	
Ratio H/L localized g1_PX1406_GM18871	
Ratio H/L nmods g1_PX1406_GM18871	
Ratio H/L variability [%] g1_PX1406_GM18871	
Ratio H/L count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM18871 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX1406_GM18871 Occupancy L	
g1_PX1406_GM18871 Occupancy H	
g1_PX1406_GM18871	The vation between two because and limbs label an article
Ratio H/L g1_PX1406_GM18907 Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX1406_GM189071 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM189072 Ratio H/L	, , ,
g1_PX1406_GM189073	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18907	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189071	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189072	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM18907 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	
Ratio H/L localized	
g1_PX1406_GM18907 Ratio H/L nmods	
g1_PX1406_GM18907 Ratio H/L variability [%]	
g1_PX1406_GM18907 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM18907 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1406_GM18907	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18907	
Occupancy L g1_PX1406_GM18907	
Occupancy H g1_PX1406_GM18907	
Ratio H/L g1_PX1406_GM18909	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189091	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189092	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189093	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18909	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM189091 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM189092 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM189093 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18909 Ratio H/L localized	
g1_PX1406_GM18909	
Ratio H/L nmods g1_PX1406_GM18909	
Ratio H/L variability [%] g1_PX1406_GM18909	
Ratio H/L count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18909	
Occupancy L g1_PX1406_GM18909	
Occupancy H	
g1_PX1406_GM18909 Ratio H/L g1_PX1406_GM18912	The ratio between two heavy and light label partners.
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Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM189121 Ratio H/L	
g1_PX1406_GM189122	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189123	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18912	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189121	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189122	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189123	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18912	
Ratio H/L localized g1 PX1406 GM18912	
Ratio H/L nmods g1_PX1406_GM18912	
Ratio H/L variability [%] g1_PX1406_GM18912	
Ratio H/L count g1 PX1406 GM18912	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for guantitation that are guantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18912	
Occupancy L g1_PX1406_GM18912	
Occupancy H g1_PX1406_GM18912	
Ratio H/L g1_PX1406_GM18913	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189131	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189132	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189133	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18913	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189131	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189132	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM189133	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM18913	
Ratio H/L localized g1_PX1406_GM18913	
Ratio H/L nmods g1_PX1406_GM18913	
Ratio H/L variability [%] g1_PX1406_GM18913	
Ratio H/L count q1 PX1406 GM18913	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for guantitation that are guantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18913	quantities and quantities that the to quantity method.
Occupancy L g1_PX1406_GM18913	
Occupancy H g1_PX1406_GM18913	
Ratio H/L g1_PX1406_GM18916	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189161	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM189162	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM189163 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM18916 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM189161	The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM189162 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM189163 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM18916 Ratio H/L localized	
g1_PX1406_GM18916	
Ratio H/L nmods g1_PX1406_GM18916	
Ratio H/L variability [%] g1_PX1406_GM18916	
Ratio H/L count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18916	
Occupancy L g1_PX1406_GM18916	
Occupancy H q1 PX1406 GM18916	
Ratio H/L g1_PX1406_GM19092	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190921 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190922 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190923 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM19092	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190921	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190922	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190923	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19092	
Ratio H/L localized g1_PX1406_GM19092	
Ratio H/L nmods g1_PX1406_GM19092	
Ratio H/L variability [%] g1_PX1406_GM19092	
Ratio H/L count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for guantitation that are guantified with the re-quantify method.
Ratio H/L type	quantitation that are quantified with the re-quantity method.
g1_PX1406'_GM19092 Occupancy L	
g1_PX1406_GM19092 Occupancy H	
g1_PX1406_GM19092	The ratio between two beauty and light label partners
Ratio H/L g1_PX1406_GM19093 Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX1406_GM190931 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190932 Ratio H/L	, , ,
g1_PX1406_GM190933	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19093	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190931	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190932	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190933	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19093	
Ratio H/L localized g1_PX1406_GM19093	
Ratio H/L nmods	
g1_PX1406_GM19093	

Ratio H/L variability [%] g1_PX1406_GM19093	
Ratio H/L count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q1 PX1406 GM19093	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	quantitation that are quantified with the re-quantity method.
g1_PX1406_GM19093 Occupancy L	
g1_PX1406_GM19093 Occupancy H	
g1_PX1406_GM19093 Ratio H/L g1_PX1406_GM19098	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190981 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190982 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM190983 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM19098 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM190981 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM190982	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190983	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19098	
Ratio H/L localized g1_PX1406_GM19098	
Ratio H/L nmods g1_PX1406_GM19098	
Ratio H/L variability [%] g1_PX1406_GM19098	
Ratio H/L count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19098	
Occupancy L g1_PX1406_GM19098	
Occupancy H g1_PX1406_GM19098	
Ratio H/L g1_PX1406_GM19099	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM190991	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM190992	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM190993	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX1406 GM19099	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190991	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190992	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM190993	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM19099 Ratio H/L localized	
g1_PX1406_GM19099 Ratio H/L nmods	
g1_PX1406_GM19099 Ratio H/L variability [%]	
g1_PX1406_GM19099 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19099 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19099 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX1406_GM19099 Occupancy L	
g1_PX1406_GM19099	

Occupancy H g1_PX1406_GM19099	
Ratio H/L g1_PX1406_GM19101	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191011	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191012	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191013	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191011	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191012	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191013	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19101	
Ratio H/L localized g1_PX1406_GM19101	
Ratio H/L nmods g1_PX1406_GM19101	
Ratio H/L variability [%] g1_PX1406_GM19101	
Ratio H/L count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19101	
Occupancy L g1_PX1406_GM19101	
Occupancy H g1_PX1406_GM19101	
Ratio H/L g1_PX1406_GM19102	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191021	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191022	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191023	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19102	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191021	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191022	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191023	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19102	
Ratio H/L localized g1_PX1406_GM19102	
Ratio H/L nmods g1_PX1406_GM19102	
Ratio H/L variability [%] g1_PX1406_GM19102	
Ratio H/L count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19102	
Occupancy L g1_PX1406_GM19102	
Occupancy H g1_PX1406_GM19102	
Ratio H/L g1_PX1406_GM19108	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191081	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191082	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191083	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM19108	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191081	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q1 PX1406 GM19108 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191083	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM19108 Ratio H/L localized	
g1_PX1406_GM19108 Ratio H/L nmods	
g1_PX1406_GM19108 Ratio H/L variability [%]	
g1_PX1406_GM19108 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19108 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19108	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19108	
Occupancy L g1_PX1406_GM19108	
Occupancy H g1_PX1406_GM19108	
Ratio H/L g1_PX1406_GM19114	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191141	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191142	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191143	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19114	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM19114 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q1 PX1406 GM19114 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191143	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19114	
Ratio H/L localized g1_PX1406_GM19114	
Ratio H/L nmods g1_PX1406_GM19114	
Ratio H/L variability [%]	
g1_PX1406_GM19114 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19114 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19114 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX1406_GM19114 Occupancy L	
g1_PX1406_GM19114 Occupancy H	
g1_PX1406_GM19114	
Ratio H/L g1_PX1406_GM19116 Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX1406_GM191161 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM191162 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM191163	
Ratio H/L normalized g1_PX1406_GM19116	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191161	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191162	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191163	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19116	

Ratio H/L localized	
g1_PX1406_GM19116 Ratio H/L nmods	
g1_PX1406_GM19116	
Ratio H/L variability [%] g1_PX1406_GM19116	
Ratio H/L count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19116	
Occupancy L	
g1_PX1406_GM19116 Occupancy H	
g1_PX1406_GM19116 Ratio H/L g1_PX1406_GM19119	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM191191 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM191192 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM191193	. , ,
Ratio H/L normalized g1_PX1406_GM19119	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191191	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19119	The median of the telah lane population has dimited to
Ratio H/L localized	
g1_PX1406_GM19119 Ratio H/L nmods	
g1_PX1406_GM19119 Ratio H/L variability [%]	
g1_PX1406_GM19119 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19119	quantitation.
Ratio H/L iso-count g1_PX1406_GM19119	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19119	
Occupancy L g1_PX1406_GM19119	
Occupancy H g1_PX1406_GM19119	
Ratio H/L g1_PX1406_GM19127	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191271	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191272	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191273	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19127	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191271	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191272	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191273	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19127	
Ratio H/L localized g1_PX1406_GM19127	
Ratio H/L nmods g1_PX1406_GM19127	
Ratio H/L variability [%]	
g1_PX1406_GM19127 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19127 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19127	quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM19127 Occupancy L	
g1_PX1406_GM19127	
Occupancy H g1_PX1406_GM19127	
Ratio H/L g1_PX1406_GM19128 Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX1406_GM191281	, , ,
Ratio H/L g1_PX1406_GM191282	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191283	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19128	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191281	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191282	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191283	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19128	
Ratio H/L localized g1_PX1406_GM19128	
Ratio H/L nmods g1_PX1406_GM19128	
Ratio H/L variability [%] g1_PX1406_GM19128	
Ratio H/L count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19128	
Occupancy L g1_PX1406_GM19128	
Occupancy H g1_PX1406_GM19128	
Ratio H/L g1_PX1406_GM19130	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191301	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191302	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191303	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19130	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191301	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191302	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191303	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19130	
Ratio H/L localized g1_PX1406_GM19130	
Ratio H/L nmods g1_PX1406_GM19130	
Ratio H/L variability [%] g1_PX1406_GM19130	
Ratio H/L count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19130	
Occupancy L g1_PX1406_GM19130	
Occupancy H g1_PX1406_GM19130	
Ratio H/L g1_PX1406_GM19131	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191311	The ratio between two heavy and light label partners.

Ratio HL The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. Normalized ratio between two fields (MS1 features) used for quantitation. Normalized ratio between two heavy and light label partners. Part Normalized ratio between two medium and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners.		
Ratio HL normalized gri EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized gri EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized gri EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized grid EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized grid EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized grid EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized grid EX1406. GM19131 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HL normalized grid EX1406. GM19131 Normalized ratio between two feedings of the total ratio population was shifted to 1. Ratio HL normalized grid EX1406. GM19131 Normalized grid EX1406. GM19131 Normalized grid EX1406. GM19131 Normalized grid EX1406. GM19137 The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. PX1406. GM19137 The ratio between two medium and light label partners. The ratio between two medium and light label partners. The ratio between two medium and light label partners. PX1406. GM19137 The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized grid Detail Ratio RM19137		The ratio between two heavy and light label partners.
Ratio H.L. normalized Normalized and to between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) The ratio between two medium and light label partners. Part 140, 60 (M1913) Part 140, 60 (M1		The ratio between two heavy and light label partners.
g1_PX1406_GM19131	Ratio H/L normalized	
Ratio HL, normalized Similar S		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L gr. PX1406_GM19137_3 The ratio between two heavy and light label partners. PX1406_GM19137_3 The ratio between two heavy and light label partners. PX1406_GM19137_3 The ratio between two heavy and light label partners. PX1406_GM19137_3 The ratio between two heavy and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19137_3 The ratio between two medium and light label partners. PX1406_GM19138_1 The ratio between two medium and light		Normalized ratio between two medium and light label partners.
Ratio H/L gr. PX1406_GM19137 The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. The ratio between two medium and light label partners. The median of the total ratio populatio	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
The fact of the		
Ratio HU, price Part Par	Ratio H/L localized	
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Company Comp	Ratio H/L g1_PX1406_GM19137	The ratio between two heavy and light label partners.
g1_PX1406_GM19137 _ 2 The ratio between two heavy and light label partners.		The ratio between two heavy and light label partners.
Ratio H/L normalized SM19137 SM10 SM19137 The median of the total ratio population was shifted to 1.		The ratio between two heavy and light label partners.
Q1_PX1406_GM19137 The median of the total ratio population was shifted to '1.		The ratio between two heavy and light label partners.
ST PX1406 GM19137 1 The median of the total ratio population was shifted to 1.		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
a1_PX1406_GM19137		
g1_PX1406_GM191373 The median of the total ratio population was Shifted to 1. Ratio H/L unmod. pep. g1_PX1406_GM19137 Ratio H/L localized g1_PX1406_GM19137 Ratio H/L variability [%] g1_PX1406_GM19137 Ratio H/L count g1_PX1406_GM19137 Ratio H/L so-count g1_PX1406_GM19137 Ratio H/L iso-count g1_PX1406_GM19137 Ratio H/L so-count g1_PX1406_GM19137 Ratio H/L g1_PX1406_GM19137 Cocupancy L g1_PX1406_GM19137 Ratio H/L g1_PX1406_GM19138 Ratio H/L normalized m1 loght label partners. Ratio H/L normalized m2 loght label partners. Ratio H/L normalized m3 loght label partners. Ratio H/L normalized m3 loght lab		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX1406_GM19137 Ratio H/L localized g1_PX1406_GM19137 Ratio H/L mords g1_PX1406_GM19137 Ratio H/L variability [%] g1_PX1406_GM19137 Ratio H/L count g1_PX1406_GM19137 Ratio H/L count g1_PX1406_GM19137 Ratio H/L iso-count g1_PX1406_GM19137 Ratio H/L iso-count g1_PX1406_GM19137 Ratio H/L type g1_PX1406_GM19137 Ratio H/L type g1_PX1406_GM19137 Ratio H/L type g1_PX1406_GM19137 Ratio H/L g1_PX1406_GM19138 The ratio between two heavy and light label partners. Ratio H/L g1_PX1406_GM19138 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H		
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g1_PX1406_GM19137 Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L count g1_PX1406_GM19137 Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L iso-count g1_PX1406_GM19137 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L type g1_PX1406_GM19137 Occupancy L g1_PX1406_GM19137 Occupancy H g1_PX1406_GM19138 The ratio between two heavy and light label partners. Ratio H/L g1_PX1406_GM19138 The ratio between two heavy and light label partners. Ratio H/L g1_PX1406_GM19138_1 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX1406_GM19138_1 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized on the total ratio population was shifted to 1. Ratio H/L normalized on the total ratio population was shifted to 1. Ratio H/L normalized on the total ratio population was shifted to 1. Ratio H/L normalized on the total ratio population was shifted to 1. Ratio H/L normalized on the total ratio population was shifted to 1. Ratio H/L normalized on the total ratio population was shifted to 1.		
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g1_PX1406_GM19137 Occupancy H g1_PX1406_GM19137 Ratio H/L g1_PX1406_GM19138 The ratio between two heavy and light label partners. Ratio H/L g1_PX1406_GM191381 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
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Ratio H/L g1_PX1406_GM191381 Ratio H/L g1_PX1406_GM191382 Ratio H/L g1_PX1406_GM191382 Ratio H/L g1_PX1406_GM191383 Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
g1_PX1406_GM191381 Ratio H/L g1_PX1406_GM191382 Ratio H/L g1_PX1406_GM191383 Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L g1_PX1406_GM19138	The ratio between two heavy and light label partners.
g1_PX1406_GM191382 Ratio H/L g1_PX1406_GM191383 Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191383 Ratio H/L normalized g1_PX1406_GM19138		The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM19138 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized g1_PX1406_GM191381 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.	Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM191381 The median of the total ratio population was šhifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
Ratio H/L normalized Normalized ratio between two medium and light label partners.		
		Normalized ratio between two medium and light label partners.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM191383 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM19138	
Ratio H/L localized g1_PX1406_GM19138	
Ratio H/L nmods g1_PX1406_GM19138	
Ratio H/L variability [%] g1_PX1406_GM19138	
Ratio H/L count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19138	
Occupancy L g1_PX1406_GM19138	
Occupancy H g1_PX1406_GM19138	
Ratio H/L g1_PX1406_GM19140	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191401	The ratio between two heavy and light label partners.
Ratio H/L g1 PX1406 GM19140 2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191403	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19140	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191401	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191402	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191403	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19140	
Ratio H/L localized g1_PX1406_GM19140	
Ratio H/L nmods g1_PX1406_GM19140	
Ratio H/L variability [%] g1_PX1406_GM19140	
Ratio H/L count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19140	
Occupancy L g1_PX1406_GM19140	
Occupancy H g1_PX1406_GM19140	
Ratio H/L g1_PX1406_GM19143	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191431	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191432	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191433	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19143	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191431	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191432	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191433	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19143	
Ratio H/L localized g1_PX1406_GM19143	
Ratio H/L nmods g1_PX1406_GM19143	
Ratio H/L variability [%] g1_PX1406_GM19143	

Ratio H/L count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19143	quantination that are quantined with the re-quantity metricus.
Occupancy L g1_PX1406_GM19143	
Occupancy H g1_PX1406_GM19143	
Ratio H/L g1_PX1406_GM19144	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191441	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191442	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191443	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19144	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191441	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191442	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191443	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19144	
Ratio H/L localized g1_PX1406_GM19144	
Ratio H/L nmods g1_PX1406_GM19144	
Ratio H/L variability [%] g1_PX1406_GM19144	
Ratio H/L count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19144	
Occupancy L g1_PX1406_GM19144	
Occupancy H g1_PX1406_GM19144	
Ratio H/L g1_PX1406_GM19147	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191471	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191472	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191473	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19147	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191471	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191472	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191473	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19147	
Ratio H/L localized g1_PX1406_GM19147	
Ratio H/L nmods g1_PX1406_GM19147	
Ratio H/L variability [%] g1_PX1406_GM19147	
Ratio H/L count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19147	
Occupancy L g1_PX1406_GM19147	
Occupancy H g1_PX1406_GM19147	

Ratio H/L g1_PX1406_GM19152	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191521	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191522	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191523	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19152	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM19152 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191523	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19152	
Ratio H/L localized g1_PX1406_GM19152	
Ratio H/L nmods g1_PX1406_GM19152	
Ratio H/L variability [%] g1_PX1406_GM19152	
Ratio H/L count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19152	
Occupancy L g1_PX1406_GM19152	
Occupancy H g1_PX1406_GM19152	
Ratio H/L g1_PX1406_GM19153	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191531	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191532	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191533	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19153	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191531	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191532	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191533	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19153	
Ratio H/L localized g1_PX1406_GM19153	
Ratio H/L nmods g1_PX1406_GM19153	
Ratio H/L variability [%] g1_PX1406_GM19153	
Ratio H/L count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19153	
Occupancy L g1_PX1406_GM19153	
Occupancy H g1_PX1406_GM19153	
Ratio H/L g1_PX1406_GM19160	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191601	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191602	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191603	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19160	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM191601 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM191602 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM191603	The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19160	
Ratio H/L localized g1_PX1406_GM19160	
Ratio H/L nmods g1_PX1406_GM19160	
Ratio H/L variability [%] g1_PX1406_GM19160	
Ratio H/L count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1 PX1406 GM19160	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX1406 GM19160	quantitation that are quantities with the re quantity method.
Occupancy L	
g1_PX1406_GM19160 Occupancy H	
g1_PX1406_GM19160 Ratio H/L g1_PX1406_GM19172	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191721	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191722	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191723	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX1406_GM19172 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM191721 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM191722 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX1406_GM191723 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX1406_GM19172 Ratio H/L localized	
g1_PX1406_GM19172 Ratio H/L pmods	
g1_PX1406_GM19172	
Ratio H/L variability [%] g1_PX1406_GM19172	
Ratio H/L count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19172	
Occupancy L g1_PX1406_GM19172	
Occupancy H g1_PX1406_GM19172	
Ratio H/L g1_PX1406_GM19192	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191921	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191922	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191923	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191921	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191922	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191923	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19192	
Ratio H/L localized g1_PX1406_GM19192	

Ratio H/L nmods	
g1_PX1406_GM19192 Ratio H/L variability [%]	
g1_PX1406_GM19192	North and the death and it has ASSA (see here)
Ratio H/L count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19192	
Occupancy L g1_PX1406_GM19192	
Occupancy H g1_PX1406_GM19192	
Ratio H/L g1_PX1406_GM19193	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191931	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191932	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM191933	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191931	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191932	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM191933	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19193	
Ratio H/L localized g1_PX1406_GM19193	
Ratio H/L nmods g1_PX1406_GM19193	
Ratio H/L variability [%] g1_PX1406_GM19193	
Ratio H/L count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19193	
Occupancy L g1_PX1406_GM19193	
Occupancy H g1_PX1406_GM19193	
Ratio H/L g1_PX1406_GM19200	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192001	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192002	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192003	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19200	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192001	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192002	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192003	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19200	
Ratio H/L localized g1_PX1406_GM19200	
Ratio H/L nmods g1_PX1406_GM19200	
Ratio H/L variability [%] g1_PX1406_GM19200	
Ratio H/L count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19200	

Occupancy L	
g1_PX1406_GM19200 Occupancy H	
g1_PX1406_GM19200 Ratio H/L g1_PX1406_GM19203	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX1406_GM192031 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM192032 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX1406_GM192033 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM19203	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192031	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192032	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192033	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19203	
Ratio H/L localized g1_PX1406_GM19203	
Ratio H/L nmods g1_PX1406_GM19203	
Ratio H/L variability [%] g1_PX1406_GM19203	
Ratio H/L count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19203	
Occupancy L q1 PX1406 GM19203	
Occupancy H q1 PX1406 GM19203	
Ratio H/L g1_PX1406_GM19204	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192041	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192042	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192043	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192041	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192042	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192043	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19204	
Ratio H/L localized g1_PX1406_GM19204	
Ratio H/L nmods g1_PX1406_GM19204	
Ratio H/L variability [%]	
Ratio H/L count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19204	
Occupancy L g1_PX1406_GM19204	
Occupancy H g1_PX1406_GM19204	
Ratio H/L g1_PX1406_GM19207	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192071	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192072	The ratio between two heavy and light label partners.

Ratio H/L g1_PX1406_GM192073	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19207	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM19207 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192072	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192073	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total fatto population was shifted to 1.
g1_PX1406_GM19207 Ratio H/L localized	
g1_PX1406_GM19207 Ratio H/L nmods	
g1_PX1406_GM19207 Ratio H/L variability [%]	
g1_PX1406_GM19207 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19207 Ratio H/L iso-count	quantitation.
g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19207	
Occupancy L g1_PX1406_GM19207	
Occupancy H g1_PX1406_GM19207	
Ratio H/L g1_PX1406_GM19209	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192091	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192092	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192093	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX1406 GM19209	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM19209 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX1406 GM19209 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192093	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX1406_GM19209	The median of the telan rane paperation had a mice to m
Ratio H/L localized g1_PX1406_GM19209	
Ratio H/L nmods g1_PX1406_GM19209	
Ratio H/L variability [%]	
g1_PX1406_GM19209 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19209 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1406_GM19209 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX1406_GM19209 Occupancy L	
g1_PX1406_GM19209 Occupancy H	
g1_PX1406_GM19209	
Ratio H/L g1_PX1406_GM19222	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192221	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192222	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192223	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19222	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192221	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192222	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192223	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Ratio H/L unmod. pep.	
g1_PX1406_GM19222	
Ratio H/L localized g1_PX1406_GM19222	
Ratio H/L nmods g1_PX1406_GM19222	
Ratio H/L variability [%] g1_PX1406_GM19222	
Ratio H/L count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19222	
Occupancy L g1_PX1406_GM19222	
Occupancy H g1_PX1406_GM19222	
Ratio H/L g1_PX1406_GM19257	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192571	The ratio between two heavy and light label partners.
Ratio H/L g1 PX1406 GM19257 2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM192573	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19257	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192571	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192572	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX1406_GM192573	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1 PX1406 GM19257	
Ratio H/L localized g1_PX1406_GM19257	
Ratio H/L nmods g1_PX1406_GM19257	
Ratio H/L variability [%] g1_PX1406_GM19257	
Ratio H/L count g1_PX1406_GM19257	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19257	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX1406 GM19257	
Occupancy L g1_PX1406_GM19257	
Occupancy H g1 PX1406 GM19257	
Ratio H/L g1_PX151_Rep1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep13 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX151_Rep1	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX151_Rep11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX151_Rep12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX151_Rep13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX151_Rep1	
Ratio H/L localized g1_PX151_Rep1	
Ratio H/L nmods g1_PX151_Rep1	
Ratio H/L variability [%] g1_PX151_Rep1	
Ratio H/L count g1_PX151_Rep1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX151_Rep1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX151_Rep1	

Occupancy L g1_PX151_Rep1	
Occupancy H g1_PX151_Rep1	
Ratio H/L g1_PX151_Rep2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep22 Ratio H/L g1_PX151_Rep23	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX151_Rep2	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX151_Rep21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX151_Rep22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX151_Rep23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX151_Rep2	
Ratio H/L localized g1_PX151_Rep2	
Ratio H/L nmods g1_PX151_Rep2	
Ratio H/L variability [%] g1_PX151_Rep2	
Ratio H/L count g1_PX151_Rep2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX151_Rep2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX151_Rep2	
Occupancy L g1_PX151_Rep2	
Occupancy H g1_PX151_Rep2	The cost's hadrones have been and Political anatoms
Ratio H/L g1_PX151_Rep3 Ratio H/L g1_PX151_Rep31	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep31	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep33	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX151_Rep3 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX151_Rep31 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX151_Rep32 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX151_Rep33	The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX151_Rep3	
Ratio H/L localized g1_PX151_Rep3	
Ratio H/L nmods g1_PX151_Rep3	
Ratio H/L variability [%] g1_PX151_Rep3	
Ratio H/L count g1_PX151_Rep3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX151_Rep3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX151_Rep3	
Occupancy L g1_PX151_Rep3	
Occupancy H g1_PX151_Rep3	
Ratio H/L g1_PX309_HCC1143-1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1143-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC1143-1	
Ratio H/L localized g1_PX309_HCC1143-1	
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Ratio H/L nmods g1_PX309_HCC1143-1	
Ratio H/L variability [%] g1_PX309_HCC1143-1	
Ratio H/L count g1_PX309_HCC1143-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1143-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-1	
Occupancy L g1_PX309_HCC1143-	
Occupancy H g1_PX309_HCC1143-1	
Ratio H/L g1_PX309_HCC1143-2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1143-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC1143-2	
Ratio H/L localized g1_PX309_HCC1143-2	
Ratio H/L nmods g1_PX309_HCC1143-2	
Ratio H/L variability [%] g1_PX309_HCC1143-2	
Ratio H/L count g1_PX309_HCC1143-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1143-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-2	
Occupancy L g1_PX309_HCC1143-	
Occupancy H g1_PX309_HCC1143-2	
Ratio H/L g1_PX309_HCC1143-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1143-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC1143-3	
Ratio H/L localized g1_PX309_HCC1143-3	
Ratio H/L nmods g1_PX309_HCC1143-3	
Ratio H/L variability [%] g1_PX309_HCC1143-3	
Ratio H/L count g1_PX309_HCC1143-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1143-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-3	

Occupancy H g1_PX309_HCC1143-3 Ratio H/L g1_PX309_HCC1599-1 The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two heavy and light label parts The ratio between two medium and light The median of the total ratio population was shift Ratio H/L normalized g1_PX309_HCC1599-1 The median of the total ratio population was shift Ratio H/L normalized g1_PX309_HCC1599-12 Ratio H/L normalized g1_PX309_HCC1599-13 Ratio H/L normalized g1_PX309_HCC1599-1 Ratio H/L unmod.pep. g1_PX309_HCC1599-1 Ratio H/L localized g1_PX309_HCC1599-1 Ratio H/L normods g1_PX309_HCC1599-1 Ratio H/L normods g1_PX309_HCC1599-1 Ratio H/L normods g1_PX309_HCC1599-1	iners. Iners. Iners. Iabel partners.
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Ratio H/L g1_PX309_HCC1599-1 Ratio H/L g1_PX309_HCC1599-1 Ratio H/L g1_PX309_HCC1599-1 Ratio H/L g1_PX309_HCC1599-1 Ratio H/L normalized g1_PX309_HCC1599-1 Ratio H/L unmod. pep. g1_PX309_HCC1599-1 Ratio H/L localized g1_PX309_HCC1599-1 Ratio H/L localized g1_PX309_HCC1599-1 Ratio H/L normals	iners. Iners. Iners. Iabel partners.
Ratio H/L g1_PX309_HCC1599- 12 Ratio H/L g1_PX309_HCC1599- 13 Ratio H/L normalized g1_PX309_HCC1599-1 Ratio H/L unmod. pep. g1_PX309_HCC1599-1 Ratio H/L localized g1_PX309_HCC1599-1 Ratio H/L localized g1_PX309_HCC1599-1 Ratio H/L normals	label partners. label partners. fed to 1. label partners. fed to 1. label partners. fed to 1. label partners. fed to 1.
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Ratio H/L variability [%] g1_PX309_HCC1599-1	
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Occupancy L g1_PX309_HCC1599-	
Occupancy H g1_PX309_HCC1599-1	
Ratio H/L g1_PX309_HCC1599-2 The ratio between two heavy and light label parts	ners.
Ratio H/L g1_PX309_HCC1599- The ratio between two heavy and light label particle.	ners.
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Ratio H/L g1_PX309_HCC1599- 23 The ratio between two heavy and light label parts	ners.
Ratio H/L normalized Normalized ratio between two medium and light g1_PX309_HCC1599-2 The median of the total ratio population was shift	label partners.
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Ratio H/L nmods g1_PX309_HCC1599-2	
Ratio H/L variability [%] g1_PX309_HCC1599-2	
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Occupancy L g1_PX309_HCC1599-	
Occupancy H g1_PX309_HCC1599-2	
Ratio H/L g1_PX309_HCC1599-3 The ratio between two heavy and light label parts	ners.
Ratio H/L g1_PX309_HCC1599- The ratio between two heavy and light label parts	ners.
Ratio H/L g1_PX309_HCC1599- 32 The ratio between two heavy and light label parts	ners.

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Ratio H/L normalized g1_PX309_HCC1937-1	Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Ratio H/L normalized g1_PX309_HCC1937-13	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
Ratio H/L unmod. pep. g1_PX309_HCC1937-1 Ratio H/L localized g1_PX309_HCC1937-1 Ratio H/L nmods g1_PX309_HCC1937-1 Ratio H/L variability [%] g1_PX309_HCC1937-1 Ratio H/L count g1_PX309_HCC1937-1 Ratio H/L iso-count g1_PX309_HCC1937-1 Ratio H/L iso-count g1_PX309_HCC1937-1 Ratio H/L soyled with the re-quantify method. Ratio H/L type g1_PX309_HCC1937-1 Occupancy L g1_PX309_HCC1937-1 Occupancy L g1_PX309_HCC1937-1 The ratio between two heavy and light label partners. Ratio H/L g1_PX309_HCC1937-2 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
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Ratio H/L nmods g1_PX309_HCC1937-1 Ratio H/L variability [%] g1_PX309_HCC1937-1 Ratio H/L count g1_PX309_HCC1937-1 Ratio H/L count g1_PX309_HCC1937-1 Ratio H/L iso-count g1_PX309_HCC1937-1 Ratio H/L type g1_PX309_HCC1937-1 Cocupancy L g1_PX309_HCC1937-1 Cocupancy L g1_PX309_HCC1937-1 Ratio H/L g1_PX309_HCC1937-2 The ratio between two heavy and light label partners. Ratio H/L g1_PX309_HCC1937-2 Ratio H/L g1_PX309_HCC1937-2 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.		
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Occupancy H g1_PX309_HCC1937-1 Ratio H/L g1_PX309_HCC1937-2 Ratio H/L g1_PX309_HCC1937-2 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_HCC1937-2 The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners.	Occupancy L g1_PX309_HCC1937-	
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Ratio H/L g1_PX309_HCC1937- 21 Ratio H/L g1_PX309_HCC1937- 22 Ratio H/L g1_PX309_HCC1937- 22 Ratio H/L g1_PX309_HCC1937- 23 Ratio H/L normalized g1_PX309_HCC1937-2 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937- 22 Ratio H/L g1_PX309_HCC1937- 23 Ratio H/L normalized g1_PX309_HCC1937-2 Ratio H/L normalized partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.	Ratio H/L g1_PX309_HCC1937-	
Ratio H/L g1_PX309_HCC1937- 23 Ratio H/L g1_PX309_HCC1937- 23 Ratio H/L normalized g1_PX309_HCC1937-2 Ratio H/L normalized g1_PX309_HCC1937-2 Ratio H/L normalized g1_PX309_HCC1937-21 Ratio H/L normalized g1_PX309_HCC1937-21 Ratio H/L normalized g1_PX309_HCC1937-22 Ratio H/L normalized g1_PX309_HCC1937-22 Ratio H/L normalized g1_PX309_HCC1937-22 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.	Ratio H/L g1_PX309_HCC1937-	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-2 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_HCC1937-21 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L g1_PX309_HCC1937-	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-21 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_HCC1937-22 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L normalized	
Ratio H/L normalized	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
	Ratio H/L normalized	Normalized ratio between two medium and light label partners.

Defeatill according	
Ratio H/L unmod. pep. g1_PX309_HCC1937-2	
Ratio H/L localized g1_PX309_HCC1937-2	
Ratio H/L nmods g1_PX309_HCC1937-2	
Ratio H/L variability [%] g1_PX309_HCC1937-2	
Ratio H/L count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-2	
Occupancy L g1_PX309_HCC1937-	
Occupancy H g1 PX309 HCC1937-2	
Ratio H/L g1_PX309_HCC1937-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-	The ratio between two heavy and light label partners.
31 Ratio H/L g1_PX309_HCC1937-	The ratio between two heavy and light label partners.
32 Ratio H/L g1_PX309_HCC1937-	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_HCC1937-3 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX309_HCC1937-31 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX309_HCC1937-32 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX309_HCC1937-33	The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC1937-3	
Ratio H/L localized g1_PX309_HCC1937-3	
Ratio H/L nmods g1_PX309_HCC1937-3	
Ratio H/L variability [%] g1_PX309_HCC1937-3	
Ratio H/L count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-3	
Occupancy L g1_PX309_HCC1937-	
Occupancy H g1_PX309_HCC1937-3	
Ratio H/L g1_PX309_HCC202-1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC202-1	The median of the total fatto population was stilled to 1.
Ratio H/L localized	
g1_PX309_HCC202-1 Ratio H/L nmods	
g1_PX309_HCC202-1 Ratio H/L variability [%]	
g1_PX309_HCC202-1 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX309_HCC202-1	quantitation.

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX309_HCC202-1 Ratio H/L type g1_PX309_HCC202-	quantitation that are quantified with the re-quantify method.
1	
Occupancy L g1_PX309_HCC202-1 Occupancy H g1_PX309_HCC202-	
1 Ratio H/L g1_PX309_HCC202-2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-	The ratio between two heavy and light label partners.
21 Ratio H/L g1_PX309_HCC202-	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202- 2 3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC202-2	
Ratio H/L localized g1_PX309_HCC202-2	
Ratio H/L nmods g1_PX309_HCC202-2 Ratio H/L variability [%]	
g1_PX309_HCC202-2	
Ratio H/L count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Occupancy L g1_PX309_HCC202-2	
Occupancy H g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC202-3 Ratio H/L g1_PX309_HCC202-	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
31	
Ratio H/L g1_PX309_HCC202- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC202-3	
Ratio H/L localized g1_PX309_HCC202-3	
Ratio H/L nmods g1_PX309_HCC202-3	
Ratio H/L variability [%] g1_PX309_HCC202-3	
Ratio H/L count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202- 3	
Occupancy L g1_PX309_HCC202-3	
Occupancy H g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC2218-1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218- 11	The ratio between two heavy and light label partners.

Ratio H.U. grl. PX309 .HCC2218- The ratio between two heavy and light label partners. Ratio H.U. grl. px309 .HCC2218- The ratio between two heavy and light label partners. Ratio H.U. promailized		
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Ratio H/L nmods g1_PX309_HCC2218-2 Ratio H/L variability [1/6] g1_PX309_HCC2218-2 Ratio H/L count g1_PX309_HCC2218-2 Ratio H/L count g1_PX309_HCC2218-2 Ratio H/L iso-count g1_PX309_HCC2218-2 Ratio H/L type g1_PX309_HCC2218-2 Occupancy L g1_PX309_HCC2218-2 Occupancy L g1_PX309_HCC2218-3 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized g1_PX309_HCC2218-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_HCC2218-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_HCC2218-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L unmod. pep. g1_PX309_HCC2218-2	
g1_PX309_HCC2218-2 Ratio H/L variability [%] g1_PX309_HCC2218-2 Ratio H/L count g1_PX309_HCC2218-2 Ratio H/L count g1_PX309_HCC2218-2 Ratio H/L iso-count g1_PX309_HCC2218-2 Ratio H/L type g1_PX309_HCC2218-2 Ratio H/L type g1_PX309_HCC2218-2 Ratio H/L g1_PX309_HCC2218-2 Ratio H/L g1_PX309_HCC2218-2 Ratio H/L g1_PX309_HCC2218-3 The ratio between two heavy and light label partners. Ratio H/L g1_PX309_HCC2218-3 The ratio between two heavy and light label partners. Ratio H/L g1_PX309_HCC2218-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. Ratio H/L g1_PX309_HCC2218-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. Ratio H/L g1_PX309_HCC2218-3 The ratio between two heavy and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two		
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g1_PX309_HCC2218-2The ratio between two heavy and light label partners.Ratio H/L g1_PX309_HCC2218-3The ratio between two heavy and light label partners.31The ratio between two heavy and light label partners.Ratio H/L g1_PX309_HCC2218-3The ratio between two heavy and light label partners.32The ratio between two heavy and light label partners.Ratio H/L g1_PX309_HCC2218-3The ratio between two heavy and light label partners.33Normalized ratio between two medium and light label partners.g1_PX309_HCC2218-3The median of the total ratio population was shifted to 1.Ratio H/L normalized g1_PX309_HCC2218-31Normalized ratio between two medium and light label partners.g1_PX309_HCC2218-31Normalized ratio between two medium and light label partners.		
Ratio H/L g1_PX309_HCC2218- 31 Ratio H/L g1_PX309_HCC2218- 32 Ratio H/L g1_PX309_HCC2218- 33 Ratio H/L g1_PX309_HCC2218- 33 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized was shifted to 1. Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized was shifted to 1. Ratio H/L normalized partners. Dormalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
Ratio H/L g1_PX309_HCC2218- 32 Ratio H/L g1_PX309_HCC2218- 33 Ratio H/L normalized g1_PX309_HCC2218-3 Ratio H/L normalized Normalized ratio between two medium and light label partners. Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L g1_PX309_HCC2218-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218- 33 Ratio H/L normalized g1_PX309_HCC2218-3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
Ratio H/L normalized STATE STA		The ratio between two heavy and light label partners.
g1_PX309_HCC2218-3The median of the total ratio population was Shifted to 1.Ratio H/L normalized g1_PX309_HCC2218-31Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.Ratio H/L normalizedNormalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
g1_PX309_HCC2218-31 The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized g1_PX309_HCC2218-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HCC2218-3	,,,,
Ratio H/L localized	
g1_PX309_HCC2218-3 Ratio H/L nmods	
g1_PX309_HCC2218-3 Ratio H/L variability [%]	
g1_PX309_HCC2218-3	
Ratio H/L count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-3	
Occupancy L g1_PX309_HCC2218-	
Occupancy H g1 PX309 HCC2218-3	
Ratio H/L g1_PX309_HMEC1-1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-	The ratio between two heavy and light label partners.
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Ratio H/L g1_PX309_HMEC1- 12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1- 13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX309 HMEC1-1 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population had difficult to 1.
Ratio H/L localized	
g1_PX309_HMEC1-1 Ratio H/L nmods	
g1_PX309_HMEC1-1	
Ratio H/L variability [%] g1_PX309_HMEC1-1	
Ratio H/L count g1_PX309_HMEC1-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Occupancy L g1_PX309_HMEC1-1	
Occupancy H g1_PX309_HMEC1-1	
Ratio H/L g1_PX309_HMEC1-2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1- 22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_HMEC1-23 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX309_HMEC1-2 Ratio H/L localized	
g1_PX309_HMEC1-2 Ratio H/L nmods	
g1_PX309_HMEC1-2 Ratio H/L variability [%]	
g1_PX309_HMEC1-2	Number of reduced and antiday (MO) (see
Ratio H/L count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX309_HMEC1-2 Ratio H/L type g1_PX309_HMEC1-	quantitation that are quantified with the re-quantify method.
Occupancy L g1_PX309_HMEC1-2	
Occupancy H g1_PX309_HMEC1-2	
Ratio H/L g1_PX309_HMEC1-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1- 31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC1-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMEC1-3	
Ratio H/L localized g1_PX309_HMEC1-3	
Ratio H/L nmods g1_PX309_HMEC1-3	
Ratio H/L variability [%] g1_PX309_HMEC1-3	
Ratio H/L count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Occupancy L g1_PX309_HMEC1-3	
Occupancy H g1_PX309_HMEC1-3	The sector between two because of Political sectors
Ratio H/L g1_PX309_HMEC2-1 Ratio H/L g1_PX309_HMEC2-	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
11	The ratio between two heavy and light laber partitions.
Ratio H/L g1_PX309_HMEC2- 12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2- 13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMEC2-1	
Ratio H/L localized g1_PX309_HMEC2-1	
Ratio H/L nmods g1_PX309_HMEC2-1	
Ratio H/L variability [%] g1_PX309_HMEC2-1	
Ratio H/L count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	
Occupancy L g1_PX309_HMEC2-1	
Occupancy H g1_PX309_HMEC2-1	
Ratio H/L g1_PX309_HMEC2-2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2- 21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2- 22 Ratio H/L g1_PX309_HMEC2-	The ratio between two heavy and light label partners.
	The ratio between two heavy and light label partners.

Ratio H/L normalized q1 PX309 HMEC2-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMEC2-2	The modal of the total ratio population was stilled to 1.
Ratio H/L localized g1_PX309_HMEC2-2	
Ratio H/L nmods	
g1_PX309_HMEC2-2 Ratio H/L variability [%]	
g1_PX309_HMEC2-2 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX309_HMEC2-2 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX309_HMEC2-2 Ratio H/L type g1_PX309_HMEC2-	quantitation that are quantified with the re-quantify method.
Occupancy L g1_PX309_HMEC2-2	
Occupancy H g1_PX309_HMEC2-2	
Ratio H/L g1_PX309_HMEC2-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2- 31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMEC2-3	
Ratio H/L localized g1_PX309_HMEC2-3	
Ratio H/L nmods g1_PX309_HMEC2-3	
Ratio H/L variability [%] g1_PX309_HMEC2-3	
Ratio H/L count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	
Occupancy L g1_PX309_HMEC2-3	
Occupancy H g1_PX309_HMEC2-3	
Ratio H/L g1_PX309_HMTS1-1 Ratio H/L g1_PX309_HMTS1-	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
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Ratio H/L g1_PX309_HMTS1- 12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1- 13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMTS1-1	
Ratio H/L localized g1_PX309_HMTS1-1	

Detic II/I remade	
Ratio H/L nmods g1_PX309_HMTS1-1	
Ratio H/L variability [%] g1_PX309_HMTS1-1	
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-1	
Occupancy L g1_PX309_HMTS1-1	
Occupancy H g1_PX309_HMTS1-1	
Ratio H/L g1_PX309_HMTS1-2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1- 21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1- 22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1- 23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMTS1-2	
Ratio H/L localized g1_PX309_HMTS1-2	
Ratio H/L nmods g1_PX309_HMTS1-2	
Ratio H/L variability [%] g1_PX309_HMTS1-2	
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-2	
Occupancy L g1_PX309_HMTS1-2	
Occupancy H g1_PX309_HMTS1-2	The ratio between two beauty and light label and are
Ratio H/L g1_PX309_HMTS1-3	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1- 31	, , ,
Ratio H/L g1_PX309_HMTS1- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_HMTS1-3	
Ratio H/L localized g1_PX309_HMTS1-3	
Ratio H/L nmods g1_PX309_HMTS1-3	
Ratio H/L variability [%] g1_PX309_HMTS1-3	
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-3	
Occupancy L g1_PX309_HMTS1-3	
Occupancy H g1_PX309_HMTS1-3	
Ratio H/L g1_PX309_MCF10a-1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a- 11	The ratio between two heavy and light label partners.

Ratio H.U. got P.X309_MCF10a-1 2 Ratio H.U. got P.X309_MCF10a-1 3 Ratio H.U. got P.X309_MCF10a-1 3 Normalized got from the total ratio population was shifted to 1. Ratio H.U. got P.X309_MCF10a-1 2 Normalized got from the total ratio population was shifted to 1. Ratio H.U. got P.X309_MCF10a-1 3 Ratio H.U. got P.X309_MCF10a-1 4 Ratio H.U. got P.X309_MCF10a-1 5 Ratio H.U. got P.X309_MCF10a-1 7 P.X309_MCF10a-1 8 Ratio H.U. got P.X309_MCF10a-1 9 Ratio H.U. got P.X309_MCF10a-2 9 Ratio H.U. got P.		
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gt_PX309_MCF10a-1		
Ratio HV. normalized gl PX309_MCF10a-1 2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L g1_PX309_MCF10a-1 Ratio H/L g1_PX309_MCF10a-2 Ratio H/L g1_PX309_MCF10a-3 Ra		Normalized ratio between two medium and light label partners.
Ratio HVI. Docalized g1_PX309_MCF10a-1 Ratio HVI. DocF10a-2 Ratio HVI. DocF10a-1 Ratio HVI. Spe g1_PX309_MCF10a-1 Ratio HVI. g1_PX309_MCF10a-1 Ratio HVI. g1_PX309_MCF10a-1 Ratio HVI. g1_PX309_MCF10a-2 Ratio HVI. normalized g1_PX309_MCF10a-2 Ratio HVI. p1_PX309_MCF10a-2 Ratio HVI. p1_PX309_MCF10a-3 Ratio HVI. g1_PX309_MCF10a-3 Ratio HVI. g1_PX3	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
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Ratio H/L count g1_PX309_MCF10a-2 Ratio H/L iso-count g1_PX309_MCF10a-2 Ratio H/L type g1_PX309_MCF10a-2 Occupancy L g1_PX309_MCF10a-2 Ratio H/L g1_PX309_MCF10a-3 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized SNormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized SNormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L variability [%]	
Ratio H/L iso-count g1_PX309_MCF10a-2 Ratio H/L type g1_PX309_MCF10a-2 Occupancy L g1_PX309_MCF10a-2 Occupancy H g1_PX309_MCF10a-2 Ratio H/L g1_PX309_MCF10a-3 Ratio H/L g1_PX309_MCF10a-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L count	
Ratio H/L type g1_PX309_MCF10a-2 Occupancy L g1_PX309_MCF10a-2 Occupancy H g1_PX309_MCF10a-2 Ratio H/L g1_PX309_MCF10a-3 Ratio H/L g1_PX309_MCF10a-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-32 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-32 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
Occupancy L g1_PX309_MCF10a-2 Occupancy H g1_PX309_MCF10a-2 Ratio H/L g1_PX309_MCF10a-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 Z Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 Z Normalized ratio between two medium and light label partners.	Ratio H/L type g1_PX309_MCF10a-	
Occupancy H g1_PX309_MCF10a-2 Ratio H/L g1_PX309_MCF10a-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-3 Z Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.		
Ratio H/L g1_PX309_MCF10a-3 Ratio H/L g1_PX309_MCF10a-3 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized ratio between two medium and light label partners.	Occupancy H g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a- 32 Ratio H/L g1_PX309_MCF10a- 33 Ratio H/L normalized g1_PX309_MCF10a-3 Ratio H/L normalized Normalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a- 33 Ratio H/L normalized g1_PX309_MCF10a-3 Ratio H/L normalized g1_PX309_MCF10a-3 Ratio H/L normalized g1_PX309_MCF10a-3 Ratio H/L normalized g1_PX309_MCF10a-3 Ratio H/L normalized g1_PX309_MCF10a-31 Ratio H/L normalized g1_PX309_MCF10a-32 Ratio H/L normalized g1_PX309_MCF10a-32 Ratio H/L normalized g1_PX309_MCF10a-32 Ratio H/L normalized medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized medium and light label partners.	Ratio H/L g1_PX309_MCF10a-	
Ratio H/L normalized g1_PX309_MCF10a-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-31 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-31 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized Normalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
g1_PX309_MCF10a-3 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-31 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-32 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		The ratio between two heavy and light label partners.
g1_PX309_MCF10a-31 The median of the total ratio population was shifted to 1. Ratio H/L normalized g1_PX309_MCF10a-32 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.		
Ratio H/L normalized Solution Normalized The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized Normalized The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.		
Ratio H/L normalized g1_PX309_MCF10a-33 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L unmod. pep.	
g1_PX309_MCF10a-3	
Ratio H/L localized g1_PX309_MCF10a-3	
Ratio H/L nmods g1_PX309_MCF10a-3	
Ratio H/L variability [%] g1_PX309_MCF10a-3	
Ratio H/L count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Occupancy L g1_PX309_MCF10a-3	
Occupancy H g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MDAMB453-1 Ratio H/L g1_PX309_MDAMB453-	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
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Ratio H/L g1_PX309_MDAMB453- 12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453- 13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_MDAMB453-1	
Ratio H/L localized g1_PX309_MDAMB453-1	
Ratio H/L nmods g1_PX309_MDAMB453-1	
Ratio H/L variability [%] g1_PX309_MDAMB453-1	
Ratio H/L count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-1	
Occupancy L g1_PX309_MDAMB453-1	
Occupancy H g1_PX309_MDAMB453-1	
Ratio H/L g1_PX309_MDAMB453-2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453- 22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453- 23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_MDAMB453-2	
Ratio H/L localized g1_PX309_MDAMB453-2	
Ratio H/L nmods g1_PX309_MDAMB453-2	
Ratio H/L variability [%] g1_PX309_MDAMB453-2	
Ratio H/L count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count	Number of redundant portides (MS1 features) used for
g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-2	
Occupancy L g1_PX309_MDAMB453-2	
Occupancy H g1_PX309_MDAMB453-2	
Ratio H/L g1_PX309_MDAMB453-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453- 31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_MDAMB453-3	
Ratio H/L localized g1_PX309_MDAMB453-3	
Ratio H/L nmods g1_PX309_MDAMB453-3	
Ratio H/L variability [%] g1_PX309_MDAMB453-3	
Ratio H/L count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-3	
Occupancy L g1_PX309_MDAMB453-3	
Occupancy H g1_PX309_MDAMB453-3	
Ratio H/L g1_PX309_MFM223-1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_MFM223-1	
Ratio H/L localized g1_PX309_MFM223-1	
Ratio H/L nmods g1_PX309_MFM223-1	
Ratio H/L variability [%] g1_PX309_MFM223-1	
Ratio H/L count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Occupancy L g1_PX309_MFM223-	
Occupancy H g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-2	The ratio between two heavy and light label partners.

Ratio H/L g1_PX309_MFM223- 21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_MFM223-2	
Ratio H/L localized g1_PX309_MFM223-2	
Ratio H/L nmods g1_PX309_MFM223-2	
Ratio H/L variability [%] g1_PX309_MFM223-2	
Ratio H/L count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223- 2	
Occupancy L g1_PX309_MFM223-	
Occupancy H g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223- 33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX309_MFM223-3	
Ratio H/L localized g1_PX309_MFM223-3	
Ratio H/L nmods g1_PX309_MFM223-3	
Ratio H/L variability [%] g1_PX309_MFM223-3	
Ratio H/L count g1_PX309_MFM223-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-3	
Occupancy L g1_PX309_MFM223-3	
Occupancy H g1_PX309_MFM223-	
Ratio H/L g1_PX359_0h_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_13	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_0h_1 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX359_0h_11	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_0h_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_0h_13	The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_0h_1	
Ratio H/L localized g1_PX359_0h_1	
Ratio H/L nmods g1_PX359_0h_1	
Ratio H/L variability [%] g1_PX359_0h_1	
Ratio H/L count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_1	
Occupancy L g1_PX359_0h_1	
Occupancy H g1_PX359_0h_1	The ratio between two because and light label northers
Ratio H/L g1_PX359_0h_2 Ratio H/L g1_PX359_0h_21	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_23	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_0h_2	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_0h_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_0h_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_0h_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_0h_2	
Ratio H/L localized g1_PX359_0h_2	
Ratio H/L nmods g1_PX359_0h_2	
Ratio H/L variability [%] g1_PX359_0h_2	
Ratio H/L count g1_PX359_0h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_2	
Occupancy L g1_PX359_0h_2	
Occupancy H g1_PX359_0h_2	
Ratio H/L g1_PX359_0h_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_31 Ratio H/L g1_PX359_0h_32	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_33	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_0h_3 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX359_0h_31 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX359_0h_32	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_0h_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_0h_3	
Ratio H/L localized g1_PX359_0h_3	
Ratio H/L nmods g1_PX359_0h_3	
Ratio H/L variability [%] g1_PX359_0h_3	
Ratio H/L count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_3	
Occupancy L g1_PX359_0h_3	
Occupancy H g1_PX359_0h_3	The method between the state of
Ratio H/L g1_PX359_BSA_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_11 Ratio H/L g1_PX359_BSA_12	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_12 Ratio H/L g1_PX359_BSA_13	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_BSA_1	The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two modium and light label norman
g1_PX359_BSA_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_BSA_1	
Ratio H/L localized g1_PX359_BSA_1	
Ratio H/L nmods q1 PX359 BSA 1	
Ratio H/L variability [%]	
g1_PX359_BSA_1 Ratio H/L count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g1_PX359_BSA_1	quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_1	quantitation that are quantities with the re quantity method.
Occupancy L g1_PX359_BSA_1	
Occupancy H g1_PX359_BSA_1	
Ratio H/L g1_PX359_BSA_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_BSA_2	
Ratio H/L localized g1_PX359_BSA_2	
Ratio H/L nmods g1_PX359_BSA_2	
Ratio H/L variability [%] g1_PX359_BSA_2	
Ratio H/L count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_2	
Occupancy L g1_PX359_BSA_2	
Occupancy H g1_PX359_BSA_2	
Ratio H/L g1_PX359_BSA_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_BSA_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_BSA_3	
Ratio H/L localized g1_PX359_BSA_3	
Ratio H/L nmods g1_PX359_BSA_3 Ratio H/L variability [%]	
g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX359_BSA_3 Ratio H/L type g1_PX359_BSA_3	quantitation that are quantified with the re-quantify method.
Occupancy L g1_PX359_BSA_3	
Occupancy H g1_PX359_BSA_3	

Datio II/I at DV250 EN 4	The ratio hattugen two heavy and light label northers
Ratio H/L g1_PX359_FN_1 Ratio H/L g1_PX359_FN_11	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_12	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_13	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_FN_1 Ratio H/L normalized	The median of the total ratio population was shifted to 1.
g1_PX359_FN_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_FN_1	
Ratio H/L localized g1_PX359_FN_1	
Ratio H/L nmods g1_PX359_FN_1	
Ratio H/L variability [%] g1_PX359_FN_1	
Ratio H/L count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_1	
Occupancy L g1_PX359_FN_1	
Occupancy H g1_PX359_FN_1	
Ratio H/L g1_PX359_FN_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_23 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX359_FN_2	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_FN_2	
Ratio H/L localized g1_PX359_FN_2	
Ratio H/L nmods g1_PX359_FN_2	
Ratio H/L variability [%] g1_PX359_FN_2	
Ratio H/L count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_2	
Occupancy L g1_PX359_FN_2	
Occupancy H g1_PX359_FN_2	
Ratio H/L g1_PX359_FN_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_FN_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_FN_3	
Ratio H/L localized g1_PX359_FN_3	
Ratio H/L nmods g1_PX359_FN_3	
Ratio H/L variability [%] g1_PX359_FN_3	
<u> </u>	

Ratio H/L count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_3	quantitation that are quantities with the re quantity method.
Occupancy L g1_PX359_FN_3	
Occupancy H g1_PX359_FN_3	
Ratio H/L g1_PX359_GFR_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_GFR_1	
Ratio H/L localized g1_PX359_GFR_1	
Ratio H/L nmods g1_PX359_GFR_1	
Ratio H/L variability [%] g1_PX359_GFR_1	
Ratio H/L count g1_PX359_GFR_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_1	
Occupancy L g1_PX359_GFR_1	
Occupancy H g1_PX359_GFR_1	
Ratio H/L g1_PX359_GFR_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_GFR_2	
Ratio H/L localized g1_PX359_GFR_2	
Ratio H/L nmods g1_PX359_GFR_2	
Ratio H/L variability [%] g1_PX359_GFR_2	
Ratio H/L count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_2	
Occupancy L g1_PX359_GFR_2	
Occupancy H g1_PX359_GFR_2	
Ratio H/L g1_PX359_GFR_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_GFR_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_GFR_33	The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_GFR_3	
Ratio H/L localized g1_PX359_GFR_3	
Ratio H/L nmods g1_PX359_GFR_3	
Ratio H/L variability [%] g1_PX359_GFR_3	
Ratio H/L count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_3	
Occupancy L g1_PX359_GFR_3	
Occupancy H g1_PX359_GFR_3 Ratio H/L g1_PX359_LAM_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_LAM_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_LAM_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_LAM_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_LAM_1	The state of the s
Ratio H/L localized g1_PX359_LAM_1	
Ratio H/L nmods g1_PX359_LAM_1	
Ratio H/L variability [%]	
Ratio H/L count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_1	
Occupancy L g1_PX359_LAM_1	
Occupancy H g1_PX359_LAM_1	
Ratio H/L g1_PX359_LAM_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_21 Ratio H/L g1_PX359_LAM_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_22 Ratio H/L g1_PX359_LAM_23	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_LAM_2 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX359_LAM_21 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX359_LAM_22	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_LAM_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_LAM_2	
Ratio H/L localized g1_PX359_LAM_2	
Ratio H/L nmods g1_PX359_LAM_2	
Ratio H/L variability [%] g1_PX359_LAM_2	
Ratio H/L count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_2	
Occupancy L g1_PX359_LAM_2	
Occupancy H g1_PX359_LAM_2	The contract of the contract of
Ratio H/L g1_PX359_LAM_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_31 Ratio H/L g1_PX359_LAM_32	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Natio	Title ratio between two neavy and light label partners.

Ratio H/L g1_PX359_LAM_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_LAM_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_LAM_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_LAM_33 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX359_LAM_3 Ratio H/L localized	
g1_PX359_LAM_3 Ratio H/L nmods g1_PX359_LAM_3	
Ratio H/L variability [%]	
g1_PX359_LAM_3 Ratio H/L count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count q1 PX359 LAM 3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_3	quantitation that are quantified with the re quantity method.
Occupancy L g1_PX359_LAM_3	
Occupancy H g1_PX359_LAM_3 Ratio H/L g1_PX359_Matr 12h_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr	The ratio between two heavy and light label partners.
12h_11 Ratio H/L g1_PX359_Matr	The ratio between two heavy and light label partners.
12h_12 Ratio H/L g1_PX359_Matr	The ratio between two heavy and light label partners.
12h_13 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_Matr 12h_1 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX359_Matr 12h_11	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr 12h_1	
Ratio H/L localized g1_PX359_Matr 12h_1	
Ratio H/L nmods g1_PX359_Matr 12h_1	
Ratio H/L variability [%] q1 PX359 Matr 12h 1	
Ratio H/L count g1_PX359_Matr	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr	qualities and qualities and the quality in the second
Occupancy L g1_PX359_Matr	
Occupancy H g1_PX359_Matr	
Ratio H/L g1_PX359_Matr 12h_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h 2 3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population was stilled to 1.
g1_PX359_Matr 12h_2 Ratio H/L localized g1_PX359_Matr	
12h_2	

Ratio H/L nmods g1_PX359_Matr 12h 2	
Ratio H/L variability [%] g1_PX359_Matr 12h_2	
Ratio H/L count g1_PX359_Matr 12h 2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_2	quarimanor anacaro quarimiou war are re quarimy meaned.
Occupancy L g1_PX359_Matr 12h 2	
Occupancy H g1_PX359_Matr 12h 2	
Ratio H/L g1_PX359_Matr 12h_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h 3 2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h 3 3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 12h_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr 12h_3	
Ratio H/L localized g1_PX359_Matr 12h_3	
Ratio H/L nmods g1_PX359_Matr 12h_3	
Ratio H/L variability [%] g1_PX359_Matr 12h_3	
Ratio H/L count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_3	
Occupancy L g1_PX359_Matr 12h_3	
Occupancy H g1_PX359_Matr 12h 3	
Ratio H/L g1_PX359_Matr 24h_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr 24h_1	
Ratio H/L localized g1_PX359_Matr 24h_1	
Ratio H/L nmods g1_PX359_Matr 24h_1	
Ratio H/L variability [%] g1_PX359_Matr 24h_1	
Ratio H/L count g1_PX359_Matr 24h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_1	

Occupancy L g1_PX359_Matr	
Occupancy H g1_PX359_Matr	
24h_1 Ratio H/L g1_PX359_Matr 24h_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr 24h_2	
Ratio H/L localized g1_PX359_Matr 24h_2	
Ratio H/L nmods g1_PX359_Matr 24h_2	
Ratio H/L variability [%] g1_PX359_Matr 24h_2	
Ratio H/L count g1_PX359_Matr 24h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_2	
Occupancy L g1_PX359_Matr 24h_2	
Occupancy H g1_PX359_Matr 24h_2	
Ratio H/L g1_PX359_Matr 24h_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 24h_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr 24h_3	
Ratio H/L localized g1_PX359_Matr 24h_3	
Ratio H/L nmods g1_PX359_Matr 24h_3	
Ratio H/L variability [%] g1_PX359_Matr 24h_3	
Ratio H/L count g1_PX359_Matr 24h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_3	
Occupancy L g1_PX359_Matr 24h_3	
Occupancy H g1_PX359_Matr 24h_3	
Ratio H/L g1_PX359_Matr 30h_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_12	The ratio between two heavy and light label partners.

Ratio H/L g1_PX359_Matr 30h_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX359_Matr 30h_13 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX359_Matr 30h_1 Ratio H/L localized g1_PX359_Matr	
30h_1 Ratio H/L nmods g1_PX359_Matr	
30h_1	
Ratio H/L variability [%] g1_PX359_Matr 30h_1	
Ratio H/L count g1_PX359_Matr 30h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 30h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h 1	
Occupancy L g1_PX359_Matr 30h_1	
Occupancy H g1_PX359_Matr 30h 1	
Ratio H/L g1_PX359_Matr 30h_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h 2 1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h 2 2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h 2 3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr 30h_2	
Ratio H/L localized g1_PX359_Matr 30h 2	
Ratio H/L nmods g1_PX359_Matr 30h 2	
Ratio H/L variability [%] g1_PX359_Matr 30h_2	
Ratio H/L count g1_PX359_Matr 30h 2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX359_Matr 30h 2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h 2	quantitation and and quantition with the to quantity motified.
Occupancy L g1_PX359_Matr 30h 2	
Occupancy H g1_PX359_Matr 30h 2	
Ratio H/L g1_PX359_Matr 30h_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr 30h_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g 7.000_man 0011_00	The median of the total ratio population was stilled to 1.

Ratio H/L unmod. pep.	
g1_PX359_Matr 30h_3 Ratio H/L localized g1 PX359 Matr	
30h_3	
Ratio H/L nmods g1_PX359_Matr 30h_3	
Ratio H/L variability [%] g1_PX359_Matr 30h_3	
Ratio H/L count g1_PX359_Matr 30h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 30h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_3	
Occupancy L g1_PX359_Matr 30h_3	
Occupancy H g1_PX359_Matr 30h_3	
Ratio H/L g1_PX359_Matr dil_1	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_11	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_12	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr dil_1	
Ratio H/L localized g1_PX359_Matr dil_1	
Ratio H/L nmods g1_PX359_Matr dil_1	
Ratio H/L variability [%] g1_PX359_Matr dil_1	
Ratio H/L count g1_PX359_Matr dil_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_1	
Occupancy L g1_PX359_Matr dil_1	
Occupancy H g1_PX359_Matr dil_1	
Ratio H/L g1_PX359_Matr dil_2	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_21	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_22	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr dil_2	
Ratio H/L localized g1_PX359_Matr dil_2	
Ratio H/L nmods g1_PX359_Matr dil_2	
Ratio H/L variability [%] g1_PX359_Matr dil_2	
Ratio H/L count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1_PX359_Matr	
dil_2	
Occupancy L g1_PX359_Matr dil_2 Occupancy H g1_PX359_Matr dil_2	
Ratio H/L g1_PX359_Matr dil_3	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_31	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_32	The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX359_Matr dil_33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX359_Matr dil_3	
Ratio H/L localized g1_PX359_Matr dil_3	
Ratio H/L nmods g1_PX359_Matr dil_3	
Ratio H/L variability [%] g1_PX359_Matr dil_3	
Ratio H/L count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_3	
Occupancy L g1_PX359_Matr dil_3	
Occupancy H g1_PX359_Matr dil_3 Ratio H/L g1_PX419_human_18507	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners.
g1_PX419_human_185071 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX419_human_185072 Ratio H/L	The ratio between two heavy and light label partners.
g1_PX419_human_185073 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX419_human_18507 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX419_human_185071 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX419_human_185072 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX419_human_185073 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX419_human_18507 Ratio H/L localized	
g1_PX419_human_18507 Ratio H/L nmods	
g1_PX419_human_18507 Ratio H/L variability [%]	
g1_PX419_human_18507 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX419_human_18507 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX419_human_18507 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX419_human_18507 Occupancy L	
g1_PX419_human_18507 Occupancy H	
g1_PX419_human_18507	
Ratio H/L g1_PX419_human_18516	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_185161	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_185162	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_185163	The ratio between two heavy and light label partners.

Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX419_human_18516 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX419_human_185161 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX419_human_185162 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX419_human_185163 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX419_human_18516 Ratio H/L localized	
g1_PX419_human_18516	
Ratio H/L nmods g1_PX419_human_18516	
Ratio H/L variability [%] g1_PX419_human_18516	
Ratio H/L count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_18516	
Occupancy L g1_PX419_human_18516	
Occupancy H g1 PX419 human 18516	
Ratio H/L g1_PX419_human_19193	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_191931	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_191932	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_191933	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX419_human_191931	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX419_human_191932	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX419_human_191933	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX419_human_19193	
Ratio H/L localized g1_PX419_human_19193	
Ratio H/L nmods g1_PX419_human_19193	
Ratio H/L variability [%]	
g1_PX419_human_19193 Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX419_human_19193 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX419_human_19193 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g1_PX419_human_19193 Occupancy L	
g1_PX419_human_19193 Occupancy H	
g1_PX419_human_19193	
Ratio H/L g1_PX419_human_19204	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g1_PX419_human_192041 Ratio H/L	, , ,
g1_PX419_human_192042	The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_192043	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX419_human_192041	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX419_human_192042	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX419_human_192043	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX419_human_19204	

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Ratio H/L localized g1_PX419_human_19204	
Ratio H/L nmods g1_PX419_human_19204	
Ratio H/L variability [%] g1_PX419_human_19204	
Ratio H/L count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_19204	
Occupancy L g1_PX419_human_19204	
Occupancy H g1_PX419_human_19204	
Ratio H/L g1_PX438_Xeno092	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno0921	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno0922	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno0923	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX438 Xeno092	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX438 Xeno092 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX438_Xeno0922 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno0923 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX438_Xeno092 Ratio H/L localized	
g1_PX438_Xeno092	
Ratio H/L nmods g1_PX438_Xeno092	
Ratio H/L variability [%] g1_PX438_Xeno092	
Ratio H/L count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno092	
Occupancy L g1_PX438_Xeno092	
Occupancy H g1_PX438_Xeno092	
Ratio H/L g1_PX438_Xeno441	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno4411	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno4412	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno4413 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno441 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno4411 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno4412 Ratio H/L normalized	The median of the total ratio population was shifted to 1.
g1_PX438_Xeno4413	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g1_PX438_Xeno441	
Ratio H/L localized g1_PX438_Xeno441	
Ratio H/L nmods g1_PX438_Xeno441	
Ratio H/L variability [%] g1_PX438_Xeno441	
Ratio H/L count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno441	
Occupancy L g1_PX438_Xeno441	
Occupancy H g1_PX438_Xeno441	
Ratio H/L g1_PX438_Xeno561	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno5611	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno5612	The ratio between two heavy and light label partners.

Ratio H/L g1_PX438_Xeno5613	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno561	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX438_Xeno5611	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX438_Xeno5612 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno5613 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX438_Xeno561 Ratio H/L localized	
g1_PX438_Xeno561 Ratio H/L nmods	
g1_PX438_Xeno561	
Ratio H/L variability [%] g1_PX438_Xeno561	
Ratio H/L count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno561	
Occupancy L st. PX438_Xeno561	
Occupancy H g1_PX438_Xeno561 Ratio H/L g1_PX438_Xeno691	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno6911	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno6912	The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno6913	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno691	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1 PX438 Xeno691 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX438_Xeno6912	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX438_Xeno6913	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g1_PX438_Xeno691 Ratio H/L localized	
g1_PX438_Xeno691 Ratio H/L nmods	
g1_PX438_Xeno691 Ratio H/L variability [%]	
g1_PX438_Xeno691	Number of reduced at a satisfact (MC4 feetures) used for
Ratio H/L count g1_PX438_Xeno691	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno691	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno691	
Occupancy L g1_PX438_Xeno691	
Occupancy H g1_PX438_Xeno691	
Ratio H/L g2_PX058_expA	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expA1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expA2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expA3 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expA Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g2_PX058_expA1 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g2_PX058_expA2 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g2_PX058_expA3	The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX058_expA	
Ratio H/L localized g2_PX058_expA	
Ratio H/L nmods g2_PX058_expA	
Ratio H/L variability [%] g2_PX058_expA	
Ratio H/L count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g2_PX058_expA	
Occupancy L g2_PX058_expA	
Occupancy H g2_PX058_expA	
Ratio H/L g2_PX058_expB	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expB1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expB2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expB3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expB	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expB1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expB2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expB3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX058_expB	
Ratio H/L localized g2_PX058_expB	
Ratio H/L nmods g2_PX058_expB	
Ratio H/L variability [%] g2_PX058_expB	
Ratio H/L count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expB	
Occupancy L g2_PX058_expB	
Occupancy H g2_PX058_expB	
Ratio H/L g2_PX058_expC	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expC1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expC2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expC3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expC	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expC1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expC2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expC3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX058_expC	
Ratio H/L localized g2_PX058_expC	
Ratio H/L nmods g2_PX058_expC	
Ratio H/L variability [%] g2_PX058_expC	
Ratio H/L count g2_PX058_expC	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g2_PX058_expC	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expC	
Occupancy L g2_PX058_expC	
Occupancy H g2_PX058_expC	
Ratio H/L g2_PX058_expD	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expD1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expD2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expD3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expD	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expD1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expD2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expD3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX058_expD	
Ratio H/L localized g2_PX058_expD	
Ratio H/L nmods g2_PX058_expD	

Ratio H/L variability [%]	
g2_PX058_expD	Nearly and an dead manifolds (MOA (actions)) and for
Ratio H/L count g2_PX058_expD	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expD	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expD	
Occupancy L g2_PX058_expD	
Occupancy H g2_PX058_expD	
Ratio H/L g2_PX058_expE	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expE1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expE2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expE3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expE1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expE2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expE3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX058_expE	
Ratio H/L localized g2_PX058_expE	
Ratio H/L nmods g2_PX058_expE	
Ratio H/L variability [%] g2_PX058_expE	
Ratio H/L count g2_PX058_expE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expE	
Occupancy L g2_PX058_expE	
Occupancy H g2_PX058_expE	
Ratio H/L g2_PX058_expF	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expF1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expF2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expF3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expF	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expF1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expF2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX058_expF3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX058_expF	
Ratio H/L localized g2_PX058_expF	
Ratio H/L nmods g2_PX058_expF	
Ratio H/L variability [%] g2_PX058_expF	
Ratio H/L count g2_PX058_expF	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expF	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expF	
Occupancy L g2_PX058_expF	
Occupancy H g2_PX058_expF	
Ratio H/L g2_PX089_Rep1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep11	The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep12	The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep13	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX089_Rep1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX089_Rep11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX089_Rep12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX089_Rep13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

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Ratio H/L unmod. pep. g2_PX089_Rep1	
Ratio H/L localized g2_PX089_Rep1	
Ratio H/L nmods g2_PX089_Rep1	
Ratio H/L variability [%]	
g2_PX089_Rep1 Ratio H/L count g2_PX089_Rep1	Number of redundant peptides (MS1 features) used for
rtaile Fine death ge_1 76065_1top 1	quantitation.
Ratio H/L iso-count g2 PX089 Rep1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX089_Rep1	
Occupancy L g2_PX089_Rep1	
Occupancy H g2_PX089_Rep1	The vetic between two begins and light label northers
Ratio H/L g2_PX089_Rep2 Ratio H/L g2_PX089_Rep21	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep22	The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep23	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX089_Rep2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX089_Rep21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX089_Rep22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX089_Rep23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX089_Rep2	
Ratio H/L localized g2_PX089_Rep2	
Ratio H/L nmods g2_PX089_Rep2	
Ratio H/L variability [%] g2_PX089_Rep2	
Ratio H/L count g2_PX089_Rep2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX089_Rep2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX089_Rep2	
Occupancy L g2_PX089_Rep2	
Occupancy H g2_PX089_Rep2 Ratio H/L g2_PX537_exp14 rep1	The ratio between two heavy and light label partners.
20h	, , ,
Ratio H/L g2_PX537_exp14 rep1 20h1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 20h2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 20h3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep1 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep1 20h1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep1 20h2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep1 20h3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX537_exp14 rep1 20h	
Ratio H/L localized g2_PX537_exp14 rep1 20h	
Ratio H/L nmods g2_PX537_exp14 rep1 20h	
Ratio H/L variability [%] g2_PX537_exp14 rep1 20h	
Ratio H/L count g2_PX537_exp14 rep1 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep1 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 20h	
Occupancy L g2_PX537_exp14 rep1 20h	
Occupancy H g2_PX537_exp14 rep1 20h	

Ratio H/L g2_PX537_exp14 rep1 6h	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 6h 1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 6h2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 6h 3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep1 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep1 6h1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep1 6h2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep1 6h3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX537_exp14 rep1 6h	
Ratio H/L localized g2_PX537_exp14 rep1 6h	
Ratio H/L nmods g2_PX537_exp14 rep1 6h	
Ratio H/L variability [%] g2_PX537_exp14 rep1 6h	
Ratio H/L count g2_PX537_exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 6h	
Occupancy L g2_PX537_exp14 rep1 6h	
Occupancy H g2_PX537_exp14 rep1 6h	
Ratio H/L g2_PX537_exp14 rep2 20h	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 20h1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 20h2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 20h3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep2 20h1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep2 20h2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep2 20h3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX537_exp14 rep2 20h	
Ratio H/L localized g2_PX537_exp14 rep2 20h	
Ratio H/L nmods g2_PX537_exp14 rep2 20h	
Ratio H/L variability [%] g2_PX537_exp14 rep2 20h	
Ratio H/L count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 20h	
Occupancy L g2_PX537_exp14 rep2 20h	
Occupancy H g2_PX537_exp14 rep2 20h	
Ratio H/L g2_PX537_exp14 rep2 6h Ratio H/L g2_PX537_exp14 rep2	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
6h1	
Ratio H/L g2_PX537_exp14 rep2 6h2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 6h3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Datio II/I parmalizad	Normalized ratio between two modium and light label northers
Ratio H/L normalized g2_PX537_exp14 rep2 6h1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep2 6h2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep2 6h3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX537_exp14 rep2 6h	
Ratio H/L localized g2_PX537_exp14 rep2 6h	
Ratio H/L nmods g2_PX537_exp14 rep2 6h	
Ratio H/L variability [%] g2_PX537_exp14 rep2 6h	
Ratio H/L count g2_PX537_exp14 rep2 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 6h	
Occupancy L g2_PX537_exp14 rep2 6h	
Occupancy H g2_PX537_exp14 rep2 6h	
Ratio H/L g2_PX537_exp14 rep3 20h	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 20h1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 20h2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 20h3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep3 20h1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep3 20h2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep3 20h3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX537_exp14 rep3 20h	
Ratio H/L localized g2_PX537_exp14 rep3 20h	
Ratio H/L nmods g2_PX537_exp14 rep3 20h	
Ratio H/L variability [%] g2_PX537_exp14 rep3 20h	
Ratio H/L count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 20h	
Occupancy L g2_PX537_exp14 rep3 20h	
Occupancy H g2_PX537_exp14 rep3 20h	
Ratio H/L g2_PX537_exp14 rep3 6h	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 6h1	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 6h2	The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 6h3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep3 6h1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep3 6h2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g2_PX537_exp14 rep3 6h3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g2_PX537_exp14 rep3 6h	

Ratio H/L localized	
g2_PX537_exp14 rep3 6h Ratio H/L nmods g2_PX537_exp14	
rep3 6h Ratio H/L variability [%]	
g2_PX537_exp14 rep3 6h	North and an included a series (MOCCO) and the series of t
Ratio H/L count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 6h	
Occupancy L g2_PX537_exp14 rep3 6h	
Occupancy H g2_PX537_exp14 rep3 6h	
Ratio M/L g3_GK1_Chromatin_A_TSA_1	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_11	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_12	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_13	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_11	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_12	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_13	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_A_TSA_1	
Ratio M/L localized g3_GK1_Chromatin_A_TSA_1	
Ratio M/L nmods g3_GK1_Chromatin_A_TSA_1	
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_1	
Ratio H/L g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_11	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_12	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_A_TSA_1	
Ratio H/L localized g3_GK1_Chromatin_A_TSA_1	
Ratio H/L nmods g3_GK1_Chromatin_A_TSA_1	
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g3_GK1_Chromatin_A_TSA_1	
Ratio H/M g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_11	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_12	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_13	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_11	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_12	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_13	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_A_TSA_1	
Ratio H/M localized g3_GK1_Chromatin_A_TSA_1	
Ratio H/M nmods g3_GK1_Chromatin_A_TSA_1	
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_A_TSA_1	
Occupancy L g3_GK1_Chromatin_A_TSA_1	
Occupancy M g3_GK1_Chromatin_A_TSA_1	
Occupancy H g3_GK1_Chromatin_A_TSA_1	
Ratio M/L g3_GK1_Chromatin_A_TSA_2	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_21	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_22	The ratio between two medium and light label partners.
Ratio M/L	The ratio between two medium and light label partners.
g3_GK1_Chromatin_A_TSA_23 Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_A_TSA_2 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_A_TSA_21 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_A_TSA_22 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_A_TSA_23 Ratio M/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_GK1_Chromatin_A_TSA_2 Ratio M/L localized	
g3_GK1_Chromatin_A_TSA_2 Ratio M/L nmods	
g3_GK1_Chromatin_A_TSA_2	Out the state of t
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_2	
Ratio H/L g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and light label partners.
Ratio H/L q3 GK1 Chromatin A TSA 2 1	The ratio between two heavy and light label partners.

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Ratio H/L g3_GK1_Chromatin_A_TSA_22	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_A_TSA_2	
Ratio H/L localized g3_GK1_Chromatin_A_TSA_2	
Ratio H/L nmods g3_GK1_Chromatin_A_TSA_2	
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_A_TSA_2	
Ratio H/M g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_21	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_22	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3 GK1 Chromatin A TSA 2	
Ratio H/M localized g3_GK1_Chromatin_A_TSA_2	
Ratio H/M nmods	
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3 GK1 Chromatin A TSA 2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_A_TSA_2	
Occupancy L g3_GK1_Chromatin_A_TSA_2	
Occupancy M g3_GK1_Chromatin_A_TSA_2	
Occupancy H g3_GK1_Chromatin_A_TSA_2	
Ratio M/L g3_GK1_Chromatin_CC_1	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_11	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_12	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_13	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_CC_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.

Ratio M/L normalized g3_GK1_Chromatin_CC_11	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_CC_12	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized q3 GK1 Chromatin CC 1 3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_CC_1	The median of the total rane population was similar to 1.
Ratio M/L localized g3_GK1_Chromatin_CC_1	
Ratio M/L nmods	
g3_GK1_Chromatin_CC_1 Ratio M/L variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count q3 GK1 Chromatin CC 1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_CC_1	quantities and quantities that are to quantity meaness
Ratio H/L	The ratio between two heavy and light label partners.
g3_GK1_Chromatin_CC_1 Ratio H/L	The ratio between two heavy and light label partners.
g3_GK1_Chromatin_CC_11 Ratio H/L	The ratio between two heavy and light label partners.
g3_GK1_Chromatin_CC_12 Ratio H/L	The ratio between two heavy and light label partners.
g3_GK1_Chromatin_CC_13 Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_GK1_Chromatin_CC_1 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g3_GK1_Chromatin_CC_11	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_CC_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_CC_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_CC_1	
Ratio H/L localized g3_GK1_Chromatin_CC_1	
Ratio H/L nmods g3_GK1_Chromatin_CC_1	
Ratio H/L variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q3 GK1 Chromatin CC 1	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_1	quantitation that are quantities with the re-quantity method.
Ratio H/M	The ratio between two heavy and medium label partners.
g3_GK1_Chromatin_CC_1 Ratio H/M	The ratio between two heavy and medium label partners.
g3_GK1_Chromatin_CC_11 Ratio H/M	The ratio between two heavy and medium label partners.
g3_GK1_Chromatin_CC_12 Ratio H/M	The ratio between two heavy and medium label partners.
g3_GK1_Chromatin_CC_13 Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_GK1_Chromatin_CC_1	partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_CC_11	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_CC_12	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_CC_13	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_CC_1	
Ratio H/M localized g3_GK1_Chromatin_CC_1	
Ratio H/M nmods g3_GK1_Chromatin_CC_1	

Ratio H/M variability [%] g3_GK1_Chromatin_CC_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_1	
Occupancy L g3_GK1_Chromatin_CC_1	
Occupancy M g3_GK1_Chromatin_CC_1	
Occupancy H g3_GK1_Chromatin_CC_1	
Ratio M/L g3_GK1_Chromatin_CC_2	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_21	The ratio between two medium and light label partners.
Ratio M/L g3 GK1 Chromatin CC 2 2	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3 GK1 Chromatin CC 2 1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_CC_22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_CC_23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_CC_2	
Ratio M/L localized g3_GK1_Chromatin_CC_2	
Ratio M/L nmods g3_GK1_Chromatin_CC_2	
Ratio M/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_CC_2	
Ratio H/L g3_GK1_Chromatin_CC_2	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_21	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_22	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_CC_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_CC_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_CC_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_CC_2	
Ratio H/L localized g3_GK1_Chromatin_CC_2	
Ratio H/L nmods g3_GK1_Chromatin_CC_2	
Ratio H/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_2	

Ratio H/M g3_GK1_Chromatin_CC_2	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_CC_21	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_CC_22	The ratio between two heavy and medium label partners.
Ratio H/M g3 GK1 Chromatin_CC 2 3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_CC_21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_CC_22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_CC_23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_CC_2	
Ratio H/M localized g3_GK1_Chromatin_CC_2	
Ratio H/M nmods g3_GK1_Chromatin_CC_2	
Ratio H/M variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_2	
Occupancy L g3_GK1_Chromatin_CC_2	
Occupancy M g3_GK1_Chromatin_CC_2	
Occupancy H g3_GK1_Chromatin_CC_2	
Ratio M/L g3_GK1_Chromatin_EHT_1	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_11	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_12	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_13	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_11	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_12	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_13	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_EHT_1	
Ratio M/L localized g3_GK1_Chromatin_EHT_1	
Ratio M/L nmods g3_GK1_Chromatin_EHT_1	
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_1	
Ratio H/L g3_GK1_Chromatin_EHT_1	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_11	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_12	The ratio between two heavy and light label partners.

Ratio H/L g3_GK1_Chromatin_EHT_13	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_EHT_1	
Ratio H/L localized g3_GK1_Chromatin_EHT_1	
Ratio H/L nmods g3_GK1_Chromatin_EHT_1	
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_1	
Ratio H/M g3_GK1_Chromatin_EHT_1	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_11	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_12	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_13	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_11	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_12	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_13	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_EHT_1	
Ratio H/M localized g3_GK1_Chromatin_EHT_1	
Ratio H/M nmods g3_GK1_Chromatin_EHT_1	
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_1	
Occupancy L g3_GK1_Chromatin_EHT_1	
Occupancy M g3_GK1_Chromatin_EHT_1	
Occupancy H g3_GK1_Chromatin_EHT_1	
Ratio M/L g3_GK1_Chromatin_EHT_2	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_21	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_22	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_21	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.

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Ratio M/L normalized g3_GK1_Chromatin_EHT_22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_EHT_2	
Ratio M/L localized g3_GK1_Chromatin_EHT_2	
Ratio M/L nmods g3 GK1 Chromatin EHT 2	
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
	naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_2	
Ratio H/L g3_GK1_Chromatin_EHT_2	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_21	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_22	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_EHT_2	
Ratio H/L localized g3_GK1_Chromatin_EHT_2	
Ratio H/L nmods g3_GK1_Chromatin_EHT_2	
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_2	
Ratio H/M g3_GK1_Chromatin_EHT_2	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_21	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_22	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_EHT_2	
Ratio H/M localized g3_GK1_Chromatin_EHT_2	
Ratio H/M nmods g3_GK1_Chromatin_EHT_2	

Ratio H/M variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3 GK1 Chromatin EHT 2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_2	, , , , , , , , , , , , , , , , , , , ,
Occupancy L g3_GK1_Chromatin_EHT_2	
Occupancy M g3 GK1 Chromatin EHT 2	
Occupancy H g3_GK1_Chromatin_EHT_2	
Ratio M/L g3_GK1_Chromatin_EHT_3	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_31	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_32	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_33	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_EHT_31 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_EHT_32 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_EHT_33 Ratio M/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_GK1_Chromatin_EHT_3 Ratio M/L localized	
g3_GK1_Chromatin_EHT_3 Ratio M/L nmods	
g3_GK1_Chromatin_EHT_3 Ratio M/L variability [%]	Coefficient of variability over all redundant quantifiable
g3_GK1_Chromatin_EHT_3	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_3	
Ratio H/L g3_GK1_Chromatin_EHT_3	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_31	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_32	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_33	The ratio between two heavy and light label partners.
Ratio H/L normalized g3 GK1 Chromatin EHT 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q3 GK1 Chromatin EHT 3 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_EHT_3	
Ratio H/L localized g3_GK1_Chromatin_EHT_3	
Ratio H/L nmods g3 GK1 Chromatin EHT 3	
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_3	

Ratio H/M g3_GK1_Chromatin_EHT_3	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_31	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_32	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_33	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_31	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_32	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_33	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_EHT_3	
Ratio H/M localized g3_GK1_Chromatin_EHT_3	
Ratio H/M nmods g3_GK1_Chromatin_EHT_3	
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_3	
Occupancy L g3_GK1_Chromatin_EHT_3	
Occupancy M g3_GK1_Chromatin_EHT_3	
Occupancy H g3_GK1_Chromatin_EHT_3	
Ratio M/L g3_GK1_Chromatin_EHT_4	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_41	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_42	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_43	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_41	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_42	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_43	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_EHT_4	
Ratio M/L localized g3_GK1_Chromatin_EHT_4	
Ratio M/L nmods g3_GK1_Chromatin_EHT_4	
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_4	
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Ratio H/L g3_GK1_Chromatin_EHT_4	The ratio between two heavy and light label partners.
Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.

Ratio H/L g3_GK1_Chromatin_EHT_43	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_42	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_GK1_Chromatin_EHT_4 Ratio H/L localized	
g3_GK1_Chromatin_EHT_4 Ratio H/L nmods	
g3_GK1_Chromatin_EHT_4 Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g3_GK1_Chromatin_EHT_4	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_4	
Ratio H/M g3_GK1_Chromatin_EHT_4	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_41	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_42	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_43	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to
Ratio H/M normalized	1.
g3_GK1_Chromatin_EHT_41	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_42	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_43	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_EHT_4	
Ratio H/M localized g3_GK1_Chromatin_EHT_4	
Ratio H/M nmods g3_GK1_Chromatin_EHT_4	
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_4	
Occupancy L g3_GK1_Chromatin_EHT_4	
Occupancy M g3_GK1_Chromatin_EHT_4	
Occupancy H g3_GK1_Chromatin_EHT_4	
Ratio M/L g3_GK1_Chromatin_EHT_5	The ratio between two medium and light label partners.
<u> </u>	
Ratio M/L g3_GK1_Chromatin_EHT_51	The ratio between two medium and light label partners.
g3_GK1_Chromatin_EHT_51 Ratio M/L	The ratio between two medium and light label partners. The ratio between two medium and light label partners.
g3_GK1_Chromatin_EHT_51 Ratio M/L g3_GK1_Chromatin_EHT_52 Ratio M/L	<u> </u>
g3_GK1_Chromatin_EHT_51 Ratio M/L g3_GK1_Chromatin_EHT_52	The ratio between two medium and light label partners.

Ratio M/L normalized g3_GK1_Chromatin_EHT_52	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_53	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_EHT_5	
Ratio M/L localized g3_GK1_Chromatin_EHT_5	
Ratio M/L nmods g3_GK1_Chromatin_EHT_5	
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_5	
Ratio H/L g3_GK1_Chromatin_EHT_5	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_51	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_52	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_53	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_51	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_52	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_53	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_EHT_5	
Ratio H/L localized g3_GK1_Chromatin_EHT_5	
Ratio H/L nmods g3_GK1_Chromatin_EHT_5	
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_5	
Ratio H/M g3_GK1_Chromatin_EHT_5	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_51	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_52	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_53	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_51	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_52	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_53	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_EHT_5	
Ratio H/M localized g3_GK1_Chromatin_EHT_5	
Ratio H/M nmods g3_GK1_Chromatin_EHT_5	

Ratio H/M variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3 GK1 Chromatin EHT 5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_5	, ,
Occupancy L g3_GK1_Chromatin_EHT_5	
Occupancy M g3_GK1_Chromatin_EHT_5	
Occupancy H g3_GK1_Chromatin_EHT_5	
Ratio M/L g3_GK1_Chromatin_EHT_6	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_61	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_62	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_63	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_EHT_61	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized q3 GK1 Chromatin EHT 6 2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
g3_GK1_Chromatin_EHT_63 Ratio M/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_GK1_Chromatin_EHT_6 Ratio M/L localized	
g3_GK1_Chromatin_EHT_6 Ratio M/L nmods	
g3_GK1_Chromatin_EHT_6 Ratio M/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_6	quantition and and quantition from the quantity means and
Ratio H/L g3_GK1_Chromatin_EHT_6	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_61	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_62	The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_63	The ratio between two heavy and light label partners.
Ratio H/L normalized q3 GK1 Chromatin EHT 6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_61	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_GK1_Chromatin_EHT_62	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q3 GK1 Chromatin EHT 6 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_GK1_Chromatin_EHT_6	
Ratio H/L localized g3_GK1_Chromatin_EHT_6	
Ratio H/L nmods g3 GK1 Chromatin EHT 6	
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_6	

Ratio H/M g3 GK1 Chromatin EHT 6	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_61	The ratio between two heavy and medium label partners.
Ratio H/M q3 GK1 Chromatin EHT 6 2	The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_63	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_61	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_62	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_GK1_Chromatin_EHT_63	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_GK1_Chromatin_EHT_6	
Ratio H/M localized g3_GK1_Chromatin_EHT_6	
Ratio H/M nmods g3_GK1_Chromatin_EHT_6	
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_6	
Occupancy L g3_GK1_Chromatin_EHT_6	
Occupancy M g3_GK1_Chromatin_EHT_6	
Occupancy H g3_GK1_Chromatin_EHT_6	
Ratio M/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_mH2A_4_5 1	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_mH2A_4_5 2	The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_mH2A_4_5 3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L localized g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L nmods g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_mH2A_4_5	

The ratio between two heavy and light label partners.
The ratio between two heavy and light label partners.
The ratio between two heavy and light label partners.
The ratio between two heavy and light label partners.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two heavy and medium label partners.
The ratio between two heavy and medium label partners.
The ratio between two heavy and medium label partners.
The ratio between two heavy and medium label partners.
Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Occupancy H	
g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L g3_KW35_ET	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET1	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_ET1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_ET2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_ET3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_ET	
Ratio M/L localized g3_KW35_ET	
Ratio M/L nmods g3_KW35_ET	
Ratio M/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_ET	
Ratio H/L g3_KW35_ET	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET1	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET3 Ratio H/L normalized g3_KW35_ET	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
0	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_ET1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_ET2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_ET3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_KW35_ET	
Ratio H/L localized g3_KW35_ET	
Ratio H/L nmods g3_KW35_ET	
Ratio H/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_ET	
Ratio H/M g3_KW35_ET	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET1	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET2	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_ET1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_ET2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_ET3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_KW35_ET	
Ratio H/M localized g3_KW35_ET	
Ratio H/M nmods g3_KW35_ET	
Ratio H/M variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/M count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET	quantitation that are quantities with the re-quantity method.
Occupancy L g3_KW35_ET	
Occupancy M g3_KW35_ET	
Occupancy H g3_KW35_ET	
Ratio M/L g3_KW35_ET_2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET_21	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET_22	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET_23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_ET_21	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_ET_22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_ET_23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_ET_2	
Ratio M/L localized g3_KW35_ET_2	
Ratio M/L nmods g3_KW35_ET_2	
Ratio M/L variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_ET_2	
Ratio H/L g3_KW35_ET_2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET_21	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET_22	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_ET_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_ET_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_ET_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_ET_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_KW35_ET_2	
Ratio H/L localized g3_KW35_ET_2	
Ratio H/L nmods g3_KW35_ET_2	
Ratio H/L variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_ET_2	
Ratio H/M g3_KW35_ET_2	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET_21	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET_22	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET_23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_ET_21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_ET_22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_ET_23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.

Ratio H/M unmod. pep. g3_KW35_ET_2	
Ratio H/M localized g3_KW35_ET_2	
Ratio H/M nmods g3_KW35_ET_2	
Ratio H/M variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET_2	
Occupancy L g3_KW35_ET_2	
Occupancy M g3_KW35_ET_2	
Occupancy H g3_KW35_ET_2	
Ratio M/L g3_KW35_nE	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE1	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_nE	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_nE1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_nE2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_nE3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_nE	
Ratio M/L localized g3_KW35_nE	
Ratio M/L nmods g3_KW35_nE	
Ratio M/L variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_nE	
Ratio H/L g3_KW35_nE	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE1	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_nE1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_nE2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_nE3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_KW35_nE	
Ratio H/L localized g3_KW35_nE Ratio H/L nmods g3_KW35_nE	
Ratio H/L variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE	
Ratio H/M g3_KW35_nE	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE1	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE2	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_nE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.

Ratio H/M normalized g3_KW35_nE1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_nE2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_nE3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_KW35_nE	1.
Ratio H/M localized g3_KW35_nE	
Ratio H/M nmods g3_KW35_nE	
Ratio H/M variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE	
Occupancy L g3_KW35_nE	
Occupancy M g3_KW35_nE	
Occupancy H g3_KW35_nE	
Ratio M/L g3_KW35_nE_2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE_21	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE_22	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE_23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_nE_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_nE_21	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_nE_22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_nE_23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_nE_2	
Ratio M/L localized g3_KW35_nE_2	
Ratio M/L nmods g3_KW35_nE_2	
Ratio M/L variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_nE_2	
Ratio H/L g3_KW35_nE_2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE_21	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE_22	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE_23 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g3_KW35_nE_2 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g3_KW35_nE_21	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_nE_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_nE_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_KW35_nE_2	
Ratio H/L localized g3_KW35_nE_2	
Ratio H/L nmods g3_KW35_nE_2	
Ratio H/L variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE_2	
Ratio H/M g3_KW35_nE_2	The ratio between two heavy and medium label partners.

Ratio H/M g3_KW35_nE_21	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE_22	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE_23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_nE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_nE_21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_nE_22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_nE_23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_KW35_nE_2	
Ratio H/M localized g3_KW35_nE_2	
Ratio H/M nmods g3_KW35_nE_2	
Ratio H/M variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE_2	
Occupancy L g3_KW35_nE_2 Occupancy M g3_KW35_nE_2	
Occupancy H g3_KW35_nE_2	
Ratio M/L g3_KW35_rot_ET	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_rot_ET1	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_rot_ET2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_rot_ET3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_rot_ET	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_rot_ET1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_rot_ET2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_rot_ET3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_rot_ET Ratio M/L localized	
g3_KW35_rot_ET	
Ratio M/L nmods g3_KW35_rot_ET	
Ratio M/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_rot_ET	
Ratio H/L g3_KW35_rot_ET	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_rot_ET1	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_rot_ET2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_rot_ET3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_rot_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_rot_ET1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_rot_ET2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_rot_ET3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_KW35_rot_ET	
Ratio H/L localized g3_KW35_rot_ET	
Ratio H/L nmods g3_KW35_rot_ET	

Ratio H/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g3_KW35_rot_ET	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g3_KW35_rot_ET	quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_rot_ET	
Ratio H/M g3_KW35_rot_ET	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_rot_ET1	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_rot_ET2	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_rot_ET3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_rot_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_rot_ET1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_rot_ET2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_rot_ET3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_KW35_rot_ET	
Ratio H/M localized g3_KW35_rot_ET	
Ratio H/M nmods g3_KW35_rot_ET	
Ratio H/M variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_rot_ET	
Occupancy L g3_KW35_rot_ET	
Occupancy M g3_KW35_rot_ET	
Occupancy H g3_KW35_rot_ET	
Ratio M/L g3_KW35_wE	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE1	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_wE1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_wE2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_wE3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_wE Ratio M/L localized q3 KW35 wE	
Ratio M/L localized g3_KW35_wE Ratio M/L nmods g3_KW35_wE	
Ratio M/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE	
Ratio H/L g3_KW35_wE	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE1	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_wE1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_wE2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized g3_KW35_wE 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_KW35_wE	
Ratio H/L localized g3_KW35_wE	
Ratio H/L nmods g3_KW35_wE	Coefficient of veriability ever all redundant avantifiable
Ratio H/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE	
Ratio H/M g3_KW35_wE	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE1	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE2	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_wE1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_wE2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_wE3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_KW35_wE	
Ratio H/M localized g3_KW35_wE	
Ratio H/M nmods g3_KW35_wE	
Ratio H/M variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE	
Occupancy L g3_KW35_wE	
Occupancy M g3_KW35_wE	
Occupancy H g3_KW35_wE	
Ratio M/L g3_KW35_wE_2	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE_21	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE_22	The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE_23 Ratio M/L normalized	The ratio between two medium and light label partners.
g3_KW35_wE_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_wE_21 Ratio M/L normalized	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
g3_KW35_wE_22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_KW35_wE_23 Retic M/L upmed_nee	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_KW35_wE_2 Patio M/L localized	
Ratio M/L localized g3_KW35_wE_2	
Ratio M/L nmods g3_KW35_wE_2	Occupation of control tiles and the control tiles are the control tiles and the control tiles are the control
Ratio M/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE_2	
Ratio H/L g3_KW35_wE_2	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE_21	The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE_22	The ratio between two heavy and light label partners.

Ratio H/L g3_KW35_wE_23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_wE_21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_wE_22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_KW35_wE_23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_KW35_wE_2	
Ratio H/L localized g3_KW35_wE_2	
Ratio H/L nmods g3_KW35_wE_2	
Ratio H/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE_2	
Ratio H/M g3_KW35_wE_2	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE_21	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE_22	The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE_23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_wE_21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_wE_22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_KW35_wE_23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_KW35_wE_2	
Ratio H/M localized g3_KW35_wE_2	
Ratio H/M nmods g3_KW35_wE_2	
Ratio H/M variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE_2	
Occupancy L g3_KW35_wE_2	
Occupancy M g3_KW35_wE_2	
Occupancy H g3_KW35_wE_2	
Ratio M/L g3_PX328_Diff3_Exp1	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp11	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp12	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp13	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff3_Exp11	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff3_Exp12	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff3_Exp13	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX328_Diff3_Exp1	
Ratio M/L localized g3_PX328_Diff3_Exp1 Ratio M/L nmods	
g3_PX328_Diff3_Exp1	

Ratio M/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count	Number of redundant peptides (MS1 features) used for
g3_PX328_Diff3_Exp1 Ratio M/L type	quantitation that are quantified with the re-quantify method.
g3_PX328_Diff3_Exp1	
Ratio H/L g3_PX328_Diff3_Exp1 Ratio H/L	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
g3_PX328_Diff3_Exp11	, , ,
Ratio H/L g3_PX328_Diff3_Exp12	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp13	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff3_Exp11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff3_Exp12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff3_Exp13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX328_Diff3_Exp1	
Ratio H/L localized g3_PX328_Diff3_Exp1	
Ratio H/L nmods g3_PX328_Diff3_Exp1	
Ratio H/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp1	
Ratio H/M g3_PX328_Diff3_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp11	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp12	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp13	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff3_Exp11	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff3_Exp12	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff3_Exp13	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX328_Diff3_Exp1	
Ratio H/M localized g3_PX328_Diff3_Exp1	
Ratio H/M nmods g3_PX328_Diff3_Exp1	
Ratio H/M variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp1	
Occupancy L g3_PX328_Diff3_Exp1	
Occupancy M g3_PX328_Diff3_Exp1	

Occupancy H	
g3_PX328_Diff3_Exp1 Ratio M/L g3_PX328_Diff3_Exp2	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp21	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp22	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff3_Exp21	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff3_Exp22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff3_Exp23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX328_Diff3_Exp2	
Ratio M/L localized g3_PX328_Diff3_Exp2	
Ratio M/L nmods g3_PX328_Diff3_Exp2	
Ratio M/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff3_Exp2	
Ratio H/L g3_PX328_Diff3_Exp2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp21	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp22	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff3_Exp21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff3_Exp22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff3_Exp23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX328_Diff3_Exp2	
Ratio H/L localized g3_PX328_Diff3_Exp2	
Ratio H/L nmods g3_PX328_Diff3_Exp2	
Ratio H/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp2	
Ratio H/M g3_PX328_Diff3_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp21	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp22	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff3_Exp21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.

Ratio H/M normalized g3_PX328_Diff3_Exp22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff3_Exp23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX328_Diff3_Exp2	
Ratio H/M localized g3_PX328_Diff3_Exp2	
Ratio H/M nmods g3_PX328_Diff3_Exp2	
Ratio H/M variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp2	
Occupancy L g3_PX328_Diff3_Exp2	
Occupancy M g3_PX328_Diff3_Exp2	
Occupancy H g3_PX328_Diff3_Exp2	
Ratio M/L g3_PX328_Diff4_Exp1	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp11	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp12	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp13	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff4_Exp11	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff4_Exp12	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff4_Exp13	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX328_Diff4_Exp1	
Ratio M/L localized g3_PX328_Diff4_Exp1	
Ratio M/L nmods g3_PX328_Diff4_Exp1	
Ratio M/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff4_Exp1	
Ratio H/L g3_PX328_Diff4_Exp1	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp11	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp12	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp13	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff4_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff4_Exp11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff4_Exp12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff4_Exp13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX328_Diff4_Exp1	
Ratio H/L localized g3_PX328_Diff4_Exp1	

Ratio H/L nmods	
g3_PX328_Diff4_Exp1 Ratio H/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff4_Exp1	
Ratio H/M g3_PX328_Diff4_Exp1 Ratio H/M	The ratio between two heavy and medium label partners. The ratio between two heavy and medium label partners.
g3_PX328_Diff4_Exp11 Ratio H/M	The ratio between two heavy and medium label partners. The ratio between two heavy and medium label partners.
g3_PX328_Diff4_Exp12 Ratio H/M	,
g3_PX328_Diff4_Exp13	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff4_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff4_Exp11	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff4_Exp12	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff4_Exp13	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX328_Diff4_Exp1	
Ratio H/M localized g3_PX328_Diff4_Exp1	
Ratio H/M nmods g3_PX328_Diff4_Exp1	
Ratio H/M variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff4_Exp1	
Occupancy L g3_PX328_Diff4_Exp1	
Occupancy M g3_PX328_Diff4_Exp1	
Occupancy H g3_PX328_Diff4_Exp1	
Ratio M/L g3_PX328_Diff4_Exp2	The ratio between two medium and light label partners.
g3_PX328_Diff4_Exp21	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp22	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff4_Exp21	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff4_Exp22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff4_Exp23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX328_Diff4_Exp2	
Ratio M/L localized g3_PX328_Diff4_Exp2	
Ratio M/L nmods g3_PX328_Diff4_Exp2	
Ratio M/L variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.

go_PX328_DH4_Exp2 Ratio HU_gb_FX328_DH4_Exp2 Ratio HU_gb_FX328_DH4_Exp2 Ratio HU_gb_FX328_DH4_Exp2 The ratio between two heavy and light label partners. Ratio HU_gb_FX328_DH4_Exp2 The ratio between two heavy and light label partners. Ratio HU_gb_FX328_DH4_Exp2 The ratio between two heavy and light label partners. Ratio HU_gb_FX328_DH4_Exp2 Ratio HU_gb_FX	Ratio M/L iso-count	Number of redundant peptides (MS1 features) used for
Ago PX328_DIM4_Exp2	·	quantitation that are quantified with the re-quantify method.
Ratio HU. Control (Lorentz Park) Ratio HU. Increase Diffe Exp2 1 Ratio HU. Increase Diffe Exp2 2 Ratio HU. Increase Diffe Exp2 2 Ratio HU. Increase Diffe Exp2 3 Ratio HU. Increase Diffe Exp2 4 Ratio HU. Increase Diffe Exp2 5 Ratio HU. Increase Diffe Exp2 7 Ratio H	g3_PX328_Diff4_Exp2	
Sage Pixilage Direct Expo	-	, , ,
9.3 PX328 Diff4 Exp2 2 The ratio between two heavy and light label partners. Ratio HL contral Ratio Ra	g3_PX328_Diff4_Exp21	, , ,
Sol. PX328_Diff4_Exp2_3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio partners. The median of the total ratio population was shifted to 1. Ratio HJL normalized ratio partners. The median of the total ratio partners are shifted to 1. Ratio HJL specular ratio partners. The ratio between two heavy and medium label partners. The ratio between two heavy and medium label partners. The ratio between two heavy and medium label partners. The ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Ratio HJM normalized ratio partners. The median of the total ratio population was shifted to 1. Ratio HJM normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Ratio HJM normalized ratio partners. The median of the total ratio population was shifted to	g3_PX328_Diff4_Exp22	The ratio between two heavy and light label partners.
Ratio HJ. normalized Ratio HJM. nor		The ratio between two heavy and light label partners.
Ratio HJ. normalized g3_PX328_Diff4_Exp2_1 The median of the total ratio population was shifted to 1. Ratio HJ. normalized g3_PX328_Diff4_Exp2_3 Ratio HJ. normalized g3_PX328_Diff4_Exp2_3 Ratio HJ. normalized g3_PX328_Diff4_Exp2_3 Ratio HJ. south to the state of the total ratio population was shifted to 1. Ratio HJ. south to the state of the total ratio population was shifted to 1. Ratio HJ. south to the state of the total ratio population was shifted to 1. Ratio HJL south to the state of the state of the state of the total ratio population was shifted to 1. Ratio HJL south to the state of the st		
Ratio HJ. normalized ga. PX328_Diff4_Exp2 and interest process of the second process of		
Ratio H/L unmod pep. 93 PX328 Diff4_Exp2 Ratio H/L unmod pep. 93 PX328 Diff4_Exp2 Ratio H/L localized 93 PX328 Diff4_Exp2 Ratio H/L count 93 PX328 Diff4_Exp2 Ratio H/R gap PX328 Diff4_Exp2 Ratio H/R normalized 93 PX328 Diff4_Exp2 Ratio H/R normalized 104 PX328 Diff4_Exp2 Ratio H/R normalized 205 PX328 Diff4_Exp2 Ratio H/R normalized 305 PX328 Diff4_Exp2 Ratio H/R normalized 405 PX328 Diff4_Exp2 Ratio H/R normalized 505 PX328 Diff4_Exp2 Ratio H/R normalized 506 PX328 Diff4_Exp2 Ratio H/R normalized 507 PX328 Diff4_Exp2 Ratio H/R normalized 507 PX328 Diff4_Exp2 Ratio H/R normalized 507		
Ratio H/I Localized Ratio H/I Ratio H/I Localized Ratio H/I Rati		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g3_PX328_Diff4_Exp2 Ratio H/L mmds g3_PX328_Diff4_Exp2 Ratio H/L mmds g3_PX328_Diff4_Exp2 Ratio H/L variability [%] g3_PX328_Diff4_Exp2 Ratio H/L variability [%] g3_PX328_Diff4_Exp2 Ratio H/L count g3_PX328_Diff4_Exp2 Ratio H/L count g3_PX328_Diff4_Exp2 Ratio H/L count g3_PX328_Diff4_Exp2 Ratio H/R normalized g3_PX328_Diff4_Exp2 Ratio H/R n		
Ga Px328_Diff4_Exp2 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g3 Px328_Diff4_Exp2 Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L iso-count g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M mg3 Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M mg3 Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g3. Px328_Diff4_Exp2 The ratio between two heavy and medium label partners. Ratio H/M normalized g4. Ratio H/M normalized g5. Ratio H/M normalized g6. Ratio H/M normalized g7. R		
gg_PX328_Diff4_Exp2 Ratio H/L count g3_PX328_Diff4_Exp2 Ratio H/M ga_PX328_Diff4_Exp2 Ratio H/M normalized g3_PX328_Diff4_Exp2 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M normalized g3_PX328_Diff4_Exp2 Ratio H/M normalized g3_PX328_Diff4_Exp2 Ratio H/M since the total ratio population was shifted to 1. Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M since the total ratio population was shifted to 1. Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M since the total ratio population was shifted to 1. Ratio H/M since the total ratio population was shifted to 1. Ratio H/M since the total ratio population was shifted to 1. Ratio H/M		
quantitation Number of redundant pepticles (MS1 features) used for ga PX328_Diff4_Exp2 quantitation that are quantified with the re-quantify method.		peptides. It is calculated as the standard deviation of the
g3_PX328_Diff4_Exp2 quantitation that are quantified with the re-quantify method.		
Ratio H/M g3_PX328_Diff4_Exp2_1 Ratio H/M g3_PX328_Diff4_Exp2_1 Ratio H/M Ra	Ratio H/L iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M g3_PX32B_Diff4_Exp22 Ratio H/M g3_PX32B_Diff4_Exp22 Ratio H/M g3_PX32B_Diff4_Exp22 Ratio H/M g3_PX32B_Diff4_Exp23 Ratio H/M normalized g3_PX32B_Diff4_Exp21 Ratio H/M normalized g3_PX32B_Diff4_Exp21 Ratio H/M normalized g3_PX32B_Diff4_Exp22 Ratio H/M normalized g3_PX32B_Diff4_Exp23 Ratio H/M coalized g3_PX32B_Diff4_Exp2 Ratio H/M normalized g3_PX32B_Diff4_Exp2 Ratio H/M normalized g3_PX32B_Diff4_Exp2 Ratio H/M scalabled g4_PX2B_Diff4_Exp2 Ratio H/M scalabled g4_PX2B_Diff4_Exp2 Ratio H/M scalabled g4_PX2B_Diff4_Exp2 Ratio H/M scalabled g4_PX2B_Diff4_Exp2 Ratio H/M g4_PX32B_Diff4_Exp2 Ratio H/M g4_PX3B_Diff4_Exp2 Ratio H/M	Ratio H/L type g3_PX328_Diff4_Exp2	
Ratio H/M Sample		The ratio between two heavy and medium label partners.
g3_PX328_Diff4_Exp2_2 Ratio H/M Sa_PX328_Diff4_Exp2_3 Ratio H/M normalized Partners. Ratio H/M unmod. Pep. Ratio H/M localized Partners. Ratio H/M normalized Partners. Ratio H/M count Partners. Ratio H/M count Partners. Ratio H/M soccount Partners. Ratio H/M soccount Partners. Ratio H/M type Partners.		The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff4_Exp2		The ratio between two heavy and medium label partners.
g3_PX328_Diff4_Exp2 Ratio H/M normalized g3_PX328_Diff4_Exp21 Ratio H/M normalized g3_PX328_Diff4_Exp21 Ratio H/M normalized g3_PX328_Diff4_Exp22 Ratio H/M normalized g3_PX328_Diff4_Exp22 Ratio H/M normalized g3_PX328_Diff4_Exp22 Ratio H/M normalized g3_PX328_Diff4_Exp23 Ratio H/M normalized g3_PX328_Diff4_Exp23 Ratio H/M unmod.pep. g3_PX328_Diff4_Exp2 Ratio H/M localized g3_PX328_Diff4_Exp2 Ratio H/M monds g3_PX328_Diff4_Exp2 Ratio H/M monds g3_PX328_Diff4_Exp2 Ratio H/M vicalized g3_PX328_Diff4_Exp2 Ratio H/M coalized g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M tiso-count g3_PX328_Diff4_Exp2 Cocupancy L g3_PX328_Diff4_Exp2 Cocupancy M g3_PX328_Diff4_Exp2 Cocupancy H g3_PX328_Diff4_Exp2 Cocupancy H g3_PX328_Diff4_Exp2 Ratio ML_g3_PX328_Difff5_Exp1 The ratio between two medium and light label partners. The ratio between two medium and light label partners.		The ratio between two heavy and medium label partners.
g3_PX328_Diff4_Exp21 Ratio H/M normalized g3_PX328_Diff4_Exp22 Ratio H/M normalized g3_PX328_Diff4_Exp22 Ratio H/M normalized g3_PX328_Diff4_Exp23 Ratio H/M unmod_pep. g3_PX328_Diff4_Exp2 Ratio H/M localized g3_PX328_Diff4_Exp2 Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M so-count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio M/M g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 The ratio between two medium and light label partners. Ratio M/L g3_PX328_Diff4_Exp2 The ratio between two medium and light label partners.		partners. The median of the total ratio population was shifted to
g3_PX328_Diff4_Exp22 Ratio H/M normalized g3_PX328_Diff4_Exp23 Ratio H/M unmod. pep. g3_PX328_Diff4_Exp2 Ratio H/M localized g3_PX328_Diff4_Exp2 Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Coccupancy L g3_PX328_Diff4_Exp2 Coccupancy M g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 The ratio between two medium and light label partners. Ratio M/L The ratio between two medium and light label partners.		Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
g3_PX328_Diff4_Exp23 Ratio H/M unmod. pep. g3_PX328_Diff4_Exp2 Ratio H/M localized g3_PX328_Diff4_Exp2 Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Cocupancy L g3_PX328_Diff4_Exp2 Cocupancy M g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff4_Exp2 Ratio M/L The ratio between two medium and light label partners. Ratio M/L The ratio between two medium and light label partners.		partners. The median of the total ratio population was shifted to
g3_PX328_Diff4_Exp2 Ratio H/M localized g3_PX328_Diff4_Exp2 Ratio H/M variability [%] Ratio H/M variability [%] Peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/M count Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 quantitation. Ratio H/M type g3_PX328_Diff4_Exp2 quantitation that are quantified with the re-quantify method. Ratio H/M type g3_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type g3_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type g3_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type g3_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type g3_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type g3_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method. Ratio H/M type G4_PX328_Diff4_Exp2 Quantitation that are quantified with the re-quantify method.		partners. The median of the total ratio population was shifted to
Ratio H/M nmods g3_PX328_Diff4_Exp2 Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy M g3_PX328_Diff4_Exp2 Occupancy M g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 The ratio between two medium and light label partners. Ratio M/L Ratio M/L Ratio between two medium and light label partners.		
Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff5_Exp1 Ratio M/L Ratio H/M synch delication of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two medium and light label partners. The ratio between two medium and light label partners.		
Ratio H/M variability [%] g3_PX328_Diff4_Exp2 Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff5_Exp1 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.	Ratio H/M nmods g3_PX328_Diff4_Exp2	
Ratio H/M count g3_PX328_Diff4_Exp2 Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy M g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff5_Exp1 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation.	Ratio H/M variability [%]	peptides. It is calculated as the standard deviation of the
Ratio H/M iso-count g3_PX328_Diff4_Exp2 Ratio H/M type g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy M g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff5_Exp1 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two medium and light label partners. The ratio between two medium and light label partners.		Number of redundant peptides (MS1 features) used for
Ratio H/M type g3_PX328_Diff4_Exp2 Occupancy L g3_PX328_Diff4_Exp2 Occupancy M g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff5_Exp1 The ratio between two medium and light label partners. Ratio M/L The ratio between two medium and light label partners.	Ratio H/M iso-count	
Occupancy L g3_PX328_Diff4_Exp2 Occupancy M g3_PX328_Diff4_Exp2 Occupancy H g3_PX328_Diff4_Exp2 Ratio M/L g3_PX328_Diff5_Exp1 The ratio between two medium and light label partners. Ratio M/L The ratio between two medium and light label partners.	Ratio H/M type	
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Ratio M/L g3_PX328_Diff5_Exp1 The ratio between two medium and light label partners. Ratio M/L The ratio between two medium and light label partners.	Occupancy H	
		The ratio between two medium and light label partners.
		The ratio between two medium and light label partners.

Ratio M/L	The ratio between two medium and light label partners.
g3_PX328_Diff5_Exp12 Ratio M/L	The ratio between two medium and light label partners.
g3_PX328_Diff5_Exp13	
Ratio M/L normalized g3_PX328_Diff5_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff5_Exp11	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff5_Exp12	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff5_Exp13	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX328_Diff5_Exp1	
Ratio M/L localized g3_PX328_Diff5_Exp1	
Ratio M/L nmods g3_PX328_Diff5_Exp1	
Ratio M/L variability [%] g3_PX328_Diff5_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff5_Exp1	
Ratio H/L g3_PX328_Diff5_Exp1	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp11	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp12	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp13	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff5_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff5_Exp11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff5_Exp12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff5_Exp13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX328_Diff5_Exp1	
Ratio H/L localized g3_PX328_Diff5_Exp1	
Ratio H/L nmods g3_PX328_Diff5_Exp1	
Ratio H/L variability [%] g3_PX328_Diff5_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff5_Exp1	
Ratio H/M g3_PX328_Diff5_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp11	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp12	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp13	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff5_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff5_Exp11	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff5_Exp12	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff5_Exp13	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
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Ratio H/M unmod. pep.	
g3_PX328_Diff5_Exp1 Ratio H/M localized	
g3_PX328_Diff5_Exp1	
Ratio H/M nmods g3_PX328_Diff5_Exp1	
Ratio H/M variability [%] g3_PX328_Diff5_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff5_Exp1	
Occupancy L g3_PX328_Diff5_Exp1	
Occupancy M g3_PX328_Diff5_Exp1	
Occupancy H g3_PX328_Diff5_Exp1	
Ratio M/L g3_PX328_Diff5_Exp2	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff5_Exp21	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff5_Exp22	The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff5_Exp23	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff5_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff5_Exp21	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff5_Exp22	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX328_Diff5_Exp23	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX328_Diff5_Exp2	
Ratio M/L localized g3_PX328_Diff5_Exp2	
Ratio M/L nmods g3_PX328_Diff5_Exp2	
Ratio M/L variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3 PX328 Diff5 Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff5_Exp2	
Ratio H/L g3_PX328_Diff5_Exp2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp21	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp22	The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp23	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff5_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff5_Exp21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff5_Exp22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX328_Diff5_Exp23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX328_Diff5_Exp2	
Ratio H/L localized g3_PX328_Diff5_Exp2	
Ratio H/L nmods g3_PX328_Diff5_Exp2	
Ratio H/L variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g3_PX328_Diff5_Exp2 Ratio H/L type	quantitation that are quantified with the re-quantify method.
g3_PX328_Diff5_Exp2	
Ratio H/M g3_PX328_Diff5_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp21	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp22	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp23	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff5_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff5_Exp21	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff5_Exp22	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX328_Diff5_Exp23	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX328_Diff5_Exp2	
Ratio H/M localized g3_PX328_Diff5_Exp2	
Ratio H/M nmods g3_PX328_Diff5_Exp2	
Ratio H/M variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff5_Exp2	
Occupancy L g3_PX328_Diff5_Exp2	
Occupancy M g3_PX328_Diff5_Exp2	
Occupancy H g3_PX328_Diff5_Exp2	
Ratio M/L g3_PX597_A1_Spr	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A1_Spr1	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A1_Spr2	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A1_Spr3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A1_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_A1_Spr1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_A1_Spr2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_A1_Spr3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX597_A1_Spr	
Ratio M/L localized g3_PX597_A1_Spr	
Ratio M/L nmods g3_PX597_A1_Spr	
Ratio M/L variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A1_Spr	
Ratio H/L g3_PX597_A1_Spr	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A1_Spr1	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A1_Spr2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A1_Spr3	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_PX597_A1_Spr	The median of the total ratio population was shifted to 1.

Ratio H/L normalized g3_PX597_A1_Spr1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_A1_Spr2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q3_PX597_A1_Spr3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX597_A1_Spr	The median of the lotar ratio population was stilled to 1.
Ratio H/L localized	
g3_PX597_A1_Spr Ratio H/L nmods	
g3_PX597_A1_Spr Ratio H/L variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A1_Spr	
Ratio H/M g3_PX597_A1_Spr	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A1_Spr1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A1_Spr2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A1_Spr3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A1_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A1_Spr1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A1_Spr2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A1_Spr3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX597_A1_Spr	
Ratio H/M localized g3_PX597_A1_Spr	
Ratio H/M nmods g3_PX597_A1_Spr	
Ratio H/M variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A1_Spr	
Occupancy L g3_PX597_A1_Spr	
Occupancy M g3_PX597_A1_Spr	
Occupancy H g3_PX597_A1_Spr	
Ratio M/L g3_PX597_A2_Spr	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A2_Spr1	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A2_Spr2	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A2_Spr3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A2_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_A2_Spr1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_A2_Spr2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_A2_Spr3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX597_A2_Spr	
Ratio M/L localized g3_PX597_A2_Spr	
Ratio M/L nmods g3_PX597_A2_Spr	
Ratio M/L variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio M/L count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A2_Spr	quantitation that are quantities with the re-quantity method.
Ratio H/L g3_PX597_A2_Spr	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A2_Spr1	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A2_Spr2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A2_Spr3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A2_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_PX597_A2_Spr1 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g3_PX597_A2_Spr2 Ratio H/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.
g3_PX597_A2_Spr3 Ratio H/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_PX597_A2_Spr Ratio H/L localized	
g3_PX597_A2_Spr Ratio H/L nmods	
g3_PX597_A2_Spr	Coefficient of veriebility ever all radius dest successful.
Ratio H/L variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A2_Spr	
Ratio H/M g3_PX597_A2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A2_Spr1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A2_Spr2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A2_Spr3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A2_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A2_Spr1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A2_Spr2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A2_Spr3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX597_A2_Spr	
Ratio H/M localized g3_PX597_A2_Spr	
Ratio H/M nmods g3_PX597_A2_Spr	
Ratio H/M variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A2_Spr	The state of the s
Occupancy L g3_PX597_A2_Spr	
Occupancy M g3_PX597_A2_Spr	
Occupancy H g3_PX597_A2_Spr	
Ratio M/L g3_PX597_A3_Spr	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A3_Spr1	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A3_Spr2	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A3_Spr3	The ratio between two medium and light label partners.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
g3_PX597_A3_Spr Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_PX597_A3_Spr1 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_PX597_A3_Spr2	The median of the total ratio population was shifted to 1.

Ratio M/L normalized g3_PX597_A3_Spr3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L unmod. pep. g3_PX597_A3_Spr	
Ratio M/L localized g3_PX597_A3_Spr	
Ratio M/L nmods g3_PX597_A3_Spr	
Ratio M/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A3_Spr	
Ratio H/L g3_PX597_A3_Spr	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A3_Spr1	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A3_Spr2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A3_Spr3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_A3_Spr1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_A3_Spr2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_A3_Spr3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX597_A3_Spr	
Ratio H/L localized g3_PX597_A3_Spr	
Ratio H/L nmods g3_PX597_A3_Spr	
Ratio H/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A3_Spr	
Ratio H/M g3_PX597_A3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A3_Spr1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A3_Spr2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A3_Spr3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A3_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A3_Spr1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A3_Spr2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_A3_Spr3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX597_A3_Spr	
Ratio H/M localized g3_PX597_A3_Spr	
Ratio H/M nmods g3_PX597_A3_Spr	
Ratio H/M variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A3_Spr	
Occupancy L g3_PX597_A3_Spr	
Occupancy M g3_PX597_A3_Spr	
Occupancy H g3_PX597_A3_Spr	

Ratio M/L g3 PX597 B1 Spr 1 Ratio M/L g3 PX597 B1 Spr 2 Ratio M/L g3 PX597 B1 Spr 3 Ratio M/L normalized Ra	D :: M// 0 DV507 D4 0	
Ratio ML g3 PX597 B1 Spr g Ratio ML g3 PX597 B1 Spr g Ratio ML g3 PX597 B1 Spr g Ratio ML normalized garden spread garden spr	Ratio M/L g3_PX597_B1_Spr	The ratio between two medium and light label partners.
Ratio ML normalized 33_PX597_B1_Spr Ratio ML normalized 33_PX597_B1_Spr Ratio ML normalized 33_PX597_B1_Spr The ratio between two needium and light label partners. Ratio ML normalized 33_PX597_B1_Spr 1		¥ .
Ratio ML count g3 PX597 B1 Spr Ratio ML count g3 PX597 B1 Spr Ratio ML g3 PX597 B1 Spr Ratio ML p3 PX597 B1 Spr Ratio ML p4 Spr Ratio ML p4 Spr Ratio ML p5 Spr R	<u> </u>	¥ .
The median of the total ratio population was shifted to 1. Ratio ML normalized g3_PX597_B1_Spr		<u> </u>
g3_PX597_B1_Spr1 The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio ML rotalised as the standard deviation of the naturally logarithmized ratios times 100. Ratio ML rotalishility (St.) Ratio ML rotalishility (St.) Ratio ML so-count (St.) Ratio ML so-count (St.) Ratio ML so-count (St.) Ratio ML so-count (St.) Ratio ML type g3 PX597_B1_Spr (St.) Ratio ML upe g3 PX597_B1_Spr (St.) Ratio ML upe g3 PX597_B1_Spr (St.) Ratio ML upe g3 PX597_B1_Spr (St.) The ratio between two heavy and light label partners. Ratio HL upe y3 PX597_B1_Spr (St.) The ratio between two heavy and light label partners. Ratio HL upe y3 PX597_B1_Spr (St.) The ratio between two heavy and light label partners. Ratio HL upe y3 PX597_B1_Spr (St.) Ratio HL upe y3 PX597_B1_Spr (St.) The ratio between two heavy and light label partners. Ratio HL upe y3 PX597_B1_Spr (St.) Ratio HL upe y3 PX597_B1_Spr (St.) The ratio between two heavy and light label partners. Ratio HL upe y3 PX597_B1_Spr (St.) Ratio HL upernalized (St.) Rat	g3_PX597_B1_Spr	The median of the total ratio population was shifted to 1.
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g3_PX597_B1_Spr3 partners. The median of the total ratio population was shifted to 1. Ratio H/M unmod. pep. g3_PX597_B1_Spr Ratio H/M localized g3_PX597_B1_Spr Ratio H/M nmods	g3_PX597_B1_Spr2	partners. The median of the total ratio population was shifted to
g3_PX597_B1_Spr Ratio H/M localized g3_PX597_B1_Spr Ratio H/M nmods		partners. The median of the total ratio population was shifted to
g3_PX597_B1_Spr Ratio H/M nmods	g3_PX597_B1_Spr	
	g3_PX597_B1_Spr	

Ratio H/M variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B1_Spr	
Occupancy L g3_PX597_B1_Spr	
Occupancy M g3_PX597_B1_Spr	
Occupancy H g3_PX597_B1_Spr	
Ratio M/L g3_PX597_B2_Spr	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B2_Spr1	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B2_Spr2	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B2_Spr3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B2_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized g3_PX597_B2_Spr1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
g3_PX597_B2_Spr3 Ratio M/L unmod. pep. g3_PX597_B2_Spr	The median of the total ratio population was shifted to 1.
Ratio M/L localized g3_PX597_B2_Spr	
Ratio M/L nmods g3_PX597_B2_Spr	
Ratio M/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for guantitation.
Ratio M/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B2_Spr	
Ratio H/L g3_PX597_B2_Spr	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B2_Spr1	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B2_Spr2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B2_Spr3	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_PX597_B2_Spr	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_B2_Spr1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_B2_Spr2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_B2_Spr3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX597_B2_Spr	
Ratio H/L localized g3_PX597_B2_Spr	
Ratio H/L nmods g3_PX597_B2_Spr	
Ratio H/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B2_Spr	
Ratio H/M g3_PX597_B2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B2_Spr1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B2_Spr2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B2_Spr3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B2_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to
Ratio H/M normalized g3_PX597_B2_Spr1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.

Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_PX597_B2_Spr2	partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_B2_Spr3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX597_B2_Spr	
Ratio H/M localized g3_PX597_B2_Spr	
Ratio H/M nmods g3_PX597_B2_Spr	
Ratio H/M variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B2_Spr	
Occupancy L g3_PX597_B2_Spr	
Occupancy M g3_PX597_B2_Spr	
Occupancy H g3_PX597_B2_Spr	The ratio between two medium and light label partners
Ratio M/L g3_PX597_B3_Spr Ratio M/L g3_PX597_B3_Spr1	The ratio between two medium and light label partners. The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B3_Spr2	The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B3_Spr3	The ratio between two medium and light label partners.
Ratio M/L normalized	Normalized ratio between two heavy and light label partners.
g3_PX597_B3_Spr Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_PX597_B3_Spr1 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_PX597_B3_Spr2 Ratio M/L normalized	The median of the total ratio population was shifted to 1. Normalized ratio between two heavy and light label partners.
g3_PX597_B3_Spr3 Ratio M/L unmod. pep.	The median of the total ratio population was shifted to 1.
g3_PX597_B3_Spr Ratio M/L localized	
g3_PX597_B3_Spr Ratio M/L nmods	
g3_PX597_B3_Spr	
Ratio M/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B3_Spr	
Ratio H/L g3_PX597_B3_Spr	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B3_Spr1 Ratio H/L g3_PX597_B3_Spr2	The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B3_Spr2 Ratio H/L g3_PX597_B3_Spr3	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g3_PX597_B3_Spr1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g3_PX597_B3_Spr2 Ratio H/L normalized g3_PX597_B3_Spr3	The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g3_PX597_B3_Spr	The median of the total ratio population was stilled to 1.
Ratio H/L localized g3_PX597_B3_Spr	
Ratio H/L nmods g3_PX597_B3_Spr	
Ratio H/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B3_Spr	

Ratio H/M g3_PX597_B3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B3_Spr1	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B3_Spr2	The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B3_Spr3	The ratio between two heavy and medium label partners.
Ratio H/M normalized	Normalized ratio between two heavy and medium label
g3_PX597_B3_Spr	partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_B3_Spr1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_B3_Spr2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M normalized g3_PX597_B3_Spr3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M unmod. pep. g3_PX597_B3_Spr	
Ratio H/M localized g3_PX597_B3_Spr	
Ratio H/M nmods g3_PX597_B3_Spr	
Ratio H/M variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B3_Spr	
Occupancy L g3_PX597_B3_Spr	
Occupancy M g3_PX597_B3_Spr	
Occupancy H g3_PX597_B3_Spr	
Ratio H/L g4_NCC_A	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_A1	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_A2	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_A3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_A	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC_A1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC_A2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC_A3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC_A	
Ratio H/L localized g4_NCC_A	
Ratio H/L nmods g4_NCC_A	
Ratio H/L variability [%] g4_NCC_A	
Ratio H/L count g4_NCC_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_A	
Occupancy L g4_NCC_A	
Occupancy H g4_NCC_A	
Ratio H/L g4_NCC_B	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_B1	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_B2	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_B3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC_B	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC_B1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC_B2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC_B3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC_B	
Ratio H/L localized g4_NCC_B	
Ratio H/L nmods g4_NCC_B	
Ratio H/L variability [%] g4_NCC_B	

Ratio HL Iso-count g4_NCC_B Ratio HL Lype g4_NCC_B Occupancy L g4_NCC_B Occupancy L g4_NCC_B Occupancy L g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL g4_NCC_C The ratio between two heavy and light label partners. Ratio HL normalized g4_NCC_C The ratio between two nedium and light label partners. Ratio HL normalized AND C6_C The ratio between two medium and light label partners. Ratio HL normalized AND C6_C The ratio between two medium and light label partners. Ratio HL normalized AND C6_C The ratio between two medium and light label partners. Ratio HL normalized AND C6_C Ratio HL normalized AND C7_C Ratio HL normalized AND C7	Ratio H/L count g4_NCC_B	Number of redundant peptides (MS1 features) used for guantitation.
Occupancy L.g.4. NCC. B Ratio HU, g.4. NCC. C. 1 Ratio HU, g.4. NCC. C. 1 Ratio HU, g.4. NCC. C. 2 Ratio HU, g.4. NCC. C. 2 Ratio HU, g.4. NCC. C. 3 Ratio HU, normalized g.4. NCC. C. 1 Ratio HU, normalized g.4. NCC. C. 2 Ratio HU, normalized g.4. NCC. C. 3 Ratio HU, normalized g.4. NCC. C. 4 Ratio HU, normalized g.4. NCC. C. 8 Ratio HU, normalized g.4. NCC. C. 9 Ratio HU, soccount g.4. NCC. C. 9 Ratio HU, commalized g.4. NCC. C. 9 Ratio HU, commalized g.4. NCC	Ratio H/L iso-count g4_NCC_B	Number of redundant peptides (MS1 features) used for
Occupancy L.g.4. NCC. B Ratio HU, g.4. NCC. C. 1 Ratio HU, g.4. NCC. C. 1 Ratio HU, g.4. NCC. C. 2 Ratio HU, g.4. NCC. C. 2 Ratio HU, g.4. NCC. C. 3 Ratio HU, normalized g.4. NCC. C. 1 Ratio HU, normalized g.4. NCC. C. 2 Ratio HU, normalized g.4. NCC. C. 3 Ratio HU, normalized g.4. NCC. C. 4 Ratio HU, normalized g.4. NCC. C. 8 Ratio HU, normalized g.4. NCC. C. 9 Ratio HU, soccount g.4. NCC. C. 9 Ratio HU, commalized g.4. NCC. C. 9 Ratio HU, commalized g.4. NCC	Ratio H/L type q4 NCC B	
Decupancy High NCC B Ratio HU, 94, NCC C The ratio between two heavy and light label partners. Ratio HU, 94, NCC C 2 The ratio between two heavy and light label partners. Ratio HU, 94, NCC C 2 The ratio between two heavy and light label partners. Ratio HU, 94, NCC C 2 The ratio between two heavy and light label partners. Ratio HU, 94, NCC C 2 The ratio between two heavy and light label partners. Ratio HU, normalized 94, NCC C The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio HU, normalized 94, NCC C 2 The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HU, normalized 94, NCC C 2 The ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio HU, unormalized 94, NCC C 2 The ratio humber of redundant peptides (MS1 features) used for quantitation. Ratio HU, variability [9] g4 NCC C Number of redundant peptides (MS1 features) used for quantitation that are quantitified with the re-quantity method. Ratio HU, pug 4, NCC C Number of redundant peptides (MS1 features) used for quantitation that are quantitified with the re-quantity method. Ratio HU, pug 4, NCC C Number of redundant peptides (MS1 features) used for quantitation that are quantitified with the re-quantity method. Ratio HU, pug 4, NCC C Number of redundant peptides (MS1 features) used for quantitation that are quantitified with the re-quantity method. Ratio HU, pug 4, NCC C Number of redundant peptides (MS1 features) used for quantitation that are quantitified with the re-quantity method. Ratio HU, pug 4, NCC C Number of redundant peptides (MS1 features) used for quantitation that are quantitified with the re-quantity method. Ratio HU, pug 4, NCC C Number of redundant peptides (MS1 features) used for quantitation of the total ratio population was shifted to 1. Normalized 44, NCC C Normalized gate between two heavy and light label		
Ratio H/L g4 NCC C Ratio H/L normalized g4 NCC C Ratio H/L user Ratio H/L normalized g4 NCC C Ratio H/L user Ratio H/L normalized g4 NCC C Ratio H/L count g4 NCC C Ratio H/L Normalized g4 NCC C Ratio H/L Count g4 NCC C Ratio H/L Robin Ratio H/L normalized g4 NCC C Ratio H/L Robin Ratio Rati		
Ratio H/L 94 NCC C 1 Ratio H/L 94 NCC C 2 Ratio H/L 94 NCC C 3 Ratio H/L normalized g4 NCC C Ratio H/L normalized g4 NCC C 1 Ratio H/L normalized g4 NCC C 2 Ratio H/L normalized g4 NCC C C 2 Ratio H/L unnod, pep. g4 NCC C C Ratio H/L unnod, pep. g4 NCC C C Ratio H/L unnod g4 NCC C Rat		The ratio between two heavy and light label partners.
Ratio HJL 94 NCC C 2 Ratio HJL 94 NCC C 2 Ratio HJL 94 NCC C 3 Ratio HJL normalized 94 NCC C Ratio HJL normalized 94 NCC C Ratio HJL normalized 94 NCC C 1 Rat		, , ,
Ratio HZL pd. NCC. C 3 Ratio HZL normalized g4_NCC_C Ratio HZL pd. NCC_CPT_s1 1 The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio HZL normalized g4_NCC_CC_C Ratio HZL normalized g4_NCC_CC_CC_CC_CC_CC_CC_CC_CC_CC_CC_CC_CC		, , ,
Ratio H/L normalized g4_NCC_C Ratio H/L seriount g4_NCC_C Ratio H/L yep g4_NCC_C Ratio H/L yep g4_NCC_C Ratio H/L yep g4_NCC_C Ratio H/L yep g4_NCC_C Ratio H/L g4_NCC_CPT_s1 Ratio H/L normalized g4_NCC_C Ratio		, , ,
The median of the total ratio population was shifted to 1. Ratio H/L normalized gd_NCC C 1 The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod.pep. g4_NCC_C Ratio H/L unmod.pep. g4_NCC_C Ratio H/L unmod.pep. g4_NCC_C Ratio H/L variability [%] gd_NCC_C Ratio H/L variability [%] gd_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L type gd_NCC_C Ratio H/L type gd_NCC_C Ratio H/L type gd_NCC_C Ratio H/L type gd_NCC_C Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 Ratio H/L gd_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L gd_NCC_CPT_s1 Ratio H/L gd_NCC_CPT_s1 Ratio H/L normalized gd_NCC_CPT_s1 Ratio H/L norm		, v v
gd_NCC_C_1 The median of the total ratio population was shifted to 1. Ratio H/L normalized gd_NCC_C_2 Ratio H/L normalized gd_NCC_C_3 Ratio H/L normalized gd_NCC_C_C Ratio H/L so-count gd_NCC_C_C_C Ratio H/L so-count gd_NCC_C_C_C Ratio H/L so-count gd_NCC_C_C_C_C Ratio H/L so-count gd_NCC_C_C_C_C Ratio H/L so-count gd_NCC_C_C_C_C Ratio H/L so-count gd_NCC_C_C_C_C_C_C_C_C_C_C_C_C_C_C_C_C_C_	3	The median of the total ratio population was shifted to 1.
Ratio H/L normalized system of the total ratio population was shifted to 1. Ratio H/L normalized system of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC_C Ratio H/L coalized g4_NCC_C Ratio H/L variability [%] g4_NCC_C Ratio H/L variability [%] g4_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L type g4_NCC_C Ratio H/L g4_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L g4_NCC_CPT_s1_3 The ratio between two heavy and light label partners. Ratio H/L g4_NCC_CPT_s1_3 The ratio between two heavy and light label partners. Ratio H/L g4_NCC_CPT_s1_3 The ratio between two heavy and light label partners. Ratio H/L normalized g4_NCC_CPT_s1_1 Ratio H/L normalized g4_NCC_CPT_s1_2 Ratio H/L normalized g4_NCC_CPT_s1_2 Ratio H/L normalized g4_NCC_CPT_s1_2 Ratio H/L so-count g4_NCC_CPT_s1_3 Ratio H/L normalized g4_NCC_CPT_s1_3 Ratio H/L so-count g4_NCC_CPT_s1_3 Ratio H/L normalized g4_NCC_CPT_s1_3 Ratio H/L so-count g4_NCC_CPT_s1_3 Ratio H/L normalized g4_NCC_CPT_s1_3 Ratio H/L normalized g4_NCC_CPT_s1_3 Ratio H/L normalized g4_NCC_CPT_s1_3 Ratio H/L so-count g4_NCC_CPT_s1_3 Ratio H/L normalized g4_NCC_CPT_s1_3 Ratio H/L g4_NCC_CPT_s2_1 Ratio H/L g4_NCC_CPT_s2_1 Ratio H/L g4_NCC_CPT_s2_1 Ratio H/L g4_NCC_CPT	g4_NCC_C1	The median of the total ratio population was shifted to 1.
gd_NCC_C_3 The median of the total ratio population was shifted to 1. Ratio H/L unmods_pep_gd_NCC_C Ratio H/L variability [%] gd_NCC_C Ratio H/L variability [%] gd_NCC_C Ratio H/L count gd_NCC_C Ratio H/L so-count gd_NCC_C Ratio H/L bypegd_NCC_C Ratio H/L bypegd_NCC_CPT_s1 Ratio H/L bypegd_NCC_CPT_s2 Ratio H/L bypegd_N	g4_NCC_C2	The median of the total ratio population was shifted to 1.
Ratio H/L localized g4_NCC_C Ratio H/L mmods g4_NCC_C Ratio H/L count g4_NCC_C Ratio H/L count g4_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L type g4_NCC_C Ratio H/L g4_NCC_CT Ratio H/L g4_NCC_CT Ratio H/L g4_NCC_CT_s1 Ratio H/L normalized g4_NCC_CT_s1 Ratio H/L s0_NCC_CT_s2 Ratio H/L s0_NCC_CT_s2 Ratio H/L g4_NCC_CT_s2 Ratio H/L normalized g4_NCC_CT_s2 Ratio H/L normalized g4_NCC_CT_s2 Ratio H/L normalized g4_NCC_CT_s3 Rat	g4_NCC_C3	
Ratio H/L nmods g4_NCC_C Ratio H/L variability [%] g4_NCC_C Ratio H/L variability [%] g4_NCC_C Ratio H/L variability [%] g4_NCC_C Ratio H/L so-count g4_NCC_C Ratio H/L g4_NCC_CPT_s1 Ratio H/L g4_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L g4_NCC_CPT_s1 Ratio H/L g4_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L g4_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L g4_NCC_CPT_s1 The ratio between two heavy and light label partners. Ratio H/L normalized g4_NCC-CPT_s1 Ratio H/L variability [%] g4_NCC-CPT_s1 Ratio H/L variability [%] g4_NCC-CPT_s1 Ratio H/L so-count g4_NCC-CPT_s1 Ratio H/L normalized g4_NCC-CPT_s1 Ratio H/L normalize		
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Ratio H/L iso-count g4_NCC- CPT_s1 Ratio H/L type g4_NCC-CPT_s1 Occupancy L g4_NCC-CPT_s1 Occupancy H g4_NCC-CPT_s1 Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s2 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s2 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s2 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s2 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC-		
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Occupancy L g4_NCC-CPT_s1 Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s21 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s22 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s23 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.		
Occupancy H g4_NCC-CPT_s1 Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s21 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s22 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s22 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod. pep. g4_NCC-	Ratio H/L type g4_NCC-CPT_s1	
Occupancy H g4_NCC-CPT_s1 Ratio H/L g4_NCC-CPT_s2 Ratio H/L g4_NCC-CPT_s21 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s22 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s22 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod. pep. g4_NCC-	Occupancy L g4_NCC-CPT_s1	
Ratio H/L g4_NCC-CPT_s2 1 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s2 1 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s2 2 The ratio between two heavy and light label partners. Ratio H/L g4_NCC-CPT_s2 3 The ratio between two heavy and light label partners. Ratio H/L normalized g4_NCC- CPT_s2		
Ratio H/L g4_NCC-CPT_s22 Ratio H/L g4_NCC-CPT_s22 The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s21 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s22 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod. pep. g4_NCC-		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s23 Ratio H/L g4_NCC-CPT_s23 The ratio between two heavy and light label partners. Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s22 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s23 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L unmod. pep. g4_NCC-		· · · · · · · · · · · · · · · · · · ·
Ratio H/L g4_NCC-CPT_s23 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L unmod. pep. g4_NCC-		· · · · · · · · · · · · · · · · · · ·
Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s2 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L normalized g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod. pep. g4_NCC-	_	· · · · · · · · · · · · · · · · · · ·
Ratio H/L normalized g4_NCC- CPT_s21 Ratio H/L normalized g4_NCC- The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod. pep. g4_NCC-	Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
Ratio H/L normalized g4_NCC- CPT_s22 Ratio H/L normalized g4_NCC- The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L unmod. pep. g4_NCC-	Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
Ratio H/L normalized g4_NCC- CPT_s23 Ratio H/L unmod. pep. g4_NCC- Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
Ratio H/L unmod. pep. g4_NCC-	Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
130 1 37		The median of the total ratio population was still out to 1.

Ratio H/L localized g4_NCC- CPT_s2	
Ratio H/L nmods g4_NCC-CPT_s2	
Ratio H/L variability [%] g4_NCC-CPT_s2	
Ratio H/L count g4_NCC-CPT_s2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- CPT_s2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s2	
Occupancy L g4_NCC-CPT_s2	
Occupancy H g4_NCC-CPT_s2	
Ratio H/L g4_NCC-CPT_s3	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s31	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s32	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s33	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT_s3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-CPT_s31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- CPT_s32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-CPT_s33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC-CPT_s3	
Ratio H/L localized g4_NCC- CPT_s3	
Ratio H/L nmods g4_NCC-CPT_s3	
Ratio H/L variability [%] g4_NCC- CPT s3	
Ratio H/L count g4_NCC-CPT_s3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-CPT_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s3	
Occupancy L g4_NCC-CPT_s3	
Occupancy H g4_NCC-CPT_s3	
Ratio H/L g4_NCC-HU_Ex1	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex11	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex12	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex13	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU_Ex1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC- HU_Ex1	
Ratio H/L localized g4_NCC- HU_Ex1	
Ratio H/L nmods g4_NCC-HU_Ex1	
Ratio H/L variability [%] g4_NCC- HU_Ex1	
Ratio H/L count g4_NCC-HU_Ex1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex1	
Occupancy L g4_NCC-HU_Ex1	
Occupancy H g4_NCC-HU_Ex1	
Ratio H/L g4_NCC-HU_Ex2	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex21	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex22	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex23	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU_Ex2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
	

Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
HU_Ex22	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC- HU_Ex2	
Ratio H/L localized g4_NCC- HU_Ex2	
Ratio H/L nmods g4_NCC-HU_Ex2	
Ratio H/L variability [%] g4_NCC- HU Ex2	
Ratio H/L count g4_NCC-HU_Ex2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex2	
Occupancy L g4_NCC-HU_Ex2	
Occupancy H g4_NCC-HU_Ex2	
Ratio H/L g4_NCC-HU_Ex3	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex31	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex32	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex33	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU_Ex3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- HU_Ex33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC- HU_Ex3	
Ratio H/L localized g4_NCC- HU_Ex3	
Ratio H/L nmods g4_NCC-HU_Ex3	
Ratio H/L variability [%] g4_NCC- HU_Ex3	
Ratio H/L count g4_NCC-HU_Ex3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex3	
Occupancy L g4_NCC-HU_Ex3	
Occupancy H g4_NCC-HU_Ex3	
Ratio H/L g4_NCC-rosco_s1	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s11	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s12	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s13	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-rosco_s1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC-rosco_s1	
Ratio H/L localized g4_NCC-rosco_s1	
Ratio H/L nmods g4_NCC-rosco_s1	
Ratio H/L variability [%] g4_NCC-rosco_s1	
Ratio H/L count g4_NCC-rosco_s1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s1	
Occupancy L g4_NCC-rosco_s1	
Occupancy H g4_NCC-rosco_s1	
Ratio H/L g4_NCC-rosco_s2	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s21	The ratio between two heavy and light label partners.

Ratio H/L g4_NCC-rosco_s22	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s23	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-rosco_s2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC-rosco_s2	
Ratio H/L localized g4_NCC-rosco_s2	
Ratio H/L nmods g4_NCC-rosco_s2	
Ratio H/L variability [%] g4_NCC-rosco_s2	
Ratio H/L count g4_NCC-rosco_s2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s2	
Occupancy L g4_NCC-rosco_s2	
Occupancy H g4_NCC-rosco_s2	The ratio hatuses the beauty and light to be a set one
Ratio H/L g4_NCC-rosco_s3	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s31 Ratio H/L g4_NCC-rosco_s32	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s33	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-rosco_s3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco s3 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco s3 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC-rosco_s33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC-rosco_s3	
Ratio H/L localized g4_NCC-rosco_s3	
Ratio H/L nmods g4_NCC-rosco_s3	
Ratio H/L variability [%] g4_NCC-	
Ratio H/L count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s3	quantitation that are quantitied with the re quantity method.
Occupancy L g4_NCC-rosco_s3	
Occupancy H g4_NCC-rosco_s3	
Ratio H/L g4_NCC-TSA_Exp1	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp11	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp12	The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp13	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- TSA_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- TSA_Exp11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- TSA_Exp12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_NCC- TSA_Exp13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_NCC- TSA_Exp1	
Ratio H/L localized g4_NCC- TSA_Exp1	
Ratio H/L nmods g4_NCC- TSA_Exp1	
Ratio H/L variability [%] g4_NCC- TSA_Exp1	
Ratio H/L count g4_NCC-TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation.

TSA_Exp1 quantitation that are quantified with the re-quantity method. Ratio Hr. byte q4 .NCC-TSA_Exp1 Occupancy H. q4 .NCC-TSA_Exp1 Ratio Hr. Lyte, NCC-TSA_Exp2 Ratio Hr. Lyte, NCC-TSA_Exp3 Ratio Hr. Lyte, NCC-	Ratio H/L iso-count g4_NCC-	Number of redundant peptides (MS1 features) used for
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Ratio H/L count g4_NCC-TSA_Exp3 Ratio H/L iso-count g4_NCC- TSA_Exp3 Ratio H/L type g4_NCC-TSA_Exp3 Occupancy L g4_NCC-TSA_Exp3 Occupancy H g4_NCC-TSA_Exp3 Occupancy H g4_NCC-TSA_Exp3 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A3 Ratio H/L g4_PX183_A3 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized g4_PX183_A1 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Romalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Romalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Romalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Romalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Romalized ratio between two medium and light label partners.		
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TSA_Exp3 quantitation that are quantified with the re-quantify method. Ratio H/L type g4_NCC-TSA_Exp3 Occupancy L g4_NCC-TSA_Exp3 Occupancy H g4_NCC-TSA_Exp3 Ratio H/L g4_PX183_A The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A_2 Ratio H/L g4_PX183_A_3 Ratio H/L normalized g4_PX183_A Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Rormalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.	Ratio H/L count g4_NCC-TSA_Exp3	
Ratio H/L type g4_NCC-TSA_Exp3 Occupancy L g4_NCC-TSA_Exp3 Occupancy H g4_NCC-TSA_Exp3 Ratio H/L g4_PX183_A Ratio H/L g4_PX183_A1 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A2 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A3 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A3 Ratio H/L normalized g4_PX183_A Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Occupancy H g4_NCC-TSA_Exp3 Ratio H/L g4_PX183_A The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A1 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A2 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A3 Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A1 Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.	Ratio H/L type g4_NCC-TSA_Exp3	
Ratio H/L g4_PX183_A The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A1 The ratio between two heavy and light label partners. Ratio H/L g4_PX183_A2 Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized y4_PX183_A2 Ratio H/L normalized y5_PX183_A2 Normalized ratio between two medium and light label partners.	Occupancy L g4_NCC-TSA_Exp3	
Ratio H/L g4_PX183_A2 Ratio H/L g4_PX183_A2 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2	Occupancy H g4_NCC-TSA_Exp3	
Ratio H/L g4_PX183_A2 Ratio H/L g4_PX183_A3 Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_BX Ratio H/L	Ratio H/L g4_PX183_A	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_A3 Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. Normalized ratio between two medium and light label partners.	Ratio H/L g4_PX183_A1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_PX183_A Ratio H/L normalized g4_PX183_A Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L g4_PX183_A2	The ratio between two heavy and light label partners.
The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized Mormalized g7 atio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.	Ratio H/L g4_PX183_A3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A1 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized g4_PX183_A2 Ratio H/L normalized Mormalized The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Normalized ratio between two medium and light label partners.	Ratio H/L normalized g4_PX183_A	
Ratio H/L normalized Superior Normalized and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L normalized Normalized Normalized ratio between two medium and light label partners.		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
		Normalized ratio between two medium and light label partners.

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Ratio H/L unmod. pep. g4_PX183_A	
Ratio H/L localized g4_PX183_A	
Ratio H/L nmods g4_PX183_A	
Ratio H/L variability [%]	
g4_PX183_A	
Ratio H/L count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_A	
Occupancy L g4_PX183_A	
Occupancy H g4_PX183_A	
Ratio H/L g4_PX183_B	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_B1	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_B2	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_B3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_B	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q4 PX183 B 1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_B2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q4 PX183 B 3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX183_B	The modulation and total ratio population was stiffed to 1.
Ratio H/L localized g4_PX183_B	
Ratio H/L nmods g4_PX183_B	
Ratio H/L variability [%] g4_PX183_B	
Ratio H/L count g4_PX183_B	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_B	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_B	
Occupancy L g4_PX183_B	
Occupancy H g4_PX183_B	
Ratio H/L g4_PX183_C	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_C1	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_C2	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_C3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_C	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_C1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_C2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_C3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX183_C	
Ratio H/L localized g4_PX183_C	
Ratio H/L nmods g4_PX183_C	
Ratio H/L variability [%] g4_PX183_C	
Ratio H/L count g4_PX183_C	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_C	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_C	
Occupancy L g4_PX183_C	
Occupancy H g4_PX183_C	
Ratio H/L g4_PX183_D	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_D1	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_D2	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_D3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_D	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_D1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g4_PX183_D2	The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_D3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. q4 PX183 D	
Ratio H/L localized g4_PX183_D	
Ratio H/L nmods g4_PX183_D	
Ratio H/L variability [%] g4 PX183 D	
Ratio H/L count g4_PX183_D	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_D	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_D	
Occupancy L g4_PX183_D	
Occupancy H g4_PX183_D	
Ratio H/L g4_PX183_E	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_E1	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_E2	The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_E3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_E	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_E1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_E2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX183_E3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX183_E	
Ratio H/L localized g4_PX183_E	
Ratio H/L nmods g4_PX183_E	
Ratio H/L variability [%] g4_PX183_E	
Ratio H/L count g4_PX183_E	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_E	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX183_E	
Occupancy L g4_PX183_E	
Occupancy H g4_PX183_E	
Ratio H/L g4_PX441_E1	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E11	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E12	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E13	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E13	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_E1	
Ratio H/L localized g4_PX441_E1 Ratio H/L nmods g4_PX441_E1	
Ratio H/L variability [%] g4_PX441_E1	
Ratio H/L count g4_PX441_E1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
	Table 10 To quality motion.
Ratio H/L type g4_PX441_E1	
Occupancy L g4_PX441_E1	
Occupancy L g4_PX441_E1 Occupancy H g4_PX441_E1	The ratio between two heavy and light label partners
Occupancy L g4_PX441_E1 Occupancy H g4_PX441_E1 Ratio H/L g4_PX441_E2	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Occupancy L g4_PX441_E1 Occupancy H g4_PX441_E1	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.

Ratio H/L normalized g4_PX441_E2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q4 PX441 E2 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_E2	The median of the total ratio population was shinted to 1.
Ratio H/L localized g4_PX441_E2	
Ratio H/L nmods q4 PX441 E2	
Ratio H/L variability [%]	
Ratio H/L count g4_PX441_E2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E2	
Occupancy L g4_PX441_E2	
Occupancy H g4_PX441_E2	
Ratio H/L g4_PX441_E3	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E31	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E32	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E33	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E31	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E32	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E33	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_E3	
Ratio H/L localized g4_PX441_E3	
Ratio H/L nmods g4_PX441_E3	
Ratio H/L variability [%] g4_PX441_E3	
Ratio H/L count g4_PX441_E3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E3	
Occupancy L g4_PX441_E3	
Occupancy H g4_PX441_E3	
Ratio H/L g4_PX441_E4	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E41	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E42	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E43	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E41	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E42	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E43	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_E4	
Ratio H/L localized g4_PX441_E4	
Ratio H/L nmods g4_PX441_E4	
Ratio H/L variability [%] g4_PX441_E4	
Ratio H/L count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E4	
Occupancy L g4_PX441_E4	
Occupancy H g4_PX441_E4	
Ratio H/L g4_PX441_E5	The ratio between two heavy and light label partners.

Ratio H/L g4_PX441_E51	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E52	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E53 Ratio H/L normalized g4_PX441_E5	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E51	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q4 PX441 E5 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_E53	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_E5	The median of the total ratio population was shinted to 1.
Ratio H/L localized g4_PX441_E5	
Ratio H/L nmods g4_PX441_E5	
Ratio H/L variability [%]	
g4_PX441_E5 Ratio H/L count g4_PX441_E5	Number of redundant peptides (MS1 features) used for
0 =	quantitation.
Ratio H/L iso-count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E5	
Occupancy L g4_PX441_E5	
Occupancy H g4_PX441_E5 Ratio H/L g4_PX441_F1	The ratio between two heavy and light label partners.
Ratio H/L g4_FX441_F1 Ratio H/L g4_PX441_F11	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F12	The ratio between two heavy and light label partners. The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F13	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_F11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized q4 PX441 F1 2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_F1	
Ratio H/L localized g4_PX441_F1	
Ratio H/L nmods g4_PX441_F1	
Ratio H/L variability [%] g4_PX441_F1	
Ratio H/L count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F1	
Occupancy L g4_PX441_F1	
Occupancy H g4_PX441_F1	
Ratio H/L g4_PX441_F2	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F21	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F22	The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F23	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_F21	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_F22	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g4_PX441_F23	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L unmod. pep. g4_PX441_F2	
Ratio H/L localized g4_PX441_F2	
Ratio H/L nmods g4_PX441_F2 Ratio H/L variability [%]	
g4_PX441_F2	Number of redundant postides (MS4 feetures) used for
Ratio H/L count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F2	

Cocupancy H 44 PX441 F3 Ratio HVL 49 PX441 F3 Ratio HVL 40 PX441 F3 Ratio HVL 50 PX441 F4 Ratio HVL 50 PX441 F	O	
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Ratio H/L iso-count g4_PX441_F4 Ratio H/L type g4_PX441_F4 Occupancy L g4_PX441_F4 Occupancy H g4_PX441_F4 Ratio H/L g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L variability [%]		
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Occupancy L g4_PX441_F4 Occupancy H g4_PX441_F4 Ratio H/L g4_PX441_F5 Ratio H/L g4_PX441_F5 Ratio H/L g4_PX441_F51 The ratio between two heavy and light label partners. Ratio H/L g4_PX441_F52 The ratio between two heavy and light label partners. Ratio H/L g4_PX441_F53 Ratio H/L normalized g4_PX441_F5 Ratio H/L variability [%]	Ratio H/L iso-count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
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Ratio H/L g4_PX441_F53 Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F51 Ratio H/L normalized g4_PX441_F51 Ratio H/L normalized g4_PX441_F52 Ratio H/L normalized g4_PX441_F53 Ratio H/L normalized g4_PX441_F53 Ratio H/L normalized g4_PX441_F53 Ratio H/L normalized g4_PX441_F5 Ratio H/L unmod. pep. g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L variability [%]	Ratio H/L g4_PX441_F51	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L normalized g4_PX441_F51 Ratio H/L normalized g4_PX441_F52 Ratio H/L normalized g4_PX441_F52 Ratio H/L normalized g4_PX441_F53 Ratio H/L normalized g4_PX441_F53 Ratio H/L normalized g4_PX441_F53 Ratio H/L normalized g4_PX441_F5 Ratio H/L variability [%]	Ratio H/L g4_PX441_F52	The ratio between two heavy and light label partners.
The median of the total ratio population was shifted to 1. Ratio H/L normalized g4_PX441_F51 Ratio H/L normalized g4_PX441_F52 Ratio H/L normalized g4_PX441_F52 Ratio H/L normalized g4_PX441_F53 Ratio H/L unmod. pep. g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L normalized g4_PX441_F5 Ratio H/L variability [%]	Ratio H/L g4_PX441_F53	The ratio between two heavy and light label partners.
g4_PX441_F51The median of the total ratio population was shifted to 1.Ratio H/L normalized g4_PX441_F52Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.Ratio H/L normalized g4_PX441_F53Normalized ratio between two medium and light label partners. 	Ratio H/L normalized g4_PX441_F5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g4_PX441_F52The median of the total ratio population was shifted to 1.Ratio H/L normalized g4_PX441_F53Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.Ratio H/L unmod. pep. g4_PX441_F5g4_PX441_F5Ratio H/L localized g4_PX441_F5Ratio H/L nmods g4_PX441_F5Ratio H/L variability [%]		The median of the total ratio population was shifted to 1.
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g4_PX441_F5 Ratio H/L localized g4_PX441_F5 Ratio H/L nmods g4_PX441_F5 Ratio H/L variability [%]		
Ratio H/L nmods g4_PX441_F5 Ratio H/L variability [%]	Ratio H/L unmod. pep. g4_PX441_F5	
Ratio H/L variability [%]	Ratio H/L localized g4_PX441_F5	
	Ratio H/L nmods g4_PX441_F5	
	Ratio H/L variability [%] g4_PX441_F5	

Ratio H/L count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F5	
Occupancy L g4_PX441_F5	
Occupancy H g4_PX441_F5	
Intensity	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L	
Ratio mod/base H	
Intensity g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_AL	
Ratio mod/base H g1_GK1_Chromatin_AL	
Intensity g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_CPT	
Ratio mod/base H g1_GK1_Chromatin_CPT	
Intensity g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_CR	
Ratio mod/base H g1_GK1_Chromatin_CR	
Intensity g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_HepHek	
Ratio mod/base H g1_GK1_Chromatin_HepHek	
Intensity g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_hiIR	
Ratio mod/base H g1_GK1_Chromatin_hiIR	

Intensity g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_loIR	
Ratio mod/base H g1_GK1_Chromatin_loIR	
Intensity g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_mH2A_1	
Ratio mod/base H g1_GK1_Chromatin_mH2A_1	
Intensity g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_mH2A_2	
Ratio mod/base H g1_GK1_Chromatin_mH2A_2	
Intensity g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_mH2A_3	
Ratio mod/base H g1_GK1_Chromatin_mH2A_3	
Intensity g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_TNFa_1	
Ratio mod/base H g1_GK1_Chromatin_TNFa_1	
Intensity g1_GK1_Chromatin_TNFa_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_TNFa_2	
Ratio mod/base H g1_GK1_Chromatin_TNFa_2	
Intensity g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_TNFa_3	
Ratio mod/base H	
g1_GK1_Chromatin_TNFa_3 Intensity g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW10_110506	
Ratio mod/base H g1_KW10_110506	
Intensity g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW10_131126	
Ratio mod/base H g1_KW10_131126	
Intensity g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW10_140117	
Ratio mod/base H g1_KW10_140117	
Intensity g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW11_130125	
Ratio mod/base H q1 KW11 130125	
Intensity g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW11_140104_nE	
Ratio mod/base H g1_KW11_140104_nE	
Intensity g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW11_140104_wE	
Ratio mod/base H g1_KW11_140104_wE	

Intensity g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_130317	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW12_130317	
Ratio mod/base H q1 KW12 130317	
Intensity g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW12_131223	
Ratio mod/base H g1_KW12_131223	
Intensity g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW13_130328	
Ratio mod/base H g1_KW13_130328	
Intensity g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW14_130317	
Ratio mod/base H g1_KW14_130317	
Intensity g1_KW15_130317	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW15_130317	
Ratio mod/base H g1_KW15_130317	
Intensity g1_KW17_130319	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW17_130319	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW17_130319	
Ratio mod/base H g1_KW17_130319	
Intensity g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW8_120517	inned to the heavy tabel partition.
Ratio mod/base H g1_KW8_120517	
Intensity g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW8_131126	
Ratio mod/base H g1_KW8_131126	
Intensity g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW8_140117	
Ratio mod/base H g1_KW8_140117	
Intensity g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW9_120425	
Ratio mod/base H g1_KW9_120425	
Intensity g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_KW9_120510	
Ratio mod/base H g1_KW9_120510	
Intensity g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H1	
Ratio mod/base H g1_PX1194_H1	
Intensity g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H10	
Ratio mod/base H g1_PX1194_H10	
Intensity g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H11 Ratio mod/base H g1_PX1194_H11	
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Intensity g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H12	
Ratio mod/base H g1_PX1194_H12	
Intensity g1_PX1194_H2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H2	
Ratio mod/base H g1_PX1194_H2	
Intensity g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H3	
Ratio mod/base H g1_PX1194_H3	
Intensity g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H4	
Ratio mod/base H g1_PX1194_H4	
Intensity g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H5	
Ratio mod/base H g1_PX1194_H5	
Intensity g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H6	
Ratio mod/base H g1_PX1194_H6	
Intensity g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H7	
Ratio mod/base H g1_PX1194_H7	
Intensity g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H8	·
Ratio mod/base H g1_PX1194_H8	
Intensity g1_PX1194_H9	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_H9	
Ratio mod/base H g1_PX1194_H9	
Intensity g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa1_1	
Ratio mod/base H g1_PX1194_PCa1_1	
Intensity g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa1_2	
Ratio mod/base H g1_PX1194_PCa1_2	
Intensity g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa2_1	
Ratio mod/base H g1_PX1194_PCa2_1	
Intensity g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa2_2	
Ratio mod/base H g1_PX1194_PCa2_2	
Intensity g1_PX1194_PCa2_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa2_3	
Ratio mod/base H g1_PX1194_PCa2_3	
Intensity g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa3_1	
Ratio mod/base H g1_PX1194_PCa3_1	
Intensity g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa3_2	
Ratio mod/base H g1_PX1194_PCa3_2	
Intensity g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa3_3	
Ratio mod/base H g1_PX1194_PCa3_3	
Intensity g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa4_1	
Ratio mod/base H g1_PX1194_PCa4_1	
Intensity g1_PX1194_PCa4_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa4_2	
Ratio mod/base H g1_PX1194_PCa4_2	
Intensity g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa4_3	
Ratio mod/base H g1_PX1194_PCa4_3	
Intensity g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa5_1	

Ratio mod/base H	
g1_PX1194_PCa5_1 Intensity g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
Intensity g1_FA1194_FGa5_2	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa5_2	
Ratio mod/base H	
g1_PX1194_PCa5_2 Intensity g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
illicitistly gr_i X1154_i Oa5_5	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa5_3	
Ratio mod/base H g1_PX1194_PCa5_3	
Intensity g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a
	labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa6_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa6_1	
Ratio mod/base H g1_PX1194_PCa6_1	
Intensity g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1194_PCa7_1	
Ratio mod/base H g1_PX1194_PCa7_1	
Intensity g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18486	
Ratio mod/base H g1_PX1406_GM18486	
Intensity g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18498	7 1
Ratio mod/base H g1_PX1406_GM18498	
Intensity g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18499	
Ratio mod/base H g1_PX1406_GM18499	
Intensity g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18501	
Ratio mod/base H q1 PX1406 GM18501	
Intensity g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18502	
Ratio mod/base H g1_PX1406_GM18502	
Intensity g1_PX1406_GM18504	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18504	
Ratio mod/base H g1_PX1406_GM18504	
Intensity g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18505	
Ratio mod/base H q1 PX1406 GM18505	
Intensity g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18507	
Ratio mod/base H g1_PX1406_GM18507	
Intensity g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18508	

Ratio mod/base H	
g1_PX1406_GM18508 Intensity g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g1_PX1406_GM18510	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity H g1_PX1406_GM18510	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1 PX1406 GM18510	illined to the fleavy label partiel.
Ratio mod/base H	
g1_PX1406_GM18510 Intensity g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18511	,
Ratio mod/base H g1_PX1406_GM18511	
Intensity g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18516	
Ratio mod/base H g1_PX1406_GM18516	
Intensity g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18517	
Ratio mod/base H g1_PX1406_GM18517	
Intensity g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18519	
Ratio mod/base H g1_PX1406_GM18519	
Intensity g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18520	
Ratio mod/base H g1_PX1406_GM18520	
Intensity g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18522	
Ratio mod/base H g1_PX1406_GM18522	
Intensity g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18523	
Ratio mod/base H g1_PX1406_GM18523	
Intensity g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18852	
Ratio mod/base H g1_PX1406_GM18852	
Intensity g1_PX1406_GM18855	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18855	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18855	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18855	
Ratio mod/base H g1_PX1406_GM18855	
Intensity g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18858	
Ratio mod/base H q1 PX1406 GM18858	
Intensity g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18861	
Ratio mod/base H g1_PX1406_GM18861	
Intensity g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18862	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18862	

Ratio mod/base H	
g1_PX1406_GM18862 Intensity g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
Intensity 91_1 X1400_GW10070	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18870	
Ratio mod/base H	
g1_PX1406_GM18870 Intensity g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
intensity gr_1 X1400_GW10071	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18871	
Ratio mod/base H g1_PX1406_GM18871	
Intensity g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18907	
Ratio mod/base H g1_PX1406_GM18907	
Intensity g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18909	
Ratio mod/base H q1 PX1406 GM18909	
Intensity g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18912	
Ratio mod/base H g1_PX1406_GM18912	
Intensity g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18913	minos to the heavy labor partitor.
Ratio mod/base H g1_PX1406_GM18913	
Intensity g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM18916	
Ratio mod/base H g1_PX1406_GM18916	
Intensity g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19092	
Ratio mod/base H q1 PX1406 GM19092	
Intensity g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19093	
Ratio mod/base H g1_PX1406_GM19093	
Intensity g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19098	
Ratio mod/base H g1_PX1406_GM19098	
Intensity g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19099	
Ratio mod/base H g1_PX1406_GM19099	
Intensity g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19101	
Ratio mod/base H g1_PX1406_GM19101	
Intensity g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19102	

Ratio mod/base H g1_PX1406_GM19102	
Intensity g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g1_PX1406_GM19108	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19108	inned to the neary label parties.
Ratio mod/base H	
g1_PX1406_GM19108 Intensity g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L q1 PX1406 GM19114	
Ratio mod/base H g1_PX1406_GM19114	
Intensity g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19116	
Ratio mod/base H g1_PX1406_GM19116	
Intensity g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19119	
Ratio mod/base H q1 PX1406 GM19119	
Intensity g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19127	
Ratio mod/base H g1_PX1406_GM19127	
Intensity g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19128	
Ratio mod/base H g1_PX1406_GM19128	
Intensity g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19130	
Ratio mod/base H g1_PX1406_GM19130	
Intensity g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19131	
Ratio mod/base H q1 PX1406 GM19131	
Intensity g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19137	
Ratio mod/base H g1_PX1406_GM19137	
Intensity g1_PX1406_GM19138	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19138	
Ratio mod/base H g1_PX1406_GM19138	
Intensity g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19140	
Ratio mod/base H q1 PX1406 GM19140	
Intensity g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19143	
Ratio mod/base H g1_PX1406_GM19143	
Intensity g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19144	

Ratio mod/base H g1_PX1406_GM19144	
Intensity g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic potentials in the label eluster.
Intensity L g1_PX1406_GM19147	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19147	inned to the neary table parallel.
Ratio mod/base H	
g1_PX1406_GM19147 Intensity g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L q1 PX1406 GM19152	
Ratio mod/base H g1_PX1406_GM19152	
Intensity g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19153	
Ratio mod/base H g1_PX1406_GM19153	
Intensity g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19160	
Ratio mod/base H q1 PX1406 GM19160	
Intensity g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19172	
Ratio mod/base H g1_PX1406_GM19172	
Intensity g1_PX1406_GM19192	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19192	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19192	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19192	
Ratio mod/base H g1_PX1406_GM19192	
Intensity g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19193	
Ratio mod/base H g1_PX1406_GM19193	
Intensity g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19200	
Ratio mod/base H g1_PX1406_GM19200	
Intensity g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19203	
Ratio mod/base H g1_PX1406_GM19203	
Intensity g1_PX1406_GM19204	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19204	
Ratio mod/base H g1_PX1406_GM19204	
Intensity g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19207	
Ratio mod/base H q1 PX1406 GM19207	
Intensity g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19209	
Ratio mod/base H g1_PX1406_GM19209	
Intensity g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19222	

Ratio mod/base H g1_PX1406_GM19222	
Intensity g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX1406_GM19257	
Ratio mod/base H g1_PX1406_GM19257	
Intensity g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX151_Rep1	
Ratio mod/base H g1_PX151_Rep1	
Intensity g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX151_Rep2	
Ratio mod/base H g1_PX151_Rep2	
Intensity g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX151_Rep3	
Ratio mod/base H g1_PX151_Rep3	
Intensity g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1143-1	
Ratio mod/base H g1_PX309_HCC1143-1	
Intensity g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1143-2	, ,
Ratio mod/base H g1_PX309_HCC1143-2	
Intensity g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1143-3	

Ratio mod/base H	
g1_PX309_HCC1143-3	
Intensity g1_PX309_HCC1599-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1599-1	
Ratio mod/base H	
g1_PX309_HCC1599-1 Intensity g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1599-2	
Ratio mod/base H g1_PX309_HCC1599-2	
Intensity g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1599-3	
Ratio mod/base H g1_PX309_HCC1599-3	
Intensity g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1937-1	
Ratio mod/base H g1_PX309_HCC1937-1	
Intensity g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1937-2	
Ratio mod/base H g1_PX309_HCC1937-2	
Intensity g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC1937-3	
Ratio mod/base H g1_PX309_HCC1937-3	
Intensity g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC202-1	
Ratio mod/base H g1_PX309_HCC202-1	
Intensity g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC202-2	
Ratio mod/base H g1_PX309_HCC202-2	
Intensity g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC202-3	
Ratio mod/base H g1_PX309_HCC202-3	
Intensity g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC2218-1	
Ratio mod/base H g1_PX309_HCC2218-1	
Intensity g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC2218-2	
Ratio mod/base H q1 PX309 HCC2218-2	
Intensity g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HCC2218-3	
Ratio mod/base H g1_PX309_HCC2218-3	
Intensity g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMEC1-1	

Ratio mod/base H	
g1_PX309_HMEC1-1 Intensity g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity L g1_PX309_HMEC1-2	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMEC1-2	mined to the fieavy label partiel.
Ratio mod/base H	
g1_PX309_HMEC1-2 Intensity g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMEC1-3	
Ratio mod/base H g1_PX309_HMEC1-3	
Intensity g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMEC2-1	
Ratio mod/base H g1_PX309_HMEC2-1	
Intensity g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMEC2-2	
Ratio mod/base H q1 PX309 HMEC2-2	
Intensity g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMEC2-3	
Ratio mod/base H g1_PX309_HMEC2-3	
Intensity g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMTS1-1	
Ratio mod/base H g1_PX309_HMTS1-1	
Intensity g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMTS1-2	
Ratio mod/base H g1_PX309_HMTS1-2	
Intensity g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_HMTS1-3	
Ratio mod/base H g1_PX309_HMTS1-3	
Intensity g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MCF10a-1	
Ratio mod/base H g1_PX309_MCF10a-1	
Intensity g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MCF10a-2	
Ratio mod/base H g1_PX309_MCF10a-2	
Intensity g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MCF10a-3	
Ratio mod/base H g1_PX309_MCF10a-3	
Intensity g1_PX309_MDAMB453-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MDAMB453-1	
Ratio mod/base H g1_PX309_MDAMB453-1	
Intensity g1_PX309_MDAMB453-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MDAMB453-2	

Ratio mod/base H g1_PX309_MDAMB453-2	
Intensity g1_PX309_MDAMB453-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MDAMB453-3	
Ratio mod/base H g1_PX309_MDAMB453-3	
Intensity g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MFM223-1	
Ratio mod/base H g1_PX309_MFM223-1	
Intensity g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MFM223-2	
Ratio mod/base H g1_PX309_MFM223-2	
Intensity g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX309_MFM223-3	
Ratio mod/base H g1_PX309_MFM223-3	
Intensity g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_0h_1 Ratio mod/base H g1_PX359_0h_1	
Intensity g1_PX359_0h_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_0h_2	
Ratio mod/base H g1_PX359_0h_2	Cummed up of trooted less Courant (VIO) of all instants destroit
Intensity g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Ratio mod/base L g1_PX359_0h_3	
Ratio mod/base H g1_PX359_0h_3	
Intensity g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_BSA_1	
Ratio mod/base H g1_PX359_BSA_1	
Intensity g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_BSA_2	
Ratio mod/base H g1_PX359_BSA_2	
Intensity g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_BSA_3	
Ratio mod/base H g1_PX359_BSA_3	
Intensity g1_PX359_FN_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_FN_1	
Ratio mod/base H g1_PX359_FN_1	
Intensity g1_PX359_FN_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_FN_2	
Ratio mod/base H g1_PX359_FN_2	
Intensity g1_PX359_FN_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_FN_3	
Ratio mod/base H g1_PX359_FN_3	
Intensity g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_GFR_1	

Ratio mod/base H g1_PX359_GFR_1	
Intensity g1_PX359_GFR_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_GFR_2	
Ratio mod/base H g1_PX359_GFR_2	
Intensity g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_GFR_3	
Ratio mod/base H g1_PX359_GFR_3	
Intensity g1_PX359_LAM_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_LAM_1	
Ratio mod/base H g1_PX359_LAM_1	
Intensity g1_PX359_LAM_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_LAM_2	
Ratio mod/base H g1_PX359_LAM_2	
Intensity g1_PX359_LAM_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_LAM_3	
Ratio mod/base H g1_PX359_LAM_3	
Intensity g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 12h_1	
Ratio mod/base H g1_PX359_Matr	
Intensity g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity H g1_PX359_Matr 12h_2	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Ratio mod/base L g1_PX359_Matr	linked to the heavy label partner.
12h_2	
Ratio mod/base H g1_PX359_Matr 12h_2	
Intensity g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 12h_3	
Ratio mod/base H g1_PX359_Matr 12h 3	
Intensity g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 24h_1	
Ratio mod/base H g1_PX359_Matr 24h_1	
Intensity g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 24h 2	
Ratio mod/base H g1_PX359_Matr 24h_2	
Intensity g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 24h_3	
Ratio mod/base H g1_PX359_Matr 24h_3	
Intensity g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 30h_1	
Ratio mod/base H g1_PX359_Matr 30h_1	
Intensity g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 30h_2	

Ratio mod/base H g1_PX359_Matr	
30h_2	
Intensity g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr 30h_3	
Ratio mod/base H g1_PX359_Matr 30h_3	
Intensity g1_PX359_Matr dil_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr dil 1	
Ratio mod/base H g1_PX359_Matr	
Intensity g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr dil 2	
Ratio mod/base H g1_PX359_Matr	
Intensity g1_PX359_Matr dil_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX359_Matr dil_3	
Ratio mod/base H g1_PX359_Matr dil_3	
Intensity g1_PX419_human_18507	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX419_human_18507	
Ratio mod/base H g1_PX419_human_18507	
Intensity g1_PX419_human_18516	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18516	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX419_human_18516	
Ratio mod/base H g1_PX419_human_18516	
Intensity g1_PX419_human_19193	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX419_human_19193	
Ratio mod/base H g1_PX419_human_19193	
Intensity g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX419_human_19204	
Ratio mod/base H g1_PX419_human_19204	
Intensity g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX438_Xeno092	
Ratio mod/base H g1_PX438_Xeno092	
Intensity g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX438_Xeno441	
Ratio mod/base H g1_PX438_Xeno441	
Intensity g1_PX438_Xeno561	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno561	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno561	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX438_Xeno561	
Ratio mod/base H g1_PX438_Xeno561	
Intensity g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_PX438_Xeno691	
Ratio mod/base H g1_PX438_Xeno691	
Intensity g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX058_expA Ratio mod/base H g2_PX058_expA	

Г	
Intensity g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX058_expB	
Ratio mod/base H g2_PX058_expB	
Intensity g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX058_expC	
Ratio mod/base H g2_PX058_expC	
Intensity g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX058_expD	
Ratio mod/base H g2_PX058_expD	
Intensity g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX058_expE	
Ratio mod/base H g2_PX058_expE	
Intensity g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX058_expF	
Ratio mod/base H g2_PX058_expF	
Intensity g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX089_Rep1	
Ratio mod/base H g2_PX089_Rep1	
Intensity g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX089_Rep2	
Ratio mod/base H g2_PX089_Rep2	
Intensity g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g2_PX537_exp14 rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX537_exp14 rep1 20h	illined to the neavy laber partner.
Ratio mod/base H g2_PX537_exp14 rep1 20h	
Intensity g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep1 6h	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX537_exp14 rep1 6h	
Ratio mod/base H g2_PX537_exp14 rep1 6h	
Intensity g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX537_exp14 rep2 20h	
Ratio mod/base H g2_PX537_exp14 rep2 20h	
Intensity g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX537_exp14 rep2 6h	
Ratio mod/base H g2_PX537_exp14 rep2 6h	
Intensity g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX537_exp14 rep3 20h	
Ratio mod/base H g2_PX537_exp14 rep3 20h	
Intensity g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g2_PX537_exp14 rep3 6h	
Ratio mod/base H g2_PX537_exp14 rep3 6h	
Intensity g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_A_TSA_1	

Detic mod/hoos M	
Ratio mod/base M g3_GK1_Chromatin_A_TSA_1	
Ratio mod/base H g3_GK1_Chromatin_A_TSA_1	
Intensity g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3 GK1 Chromatin A TSA 2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_A_TSA_2	
Ratio mod/base M g3_GK1_Chromatin_A_TSA_2	
Ratio mod/base H q3 GK1 Chromatin A TSA 2	
Intensity g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_CC_1	
Ratio mod/base M g3_GK1_Chromatin_CC_1	
Ratio mod/base H g3_GK1_Chromatin_CC_1	
Intensity g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_CC_2	
Ratio mod/base M g3_GK1_Chromatin_CC_2	
Ratio mod/base H g3_GK1_Chromatin_CC_2	
Intensity g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_EHT_1	
Ratio mod/base M g3_GK1_Chromatin_EHT_1	
Ratio mod/base H g3_GK1_Chromatin_EHT_1	
Intensity g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Ratio mod/base L g3_GK1_Chromatin_EHT_2	
Ratio mod/base M g3_GK1_Chromatin_EHT_2	
Ratio mod/base H g3_GK1_Chromatin_EHT_2	
Intensity g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_EHT_3	
Ratio mod/base M g3_GK1_Chromatin_EHT_3	
Ratio mod/base H g3_GK1_Chromatin_EHT_3	
Intensity g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_EHT_4	
Ratio mod/base M g3_GK1_Chromatin_EHT_4	
Ratio mod/base H g3_GK1_Chromatin_EHT_4	
Intensity g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_EHT_5	
Ratio mod/base M g3_GK1_Chromatin_EHT_5	
Ratio mod/base H g3_GK1_Chromatin_EHT_5	
Intensity g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_EHT_6	
Ratio mod/base M g3_GK1_Chromatin_EHT_6	
Ratio mod/base H g3_GK1_Chromatin_EHT_6	
Intensity g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.

Binked to the heavy label partner.	Intensity H	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK1_Chromatin_mH2A_4_5 g3_GK3_ET Summed up eXtracted ion Current (XIC) of all isotopic cluster associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic cluster intensity all gap and the intensity of all the isotopic cluster intensity M g3_KW35_ET Summed up eXtracted for Current (XIC) of the isotopic cluster intensity H g3_KW35_ET Summed up eXtracted ion Current (XIC) of the isotopic cluster intensity H g3_KW35_ET Ratio modbase M g3_KW35_ET Ratio modbase M g3_KW35_ET Intensity L g3_KW35_ET_2 Intensity L g3_KW35_ET_2 Intensity M g3_KW35_ET_2 Ratio modbase M g3_KW35_ET_2 Intensity M g3_KW35_ET_2 Ratio modbase M g3_KW35_ET_2 Intensity M g3_KW35_ET_2 Intensity M g3_KW35_ET_2 Intensity M g3_KW35_ET_2 Intensity M g3_KW35_ET_2	g3_GK1_Chromatin_mH2A_4_5	
Section Chromatin, mH2A, 4, 5 Ratio mod/base H g3, GHT, Chromatin, mH2A, 4, 5 Intensity g3, KW35_ET Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a isobeled experiment this is the total intensity of all the isotopic cluster intensity of all the isotopic cluster linked to the light label partner. Intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Intensity H g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity all partner. Ratio mod/base L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked ion the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked ion the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked ion the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity all partner. Intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity all partner. Ratio mod/base L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity all the isotopic cluster linked to the intensity all partner. Ratio mod/base L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the intensity all partner. Intensity L g3, KW35_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the linked ion the intensity	Ratio mod/base L g3_GK1_Chromatin_mH2A_4_5	
Summed up extracted ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_ET	Ratio mod/base M g3_GK1_Chromatin_mH2A_4_5	
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Ratio mod/base H g3_KW35_nE_2 Intensity g3_KW35_nE_2 Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Ratio mod/base L g3_KW35_nE_2 Ratio mod/base M g3_KW35_rot_ET Intensity L	Ratio mod/base L g3_KW35_nE	
Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Ratio mod/base L g3_KW35_nE_2 Ratio mod/base M g3_KW35_nE_2 Intensity G3_KW35_rot_ET Intensity L g3_KW35_rot_ET Intensity L g3_KW35_rot_ET Intensity M g3_KW35_rot_ET	Ratio mod/base M g3_KW35_nE	
associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity H g3_KW35_nE_2 Intensity M g3_KW35_nE_2 Ratio mod/base L g3_KW35_nE_2 Ratio mod/base H g3_KW35_nE_2 Intensity g3_KW35_rot_ET Intensity L g3_KW35_rot_ET Intensity L g3_KW35_rot_ET Intensity L g3_KW35_rot_ET Intensity M g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Ratio mod/base H g3_KW35_nE	
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linked to the medium label partner.	Intensity L g3_KW35_nE_2	
linked to the heavy label partner. Ratio mod/base L g3_KW35_nE_2 Ratio mod/base M g3_KW35_nE_2 Ratio mod/base H g3_KW35_nE_2 Intensity g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Intensity M g3_KW35_nE_2	
Ratio mod/base M g3_KW35_nE_2 Ratio mod/base H g3_KW35_nE_2 Intensity g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Intensity H g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base H g3_KW35_nE_2 Intensity g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Ratio mod/base L g3_KW35_nE_2	
Intensity g3_KW35_rot_ET Summed up eXtracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_rot_ET Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Ratio mod/base M g3_KW35_nE_2	
associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster. Intensity L g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Ratio mod/base H g3_KW35_nE_2	
Intensity L g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Intensity g3_KW35_rot_ET	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
Intensity M g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Intensity L g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity H g3_KW35_rot_ET Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner. Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Intensity M g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Ratio mod/base L g3_KW35_rot_ET Ratio mod/base M g3_KW35_rot_ET Ratio mod/base H	Intensity H g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
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	Ratio mod/base M g3_KW35_rot_ET	
g3_KW35_rot_ET	Ratio mod/base H g3_KW35_rot_ET	

Intensity of KW25 wE	Summed up attracted lon Current (VIC) of all instance allegans
Intensity g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_KW35_wE	
Ratio mod/base M g3_KW35_wE	
Ratio mod/base H g3_KW35_wE	
Intensity g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_KW35_wE_2	
Ratio mod/base M g3_KW35_wE_2	
Ratio mod/base H g3_KW35_wE_2	0
Intensity g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX328_Diff3_Exp1	
Ratio mod/base M g3_PX328_Diff3_Exp1	
Ratio mod/base H g3_PX328_Diff3_Exp1	
Intensity g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX328_Diff3_Exp2	
Ratio mod/base M g3_PX328_Diff3_Exp2	
Ratio mod/base H g3_PX328_Diff3_Exp2	
Intensity g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX328_Diff4_Exp1	
Ratio mod/base M g3_PX328_Diff4_Exp1	
Ratio mod/base H g3_PX328_Diff4_Exp1	
Intensity g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity M g3_PX328_Diff4_Exp2	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
, 0 = = = 1	linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX328_Diff4_Exp2	
Ratio mod/base M g3_PX328_Diff4_Exp2	
Ratio mod/base H q3 PX328 Diff4 Exp2	
Intensity g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX328_Diff5_Exp1	initiod to the floary face partition
Ratio mod/base M	
g3_PX328_Diff5_Exp1 Ratio mod/base H_	
g3_PX328_Diff5_Exp1 Intensity g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
IIIIGIISILY GS_I X320_DIII3_LXP2	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX328_Diff5_Exp2	
Ratio mod/base M g3_PX328_Diff5_Exp2	
Ratio mod/base H q3 PX328 Diff5 Exp2	
Intensity g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX597_A1_Spr	
Ratio mod/base M g3_PX597_A1_Spr	
Ratio mod/base H g3_PX597_A1_Spr	
Intensity g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
· · · ·	linked to the heavy label partner.
Ratio mod/base L g3_PX597_A2_Spr	
Ratio mod/base L	

Intensity g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX597_A3_Spr	
Ratio mod/base M g3_PX597_A3_Spr	
Ratio mod/base H	
g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
Intensity g3_PX597_B1_Spr	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX597_B1_Spr	mined to the risery has or parametri
Ratio mod/base M	
g3_PX597_B1_Spr Ratio mod/base H	
g3_PX597_B1_Spr	
Intensity g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B2_Spr	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX597_B2_Spr	
Ratio mod/base M g3_PX597_B2_Spr	
Ratio mod/base H g3_PX597_B2_Spr	
Intensity g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_PX597_B3_Spr	
Ratio mod/base M g3_PX597_B3_Spr	
Ratio mod/base H g3_PX597_B3_Spr	
Intensity g4_NCC_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC_A	, , , , , , , , , , , , , , , , , , , ,
Ratio mod/base H g4_NCC_A	
Intensity g4_NCC_B	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g4_NCC_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC_B	
Ratio mod/base H g4_NCC_B	
Intensity g4_NCC_C	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC_C	
Ratio mod/base H g4_NCC_C	
Intensity g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC-CPT_s1	
Ratio mod/base H g4_NCC-CPT_s1	
Intensity g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC-CPT_s2	
Ratio mod/base H g4_NCC-CPT_s2	
Intensity g4_NCC-CPT_s3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC-CPT_s3	
Ratio mod/base H g4_NCC-CPT_s3	
Intensity g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC-HU_Ex1	
Ratio mod/base H g4_NCC- HU_Ex1	
Intensity g4_NCC-HU_Ex2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC-HU_Ex2	,
Ratio mod/base H g4_NCC- HU_Ex2	
Intensity g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC-HU_Ex3	

Ratio mod/base H g4_NCC-	
HU_Ex3 Intensity g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC- rosco_s1	mined to the neavy laber partition.
Ratio mod/base H g4_NCC-rosco_s1	
Intensity g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC- rosco s2	mined to the risery raser parametri
Ratio mod/base H g4_NCC- rosco s2	
Intensity g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC- rosco s3	,
Ratio mod/base H g4_NCC-rosco_s3	
Intensity g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC- TSA_Exp1	
Ratio mod/base H g4_NCC- TSA_Exp1	
Intensity g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC- TSA_Exp2	
Ratio mod/base H g4_NCC- TSA_Exp2	
Intensity g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_NCC- TSA_Exp3	, and the state of
Ratio mod/base H g4_NCC- TSA_Exp3	
Intensity g4_PX183_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX183_A	
Ratio mod/base H g4_PX183_A	
Intensity g4_PX183_B	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX183_B	
Ratio mod/base H g4_PX183_B	
Intensity g4_PX183_C	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX183_C	
Ratio mod/base H g4_PX183_C	
Intensity g4_PX183_D	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX183_D	
Ratio mod/base H g4_PX183_D	
Intensity g4_PX183_E	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX183_E	
Ratio mod/base H g4_PX183_E	
Intensity g4_PX441_E1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_E1	
Ratio mod/base H g4_PX441_E1	
Intensity g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_E2	
Ratio mod/base H g4_PX441_E2	
Intensity g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_E3	
Ratio mod/base H g4_PX441_E3	

Intensity g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters
microny gr_i X441_E4	associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_E4	
Ratio mod/base H g4_PX441_E4	
Intensity g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_E5	
Ratio mod/base H g4_PX441_E5	
Intensity g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_F1	
Ratio mod/base H g4_PX441_F1	
Intensity g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_F2	
Ratio mod/base H g4_PX441_F2	
Intensity g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_F3	
Ratio mod/base H g4_PX441_F3	
Intensity g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_F4	
Ratio mod/base H g4_PX441_F4	
Intensity g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g4_PX441_F5 Ratio mod/base H g4_PX441_F5	
Reverse	When marked with '+', this particular peptide was found to be
IVEAGISE	part of a protein derived from the reversed part of the protein sequence database. These should be removed for further data analysis.
Potential contaminant	When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.

id	A unique (consecutive) identifier for each row in the site table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs	The identifier of the protein-group this peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple id's can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Positions	The positions of the modifications in the protein amino acid sequence.
Position	The position of the modification in the protein amino acid sequence.
Peptide IDs	Identifier(s) of the associated peptide sequence(s) summary, which can be found in the file 'peptides.txt'.
Mod. peptide IDs	Identifier(s) of the associated peptide sequence(s) summary, which can be found in the file 'modificationSpecificPeptides.txt'.
Evidence IDs	Identifier(s) for analyzed peptide evidence associated with the protein group referenced against the evidences table.
MS/MS IDs	The identifiers of the MS/MS scans identifying this peptide, referenced against the msms table.
Best localization evidence ID	
Best localization MS/MS ID	
Best localization raw file	
Best localization scan number	
Best score evidence ID	
Best score MS/MS ID	
Best score raw file	
Best score scan number	
Best PEP evidence ID	
Best PEP MS/MS ID	
Best PEP raw file	
Best PEP scan number	

Protein groups

The Protein Groups table contains information on the identified proteins in the processed raw-files. Each single row contains the group of proteins that could be reconstructed from a set of peptides.

Name	Separator	Description
Protein IDs		Identifier(s) of protein(s) contained in the protein group. They are sorted by number of identified peptides in descending order.
Majority protein IDs		These are the IDs of those proteins that have at least half of the peptides that the leading protein has.
Peptide counts (all)		Number of peptides associated with each protein in protein group, occuring in the order as the protein IDs occur in the 'Protein IDs' column. Here distinct peptide sequences are counted. Modified forms or different charges are counted as one peptide.
Peptide counts (razor+unique)		Number of peptides associated with each protein in protein group, occuring in the order as the protein IDs occur in the 'Protein IDs' column. Here distinct peptide sequences are counted. Modified forms or different charges are counted as one peptide.
Peptide counts (unique)		Number of peptides associated with each protein in protein group, occuring in the order as the protein IDs occur in the 'Protein IDs' column. Here distinct peptide sequences are counted. Modified forms or different charges are counted as one peptide.
Protein names		Name(s) of protein(s) contained within the group.
Gene names		Name(s) of the gene(s) associated to the protein(s) contained within the group.
Fasta headers		Fasta headers(s) of protein(s) contained within the group.
Number of proteins		Number of proteins contained within the group. This corresponds to the number of entries in the colum 'Protein IDs'.
Peptides		The total number of peptide sequences associated with the protein group (i.e. for all the proteins in the group).
Razor + unique peptides		The total number of razor + unique peptides associated with the protein group (i.e. these peptides are shared with another protein group).
Unique peptides		The total number of unique peptides associated with the protein group (i.e. these peptides are not shared with another protein group).
Peptides g1_GK1_Chromatin_AL		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL
Peptides g1_GK1_Chromatin_CPT		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT
Peptides g1_GK1_Chromatin_CR		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CR
Peptides g1_GK1_Chromatin_HepHek		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_HepHek
Peptides g1_GK1_Chromatin_hilR		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_hilR
Peptides g1_GK1_Chromatin_loIR		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_loIR
Peptides g1_GK1_Chromatin_mH2A_1		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_1
Peptides g1_GK1_Chromatin_mH2A_2		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_2
Peptides g1_GK1_Chromatin_mH2A_3		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_3
Peptides g1_GK1_Chromatin_TNFa_1		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_1
Peptides g1_GK1_Chromatin_TNFa_2		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_2
Peptides g1_GK1_Chromatin_TNFa_3		Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_3
Peptides g1_KW10_110506		Number of peptides (distinct peptide sequences) in experiment g1_KW10_110506
Peptides g1_KW10_131126		Number of peptides (distinct peptide sequences) in experiment g1_KW10_131126
Peptides g1_KW10_140117		Number of peptides (distinct peptide sequences) in experiment g1_KW10_140117
Peptides g1_KW11_130125		Number of peptides (distinct peptide sequences) in experiment g1_KW11_130125
Peptides g1_KW11_140104_nE		Number of peptides (distinct peptide sequences) in experiment g1_KW11_140104_nE

Peptides g1_KW11_140104_wE	Number of peptides (distinct peptide sequences) in experiment g1_KW11_140104_wE
Peptides g1_KW12_130317	Number of peptides (distinct peptide sequences) in experiment g1_KW12_130317
Peptides g1_KW12_131223	Number of peptides (distinct peptide sequences) in experiment q1 KW12 131223
Peptides g1_KW13_130328	Number of peptides (distinct peptide sequences) in experiment g1_KW13_130328
Peptides g1_KW14_130317	Number of peptides (distinct peptide sequences) in experiment q1 KW14 130317
Peptides g1_KW15_130317	Number of peptides (distinct peptide sequences) in experiment q1 KW15 130317
Peptides g1_KW17_130319	Number of peptides (distinct peptide sequences) in experiment g1_KW17_130319
Peptides g1_KW8_120517	Number of peptides (distinct peptide sequences) in experiment g1_KW8_120517
Peptides g1_KW8_131126	Number of peptides (distinct peptide sequences) in experiment q1 KW8 131126
Peptides g1_KW8_140117	Number of peptides (distinct peptide sequences) in experiment g1_KW8_140117
Peptides g1_KW9_120425	Number of peptides (distinct peptide sequences) in experiment q1 KW9 120425
Peptides g1_KW9_120510	Number of peptides (distinct peptide sequences) in experiment g1 KW9 120510
Peptides g1_PX1194_H1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H1
Peptides g1_PX1194_H10	Number of peptides (distinct peptide sequences) in experiment g1 PX1194 H10
Peptides g1_PX1194_H11	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H11
Peptides g1_PX1194_H12	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H12
Peptides g1_PX1194_H2	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H2
Peptides g1_PX1194_H3	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H3
Peptides g1_PX1194_H4	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H4
Peptides g1_PX1194_H5	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H5
Peptides g1_PX1194_H6	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H6
Peptides g1_PX1194_H7	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H7
Peptides g1_PX1194_H8	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H8
Peptides g1_PX1194_H9	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_H9
Peptides g1_PX1194_PCa1_1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa1_1
Peptides g1_PX1194_PCa1_2	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa1_2
Peptides g1_PX1194_PCa2_1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa2_1
Peptides g1_PX1194_PCa2_2	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa2_2
Peptides g1_PX1194_PCa2_3	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa2_3
Peptides g1_PX1194_PCa3_1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa3_1
Peptides g1_PX1194_PCa3_2	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa3_2
Peptides g1_PX1194_PCa3_3	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa3_3
Peptides g1_PX1194_PCa4_1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa4_1
Peptides g1_PX1194_PCa4_2	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa4_2
Peptides g1_PX1194_PCa4_3	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa4_3
Peptides g1_PX1194_PCa5_1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa5_1
Peptides g1_PX1194_PCa5_2	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa5_2
Peptides g1_PX1194_PCa5_3	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa5_3

Peptides g1_PX1194_PCa6_1	Number of peptides (distinct peptide sequences) in experiment
	g1_PX1194_PCa6_1
Peptides g1_PX1194_PCa7_1	Number of peptides (distinct peptide sequences) in experiment g1_PX1194_PCa7_1
Peptides g1_PX1406_GM18486	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18486
Peptides g1_PX1406_GM18498	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18498
Peptides g1_PX1406_GM18499	Number of peptides (distinct peptide sequences) in experiment g1 PX1406 GM18499
Peptides g1_PX1406_GM18501	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18501
Peptides g1_PX1406_GM18502	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18502
Peptides g1_PX1406_GM18504	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18504
Peptides g1_PX1406_GM18505	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18505
Peptides g1_PX1406_GM18507	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18507
Peptides g1_PX1406_GM18508	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18508
Peptides g1_PX1406_GM18510	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18510
Peptides g1_PX1406_GM18511	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18516	g1_PX1406_GM18511 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18517	g1_PX1406_GM18516 Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18517
Peptides g1_PX1406_GM18519	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18520	g1_PX1406_GM18519 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18522	g1_PX1406_GM18520 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18523	g1_PX1406_GM18522 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18852	g1_PX1406_GM18523 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18855	g1_PX1406_GM18852 Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18855
Peptides g1_PX1406_GM18858	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18858
Peptides g1_PX1406_GM18861	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18861
Peptides g1_PX1406_GM18862	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM18862
Peptides g1_PX1406_GM18870	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18870
Peptides g1_PX1406_GM18871	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18871
Peptides g1_PX1406_GM18907	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18907
Peptides g1_PX1406_GM18909	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18909
Peptides g1_PX1406_GM18912	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM18912
Peptides g1_PX1406_GM18913	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM18916	g1_PX1406_GM18913 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM19092	g1_PX1406_GM18916 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM19093	g1_PX1406_GM19092 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM19098	g1_PX1406_GM19093 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM19099	g1_PX1406_GM19098 Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19099
Peptides g1_PX1406_GM19101	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM19102	g1_PX1406_GM19101 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX1406_GM19108	g1_PX1406_GM19102 Number of peptides (distinct peptide sequences) in experiment
	g1_PX1406_GM19108

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Peptides g1_PX1406_GM19114	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19114
Peptides g1_PX1406_GM19116	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19116
Peptides g1_PX1406_GM19119	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19119
Peptides g1_PX1406_GM19127	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19127
Peptides g1_PX1406_GM19128	Number of peptides (distinct peptide sequences) in experiment a1 PX1406 GM19128
Peptides g1_PX1406_GM19130	Number of peptides (distinct peptide sequences) in experiment g1 PX1406 GM19130
Peptides g1_PX1406_GM19131	Number of peptides (distinct peptide sequences) in experiment g1 PX1406 GM19131
Peptides g1_PX1406_GM19137	Number of peptides (distinct peptide sequences) in experiment g1 PX1406 GM19137
Peptides g1_PX1406_GM19138	Number of peptides (distinct peptide sequences) in experiment g1 PX1406 GM19138
Peptides g1_PX1406_GM19140	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19140
Peptides g1_PX1406_GM19143	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19143
Peptides g1_PX1406_GM19144	Number of peptides (distinct peptide sequences) in experiment at PX1406 GM19144
Peptides g1_PX1406_GM19147	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19147
Peptides g1_PX1406_GM19152	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19152
Peptides g1_PX1406_GM19153	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19153
Peptides g1_PX1406_GM19160	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19160
Peptides g1_PX1406_GM19172	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19172
Peptides g1_PX1406_GM19192	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19192
Peptides g1_PX1406_GM19193	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19193
Peptides g1_PX1406_GM19200	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19200
Peptides g1_PX1406_GM19203	Number of peptides (distinct peptide sequences) in experiment q1 PX1406 GM19203
Peptides g1_PX1406_GM19204	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19204
Peptides g1_PX1406_GM19207	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19207
Peptides g1_PX1406_GM19209	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19209
Peptides g1_PX1406_GM19222	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19222
Peptides g1_PX1406_GM19257	Number of peptides (distinct peptide sequences) in experiment g1_PX1406_GM19257
Peptides g1_PX151_Rep1	Number of peptides (distinct peptide sequences) in experiment q1 PX151 Rep1
Peptides g1_PX151_Rep2	Number of peptides (distinct peptide sequences) in experiment g1_PX151_Rep2
Peptides g1_PX151_Rep3	Number of peptides (distinct peptide sequences) in experiment g1_PX151_Rep3
Peptides g1_PX309_HCC1143-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-1
Peptides g1_PX309_HCC1143-2	Number of peptides (distinct peptide sequences) in experiment q1 PX309 HCC1143-2
Peptides g1_PX309_HCC1143-3	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-3
Peptides g1_PX309_HCC1599-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC1599-1
Peptides g1_PX309_HCC1599-2	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC1599-2
Peptides g1_PX309_HCC1599-3	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC1599-3
Peptides g1_PX309_HCC1937-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC1937-1
Peptides g1_PX309_HCC1937-2	Number of peptides (distinct peptide sequences) in experiment q1 PX309 HCC1937-2
Peptides g1_PX309_HCC1937-3	Number of peptides (distinct peptide sequences) in experiment q1 PX309 HCC1937-3

Peptides g1_PX309_HCC202-1	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_HCC202-2	g1_PX309_HCC202-1 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_HCC202-3	g1_PX309_HCC202-2 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_HCC2218-1	g1_PX309_HCC202-3 Number of peptides (distinct peptide sequences) in experiment
	g1_PX309_HCC2218-1
Peptides g1_PX309_HCC2218-2	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-2
Peptides g1_PX309_HCC2218-3	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-3
Peptides g1_PX309_HMEC1-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-1
Peptides g1_PX309_HMEC1-2	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-2
Peptides g1_PX309_HMEC1-3	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-3
Peptides g1_PX309_HMEC2-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-1
Peptides g1_PX309_HMEC2-2	Number of peptides (distinct peptide sequences) in experiment a1 PX309 HMEC2-2
Peptides g1_PX309_HMEC2-3	Number of peptides (distinct peptide sequences) in experiment g1 PX309 HMEC2-3
Peptides g1_PX309_HMTS1-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_HMTS1-1
Peptides g1_PX309_HMTS1-2	Number of peptides (distinct peptide sequences) in experiment q1 PX309 HMTS1-2
Peptides g1_PX309_HMTS1-3	Number of peptides (distinct peptide sequences) in experiment q1 PX309 HMTS1-3
Peptides g1_PX309_MCF10a-1	Number of peptides (distinct peptide sequences) in experiment g1_PX309_MCF10a-1
Peptides g1_PX309_MCF10a-2	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_MCF10a-3	g1_PX309_MCF10a-2 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_MDAMB453-1	g1_PX309_MCF10a-3 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_MDAMB453-2	g1_PX309_MDAMB453-1 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_MDAMB453-3	g1_PX309_MDAMB453-2 Number of peptides (distinct peptide sequences) in experiment g1 PX309 MDAMB453-3
Peptides g1_PX309_MFM223-1	Number of peptides (distinct peptide sequences) in experiment g1 PX309 MFM223-1
Peptides g1_PX309_MFM223-2	Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX309_MFM223-3	g1_PX309_MFM223-2 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX359_0h_1	g1_PX309_MFM223-3 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX359_0h_2	g1_PX359_0h_1 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX359_0h_3	g1_PX359_0h_2 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX359_BSA_1	g1_PX359_0h_3 Number of peptides (distinct peptide sequences) in experiment
Peptides g1_PX359_BSA_2	g1_PX359_BSA_1 Number of peptides (distinct peptide sequences) in experiment
	g1_PX359_BSA_2
Peptides g1_PX359_BSA_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_BSA_3
Peptides g1_PX359_FN_1	Number of peptides (distinct peptide sequences) in experiment g1_PX359_FN_1
Peptides g1_PX359_FN_2	Number of peptides (distinct peptide sequences) in experiment g1_PX359_FN_2
Peptides g1_PX359_FN_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_FN_3
Peptides g1_PX359_GFR_1	Number of peptides (distinct peptide sequences) in experiment g1_PX359_GFR_1
Peptides g1_PX359_GFR_2	Number of peptides (distinct peptide sequences) in experiment g1_PX359_GFR_2
Peptides g1_PX359_GFR_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_GFR_3
Peptides g1_PX359_LAM_1	Number of peptides (distinct peptide sequences) in experiment g1_PX359_LAM_1
Peptides g1_PX359_LAM_2	Number of peptides (distinct peptide sequences) in experiment g1 PX359 LAM 2
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Peptides g1_PX359_LAM_3	Number of peptides (distinct peptide sequences) in experiment
	g1_PX359_LAM_3
Peptides g1_PX359_Matr 12h_1	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 12h_1
Peptides g1_PX359_Matr 12h_2	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 12h_2
Peptides g1_PX359_Matr 12h_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 12h_3
Peptides g1_PX359_Matr 24h_1	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 24h_1
Peptides g1_PX359_Matr 24h_2	Number of peptides (distinct peptide sequences) in experiment q1 PX359 Matr 24h 2
Peptides g1_PX359_Matr 24h_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 24h_3
Peptides g1_PX359_Matr 30h_1	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_1
Peptides g1_PX359_Matr 30h_2	Number of peptides (distinct peptide sequences) in experiment q1 PX359 Matr 30h 2
Peptides g1_PX359_Matr 30h_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_3
Peptides g1_PX359_Matr dil_1	Number of peptides (distinct peptide sequences) in experiment g1 PX359 Matr dil 1
Peptides g1_PX359_Matr dil_2	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_2
Peptides g1_PX359_Matr dil_3	Number of peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_3
Peptides g1_PX419_human_18507	Number of peptides (distinct peptide sequences) in experiment g1_PX419_human_18507
Peptides g1_PX419_human_18516	Number of peptides (distinct peptide sequences) in experiment g1_PX419_human_18516
Peptides g1_PX419_human_19193	Number of peptides (distinct peptide sequences) in experiment g1_PX419_human_19193
Peptides g1_PX419_human_19204	Number of peptides (distinct peptide sequences) in experiment g1_PX419_human_19204
Peptides g1_PX438_Xeno092	Number of peptides (distinct peptide sequences) in experiment g1_PX438_Xeno092
Peptides g1_PX438_Xeno441	Number of peptides (distinct peptide sequences) in experiment g1_PX438_Xeno441
Peptides g1_PX438_Xeno561	Number of peptides (distinct peptide sequences) in experiment g1_PX438_Xeno561
Peptides g1_PX438_Xeno691	Number of peptides (distinct peptide sequences) in experiment g1_PX438_Xeno691
Peptides g2_PX058_expA	Number of peptides (distinct peptide sequences) in experiment g2_PX058_expA
Peptides g2_PX058_expB	Number of peptides (distinct peptide sequences) in experiment g2_PX058_expB
Peptides g2_PX058_expC	Number of peptides (distinct peptide sequences) in experiment g2_PX058_expC
Peptides g2_PX058_expD	Number of peptides (distinct peptide sequences) in experiment g2_PX058_expD
Peptides g2_PX058_expE	Number of peptides (distinct peptide sequences) in experiment q2_PX058_expE
Peptides g2_PX058_expF	Number of peptides (distinct peptide sequences) in experiment g2_PX058_expF
Peptides g2_PX089_Rep1	Number of peptides (distinct peptide sequences) in experiment g2_PX089_Rep1
Peptides g2_PX089_Rep2	Number of peptides (distinct peptide sequences) in experiment g2_PX089_Rep2
Peptides g2_PX537_exp14 rep1 20h	Number of peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep1 20h
Peptides g2_PX537_exp14 rep1 6h	Number of peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep1 6h
Peptides g2_PX537_exp14 rep2 20h	Number of peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep2 20h
Peptides g2_PX537_exp14 rep2 6h	Number of peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep2 6h
Peptides g2_PX537_exp14 rep3 20h	Number of peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep3 20h
Peptides g2_PX537_exp14 rep3 6h	Number of peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep3 6h
Peptides g3_GK1_Chromatin_A_TSA_1	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_A_TSA_1
Peptides g3_GK1_Chromatin_A_TSA_2	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_A_TSA_2
Peptides g3_GK1_Chromatin_CC_1	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_CC_1
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Peptides g3_GK1_Chromatin_CC_2	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_CC_2
Peptides g3_GK1_Chromatin_EHT_1	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_1
Peptides g3_GK1_Chromatin_EHT_2	Number of peptides (distinct peptide sequences) in experiment q3 GK1 Chromatin EHT 2
Peptides g3_GK1_Chromatin_EHT_3	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_3
Peptides g3_GK1_Chromatin_EHT_4	Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_4
Peptides	Number of peptides (distinct peptide sequences) in experiment a3 GK1 Chromatin EHT 5
g3_GK1_Chromatin_EHT_5 Peptides	Number of peptides (distinct peptide sequences) in experiment
g3_GK1_Chromatin_EHT_6 Peptides	g3_GK1_Chromatin_EHT_6 Number of peptides (distinct peptide sequences) in experiment
g3_GK1_Chromatin_mH2A_4_5 Peptides g3_KW35_ET	g3_GK1_Chromatin_mH2A_4_5 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_KW35_ET_2	g3_KW35_ET Number of peptides (distinct peptide sequences) in experiment
Peptides g3_KW35_nE	g3_KW35_ET_2 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_KW35_nE_2	g3_KW35_nE Number of peptides (distinct peptide sequences) in experiment
Peptides g3_KW35_rot_ET	g3_KW35_nE_2 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_KW35_wE	g3_KW35_rot_ET Number of peptides (distinct peptide sequences) in experiment
Peptides g3_KW35_wE_2	g3_KW35_wE Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX328_Diff3_Exp1	g3_KW35_wE_2 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX328_Diff3_Exp2	g3_PX328_Diff3_Exp1 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX328_Diff4_Exp1	g3_PX328_Diff3_Exp2 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX328_Diff4_Exp2	g3_PX328_Diff4_Exp1 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX328_Diff5_Exp1	g3_PX328_Diff4_Exp2 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX328_Diff5_Exp2	g3_PX328_Diff5_Exp1 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX597_A1_Spr	g3_PX328_Diff5_Exp2 Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX597_A2_Spr	g3_PX597_A1_Spr Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX597_A3_Spr	g3_PX597_A2_Spr Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX597_B1_Spr	g3_PX597_A3_Spr Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX597_B2_Spr	g3_PX597_B1_Spr Number of peptides (distinct peptide sequences) in experiment
Peptides g3_PX597_B3_Spr	g3_PX597_B2_Spr Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC_A	g3_PX597_B3_Spr Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC_B	g4_NCC_A Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC_C	g4_NCC_B Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-CPT_s1	g4_NCC_C Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-CPT_s2	g4_NCC-CPT_s1 Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-CPT_s3	g4_NCC-CPT_s2 Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-HU_Ex1	g4_NCC-CPT_s3 Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-HU_Ex2	g4_NCC-HU_Ex1 Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-HU_Ex3	g4_NCC-HU_Ex2 Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-rosco_s1	g4_NCC-HU_Ex3 Number of peptides (distinct peptide sequences) in experiment
Peptides g4_NCC-rosco_s2	g4_NCC-rosco_s1 Number of peptides (distinct peptide sequences) in experiment
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Peptides g4_NCCTSA_Exp2 Peptides g4_NCCTSA_Exp2 Peptides g4_NCCTSA_Exp2 Peptides g4_NCCTSA_Exp3 Peptides g4_NCTSA_Exp3 Peptides	Peptides g4_NCC-rosco_s3	Number of peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s3
Poptides g4_NCCTSA_Exp2 Poptides g4_NCCTSA_Exp3 Poptides g4_NCCTSA_Exp3 Poptides g4_PX183_A Poptides g4_PX183_A Poptides g4_PX183_A Poptides g4_PX183_B Poptides g4_PX183_D Poptides g4_PX	Peptides g4_NCC-TSA_Exp1	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX183_A Peptides g4_PX183_A Peptides g4_PX183_B Peptides g4_PX183_B Peptides g4_PX183_B Peptides g4_PX183_C Peptides g4_PX183_C Peptides g4_PX183_D Peptides g4_PX183_E Peptides g4_PX184_E1 Peptides g4_PX184_E2 Peptides g4_PX184_E3 Peptides g4_PX184_E3 Peptides g4_PX184_E3 Peptides g4_PX184_E3 Peptides g4_PX184_E4 Peptides g4_PX184_E5 Peptides g4_PX184_E6 Number of peptides sequences) in experiment g4_PX184_E7 Peptides g4_PX18_E7 Peptides g6_E7 Number of peptides sequences) in experiment g4_PX18_E7 Peptides g6_E7 Number of peptides sequences) in experiment g6_E7 Peptides g6_E7 Number of peptides sequences) in experiment g6_E7 Peptides g7 Peptides g7 Peptides Peptid	Peptides g4_NCC-TSA_Exp2	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX183_A Peptides g4_PX183_B Peptides g4_PX183_B Peptides g4_PX183_C Peptides g4_PX183_C Peptides g4_PX183_C Peptides g4_PX183_C Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_E Peptides g4_PX141_E1 Peptides g4_EX14_E1 Peptid	Peptides g4_NCC-TSA_Exp3	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX183_B Peptides g4_PX183_C Peptides g4_PX183_C Peptides g4_PX183_C Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_E Peptides g4_PX184_E1 Peptides g4_PX184_E1 Peptides g4_PX184_E2 Reptides g4_PX184_E2 Reptides g4_PX18_E Peptides g4_PX18_E Peptides g4_PX18_E Peptides g4_PX18_E Peptides g4_PX18_E3 Reptides g4_PX18_E3 Reptides g4_PX18_E3 Reptides g4_PX18_E3 Reptides g4_PX18_E3 Reptides g4_PX18_E4 Reptides g4_PX18_E5 Reptides g4_PX18_E5 Reptides g4_PX18_E6 Reptides g4_PX18_E6 Reptides g4_PX18_E6 Reptides g4_PX18_E7 Reptid	Peptides g4_PX183_A	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX183_C Peptides g4_PX183_D Peptides g4_PX183_D Peptides g4_PX183_E Peptides g4_PX183_E Peptides g4_PX183_E Peptides g4_PX183_E Peptides g4_PX41_E1 Peptides g4_PX41_E1 Peptides g4_PX41_E2 Peptides g4_PX41_E3 Peptides g4_PX41_E3 Peptides g4_PX41_E3 Peptides g4_PX41_E3 Peptides g4_PX41_E4 Peptides g4_PX41_E3 Peptides g4_PX41_E4 Peptides g4_PX41_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E5 Peptides g4_PX41_E5 Peptides g4_PX41_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E5 Peptides g4_PX41_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E6 Peptides g4_PX41_E6 Peptides g4_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E6 Peptides g4_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g4_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g6_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g6_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g6_PX41_E6 Peptides g4_PX41_E6 Number of peptides (distinct peptide sequences) in experiment g6_PX41_E6 Number of peptides (distinct peptides sequences) in experiment g6_PX41_E6 Number of peptides (distinct peptides sequences) in experiment g6_PX41_E6 Number of peptides (distinct peptid	Peptides g4_PX183_B	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX183_D Number of peptides (distinct peptide sequences) in experiment g4_PX183_D Peptides g4_PX183_E Number of peptides (distinct peptide sequences) in experiment g4_PX183_E Peptides g4_PX441_E1 Number of peptides (distinct peptide sequences) in experiment g4_PX411_E1 Peptides g4_PX441_E2 Number of peptides (distinct peptide sequences) in experiment g4_PX411_E1 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX411_E2 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E6 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_F1 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F1 Peptides g4_PX441_F2 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F1 Peptides g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F2 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Number of peptides g4_PX441_F4 Number of peptides	Peptides g4_PX183_C	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_E1 Peptides g4_PX441_E2 Peptides g4_PX441_E3 Peptides g4_PX441_E3 Peptides g4_PX441_E3 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E3 Peptides g4_PX441_E3 Peptides g4_PX441_E4 Peptides g4_PX441_E4 Peptides g4_PX441_E4 Peptides g4_PX441_E4 Peptides g4_PX441_E6 Peptides g4_PX441_E6 Peptides g4_PX441_E6 Peptides g4_PX441_E7 Peptides g4_PX441_E6 Peptides g4_PX441_E7 Peptides g4_PX441_E7 Peptides g4_PX441_E7 Peptides g4_PX441_E7 Peptides g4_PX441_F1 Peptides g4_PX441_F2 Peptides g4_PX441_F2 Peptides g4_PX441_F2 Peptides g4_PX441_F3 Peptides g4_PX441_F	Peptides g4_PX183_D	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_E1 Peptides g4_PX441_E2 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E4 Peptides g4_PX441_E5 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E1 Peptides g4_PX441_E1 Peptides g4_PX441_E1 Peptides g4_PX441_E2 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_E3 Peptides g4_PX441_E3 Peptides g4_PX441_E3 Peptides g4_PX441_E4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_A1 Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CR Razor + unique peptides Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT Razor + unique peptides Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_NEA Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_NEA Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_Mil2_1 Number of razor + unique peptides (distinct peptide sequence	Peptides g4_PX183_E	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_E2 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E2 Peptides g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_F1 Peptides g4_PX441_F2 Peptides g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Peptides g4_PX441_F3 Peptides g4_PX441_F3 Peptides g4_PX441_F4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Peptides g4_PX441_F4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F4 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F4 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F4 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL Razor + unique peptides Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT Razor + unique peptides Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT Razor + unique peptides Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_PTA Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_PTA Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_Inplied Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_Inplied Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_C	Peptides g4_PX441_E1	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_E3 Peptides g4_PX441_E4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E5 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_F1 Peptides g4_PX441_F2 Peptides g4_PX441_F2 Peptides g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F2 Peptides g4_PX441_F3 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Peptides g4_PX441_F4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F4 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin. At sequences) in experiment g1_GK1_Chromatin. CPT Razor + unique peptides g1_GK1_Chromatin. CPT Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin. CPT Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin. PRP Razor + unique peptides g1_GK1_Chromatin. HepHek Razor + unique peptides g1_GK1_Chromatin. MiR Razor + unique peptides g1_GK1_Chromatin. MiR2_1 Razor + unique peptides g1_GK1_Chromatin. MiR2_2 Razor + unique peptides g1_GK1_Chromatin. MiR2_3 Number of razor + unique peptides (distinct peptide sequences)	Peptides g4_PX441_E2	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_E4 Peptides g4_PX441_E5 Peptides g4_PX441_E5 Peptides g4_PX441_E5 Peptides g4_PX441_E5 Peptides g4_PX441_E5 Peptides g4_PX441_E1 Peptides g4_PX441_E1 Peptides g4_PX441_E1 Peptides g4_PX441_E2 Peptides g4_PX441_E3 Peptides g4_PX441_E4 Peptides g4_PX441_E4 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E3 Peptides g4_PX441_E5 Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL Razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_DilR Razor + unique peptides g1_GK1_Chromatin_DilR Razor + unique peptides g1_GK1_Chromatin_DilR Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_DilR Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHex Razor + unique peptides g1_G	Peptides g4_PX441_E3	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment d4_PX441_E5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_E1 Peptides g4_PX441_F2	Peptides g4_PX441_E4	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_F1 Peptides g4_PX441_F2 Peptides g4_PX441_F3 Peptides g4_PX441_F3 Peptides g4_PX441_F3 Peptides g4_PX441_F3 Peptides g4_PX441_F4 Peptides g4_PX441_F4 Peptides g4_PX441_F5 Razor + unique peptides g1_GK1_Chromatin_AL Razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_H2A Razor + unique peptides g1_GK1_Chromatin_TH2A Razor + unique peptides g1_GK1_Chromatin_TNFa_2 Razor + unique peptides g1_GK1_Chromatin_TNFa_3 Razor + unique peptide	Peptides g4_PX441_E5	Number of peptides (distinct peptide sequences) in experiment
Peptides g4_PX441_F3 Peptides g4_PX441_F4 Peptides g4_PX441_F4 Peptides g4_PX441_F5 Razor + unique peptides g1_GK1_Chromatin_AL Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_Inle Razor + unique peptides g1_GK1_Chroma	Peptides g4_PX441_F1	Number of peptides (distinct peptide sequences) in experiment q4 PX441 F1
Peptides g4_PX441_F3 Peptides g4_PX441_F4 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F3 Peptides g4_PX441_F5 Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g4_PX441_F4 Peptides g4_PX441_F5 Razor + unique peptides g1_GK1_Chromatin_AL Razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_DPT Razor + unique peptides g1_GK1_Chromatin_HPHek Razor + unique peptides g1_GK1_Chromatin_HPHek Razor + unique peptides g1_GK1_Chromatin_HilR Razor + unique peptides g1_GK1_Chromatin_HilR Razor + unique peptides g1_GK1_Chromatin_HIR Razor + unique peptides g1_GK1_Chromatin_TNFa_1 Sequences) in experiment g1_GK1_Chromatin_HIR_A Sequences) in experiment g1_GK1_Chromatin_ThFa_3 Razor + unique peptides g	Peptides g4_PX441_F2	Number of peptides (distinct peptide sequences) in experiment q4 PX441 F2
Peptides g4_PX441_F5 Number of peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL Razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_hilR Razor + unique	Peptides g4_PX441_F3	Number of peptides (distinct peptide sequences) in experiment
Razor + unique peptides Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL	Peptides g4_PX441_F4	Number of peptides (distinct peptide sequences) in experiment
Razor + unique peptides g1_GK1_Chromatin_AL sequences) in experiment g1_GK1_Chromatin_AL sequences) in experiment g1_GK1_Chromatin_AL Number of razor + unique peptides g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_HepHek Number of razor + unique peptides (distinct peptide g1_GK1_Chromatin_HepHek sequences) in experiment g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_HepHek sequences) in experiment g1_GK1_Chromatin_HepHek Number of razor + unique peptides (distinct peptide g1_GK1_Chromatin_HepHek sequences) in experiment g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_lolR Razor + unique peptides g1_GK1_Chromatin_lolR Razor + unique peptides g1_GK1_Chromatin_lolR Razor + unique peptides g1_GK1_Chromatin_mH2A_1 sequences) in experiment g1_GK1_Chromatin_lolR Razor + unique peptides g1_GK1_Chromatin_mH2A_1 sequences) in experiment g1_GK1_Chromatin_mH2A_1 sequences) in experiment g1_GK1_Chromatin_mH2A_1 sequences) in experiment g1_GK1_Chromatin_mH2A_2 Razor + unique peptides g1_GK1_Chromatin_mH2A_3 Razor + unique peptides g1_GK1_Chromatin_TNFa_1 sequences) in experiment g1_GK1_Chromatin_mH2A_3 Razor + unique peptides g1_GK1_Chromatin_TNFa_1 sequences) in experiment g1_GK1_Chromatin_TNFa_1 sequences) in experiment g1_GK1_Chromatin_TNFa_1 sequences) in experiment g1_GK1_Chromatin_TNFa_1 sequences) in experiment g1_GK1_Chromatin_TNFa_1 Razor + unique peptides g1_GK1_Chromatin_TNFa_3 Razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_2 Razor + unique peptides g1_GK1_Chromatin_TNFa_3 Razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_3 Razor + unique peptides g1_KW10_110506 Razor + unique peptides g1_KW10_110506 Razor + unique pe	Peptides g4_PX441_F5	Number of peptides (distinct peptide sequences) in experiment g4_PX441_F5
g1_GK1_Chromatin_CPT Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_CR Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_HepHek Razor + unique peptides g1_GK1_Chromatin_hilR Razor + unique peptides g1_GK1_Chromatin_hilR Razor + unique peptides g1_GK1_Chromatin_hilR Razor + unique peptides g1_GK1_Chromatin_lolR Razor + unique peptides g1_GK1_Chromatin_mH2A_1 Razor + unique peptides g1_GK1_Chromatin_mH2A_1 Razor + unique peptides g1_GK1_Chromatin_mH2A_2 Razor + unique peptides g1_GK1_Chromatin_mH2A_2 Razor + unique peptides g1_GK1_Chromatin_mH2A_2 Razor + unique peptides g1_GK1_Chromatin_mH2A_3 Razor + unique peptides g1_GK1_Chromatin_TNFa_1 Razor + unique peptides g1_GK1_Chromatin_TNFa_1 Razor + unique peptides g1_GK1_Chromatin_TNFa_1 Razor + unique peptides g1_GK1_Chromatin_TNFa_2 Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_2 Razor + unique peptides g1_KW10_110506 Razor + unique peptides g1_KW10_110506		
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g1_PX1406_GM18498 Razor + unique peptides	sequences) in experiment g1_PX1406_GM18498 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM18499 Razor + unique peptides	sequences) in experiment g1_PX1406_GM18499 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM18501 Razor + unique peptides	sequences) in experiment g1_PX1406_GM18501 Number of razor + unique peptides (distinct peptide
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Razor + unique peptides g1_PX1406_GM18510	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18510
Razor + unique peptides g1_PX1406_GM18511	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18511
Razor + unique peptides g1_PX1406_GM18516	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18516
Razor + unique peptides g1_PX1406_GM18517	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18517
Razor + unique peptides g1_PX1406_GM18519	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18519
Razor + unique peptides g1_PX1406_GM18520	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18520
Razor + unique peptides g1_PX1406_GM18522	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18522
Razor + unique peptides g1_PX1406_GM18523	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18523
Razor + unique peptides g1_PX1406_GM18852	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18852
Razor + unique peptides g1_PX1406_GM18855	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18855
Razor + unique peptides q1 PX1406 GM18858	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18858
Razor + unique peptides g1_PX1406_GM18861	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18861
Razor + unique peptides g1_PX1406_GM18862	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18862
Razor + unique peptides g1_PX1406_GM18870	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18870
Razor + unique peptides g1_PX1406_GM18871	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18871
Razor + unique peptides g1_PX1406_GM18907	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18907
Razor + unique peptides g1_PX1406_GM18909	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18909
Razor + unique peptides g1_PX1406_GM18912	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18912
Razor + unique peptides g1_PX1406_GM18913	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18913
Razor + unique peptides q1 PX1406 GM18916	Number of razor + unique peptides (distinct peptide sequences) in experiment q1 PX1406 GM18916
Razor + unique peptides g1_PX1406_GM19092	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19092
Razor + unique peptides g1_PX1406_GM19093	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19093
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19098
Razor + unique peptides g1_PX1406_GM19099	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19099
Razor + unique peptides g1_PX1406_GM19101	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19101
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19102
Razor + unique peptides g1_PX1406_GM19108	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19108
Razor + unique peptides g1_PX1406_GM19114	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19114
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19116
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Razor + unique peptides g1_PX1406_GM19119	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19119
Razor + unique peptides g1_PX1406_GM19127	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19127
Razor + unique peptides q1 PX1406 GM19128	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19128
Razor + unique peptides g1_PX1406_GM19130	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19130
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19131 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19131 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19137 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19137 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19138 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19138 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19140 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19140 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19143 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19143 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19144 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19144 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19147 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19147 Number of razor + unique peptides (distinct peptide
g1_PX1406_GM19152 Razor + unique peptides	sequences) in experiment g1_PX1406_GM19152
g1_PX1406_GM19153	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19153
Razor + unique peptides g1_PX1406_GM19160	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19160
Razor + unique peptides g1_PX1406_GM19172	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19172
Razor + unique peptides g1_PX1406_GM19192	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19192
Razor + unique peptides g1_PX1406_GM19193	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19193
Razor + unique peptides g1_PX1406_GM19200	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19200
Razor + unique peptides g1_PX1406_GM19203	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19203
Razor + unique peptides g1_PX1406_GM19204	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19204
Razor + unique peptides g1_PX1406_GM19207	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19207
Razor + unique peptides g1_PX1406_GM19209	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19209
Razor + unique peptides g1_PX1406_GM19222	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19222
Razor + unique peptides q1 PX1406 GM19257	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19257
Razor + unique peptides g1_PX151_Rep1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX151_Rep1
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment q1 PX151 Rep2
Razor + unique peptides g1_PX151_Rep3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX151_Rep3
Razor + unique peptides g1_PX309_HCC1143-1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-1
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment q1 PX309 HCC1143-2
Razor + unique peptides g1_PX309_HCC1143-3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-3
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g1_PX309_HCC1599-1 Razor + unique peptides g1_PX309_HCC1599-2	sequences) in experiment g1_PX309_HCC1599-1 Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1599-2
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g1_PX309_HCC1599-3 Razor + unique peptides	sequences) in experiment g1_PX309_HCC1599-3 Number of razor + unique peptides (distinct peptide
g1_PX309_HCC1937-1 Razor + unique peptides	Sequences) in experiment g1_PX309_HCC1937-1 Number of razor + unique peptides (distinct peptide
g1_PX309_HCC1937-2 Razor + unique peptides	sequences) in experiment g1_PX309_HCC1937-2 Number of razor + unique peptides (distinct peptide
g1_PX309_HCC1937-3 Razor + unique peptides	sequences) in experiment g1_PX309_HCC1937-3 Number of razor + unique peptides (distinct peptide
g1_PX309_HCC202-1 Razor + unique peptides	sequences) in experiment g1_PX309_HCC202-1 Number of razor + unique peptides (distinct peptide
g1_PX309_HCC202-2	sequences) in experiment g1_PX309_HCC202-2

Dozor I unique pontidos	Number of record unique poptides (distinct poptide
Razor + unique peptides g1_PX309_HCC202-3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC202-3
Razor + unique peptides g1_PX309_HCC2218-1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-1
Razor + unique peptides g1_PX309_HCC2218-2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-2
Razor + unique peptides g1_PX309_HCC2218-3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-3
Razor + unique peptides g1_PX309_HMEC1-1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-1
Razor + unique peptides g1_PX309_HMEC1-2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-2
Razor + unique peptides g1_PX309_HMEC1-3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-3
Razor + unique peptides g1_PX309_HMEC2-1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-1
Razor + unique peptides g1_PX309_HMEC2-2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-2
Razor + unique peptides q1 PX309 HMEC2-3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-3
Razor + unique peptides g1_PX309_HMTS1-1	Number of razor + unique peptides (distinct peptide sequences) in experiment q1 PX309 HMTS1-1
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_HMTS1-2
Razor + unique peptides g1 PX309 HMTS1-3	Number of razor + unique peptides (distinct peptide
Razor + unique peptides	sequences) in experiment g1_PX309_HMTS1-3 Number of razor + unique peptides (distinct peptide
g1_PX309_MCF10a-1 Razor + unique peptides	sequences) in experiment g1_PX309_MCF10a-1 Number of razor + unique peptides (distinct peptide
g1_PX309_MCF10a-2 Razor + unique peptides	sequences) in experiment g1_PX309_MCF10a-2 Number of razor + unique peptides (distinct peptide
g1_PX309_MCF10a-3 Razor + unique peptides	sequences) in experiment g1_PX309_MCF10a-3 Number of razor + unique peptides (distinct peptide
g1_PX309_MDAMB453-1 Razor + unique peptides	sequences) in experiment g1_PX309_MDAMB453-1 Number of razor + unique peptides (distinct peptide
g1_PX309_MDAMB453-2 Razor + unique peptides	sequences) in experiment g1_PX309_MDAMB453-2 Number of razor + unique peptides (distinct peptide
g1_PX309_MDAMB453-3 Razor + unique peptides	sequences) in experiment g1_PX309_MDAMB453-3 Number of razor + unique peptides (distinct peptide
g1_PX309_MFM223-1	sequences) in experiment g1_PX309_MFM223-1
Razor + unique peptides g1_PX309_MFM223-2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_MFM223-2
Razor + unique peptides g1_PX309_MFM223-3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX309_MFM223-3
Razor + unique peptides g1_PX359_0h_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_0h_1
Razor + unique peptides g1_PX359_0h_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_0h_2
Razor + unique peptides g1_PX359_0h_3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_0h_3
Razor + unique peptides g1_PX359_BSA_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_BSA_1
Razor + unique peptides g1_PX359_BSA_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_BSA_2
Razor + unique peptides g1_PX359_BSA_3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_BSA_3
Razor + unique peptides g1_PX359_FN_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_FN_1
Razor + unique peptides g1_PX359_FN_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_FN_2
Razor + unique peptides g1_PX359_FN_3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_FN_3
Razor + unique peptides g1_PX359_GFR_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_GFR_1
Razor + unique peptides g1_PX359_GFR_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_GFR_2
Razor + unique peptides g1_PX359_GFR_3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_GFR_3
Razor + unique peptides g1_PX359_LAM_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_LAM_1
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g1_PX359_LAM_2 Razor + unique peptides	Sequences) in experiment g1_PX359_LAM_2 Number of razor + unique peptides (distinct peptide
g1_PX359_LAM_3 Razor + unique peptides	sequences) in experiment g1_PX359_LAM_3 Number of razor + unique peptides (distinct peptide
g1_PX359_Matr 12h_1	sequences) in experiment g1_PX359_Matr 12h_1

Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g1_PX359_Matr 12h_2 Razor + unique peptides	sequences) in experiment g1_PX359_Matr 12h_2 Number of razor + unique peptides (distinct peptide
g1_PX359_Matr 12h_3 Razor + unique peptides	sequences) in experiment g1_PX359_Matr 12h_3 Number of razor + unique peptides (distinct peptide
g1_PX359_Matr 24h_1 Razor + unique peptides	sequences) in experiment g1_PX359_Matr 24h_1 Number of razor + unique peptides (distinct peptide
g1_PX359_Matr 24h_2 Razor + unique peptides	sequences) in experiment g1_PX359_Matr 24h_2 Number of razor + unique peptides (distinct peptide
g1_PX359_Matr 24h_3	sequences) in experiment g1_PX359_Matr 24h_3
Razor + unique peptides g1_PX359_Matr 30h_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_1
Razor + unique peptides g1_PX359_Matr 30h_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_2
Razor + unique peptides g1_PX359_Matr 30h_3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_3
Razor + unique peptides g1_PX359_Matr dil_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_1
Razor + unique peptides g1_PX359_Matr dil_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_2
Razor + unique peptides g1_PX359_Matr dil_3	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_3
Razor + unique peptides g1_PX419_human_18507	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX419_human_18507
Razor + unique peptides g1_PX419_human_18516	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX419_human_18516
Razor + unique peptides g1_PX419_human_19193	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX419_human_19193
Razor + unique peptides g1_PX419_human_19204	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX419_human_19204
Razor + unique peptides g1_PX438_Xeno092	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno092
Razor + unique peptides g1_PX438_Xeno441	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno441
Razor + unique peptides g1_PX438_Xeno561	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno561
Razor + unique peptides g1_PX438_Xeno691	Number of razor + unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno691
Razor + unique peptides g2_PX058_expA	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX058_expA
Razor + unique peptides g2_PX058_expB	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX058_expB
Razor + unique peptides g2_PX058_expC	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX058_expC
Razor + unique peptides g2_PX058_expD	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX058_expD
Razor + unique peptides g2_PX058_expE	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX058_expE
Razor + unique peptides g2_PX058_expF	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX058_expF
Razor + unique peptides g2_PX089_Rep1	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX089_Rep1
Razor + unique peptides g2_PX089_Rep2	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX089_Rep2
Razor + unique peptides g2_PX537_exp14 rep1 20h	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep1 20h
Razor + unique peptides g2_PX537_exp14 rep1 6h	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep1 6h
Razor + unique peptides g2_PX537_exp14 rep2 20h	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep2 20h
Razor + unique peptides g2_PX537_exp14 rep2 6h	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep2 6h
Razor + unique peptides g2_PX537_exp14 rep3 20h	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep3 20h
Razor + unique peptides g2_PX537_exp14 rep3 6h	Number of razor + unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep3 6h
Razor + unique peptides g3_GK1_Chromatin_A_TSA_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_A_TSA_1
Razor + unique peptides g3_GK1_Chromatin_A_TSA_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_A_TSA_2
Razor + unique peptides g3_GK1_Chromatin_CC_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_CC_1
Razor + unique peptides g3_GK1_Chromatin_CC_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_CC_2
Razor + unique peptides g3_GK1_Chromatin_EHT_1	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_1

Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g3_GK1_Chromatin_EHT_2 Razor + unique peptides	sequences) in experiment g3_GK1_Chromatin_EHT_2 Number of razor + unique peptides (distinct peptide
g3_GK1_Chromatin_EHT_3 Razor + unique peptides	sequences) in experiment g3_GK1_Chromatin_EHT_3 Number of razor + unique peptides (distinct peptide
g3_GK1_Chromatin_EHT_4	sequences) in experiment g3_GK1_Chromatin_EHT_4
Razor + unique peptides g3_GK1_Chromatin_EHT_5	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_5
Razor + unique peptides g3_GK1_Chromatin_EHT_6	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_6
Razor + unique peptides g3_GK1_Chromatin_mH2A_4_5	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_mH2A_4_5
Razor + unique peptides g3_KW35_ET	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_KW35_ET
Razor + unique peptides g3_KW35_ET_2	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_KW35_ET_2
Razor + unique peptides g3_KW35_nE	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_KW35_nE
Razor + unique peptides g3 KW35_nE_2	Number of razor + unique peptides (distinct peptide sequences) in experiment q3 KW35 nE 2
Razor + unique peptides q3 KW35 rot ET	Number of razor + unique peptides (distinct peptide sequences) in experiment q3 KW35 rot ET
Razor + unique peptides g3 KW35 wE	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_KW35_wE
Razor + unique peptides g3 KW35 wE 2	Number of razor + unique peptides (distinct peptide sequences) in experiment q3 KW35 wE 2
Razor + unique peptides g3_PX328_Diff3_Exp1	Number of razor + unique peptides (distinct peptide sequences) in experiment q3 PX328 Diff3 Exp1
Razor + unique peptides g3_PX328_Diff3_Exp2	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff3_Exp2
Razor + unique peptides g3_PX328_Diff4_Exp1	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff4_Exp1
Razor + unique peptides g3_PX328_Diff4_Exp2	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff4_Exp2
Razor + unique peptides g3_PX328_Diff5_Exp1	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff5_Exp1
Razor + unique peptides g3_PX328_Diff5_Exp2	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff5_Exp2
Razor + unique peptides g3_PX597_A1_Spr	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX597_A1_Spr
Razor + unique peptides q3 PX597 A2 Spr	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX597_A2_Spr
Razor + unique peptides g3_PX597_A3_Spr	Number of razor + unique peptides (distinct peptide sequences) in experiment g3_PX597_A3_Spr
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g3_PX597_B1_Spr Razor + unique peptides	Sequences) in experiment g3_PX597_B1_Spr Number of razor + unique peptides (distinct peptide
g3_PX597_B2_Spr Razor + unique peptides	Sequences) in experiment g3_PX597_B2_Spr Number of razor + unique peptides (distinct peptide
g3_PX597_B3_Spr Razor + unique peptides	sequences) in experiment g3_PX597_B3_Spr Number of razor + unique peptides (distinct peptide
g4_NCC_A Razor + unique peptides	sequences) in experiment g4_NCC_A Number of razor + unique peptides (distinct peptide
g4_NCC_B Razor_+ unique peptides	sequences) in experiment g4_NCC_B Number of razor + unique peptides (distinct peptide
g4_NCC_C Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC_C Number of razor + unique peptides (distinct peptide
CPT_s1 Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC-CPT_s1 Number of razor + unique peptides (distinct peptide
CPT_s2 Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC-CPT_s2 Number of razor + unique peptides (distinct peptide
CPT_s3 Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC-CPT_s3 Number of razor + unique peptides (distinct peptide
HU_Ex1 Razor + unique peptides g4_NCC-	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex1 Number of razor + unique peptides (distinct peptide
HU_Ex2 Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC-HU_Ex2 Number of razor + unique peptides (distinct peptide
HU_Ex3 Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC-HU_Ex3
rosco_s1 Razor + unique peptides g4_NCC-	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s1 Number of razor + unique peptides (distinct peptide
rosco_s2 Razor + unique peptides g4_NCC-	sequences) in experiment g4_NCC-rosco_s2 Number of razor + unique peptides (distinct peptide
rosco_s3	sequences) in experiment g4_NCC-rosco_s3
Razor + unique peptides g4_NCC- TSA_Exp1	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp1

Razor + unique peptides g4_NCC- TSA_Exp2	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp2
Razor + unique peptides g4_NCC- TSA_Exp3	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp3
Razor + unique peptides	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX183_A
Razor + unique peptides g4_PX183_B	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX183_B
Razor + unique peptides g4_PX183_C	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX183_C
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g4_PX183_D Razor + unique peptides g4_PX183_E	sequences) in experiment g4_PX183_D Number of razor + unique peptides (distinct peptide
Razor + unique peptides g4_PX441_E1	sequences) in experiment g4_PX183_E Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX441_E1
Razor + unique peptides q4_PX441_E2	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX441_E2
Razor + unique peptides q4_PX441_E3	Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX441_E3
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g4_PX441_E4 Razor + unique peptides	sequences) in experiment g4_PX441_E4 Number of razor + unique peptides (distinct peptide
g4_PX441_É5 Razor + unique peptides	sequences) in experiment g4_PX441_E5 Number of razor + unique peptides (distinct peptide
g4_PX441_F1 Razor + unique peptides	sequences) in experiment g4_PX441_F1 Number of razor + unique peptides (distinct peptide
g4_PX441_F2 Razor + unique peptides	sequences) in experiment g4_PX441_F2 Number of razor + unique peptides (distinct peptide
g4_PX441_F3 Razor + unique peptides g4_PX441_F4	sequences) in experiment g4_PX441_F3 Number of razor + unique peptides (distinct peptide sequences) in experiment g4_PX441_F4
Razor + unique peptides	Number of razor + unique peptides (distinct peptide
g4_PX441_F5 Unique peptides g1_GK1_Chromatin_AL	sequences) in experiment g4_PX441_F5 Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL
Unique peptides g1_GK1_Chromatin_CPT	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT
Unique peptides q1 GK1 Chromatin CR	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CR
Unique peptides g1_GK1_Chromatin_HepHek	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_HepHek
Unique peptides g1_GK1_Chromatin_hilR	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_hilR
Unique peptides q1 GK1 Chromatin IoIR	Number of unique peptides (distinct peptide sequences) in experiment q1 GK1 Chromatin IoIR
Unique peptides g1_GK1_Chromatin_mH2A_1	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_1
Unique peptides g1_GK1_Chromatin_mH2A_2	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_2
Unique peptides g1_GK1_Chromatin_mH2A_3	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_3
Unique peptides g1_GK1_Chromatin_TNFa_1	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_1
Unique peptides g1_GK1_Chromatin_TNFa_2	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_2
Unique peptides g1_GK1_Chromatin_TNFa_3	Number of unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFa_3
Unique peptides g1_KW10_110506	Number of unique peptides (distinct peptide sequences) in experiment g1_KW10_110506
Unique peptides g1_KW10_131126	Number of unique peptides (distinct peptide sequences) in experiment g1_KW10_131126
Unique peptides g1_KW10_140117	Number of unique peptides (distinct peptide sequences) in experiment g1_KW10_140117
Unique peptides g1_KW11_130125	Number of unique peptides (distinct peptide sequences) in experiment g1_KW11_130125
Unique peptides g1_KW11_140104_nE	Number of unique peptides (distinct peptide sequences) in experiment g1_KW11_140104_nE
Unique peptides g1_KW11_140104_wE	Number of unique peptides (distinct peptide sequences) in experiment g1_KW11_140104_wE
Unique peptides g1_KW12_130317	Number of unique peptides (distinct peptide sequences) in experiment g1_KW12_130317
Unique peptides g1_KW12_131223	Number of unique peptides (distinct peptide sequences) in experiment g1_KW12_131223
Unique peptides g1_KW13_130328	Number of unique peptides (distinct peptide sequences) in experiment g1_KW13_130328
	10.000111 10.100020

Unique peptides g1_KW14_130317	Number of unique peptides (distinct peptide sequences) in experiment g1_KW14_130317
Unique peptides g1_KW15_130317	Number of unique peptides (distinct peptide sequences) in experiment q1_KW15_130317
Unique peptides g1_KW17_130319	Number of unique peptides (distinct peptide sequences) in experiment g1_KW17_130319
Unique peptides g1_KW8_120517	Number of unique peptides (distinct peptide sequences) in experiment g1_KW8_120517
Unique peptides g1_KW8_131126	Number of unique peptides (distinct peptide sequences) in experiment g1_KW8_131126
Unique peptides g1_KW8_140117	Number of unique peptides (distinct peptide sequences) in experiment g1_KW8_140117
Unique peptides g1_KW9_120425	Number of unique peptides (distinct peptide sequences) in experiment g1_KW9_120425
Unique peptides g1_KW9_120510	Number of unique peptides (distinct peptide sequences) in experiment g1_KW9_120510
Unique peptides g1_PX1194_H1	Number of unique peptides (distinct peptide sequences) in experiment q1_PX1194_H1
Unique peptides g1_PX1194_H10	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H10
Unique peptides g1_PX1194_H11	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H11
Unique peptides g1_PX1194_H12	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H12
Unique peptides g1_PX1194_H2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H2
Unique peptides g1_PX1194_H3	Number of unique peptides (distinct peptide sequences) in experiment q1 PX1194 H3
Unique peptides g1_PX1194_H4	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H4
Unique peptides g1_PX1194_H5	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H5
Unique peptides g1_PX1194_H6	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H6
Unique peptides g1_PX1194_H7	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H7
Unique peptides g1_PX1194_H8	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_H8
Unique peptides g1_PX1194_H9	Number of unique peptides (distinct peptide sequences) in experiment q1_PX1194_H9
Unique peptides g1_PX1194_PCa1_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa1_1
Unique peptides g1_PX1194_PCa1_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa1_2
Unique peptides g1_PX1194_PCa2_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa2_1
Unique peptides g1_PX1194_PCa2_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa2_2
Unique peptides g1_PX1194_PCa2_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa2_3
Unique peptides g1_PX1194_PCa3_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa3_1
Unique peptides g1_PX1194_PCa3_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa3_2
Unique peptides g1_PX1194_PCa3_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa3_3
Unique peptides g1_PX1194_PCa4_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa4_1
Unique peptides g1_PX1194_PCa4_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa4_2
Unique peptides g1_PX1194_PCa4_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa4_3
Unique peptides g1_PX1194_PCa5_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa5_1
Unique peptides g1_PX1194_PCa5_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa5_2
Unique peptides g1_PX1194_PCa5_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa5_3
Unique peptides g1_PX1194_PCa6_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa6_1
Unique peptides g1_PX1194_PCa7_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1194_PCa7_1
Unique peptides g1_PX1406_GM18486	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18486
Unique peptides g1_PX1406_GM18498	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18498

Unique peptides g1 PX1406 GM18499	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18499
Unique peptides g1_PX1406_GM18501	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18501
Unique peptides g1 PX1406 GM18502	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18502
Unique peptides g1 PX1406 GM18504	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18504
Unique peptides g1 PX1406 GM18505	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18505
Unique peptides g1_PX1406_GM18507	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18507
Unique peptides g1 PX1406 GM18508	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18508
Unique peptides g1 PX1406 GM18510	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18510
Unique peptides g1_PX1406_GM18511	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18511
Unique peptides g1 PX1406 GM18516	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18516
Unique peptides g1 PX1406 GM18517	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18517
Unique peptides g1_PX1406_GM18519	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18519
Unique peptides g1_PX1406_GM18520	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18520
Unique peptides g1_PX1406_GM18522	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18522
Unique peptides g1_PX1406_GM18523	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18523
Unique peptides g1_PX1406_GM18852	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18852
Unique peptides g1_PX1406_GM18855	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18855
Unique peptides g1_PX1406_GM18858	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18858
Unique peptides g1_PX1406_GM18861	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18861
Unique peptides g1_PX1406_GM18862	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18862
Unique peptides g1_PX1406_GM18870	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18870
Unique peptides g1_PX1406_GM18871	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18871
Unique peptides g1_PX1406_GM18907	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18907
Unique peptides g1_PX1406_GM18909	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18909
Unique peptides g1_PX1406_GM18912	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18912
Unique peptides g1_PX1406_GM18913	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18913
Unique peptides g1_PX1406_GM18916	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM18916
Unique peptides g1_PX1406_GM19092	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19092
Unique peptides g1_PX1406_GM19093	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19093
Unique peptides g1_PX1406_GM19098	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19098
Unique peptides g1_PX1406_GM19099	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19099
Unique peptides g1_PX1406_GM19101	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19101
Unique peptides g1_PX1406_GM19102	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19102
Unique peptides g1_PX1406_GM19108	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19108
Unique peptides g1_PX1406_GM19114	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19114
Unique peptides g1_PX1406_GM19116	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19116
Unique peptides g1_PX1406_GM19119	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19119
Unique peptides g1_PX1406_GM19127	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19127

Unique peptides	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19128
g1_PX1406_GM19128 Unique peptides g1_PX1406_GM19130	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19130
Unique peptides g1_PX1406_GM19131	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19131
Unique peptides g1_PX1406_GM19137	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19137
Unique peptides g1_PX1406_GM19138	Number of unique peptides (distinct peptide sequences) in
Unique peptides	experiment g1_PX1406_GM19138 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19140 Unique peptides	experiment g1_PX1406_GM19140 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19143 Unique peptides	experiment g1_PX1406_GM19143 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19144 Unique peptides	experiment g1_PX1406_GM19144 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19147 Unique peptides	experiment g1_PX1406_GM19147 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19152 Unique peptides	experiment g1_PX1406_GM19152 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19153 Unique peptides	experiment g1_PX1406_GM19153 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19160 Unique peptides	experiment g1_PX1406_GM19160 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19172 Unique peptides	experiment g1_PX1406_GM19172 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19192 Unique peptides	experiment g1_PX1406_GM19192 Number of unique peptides (distinct peptide sequences) in
g1_PX1406_GM19193	experiment g1_PX1406_GM19193
Unique peptides g1_PX1406_GM19200	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19200
Unique peptides g1_PX1406_GM19203	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19203
Unique peptides g1_PX1406_GM19204	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19204
Unique peptides g1_PX1406_GM19207	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19207
Unique peptides g1_PX1406_GM19209	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19209
Unique peptides g1_PX1406_GM19222	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19222
Unique peptides g1_PX1406_GM19257	Number of unique peptides (distinct peptide sequences) in experiment g1_PX1406_GM19257
Unique peptides g1_PX151_Rep1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX151_Rep1
Unique peptides g1_PX151_Rep2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX151_Rep2
Unique peptides g1_PX151_Rep3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX151_Rep3
Unique peptides g1_PX309_HCC1143-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-1
Unique peptides g1_PX309_HCC1143-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-2
Unique peptides g1_PX309_HCC1143-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1143-3
Unique peptides g1_PX309_HCC1599-1	Number of unique peptides (distinct peptide sequences) in experiment g1 PX309 HCC1599-1
Unique peptides g1_PX309_HCC1599-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1599-2
Unique peptides g1_PX309_HCC1599-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1599-3
Unique peptides g1_PX309_HCC1937-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1937-1
Unique peptides g1_PX309_HCC1937-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1937-2
Unique peptides g1_PX309_HCC1937-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC1937-3
Unique peptides g1_PX309_HCC202-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC202-1
Unique peptides	Number of unique peptides (distinct peptide sequences) in
g1_PX309_HCC202-2 Unique peptides	experiment g1_PX309_HCC202-2 Number of unique peptides (distinct peptide sequences) in
g1_PX309_HCC202-3 Unique peptides	experiment g1_PX309_HCC202-3 Number of unique peptides (distinct peptide sequences) in
g1_PX309_HCC2218-1	experiment g1_PX309_HCC2218-1

Unique peptides g1_PX309_HCC2218-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-2
Unique peptides g1_PX309_HCC2218-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HCC2218-3
Unique peptides g1_PX309_HMEC1-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-1
Unique peptides g1_PX309_HMEC1-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-2
Unique peptides g1_PX309_HMEC1-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC1-3
Unique peptides g1_PX309_HMEC2-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-1
Unique peptides g1_PX309_HMEC2-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-2
Unique peptides g1_PX309_HMEC2-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMEC2-3
Unique peptides g1_PX309_HMTS1-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMTS1-1
Unique peptides g1_PX309_HMTS1-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMTS1-2
Unique peptides g1_PX309_HMTS1-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_HMTS1-3
Unique peptides g1_PX309_MCF10a-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MCF10a-1
Unique peptides g1_PX309_MCF10a-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MCF10a-2
Unique peptides g1_PX309_MCF10a-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MCF10a-3
Unique peptides g1_PX309_MDAMB453-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MDAMB453-1
Unique peptides g1_PX309_MDAMB453-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MDAMB453-2
Unique peptides g1_PX309_MDAMB453-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MDAMB453-3
Unique peptides g1_PX309_MFM223-1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MFM223-1
Unique peptides g1_PX309_MFM223-2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MFM223-2
Unique peptides g1_PX309_MFM223-3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX309_MFM223-3
Unique peptides g1_PX359_0h_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_0h_1
Unique peptides g1_PX359_0h_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_0h_2
Unique peptides g1_PX359_0h_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_0h_3
Unique peptides g1_PX359_BSA_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_BSA_1
Unique peptides g1_PX359_BSA_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_BSA_2
Unique peptides g1_PX359_BSA_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_BSA_3
Unique peptides g1_PX359_FN_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_FN_1
Unique peptides g1_PX359_FN_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_FN_2
Unique peptides g1_PX359_FN_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_FN_3
Unique peptides g1_PX359_GFR_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_GFR_1
Unique peptides g1_PX359_GFR_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_GFR_2
Unique peptides g1_PX359_GFR_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_GFR_3
Unique peptides g1_PX359_LAM_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_LAM_1
Unique peptides g1_PX359_LAM_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_LAM_2
Unique peptides g1_PX359_LAM_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_LAM_3
Unique peptides g1_PX359_Matr 12h_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 12h_1
Unique peptides g1_PX359_Matr 12h_2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 12h_2
Unique peptides g1_PX359_Matr 12h_3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 12h_3

Unique peptides g1_PX359_Matr 24h 1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 24h_1
Unique peptides g1_PX359_Matr 24h 2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 24h_2
Unique peptides g1_PX359_Matr 24h 3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 24h_3
Unique peptides g1_PX359_Matr 30h_1	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_1
Unique peptides g1_PX359_Matr 30h 2	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_2
Unique peptides g1_PX359_Matr 30h 3	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr 30h_3
Unique peptides g1_PX359_Matr	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_1
Unique peptides g1_PX359_Matr	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_2
Unique peptides g1_PX359_Matr	Number of unique peptides (distinct peptide sequences) in experiment g1_PX359_Matr dil_3
Unique peptides g1_PX419_human_18507	Number of unique peptides (distinct peptide sequences) in experiment g1_PX419_human_18507
Unique peptides g1_PX419_human_18516	Number of unique peptides (distinct peptide sequences) in experiment g1_PX419_human_18516
Unique peptides g1_PX419_human_19193	Number of unique peptides (distinct peptide sequences) in experiment g1_PX419_human_19193
Unique peptides g1_PX419_human_19204	Number of unique peptides (distinct peptide sequences) in experiment g1_PX419_human_19204
Unique peptides q1 PX438 Xeno092	Number of unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno092
Unique peptides g1_PX438_Xeno441	Number of unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno441
Unique peptides g1_PX438_Xeno561	Number of unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno561
Unique peptides g1_PX438_Xeno691	Number of unique peptides (distinct peptide sequences) in experiment g1_PX438_Xeno691
Unique peptides g2_PX058_expA	Number of unique peptides (distinct peptide sequences) in experiment g2_PX058_expA
Unique peptides g2_PX058_expB	Number of unique peptides (distinct peptide sequences) in experiment g2_PX058_expB
Unique peptides g2_PX058_expC	Number of unique peptides (distinct peptide sequences) in experiment g2_PX058_expC
Unique peptides g2_PX058_expD	Number of unique peptides (distinct peptide sequences) in experiment g2_PX058_expD
Unique peptides g2_PX058_expE	Number of unique peptides (distinct peptide sequences) in experiment g2_PX058_expE
Unique peptides g2_PX058_expF	Number of unique peptides (distinct peptide sequences) in experiment g2_PX058_expF
Unique peptides g2_PX089_Rep1	Number of unique peptides (distinct peptide sequences) in experiment g2_PX089_Rep1
Unique peptides g2_PX089_Rep2	Number of unique peptides (distinct peptide sequences) in experiment g2_PX089_Rep2
Unique peptides g2_PX537_exp14 rep1 20h	Number of unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep1 20h
Unique peptides g2_PX537_exp14 rep1 6h	Number of unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep1 6h
Unique peptides g2_PX537_exp14 rep2 20h	Number of unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep2 20h
Unique peptides g2_PX537_exp14 rep2 6h	Number of unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep2 6h
Unique peptides g2_PX537_exp14 rep3 20h	Number of unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep3 20h
Unique peptides g2_PX537_exp14 rep3 6h	Number of unique peptides (distinct peptide sequences) in experiment g2_PX537_exp14 rep3 6h
Unique peptides g3_GK1_Chromatin_A_TSA_1	Number of unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_A_TSA_1
Unique peptides g3_GK1_Chromatin_A_TSA_2	Number of unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_A_TSA_2
Unique peptides g3_GK1_Chromatin_CC_1	Number of unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_CC_1
Unique peptides	Number of unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_CC_2
g3_GK1_Chromatin_CC_2	rexperiment gs_GK1_Chromatin_CC_2
g3_GK1_Chromatin_CC_2 Unique peptides g3_GK1_Chromatin_EHT_1	Number of unique peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_1
Unique peptides	Number of unique peptides (distinct peptide sequences) in

Unique peptides	Number of unique peptides (distinct peptide sequences) in
g3_GK1_Chromatin_EHT_4 Unique peptides	experiment g3_GK1_Chromatin_EHT_4 Number of unique peptides (distinct peptide sequences) in
g3_GK1_Chromatin_EHT_5 Unique peptides	experiment g3_GK1_Chromatin_EHT_5 Number of unique peptides (distinct peptide sequences) in
g3_ĠK1_Ċhromatin_EHT_6 Unique peptides	experiment g3_GK1_Chromatin_EHT_6 Number of unique peptides (distinct peptide sequences) in
g3_GK1_Chromatin_mH2A_4_5	experiment g3_GK1_Chromatin_mH2A_4_5
Unique peptides g3_KW35_ET	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_ET
Unique peptides g3_KW35_ET_2	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_ET_2
Unique peptides g3_KW35_nE	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_nE
Unique peptides g3_KW35_nE_2	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_nE_2
Unique peptides g3_KW35_rot_ET	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_rot_ET
Unique peptides g3_KW35_wE	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_wE
Unique peptides g3_KW35_wE_2	Number of unique peptides (distinct peptide sequences) in experiment g3_KW35_wE_2
Unique peptides g3_PX328_Diff3_Exp1	Number of unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff3_Exp1
Unique peptides g3_PX328_Diff3_Exp2	Number of unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff3_Exp2
Unique peptides g3_PX328_Diff4_Exp1	Number of unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff4_Exp1
Unique peptides g3_PX328_Diff4_Exp2	Number of unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff4_Exp2
Unique peptides g3_PX328_Diff5_Exp1	Number of unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff5_Exp1
Unique peptides g3_PX328_Diff5_Exp2	Number of unique peptides (distinct peptide sequences) in experiment g3_PX328_Diff5_Exp2
Unique peptides g3_PX597_A1_Spr	Number of unique peptides (distinct peptide sequences) in experiment g3_PX597_A1_Spr
Unique peptides g3_PX597_A2_Spr	Number of unique peptides (distinct peptide sequences) in experiment g3_PX597_A2_Spr
Unique peptides g3_PX597_A3_Spr	Number of unique peptides (distinct peptide sequences) in experiment g3_PX597_A3_Spr
Unique peptides g3_PX597_B1_Spr	Number of unique peptides (distinct peptide sequences) in experiment g3_PX597_B1_Spr
Unique peptides g3_PX597_B2_Spr	Number of unique peptides (distinct peptide sequences) in experiment g3_PX597_B2_Spr
Unique peptides g3_PX597_B3_Spr	Number of unique peptides (distinct peptide sequences) in experiment g3_PX597_B3_Spr
Unique peptides g4_NCC_A	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC_A
Unique peptides g4_NCC_B	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC_B
Unique peptides g4_NCC_C	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC_C
Unique peptides g4_NCC-CPT_s1	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-CPT_s1
Unique peptides g4_NCC-CPT_s2	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-CPT_s2
Unique peptides g4_NCC-CPT_s3	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-CPT_s3
Unique peptides g4_NCC-HU_Ex1	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex1
Unique peptides g4_NCC-HU_Ex2	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex2
Unique peptides g4_NCC-HU_Ex3	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex3
Unique peptides g4_NCC-rosco_s1	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s1
Unique peptides g4_NCC-rosco_s2	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s2
Unique peptides g4_NCC-rosco_s3	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s3
Unique peptides g4_NCC-TSA_Exp1	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp1
Unique peptides g4_NCC- TSA_Exp2	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp2
Unique peptides g4_NCC-TSA_Exp3	Number of unique peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp3

Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_A
Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_B
Number of unique peptides (distinct peptide sequences) in experiment q4 PX183 C
Number of unique peptides (distinct peptide sequences) in
experiment g4_PX183_D Number of unique peptides (distinct peptide sequences) in
experiment g4_PX183_E Number of unique peptides (distinct peptide sequences) in
experiment g4_PX441_E1 Number of unique peptides (distinct peptide sequences) in
experiment g4_PX441_E2 Number of unique peptides (distinct peptide sequences) in
experiment g4_PX441_E3 Number of unique peptides (distinct peptide sequences) in
experiment g4_PX441_E4 Number of unique peptides (distinct peptide sequences) in
experiment g4_PX441_E5 Number of unique peptides (distinct peptide sequences) in
experiment g4_PX441_F1
Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F2
Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F3
Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F4
Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F5
Percentage of the sequence that is covered by the identified peptides of the best protein sequence contained in the group.
Percentage of the sequence that is covered by the identified unique and razor peptides of the best protein sequence contained in the group.
Percentage of the sequence that is covered by the identified unique peptides of the best protein sequence contained in the group.
Molecular weight of the leading protein sequence contained in the protein group.
The length of the leading protein sequence contained in the group.
The length of all sequences of the proteins contained in the group.
This is the ratio of reverse to forward protein groups.
Protein score which is derived from peptide posterior error probabilities.
The ratio between two heavy and light label partners.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for quantitation.
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
The ratio between two heavy and light label partners.
Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Number of redundant peptides (MS1 features) used for
quantitation.
quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Number of redundant peptides (MS1 features) used for
Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Number of redundant peptides (MS1 features) used for

Ratio H/L count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CPT	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 GK1 Chromatin CPT	quantities and quantities in the confidence quantity in the confidence quantities and the confidence quantities and the confidence quantities are confidence quantities are confidence quantities and the confidence quantities are
Ratio H/L g1_GK1_Chromatin_CR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_CR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_CR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_CR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_CR	
Ratio H/L g1_GK1_Chromatin_HepHek	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_HepHek	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_HepHek	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_HepHek	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_HepHek	
Ratio H/L g1_GK1_Chromatin_hiIR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_hilR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_hilR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_hiIR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_hilR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_hiIR	
Ratio H/L g1_GK1_Chromatin_loIR	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_loIR	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_loIR	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_loIR	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_loIR	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_loIR	
Ratio H/L g1_GK1_Chromatin_mH2A_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_1	
Ratio H/L g1_GK1_Chromatin_mH2A_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_2	Number of redundant peptides (MS1 features) used for quantitation.

Datia IIII inc. anima	Number of reduced as the articles (MC4 feetures) used for
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_2	
Ratio H/L g1_GK1_Chromatin_mH2A_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_mH2A_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_mH2A_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_mH2A_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_mH2A_3	
Ratio H/L g1_GK1_Chromatin_TNFa_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_1	
Ratio H/L g1_GK1_Chromatin_TNFa_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_2	
Ratio H/L g1_GK1_Chromatin_TNFa_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_GK1_Chromatin_TNFa_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_GK1_Chromatin_TNFa_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_GK1_Chromatin_TNFa_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_GK1_Chromatin_TNFa_3	
Ratio H/L g1_KW10_110506	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_110506	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_110506	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_110506	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_110506	
Ratio H/L g1_KW10_131126	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_131126	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1_KW10_131126	
Ratio H/L g1_KW10_140117	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW10_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW10_140117	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW10_140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW10_140117	
Ratio H/L g1_KW11_130125 Ratio H/L normalized g1_KW11_130125	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_130125	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_130125	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_130125	
Ratio H/L g1_KW11_140104_nE	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW11_140104_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_140104_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_nE	
Ratio H/L g1_KW11_140104_wE	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 KW11 140104 wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW11_140104_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW11_140104_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW11_140104_wE	
Ratio H/L g1_KW12_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW12_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW12_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_130317	
Ratio H/L g1_KW12_131223	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW12_131223	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW12_131223	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW12_131223	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW12_131223	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW12_131223	
Ratio H/L g1_KW13_130328	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW13_130328	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW13_130328	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_KW13_130328	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW13_130328	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW13_130328	
Ratio H/L g1_KW14_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW14_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW14_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW14_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW14_130317	
Ratio H/L g1_KW15_130317	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW15_130317	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW15_130317	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW15_130317	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW15_130317	
Ratio H/L g1_KW17_130319	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW17_130319	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW17_130319	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW17_130319	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW17_130319	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW17_130319	
Ratio H/L g1_KW8_120517	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_120517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW8_120517	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW8_120517	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_120517	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_120517	
Ratio H/L g1_KW8_131126	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_131126	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW8_131126	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW8_131126	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_131126	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_131126	
Ratio H/L g1_KW8_140117	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW8_140117	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW8_140117	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW8_140117	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW8_140117	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW8_140117	
Ratio H/L g1_KW9_120425	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_KW9_120425	I ne median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_KW9_120425	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW9_120425	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW9_120425	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW9_120425	
Ratio H/L g1_KW9_120510	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW9_120510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_KW9_120510	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_KW9_120510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_KW9_120510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_KW9_120510	
Ratio H/L q1 PX1194 H1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H1	
Ratio H/L g1_PX1194_H10	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H10	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H10	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H10	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H10	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H10	
Ratio H/L g1_PX1194_H11	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H11	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H11	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H11	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H11	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H11	
Ratio H/L g1_PX1194_H12	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H12	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H12	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H12	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H12	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H12	
Ratio H/L g1_PX1194_H2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H2	
Ratio H/L g1_PX1194_H3	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1194_H3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H3	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H3	
Ratio H/L g1_PX1194_H4	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1194_H4 Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g1_PX1194_H4	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H4	
Ratio H/L g1_PX1194_H5	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H5	
Ratio H/L g1_PX1194_H6	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H6	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H6	
Ratio H/L g1_PX1194_H7	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H7	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H7	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H7	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H7	
Ratio H/L g1_PX1194_H8	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H8	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H8	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H8	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_H8	
Ratio H/L g1_PX1194_H9	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_H9	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_H9	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_H9	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1_PX1194_H9	
Ratio H/L g1_PX1194_PCa1_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa1_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_1	
Ratio H/L g1_PX1194_PCa1_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa1_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa1_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa1_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa1_2	
Ratio H/L g1_PX1194_PCa2_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_1	
Ratio H/L g1_PX1194_PCa2_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa2_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_2	
Ratio H/L g1_PX1194_PCa2_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa2_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa2_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa2_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q1 PX1194 PCa2 3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa2_3	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX1194_PCa3_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa3_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count q1 PX1194 PCa3 1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
g1_PX1194_PCa3_1 Ratio H/L type g1_PX1194_PCa3_1	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX1194_PCa3_2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g1_PX1194_PCa3_2 Ratio H/L variability [%] g1_PX1194_PCa3_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa3_2	quantitation.

Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa3_2	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_2	The section between two because of Political and con-
Ratio H/L g1_PX1194_PCa3_3 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX1194_PCa3_3	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa3_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa3_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa3_3	
Ratio H/L g1_PX1194_PCa4_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_1	
Ratio H/L g1_PX1194_PCa4_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_2	
Ratio H/L g1_PX1194_PCa4_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa4_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa4_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1 PX1194 PCa4 3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa4_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_3	
Ratio H/L g1_PX1194_PCa5_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_1	
Ratio H/L g1_PX1194_PCa5_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation
g1_PX1194_PCa5_2 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX1194_PCa5_2 Ratio H/L type g1_PX1194_PCa5_2	quantitation that are quantified with the re-quantify method.
Ratio H/L g1_PX1194_PCa5_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa5_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa5_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa5_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa5_3	quantitation that are quantined with the re-quantity method.
Ratio H/L g1_PX1194_PCa6_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa6_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa6_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa6_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa6_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa6_1	
Ratio H/L g1_PX1194_PCa7_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1194_PCa7_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1194_PCa7_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1194_PCa7_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1194_PCa7_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa7_1	
Ratio H/L g1_PX1406_GM18486	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18486	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18486	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18486	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18486	
Ratio H/L g1_PX1406_GM18498	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18498	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18498	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18498	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18498	
Ratio H/L g1_PX1406_GM18499	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18499	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18499	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18499	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18499	
Ratio H/L g1_PX1406_GM18501	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18501	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18501	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18501	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18501	
Ratio H/L g1_PX1406_GM18502	The ratio between two heavy and light label partners.

Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX1406_GM18502 Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g1_PX1406_GM18502	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18502	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX1406 GM18502	
Ratio H/L g1 PX1406 GM18504	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18504	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18504	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18504	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18504	
Ratio H/L g1_PX1406_GM18505	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18505	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18505	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18505	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18505	
Ratio H/L g1_PX1406_GM18507	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18507	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18507	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18507	
Ratio H/L g1_PX1406_GM18508	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18508	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18508	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18508	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18508	
Ratio H/L g1_PX1406_GM18510	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18510	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18510	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18510	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18510	
Ratio H/L g1_PX1406_GM18511	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18511	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18511	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18511	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	quantitation that are quantitied with the re-quantity method.
g1_PX1406_GM18511 Ratio H/L g1_PX1406_GM18516	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18516	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18516	
Ratio H/L g1_PX1406_GM18517	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18517	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18517	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18517	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18517	
Ratio H/L g1_PX1406_GM18519	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18519	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18519	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18519	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18519	
Ratio H/L g1_PX1406_GM18520	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18520	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18520	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18520	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18520	
Ratio H/L g1_PX1406_GM18522	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18522	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18522	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18522	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18522	
Ratio H/L g1_PX1406_GM18523	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18523	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18523	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18523	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM18523 Ratio H/L g1_PX1406_GM18852	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX1406 GM18852	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18852	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18852	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1 PX1406 GM18852	
Ratio H/L g1_PX1406_GM18855	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18855	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18855	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18855	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18855	
Ratio H/L g1_PX1406_GM18858	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18858	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18858	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18858	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18858	
Ratio H/L g1_PX1406_GM18861	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18861	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18861	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18861	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18861	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18861	
Ratio H/L g1_PX1406_GM18862	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18862	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18862	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18862	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18862	
Ratio H/L g1_PX1406_GM18870	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18870	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18870	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18870	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18870	
Ratio H/L g1_PX1406_GM18871	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM18871	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18871	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18871	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18871	
Ratio H/L g1_PX1406_GM18907	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18907	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18907	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18907	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18907	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18907	
Ratio H/L g1_PX1406_GM18909	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18909	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18909	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18909	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18909	
Ratio H/L g1_PX1406_GM18912	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18912	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18912	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18912	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18912	
Ratio H/L g1_PX1406_GM18913	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18913	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18913	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18913	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18913	
Ratio H/L g1_PX1406_GM18916	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM18916	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM18916	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM18916	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18916	
Ratio H/L g1_PX1406_GM19092	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19092	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19092	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19092	
Ratio H/L g1_PX1406_GM19093	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19093	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19093	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19093	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19093	
Ratio H/L g1_PX1406_GM19098	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19098	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19098	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19098	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19098	
Ratio H/L g1_PX1406_GM19099	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19099	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19099	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19099	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19099	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19099	
Ratio H/L g1_PX1406_GM19101	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19101	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19101	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19101	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19101	
Ratio H/L g1_PX1406_GM19102	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19102	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19102	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19102	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19102	
Ratio H/L g1_PX1406_GM19108	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19108	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19108	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19108	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19108	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type g1 PX1406 GM19108	
Ratio H/L g1_PX1406_GM19114	The ratio between two heavy and light label partners.
Ratio H/L normalized g1 PX1406 GM19114	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19114	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19114	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19114	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19114	
Ratio H/L g1_PX1406_GM19116	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19116	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19116	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19116	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19116	
Ratio H/L g1_PX1406_GM19119	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19119	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19119	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19119	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1 PX1406 GM19119	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19119	quantitude war are quantitude war are to quantity monitor.
Ratio H/L g1_PX1406_GM19127	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19127	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19127	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19127	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19127	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19127	
Ratio H/L g1_PX1406_GM19128	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19128	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19128	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19128	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19128	
Ratio H/L g1_PX1406_GM19130	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19130	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19130	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19130	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19130	
Ratio H/L g1_PX1406_GM19131	The ratio between two heavy and light label partners.

Ratio H/L normalized g1_PX1406_GM19131	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19131	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19131	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19131	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19131	
Ratio H/L g1_PX1406_GM19137	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19137	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19137	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19137	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19137	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19137	
Ratio H/L g1_PX1406_GM19138	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19138	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19138	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19138	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19138	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g1_PX1406_GM19140	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19140	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19140	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19140	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19140	
Ratio H/L g1_PX1406_GM19143	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19143	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19143	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19143	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19143	
Ratio H/L g1_PX1406_GM19144	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19144	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19144	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19144	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19144	
Ratio H/L g1_PX1406_GM19147	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19147	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19147	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
<u> </u>	naturally logarithmized ratios times 100.

Ratio H/L count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19147	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19147	
Ratio H/L g1_PX1406_GM19152	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19152	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19152	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19152	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19152	
Ratio H/L g1_PX1406_GM19153	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19153	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19153	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19153	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19153	
Ratio H/L g1_PX1406_GM19160	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19160	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19160	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19160	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19160	
Ratio H/L g1_PX1406_GM19172	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19172	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19172	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19172	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19172	
Ratio H/L g1_PX1406_GM19192	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19192	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19192	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19192	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19192	
Ratio H/L g1_PX1406_GM19193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19193	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type	
g1_PX1406_GM19193 Ratio H/L g1_PX1406_GM19200	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19200	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19200	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19200	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19200	
Ratio H/L g1_PX1406_GM19203	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19203	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19203	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19203	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19203	
Ratio H/L g1_PX1406_GM19204	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19204	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19204	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19204	
Ratio H/L g1_PX1406_GM19207	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19207	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19207	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19207	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19207	
Ratio H/L g1_PX1406_GM19209	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19209	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19209	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19209	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19209	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19209	
Ratio H/L g1_PX1406_GM19222	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX1406_GM19222	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX1406_GM19222	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX1406_GM19222	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19222	
Ratio H/L g1_PX1406_GM19257	The ratio between two heavy and light label partners.

Ratio H.L. Quarbellity [95] gray 1, 1406, GM19257 Ratio H.L. Quantified the peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H.L. Quantified the peptides (MS1 features) used for quantifiation. Number of redundant peptides (MS1 features) used for quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantify method. Ratio H.L. Quantified the period of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantifiation that are quantified with the re-quantified puantified of quantified of quantifiation that are quantifie	Ratio H/L normalized g1_PX1406_GM19257	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
naturally logarithmized ratios times 100. Ratio HJL count of 1, PX1406_GM19257 Ratio HJL count of 1, PX1406_GM19257 Ratio HJL count of 1, PX1406_GM19257 Ratio HJL preserved the state of the state	Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX1406_GM19257 Again HL iso-count g1_PX151_Rep1 Again HL iso-count g1_PX151_Rep2 Again HL iso-count g1_PX151_Rep3 Again HL iso-coun		naturally logarithmized ratios times 100.
guentitation that are quantified with the re-quantity method. Ratio H.U. ppc gl. PX151 Rep1 The ratio between two heavy and light label partners. Ratio H.U. q. PX151 Rep1 Ratio H.U. arisability [%] gl. pX151 Rep1 Ratio H.U. varisability [%] gl. pX151 Rep1 Ratio H.U. varisability [%] gl. pX151 Rep1 Ratio H.U. varisability [%] gl. pX151 Rep1 Ratio H.U. count gl. pX151_Rep1 Ratio H.U. count gl. pX151_Rep1 Ratio H.U. count gl. pX151_Rep1 Ratio H.U. arisability [%] gl. pX151 Rep1 Ratio H.U. arisability [%] gl. pX151 Rep1 Ratio H.U. gl. pX151_Rep1 Ratio H.U. gl. pX151_Rep1 Ratio H.U. gl. pX151_Rep2 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep2 The ratio between two medium and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep2 The ratio between two medium and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep2 Ratio H.U. count gl. pX151_Rep2 Ratio H.U. arisability [%] gl. pX151_Rep2 Ratio H.U. count gl. pX151_Rep2 Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. arisability [%] gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. count gl. pX151_Rep3 The ratio between two heavy and light label partners. Ratio H.U. count gl. pX151_Rep3 Ratio H.U. arisability [%] gl. pX309_HCC1143-1 The	1	
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Ratio H/L q1 PX151 Rep1 Ratio H/L q1 PX151 Rep1 Ratio H/L q1 normalized g1/PX151 Rep1 Ratio H/L variability (%) g1/PX151 Rep1 Ratio H/L variability (%) g1/PX151 Rep1 Ratio H/L count g1 PX151 Rep1 Ratio H/L count g1 PX151 Rep1 Ratio H/L q1 PX151 Rep2 Ratio H/L q1 PX151 Rep3 Ratio H/L q1 PX151 R	Ratio H/L type	
The median of the total ratio population was shirted to 1. Ratio H/L variability (%) g1_PX151_Rep1 Ratio H/L solid to 1. Ratio H/L sol	3 =	The ratio between two heavy and light label partners.
peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g1_PX151_Rep1 Ratio H/L iso-count g1_PX151_Rep1 Ratio H/L nype g1_PX151_Rep1 Ratio H/L nype g1_PX151_Rep2 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX151_Rep2 The median of the total ratio population was shifted to 1. Ratio H/L so-count g1_PX151_Rep2 Ratio H/L count g1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep2 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L g1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L count g1_PX151_Rep3 Ratio H/L so-count q1_PX151_Rep3 Ratio H/L count g1_PX151_Rep3 Ratio H/L g1_PX309_HCC1143-1 Ratio H/L g1_PX309_HCC1143-1 Ratio H/L count g1_PX309_HCC1143-2 Ratio H/L count g1_PX309_HCC1143-2 Ratio H/L count g1_PX309_HCC1143-3 Ratio H/L count g1_PX309_HCC1143-3 Ratio H/L coun	· · · · · · · · · · · · · · · · · ·	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L count g1_PX151_Rep1 Ratio H/L iso-count g1_PX151_Rep1 Ratio H/L ype g1_PX151_Rep1 Ratio H/L ype g1_PX151_Rep2 The ratio between two heavy and light label partners. Ratio H/L ype g1_PX151_Rep2 The median of the total ratio population was shifted to 1. Ratio H/L count g1_PX151_Rep2 Ratio H/L count g1_PX151_Rep2 The ratio between two heavy and light label partners. Ratio H/L count g1_PX151_Rep2 Ratio H/L ship Rep2 Ratio H/L g1_PX151_Rep2 Ratio H/L g1_PX151_Rep3 Ratio H/L ship Rep3 Ratio H/L shi	Ratio H/L variability [%] g1_PX151_Rep1	peptides. It is calculated as the standard deviation of the
gt_PX151_Rep1 Ratio H/L ype_gt_PX151_Rep2 Ratio H/L ype_gt_PX151_Rep2 Ratio H/L pye_gt_PX151_Rep2 Ratio H/L pye_gt_PX151_Rep2 Ratio H/L pye_gt_PX151_Rep2 Ratio H/L normalized Ratio H/L variability [%] gt_PX151_Rep2 Ratio H/L so-count gt_PX151_Rep2 Ratio H/L so-count gt_PX151_Rep2 Ratio H/L ype_gt_PX151_Rep2 Ratio H/L ype_gt_PX151_Rep2 Ratio H/L ype_gt_PX151_Rep2 Ratio H/L ype_gt_PX151_Rep3 Ratio H/L ype_gt_PX151_Rep3 Ratio H/L variability [%] gt_PX151_Rep3 Ratio H/L ype_gt_PX151_Rep3 R	Ratio H/L count g1_PX151_Rep1	Number of redundant peptides (MS1 features) used for
Ratio H/L type g1_PX151_Rep2 Ratio H/L g1_PX151_Rep2 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX151_Rep2 Ratio H/L normalized g1_PX151_Rep2 Ratio H/L variability (%) g1_PX151_Rep3 Ratio H/L count g1_PX151_Rep3 Ratio H/L count g1_PX151_Rep3 Ratio H/L variability (%) g1_PX151_Rep3 Ratio H/L variability (%) g1_PX151_Rep3 Ratio H/L count g1_PX309_HCC1143-1 Ratio H/L count g1_PX309_HCC1143-1 Ratio H/L count g1_PX309_HCC1143-1 Ratio H/L count g1_PX309_HCC1143-2 Ratio H/L count g1_PX309_HCC1143-2 Ratio H/L g1_PX309_HCC1143-3 Ratio H/L count g1_PX309_HCC1143-3	· · · · · · · · - · · · · ·	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
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Ratio H/L count g1_PX309_HCC1143-2 Ratio H/L iso-count g1_PX309_HCC1143-2 Ratio H/L type g1_PX309_HCC1143-2 Ratio H/L type g1_PX309_HCC1143-2 Ratio H/L g1_PX309_HCC1143-3 Ratio H/L normalized g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L count Number of redundant peptides (MS1 features) used for		peptides. It is calculated as the standard deviation of the
g1_PX309_HCC1143-2 Ratio H/L type g1_PX309_HCC1143-2 Ratio H/L g1_PX309_HCC1143-3 Ratio H/L normalized g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L count Number of redundant peptides (MS1 features) used for		Number of redundant peptides (MS1 features) used for
Ratio H/L type g1_PX309_HCC1143-2 Ratio H/L g1_PX309_HCC1143-3 The ratio between two heavy and light label partners. Ratio H/L normalized g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L count Number of redundant peptides (MS1 features) used for		
Ratio H/L g1_PX309_HCC1143-3 Ratio H/L g1_PX309_HCC1143-3 Ratio H/L normalized g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L count Number of redundant peptides (MS1 features) used for	Ratio H/L type	
Ratio H/L normalized g1_PX309_HCC1143-3 Ratio H/L variability [%] g1_PX309_HCC1143-3 Ratio H/L variability [%] Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count Number of redundant peptides (MS1 features) used for	<u> </u>	The ratio between two heavy and light label partners.
Ratio H/L variability [%] g1_PX309_HCC1143-3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count Number of redundant peptides (MS1 features) used for	Ratio H/L normalized	Normalized ratio between two medium and light label partners.
Ratio H/L count Number of redundant peptides (MS1 features) used for	Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
IUI PASUS ITUUTT43-3 I IUUANTITATION.	Ratio H/L count g1_PX309_HCC1143-3	

Ratio H/L iso-count g1_PX309_HCC1143-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1143-3	
Ratio H/L g1_PX309_HCC1599-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1599-1	
Ratio H/L g1_PX309_HCC1599-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX309 HCC1599-2	
Ratio H/L g1_PX309_HCC1599-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1599-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1599-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1599-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1599-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX309 HCC1599-3	
Ratio H/L g1_PX309_HCC1937-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-1	
Ratio H/L g1_PX309_HCC1937-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-2	
Ratio H/L g1_PX309_HCC1937-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC1937-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC1937-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC1937-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC1937-3	

Ratio H/L g1_PX309_HCC202-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-1	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_HCC202-1	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC202-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC202-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC202-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC202-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC202-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC202-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-	
Ratio H/L g1_PX309_HCC2218-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-1	
Ratio H/L g1_PX309_HCC2218-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-2	
Ratio H/L g1_PX309_HCC2218-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HCC2218-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HCC2218-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HCC2218-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC2218-3	
Ratio H/L g1_PX309_HMEC1-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
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Ratio H/L variability [%] g1_PX309_HMEC1-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
g1_PX309_HMEC1-1	quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC1-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC1-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC1-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC1-	
Ratio H/L g1_PX309_HMEC2-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_HMEC2-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	quarintation and quarintou wan are to quarinty mounds.
Ratio H/L g1_PX309_HMEC2-2	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 HMEC2-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g1_PX309_HMEC2-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	quantity morror.
Ratio H/L g1_PX309_HMEC2-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMEC2-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMEC2-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMEC2-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMEC2-	gammy manage
Ratio H/L g1_PX309_HMTS1-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
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Ratio H/L iso-count g1_PX309_HMTS1-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-1	quantitation that are quantitied with the re-quantity method.
Ratio H/L g1_PX309_HMTS1-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-2	
Ratio H/L g1_PX309_HMTS1-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_HMTS1-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_HMTS1-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_HMTS1-	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_HMTS1-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HMTS1-3	
Ratio H/L g1_PX309_MCF10a-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MCF10a-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MCF10a-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-	
Ratio H/L g1_PX309_MCF10a-3	The ratio between two heavy and light label partners.
Ratio H/L normalized q1 PX309 MCF10a-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MCF10a-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MCF10a-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MCF10a-3	
Ratio H/L g1_PX309_MDAMB453-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g1_PX309_MDAMB453-2	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g1_PX309_MDAMB453-2	The median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_PX309_MDAMB453-2	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-2	
Ratio H/L g1_PX309_MDAMB453-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MDAMB453-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MDAMB453-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MDAMB453-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MDAMB453-3	
Ratio H/L g1_PX309_MFM223-1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX309_MFM223-3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX309_MFM223-3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX309_MFM223-3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX309_MFM223-3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX309_MFM223-3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_MFM223-	
Ratio H/L g1_PX359_0h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_1	
Ratio H/L g1_PX359_0h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_2	Number of redundant peptides (MS1 features) used for quantitation.

	Number of redundant peptides (MS1 features) used for
Ratio H/L iso-count g1_PX359_0h_2	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_2	
Ratio H/L g1_PX359_0h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_0h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_0h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_0h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_0h_3	
Ratio H/L g1_PX359_BSA_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_1	
Ratio H/L g1_PX359_BSA_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_2	
Ratio H/L g1_PX359_BSA_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_BSA_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_BSA_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_BSA_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_BSA_3	
Ratio H/L g1_PX359_FN_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_1	
Ratio H/L g1_PX359_FN_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_2	
Ratio H/L g1_PX359_FN_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_FN_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_FN_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_FN_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_FN_3	quarintainen inat are quarintee mir ine te quarinty menteur
Ratio H/L g1_PX359_GFR_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_1	
Ratio H/L g1_PX359_GFR_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_2	
Ratio H/L g1_PX359_GFR_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_GFR_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_GFR_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_GFR_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_GFR_3	
Ratio H/L g1_PX359_LAM_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_1	
Ratio H/L g1_PX359_LAM_2 Ratio H/L normalized	The ratio between two heavy and light label partners.
g1_PX359_LAM_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_2	
Ratio H/L g1_PX359_LAM_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_LAM_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_LAM_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_LAM_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_LAM_3	
Ratio H/L g1_PX359_Matr 12h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g1_PX359_Matr 12h_1	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_1	
Ratio H/L g1_PX359_Matr 12h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_2	
Ratio H/L g1_PX359_Matr 12h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 12h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 12h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 12h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 12h_3	
Ratio H/L g1_PX359_Matr 24h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 24h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_1	
Ratio H/L g1_PX359_Matr 24h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 24h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 24h 2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_2	
Ratio H/L g1_PX359_Matr 24h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 24h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 24h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 24h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 24h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 24h_3	
Ratio H/L g1_PX359_Matr 30h_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 30h_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 30h_1	Number of redundant peptides (MS1 features) used for quantitation.
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Ratio H/L iso-count g1_PX359_Matr 30h_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_1	
Ratio H/L g1_PX359_Matr 30h_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 30h_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 30h_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 30h_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_2	
Ratio H/L g1_PX359_Matr 30h_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr 30h_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr 30h_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr 30h_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr 30h_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr 30h_3	
Ratio H/L g1_PX359_Matr dil_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_1	
Ratio H/L g1_PX359_Matr dil_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_2	
Ratio H/L g1_PX359_Matr dil_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX359_Matr dil_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX359_Matr dil_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX359_Matr dil_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX359_Matr dil_3	
Ratio H/L g1_PX419_human_18507	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_18507	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_18507	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_18507	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18507	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_18507	

Ratio H/L g1_PX419_human_18516	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_18516	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_18516	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_18516	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q1 PX419 human 18516	quantition in a series of the
Ratio H/L g1_PX419_human_19193	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19193	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_19193	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_19193	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_19193	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_19193	
Ratio H/L g1_PX419_human_19204	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX419_human_19204	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX419_human_19204	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX419_human_19204	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX419_human_19204	
Ratio H/L g1_PX438_Xeno092	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno092	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno092	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno092	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno092	
Ratio H/L g1_PX438_Xeno441 Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g1_PX438_Xeno441	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno441	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno441	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno441	
Ratio H/L g1_PX438_Xeno561	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno561	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno561	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g1_PX438_Xeno561	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno561	
Ratio H/L g1_PX438_Xeno691	The ratio between two heavy and light label partners.
Ratio H/L normalized g1_PX438_Xeno691	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g1_PX438_Xeno691	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count	Number of redundant peptides (MS1 features) used for
g1_PX438_Xeno691 Ratio H/L iso-count	quantitation. Number of redundant peptides (MS1 features) used for
g1_PX438_Xeno691	quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX438_Xeno691	The ratio between two beauty and light label partners
Ratio H/L g2_PX058_expA Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expA	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expA	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expA	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expA	
Ratio H/L g2_PX058_expB	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expB	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expB	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expB	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expB	The watis hadroness to be a second light label and second
Ratio H/L g2_PX058_expC Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expC	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expC	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expC	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expC	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expC	The watis hadroness to be a second light label and second
Ratio H/L g2_PX058_expD Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expD	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expD	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expD	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expD	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expD	The water hadroness to be accorded back label and some
Ratio H/L g2_PX058_expE Ratio H/L normalized	The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
g2_PX058_expE	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expE	
Ratio H/L g2_PX058_expF	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX058_expF	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX058_expF	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX058_expF	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX058_expF	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX058_expF	
Ratio H/L g2_PX089_Rep1	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX089_Rep1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] g2_PX089_Rep1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX089_Rep1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX089_Rep1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX089_Rep1	
Ratio H/L g2_PX089_Rep2	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX089_Rep2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX089_Rep2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX089_Rep2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g2_PX089_Rep2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX089_Rep2	quantitation that are quantified with the re-quantity method.
Ratio H/L g2_PX537_exp14 rep1	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners.
g2_PX537_exp14 rep1 20h Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g2_PX537_exp14 rep1 20h	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep1 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep1 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 20h	
Ratio H/L g2_PX537_exp14 rep1 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep1 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep1 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count q2 PX537 exp14 rep1 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep1 6h	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g2_PX537_exp14 rep2	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep2 20h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 20h	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L g2_PX537_exp14 rep2 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep2 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep2 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g2_PX537_exp14 rep2 6h	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep2 6h	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep2 6h	quantity monod.
Ratio H/L g2_PX537_exp14 rep3	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 20h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep3 20h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
92_11/0001_exp 14 1epo 2011	naturally logarithmized ratios times 100.

Ratio H/L count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 20h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 20h	
Ratio H/L g2_PX537_exp14 rep3 6h	The ratio between two heavy and light label partners.
Ratio H/L normalized g2_PX537_exp14 rep3 6h	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g2_PX537_exp14 rep3 6h	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g2_PX537_exp14 rep3 6h	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g2_PX537_exp14 rep3 6h	
Ratio M/L g3_GK1_Chromatin_A_TSA_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_1	
Ratio H/L g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_A_TSA_1	
Ratio H/M g3_GK1_Chromatin_A_TSA_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_A_TSA_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_A_TSA_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_A_TSA_1	
Ratio M/L g3_GK1_Chromatin_A_TSA_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_A_TSA_2	
Ratio H/L g3_GK1_Chromatin_A_TSA_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_A_TSA_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
	naturally logarithmized ratios times 100.

Ratio H.L. Be-count 2.0 KCL Chromatin A. TSA. 2 2.0 GKL Chromatin A. TSA. 2 2.0 Normalized an observation of the state of t	Ratio H/L count g3_GK1_Chromatin_A_TSA_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio HL Dype 3, GK1 Chromatin A, TSA, 2 Ratio HM 3, GK1 Chromatin A, TSA, 2 Ratio HM normalized 3, GK1 Chromatin A, TSA, 2 Ratio HM normalized 3, GK1 Chromatin A, TSA, 2 Ratio HM variability [%] 3, GK1 Chromatin A, TSA, 2 Ratio HM variability [%] 3, GK1 Chromatin A, TSA, 2 Ratio HM variability [%] 3, GK1 Chromatin A, TSA, 2 Ratio HM variability [%] 3, GK1 Chromatin A, TSA, 2 Ratio HM variability [%] 3, GK1 Chromatin A, TSA, 2 Ratio HM variability [%] 3, GK1 Chromatin A, TSA, 2 Ratio HM variability (%) 3, GK1 Chromatin A, TSA, 2 Ratio HM variability (%) 3, GK1 Chromatin A, TSA, 2 Ratio HM variability (%) 3, GK1 Chromatin A, TSA, 2 Ratio HM variability (%) 3, GK1 Chromatin A, TSA, 2 Ratio HM variability (%) 3, GK1 Chromatin A, TSA, 2 Ratio HM, Variability (%) 3, GK1 Chromatin A, TSA, 2 Ratio HM, Variability (%) 3, GK1 Chromatin C, 1 Ratio HM, Count (%) 3, GK1	Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
Ratio H/M pormalin. A_TSA_2 Ratio H/M normalized and the total ratio between two heavy and medium label partners. 30, 6K1. Chromatin. A_TSA_2 Ratio H/M variability [%] 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M count 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M count 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M count 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M so-count 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M iso-count 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M ype 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M pye 9.3. GK1. Chromatin. A_TSA_2 Ratio H/M. 9.3. GK1. Chromatin. A_TSA_2 Ratio H/L 8. Ratio H/M pye 9.3. GK1. Chromatin. CC_1 Ratio H/L variability [%] 9.3. GK1. Chromatin. CC_1 Ratio H/L count 9.3. GK1. Chromatin. CC_1 Ratio H/L count 9.3. GK1. Chromatin. CC_1 Ratio H/L count 1. Ratio H/L count 2. GK1. Chromatin. CC_1 Ratio H/L count 2. GK1	Ratio H/L type	quantitation that are quantities with the re-quantity method.
Ratio HM normalized gard tho between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Ratio HM variability [76] g3_GK1_Chromatin_A_TSA_2	Ratio H/M	The ratio between two heavy and medium label partners.
Ratio HM court 3. GKI_Chromatin_A_TSA_2 Ratio HM court 3. GKI_Chromatin_A_TSA_2 Ratio HM court 3. GKI_Chromatin_A_TSA_2 Ratio HM scount 3. GKI_Chromatin_A_TSA_2 Ratio HM_scount 3. GKI_Chromatin_A_TSA_2 Ratio HM_scount 3. GKI_Chromatin_CC_1 Ratio HM_variability PSi_GKI_Chromatin_CC_1 Ratio HM_variability PSi_GKI_Chromatin_CC_2 Ratio HM_var	Ratio H/M normalized	partners. The median of the total ratio population was shifted to
Ratio ML count 3,0 KM . Chromatin A TSA 2 Ratio HM size-count 3,0 KM . Chromatin A TSA 2 Ratio HM size-count 3,0 CK1 . Chromatin A TSA 2 Ratio HM size-count 3,0 CK1 . Chromatin A TSA 2 Ratio HM size-count 3,0 CK1 . Chromatin A TSA 2 Ratio HM size-count 3,0 CK1 . Chromatin A TSA 2 Ratio ML control Ratio May an according to the size of the si	Ratio H/M variability [%] g3_GK1_Chromatin_A_TSA_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio Mt. Control of the control of		Number of redundant peptides (MS1 features) used for
g3_GK1_Chromatin_CC_1	Ratio H/M iso-count	
Ratio ML promatic CC. 1 Ratio ML command promatic CC. 1 Ratio ML command promatic CC. 1 Ratio ML command promatic CC. 1 Ratio ML count Ratio ML so-count Ratio ML iso-count Ratio ML iso-count Ratio ML type Ratio ML type Ratio ML promatic CC. 1 Ratio ML type Ratio ML type Ratio ML rormatic CC. 1 Ratio ML rormatic CC. 1 Ratio ML rormatic CC. 1 Ratio ML type Ratio ML rormatic CC. 1 Ratio HL rormatic CC. 1 Ratio HL rormatic CC. 1 Ratio HL count Ratio HL iso-count Ratio HL iso-count Ratio HL iso-count Ratio HL rormatic CC. 1 Ratio HL rormatic CC. 1 Ratio HL solution in CC. 1 Ratio HL solution in CC. 1 Ratio HL rormatic CC. 1 Ratio HL rormatic CC. 1 Ratio HL solution in CC. 1 Ratio HL solution in CC. 1 Ratio HL solution in CC. 1 Ratio HL rormatic CC. 1 Ratio HL solution in CC. 1 Ratio HL solution in CC. 1 Ratio HL rormatic C	Ratio H/M type g3_GK1_Chromatin_A_TSA_2	
Ratio M.I. normalized g3_GK1_Chromatin_CC_1 Ratio M.I. variability [%] g3_GK1_Chromatin_CC_1 Ratio M.I. variability [%] g3_GK1_Chromatin_CC_1 Ratio M.I. count Ratio M.I. commain_CC_1 Ratio M.I. count Ratio M.I. coun	Ratio M/L	The ratio between two medium and light label partners.
ga3_GK1_Chromatin_CC_1 Ratio ML count g3_GK1_Chromatin_CC_1 Ratio ML iso-count g3_GK1_Chromatin_CC_2 Ratio ML iso-count		
quantitation. quantitation. quantitation. quantitation. quantitation. quantitation. quantitation. quantitation. quantitation that are quantified with the re-quantity method. quantitation. quantitation quan		peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method.		
G3 GK1 Chromatin CC 1 The ratio between two heavy and light label partners.		
Ratio H/L Sa_GK1_Chromatin_CC_1 The ratio between two heavy and light label partners.	Ratio M/L type g3_GK1_Chromatin_CC_1	
Gas GK1_Chromatin_CC_1 The median of the total ratio population was shifted to 1.	Ratio H/L	The ratio between two heavy and light label partners.
g3_GK1_Chromatin_CC_1 Ratio H/L count g3_GK1_Chromatin_CC_1 Ratio H/L count g3_GK1_Chromatin_CC_1 Ratio H/L iso-count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_C	Ratio H/L normalized	
g3_GK1_Chromatin_CC_1 Ratio H/L iso-count g3_GK1_Chromatin_CC_1 Ratio H/L type g3_GK1_Chromatin_CC_1 Ratio H/L type g3_GK1_Chromatin_CC_1 Ratio H/M mormalized g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio M/L g3_GK1_Chromatin_CC_1 Ratio M/L g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L pormalized Ratio H/L pormalized Ratio H/L normalized	Ratio H/L variability [%]	peptides. It is calculated as the standard deviation of the
g3_GK1_Chromatin_CC_1 Ratio H/L type g3_GK1_Chromatin_CC_1 Ratio H/M normalized g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio M/L sor-count g3_GK1_Chromatin_CC_2 Ratio M/L count g4_Ration		Number of redundant peptides (MS1 features) used for
GAL Chromatin CC 1		
Ratio H/M g3_GK1_Chromatin_CC_1 Ratio H/M normalized g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_2 Ratio M/L normalized gain M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L normalized gain for the total ratio population was shifted to 1. Ratio H/M so-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_2 Ratio M/L normalized gain for the total ratio population was shifted to 1. Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L so-count g3_GK1_Chromatin_CC_2 Ratio M/L so-count g3_GK1_Chromatin_CC_2 Ratio M/L so-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized Normalized ratio between two heavy and light label partners. The ratio between two heavy and light label partners.		
g3_GK1_Chromatin_CC_1 Ratio H/M variability [%] g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M so-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized Normalized ratio between two heavy and light label partners.	Ratio H/M	The ratio between two heavy and medium label partners.
g3_GK1_Chromatin_CC_1 Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_2 Ratio M/L normalized g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L chromatin_CC_2 Ratio M/L chromatin_CC_2 Ratio M/L chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L chromatin_CC_2 Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/M normalized	partners. The median of the total ratio population was shifted to
Ratio H/M count g3_GK1_Chromatin_CC_1 Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio M/L g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L normalized Normalized ratio between two medium and light label partners.		peptides. It is calculated as the standard deviation of the
Ratio H/M iso-count g3_GK1_Chromatin_CC_1 Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio M/L g3_GK1_Chromatin_CC_2 Ratio M/L normalized g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L Ratio H/L Ratio H/L Ratio H/L normalized Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.		Number of redundant peptides (MS1 features) used for
Ratio H/M type g3_GK1_Chromatin_CC_1 Ratio M/L g3_GK1_Chromatin_CC_2 Ratio M/L normalized g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/M iso-count	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio M/L g3_GK1_Chromatin_CC_2 Ratio M/L normalized g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized The ratio between two medium and light label partners. The ratio between two medium and light label partners.	Ratio H/M type	
Ratio M/L normalized g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L variability [%] g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized Normalized ratio between two heavy and light label partners. Normalized ratio between two heavy and light label partners. Romatic model is the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.	Ratio M/L	The ratio between two medium and light label partners.
g3_GK1_Chromatin_CC_2 Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners.		
Ratio M/L count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners.	Ratio M/L variability [%]	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio M/L iso-count g3_GK1_Chromatin_CC_2 Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners.		Number of redundant peptides (MS1 features) used for
Ratio M/L type g3_GK1_Chromatin_CC_2 Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.	Ratio M/L iso-count	Number of redundant peptides (MS1 features) used for
Ratio H/L g3_GK1_Chromatin_CC_2 Ratio H/L normalized The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.	Ratio M/L type	, , , , , , , , , , , , , , , , , , , ,
Ratio H/L normalized Normalized ratio between two medium and light label partners.	Ratio H/L	The ratio between two heavy and light label partners.
	Ratio H/L normalized	

Ratio H/L variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_CC_2	
Ratio H/M g3_GK1_Chromatin_CC_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_CC_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_CC_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_CC_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_CC_2	
Ratio M/L g3_GK1_Chromatin_EHT_1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_1	
Ratio H/L g3_GK1_Chromatin_EHT_1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_1	, , , , , , , , , , , , , , , , , , , ,
Ratio H/M g3_GK1_Chromatin_EHT_1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_1	
Ratio M/L g3_GK1_Chromatin_EHT_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_2	
Ratio H/L g3_GK1_Chromatin_EHT_2	The ratio between two heavy and light label partners.

Ratio H/L normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_2	
Ratio H/M g3_GK1_Chromatin_EHT_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_2	
Ratio M/L g3_GK1_Chromatin_EHT_3	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_3	
Ratio H/L g3_GK1_Chromatin_EHT_3	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_3	
Ratio H/M g3_GK1_Chromatin_EHT_3	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_3	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_3	
Ratio M/L g3_GK1_Chromatin_EHT_4	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_4	

Ratio H/L g3_GK1_Chromatin_EHT_4	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_4	
Ratio H/M g3_GK1_Chromatin_EHT_4	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_4	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_4	
Ratio M/L g3_GK1_Chromatin_EHT_5	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_EHT_5	
Ratio H/L g3_GK1_Chromatin_EHT_5	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_5	
Ratio H/M g3_GK1_Chromatin_EHT_5	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_5	
Ratio M/L g3_GK1_Chromatin_EHT_6	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

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Ratio M/L type g3_GK1_Chromatin_EHT_6	
Ratio H/L g3_GK1_Chromatin_EHT_6	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_EHT_6	
Ratio H/M g3_GK1_Chromatin_EHT_6	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_EHT_6	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_EHT_6	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_EHT_6	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_EHT_6	
Ratio M/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two medium and light label partners.
Ratio M/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_GK1_Chromatin_mH2A_4_5	
Ratio H/L g3_GK1_Chromatin_mH2A_4_5	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_GK1_Chromatin_mH2A_4_5	
Ratio H/M g3_GK1_Chromatin_mH2A_4_5	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_GK1_Chromatin_mH2A_4_5	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_GK1_Chromatin_mH2A_4_5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_GK1_Chromatin_mH2A_4_5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_GK1_Chromatin_mH2A_4_5	
Ratio M/L g3_KW35_ET	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.

Ratio M/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_ET	
Ratio H/L g3_KW35_ET	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type q3 KW35 ET	
Ratio H/M g3_KW35_ET	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET	
Ratio M/L g3_KW35_ET_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_ET_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_ET_2	
Ratio H/L g3_KW35_ET_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_ET_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_ET_2	
Ratio H/M g3_KW35_ET_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_ET_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_ET_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_ET_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET_2	
Ratio M/L g3_KW35_nE	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_nE	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_nE	
Ratio H/L g3_KW35_nE	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_nE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%]	Coefficient of variability over all redundant quantifiable
g3_KW35_nE	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE	
Ratio H/M g3_KW35_nE	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_nE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_nE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE	
Ratio M/L g3_KW35_nE_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_nE_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_nE_2	
Ratio H/L g3_KW35_nE_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_nE_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_nE_2	
Ratio H/M g3_KW35_nE_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_nE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_nE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_nE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_nE_2	
Ratio M/L g3_KW35_rot_ET	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_rot_ET	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_rot_ET	
Ratio H/L g3_KW35_rot_ET	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_rot_ET	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_rot_ET	

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Ratio H/M g3_KW35_rot_ET	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_rot_ET	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_rot_ET	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_rot_ET	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_rot_ET	
Ratio M/L g3_KW35_wE	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE	
Ratio H/L g3_KW35_wE	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE	
Ratio H/M g3_KW35_wE	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_wE	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE	
Ratio M/L g3_KW35_wE_2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_KW35_wE_2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_KW35_wE_2	
Ratio H/L g3_KW35_wE_2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_KW35_wE_2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_KW35_wE_2	
Ratio H/M g3_KW35_wE_2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_KW35_wE_2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_KW35_wE_2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/M count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_KW35_wE_2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_wE_2	
Ratio M/L g3_PX328_Diff3_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff3_Exp1	
Ratio H/L g3_PX328_Diff3_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp1	
Ratio H/M g3_PX328_Diff3_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff3_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff3_Exp1	
Ratio M/L g3_PX328_Diff3_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff3_Exp2	
Ratio H/L g3_PX328_Diff3_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff3_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff3_Exp2	
Ratio H/M g3_PX328_Diff3_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff3_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff3_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff3_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/M type	
g3_PX328_Diff3_Exp2 Ratio M/L g3_PX328_Diff4_Exp1	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff4_Exp1	
Ratio H/L g3_PX328_Diff4_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff4_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff4_Exp1	
Ratio H/M g3_PX328_Diff4_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff4_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff4_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff4_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff4_Exp1	
Ratio M/L g3_PX328_Diff4_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff4_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff4_Exp2	
Ratio H/L g3_PX328_Diff4_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff4_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff4_Exp2	
Ratio H/M g3_PX328_Diff4_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff4_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff4_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff4_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff4_Exp2	
Ratio M/L g3_PX328_Diff5_Exp1	The ratio between two medium and light label partners.

Ratio M/L normalized g3_PX328_Diff5_Exp1	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff5_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff5_Exp1	
Ratio H/L g3_PX328_Diff5_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff5_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff5_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for guantitation that are guantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff5_Exp1	
Ratio H/M g3_PX328_Diff5_Exp1	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff5_Exp1	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff5_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff5_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff5_Exp1	
Ratio M/L g3_PX328_Diff5_Exp2	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX328_Diff5_Exp2	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio M/L iso-count q3 PX328 Diff5 Exp2	Number of redundant peptides (MS1 features) used for guantitation that are guantified with the re-quantify method.
Ratio M/L type g3_PX328_Diff5_Exp2	quantitation that are quantified with the re-quantity method.
Ratio H/L g3_PX328_Diff5_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX328_Diff5_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX328_Diff5_Exp2	
Ratio H/M g3_PX328_Diff5_Exp2	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX328_Diff5_Exp2	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX328_Diff5_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX328_Diff5_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX328_Diff5_Exp2	
Ratio M/L g3_PX597_A1_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A1_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.

Ratio M/L variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A1_Spr	
Ratio H/L g3_PX597_A1_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A1_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A1_Spr	
Ratio H/M g3_PX597_A1_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A1_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A1_Spr	
Ratio M/L g3_PX597_A2_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A2_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A2_Spr	
Ratio H/L g3_PX597_A2_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_A2_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A2_Spr	
Ratio H/M g3_PX597_A2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A2_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A2_Spr	
Ratio M/L g3_PX597_A3_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_A3_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_A3_Spr	quantity monde.

Ratio H/L g3_PX597_A3_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
g3_PX597_A3_Spr Ratio H/L variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_A3_Spr	
Ratio H/M g3_PX597_A3_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_A3_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_A3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_A3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_A3_Spr	
Ratio M/L g3_PX597_B1_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B1_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B1_Spr	The section between two because of Polytheles and control
Ratio H/L g3_PX597_B1_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B1_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B1_Spr	
Ratio H/M g3_PX597_B1_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B1_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B1_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/M iso-count g3_PX597_B1_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B1_Spr	
Ratio M/L g3_PX597_B2_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B2_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B2_Spr	
Ratio H/L g3_PX597_B2_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B2_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
<u> </u>	quantitation that are quantitied with the re-quantity method.
Ratio H/L type g3_PX597_B2_Spr	The set's hadron of the harmonial and the latest and the
Ratio H/M g3_PX597_B2_Spr	The ratio between two heavy and medium label partners.
Ratio H/M normalized g3_PX597_B2_Spr	Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1.
Ratio H/M variability [%] g3_PX597_B2_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/M count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/M iso-count g3_PX597_B2_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_PX597_B2_Spr	
Ratio M/L g3_PX597_B3_Spr	The ratio between two medium and light label partners.
Ratio M/L normalized g3_PX597_B3_Spr	Normalized ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1.
Ratio M/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio M/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio M/L iso-count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio M/L type g3_PX597_B3_Spr	
Ratio H/L g3_PX597_B3_Spr	The ratio between two heavy and light label partners.
Ratio H/L normalized g3_PX597_B3_Spr	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g3_PX597_B3_Spr	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g3_PX597_B3_Spr	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count	Number of redundant peptides (MS1 features) used for
g3_PX597_B3_Spr	quantitation that are quantified with the re-quantify method.
g3_PX597_B3_Spr Ratio H/L type g3_PX597_B3_Spr	quantitation that are quantified with the re-quantify method.
<u> </u>	quantitation that are quantified with the re-quantify method. The ratio between two heavy and medium label partners.
Ratio H/L type g3_PX597_B3_Spr	
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%]	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners.
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L normalized g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A Ratio H/L iso-count g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A Ratio H/L iso-count g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A Ratio H/L iso-count g4_NCC_A Ratio H/L type g4_NCC_A	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A Ratio H/L iso-count g4_NCC_A Ratio H/L type g4_NCC_A Ratio H/L type g4_NCC_B Ratio H/L g4_NCC_B	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A Ratio H/L iso-count g4_NCC_A Ratio H/L type g4_NCC_A Ratio H/L type g4_NCC_B Ratio H/L p4_NCC_B Ratio H/L variability [%] g4_NCC_B	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L count g4_NCC_A Ratio H/L iso-count g4_NCC_A Ratio H/L type g4_NCC_A Ratio H/L d4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L type g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L count g4_NCC_B Ratio H/L type g4_NCC_B	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for
Ratio H/L type g3_PX597_B3_Spr Ratio H/M g3_PX597_B3_Spr Ratio H/M normalized g3_PX597_B3_Spr Ratio H/M variability [%] g3_PX597_B3_Spr Ratio H/M count g3_PX597_B3_Spr Ratio H/M iso-count g3_PX597_B3_Spr Ratio H/M type g3_PX597_B3_Spr Ratio H/L g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L variability [%] g4_NCC_A Ratio H/L iso-count g4_NCC_A Ratio H/L type g4_NCC_A Ratio H/L type g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L type g4_NCC_B Ratio H/L variability [%] g4_NCC_B Ratio H/L variability [%] g4_NCC_B	The ratio between two heavy and medium label partners. Normalized ratio between two heavy and medium label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for

Ratio H/L variability [%] g4_NCC_C	Coefficient of variability over all redundant quantifiable
	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC_C	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC_C	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC_C	
Ratio H/L g4_NCC-CPT_s1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT_s1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- CPT_s1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s1	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g4_NCC- CPT_s1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s1	
Ratio H/L g4_NCC-CPT_s2	The ratio between two heavy and light label partners.
	, , , , , , , , , , , , , , , , , , ,
Ratio H/L normalized g4_NCC- CPT_s2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-CPT_s2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- CPT_s2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s2	
Ratio H/L g4_NCC-CPT_s3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- CPT s3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-CPT_s3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-CPT_s3	Number of redundant peptides (MS1 features) used for guantitation.
Ratio H/L iso-count g4_NCC- CPT_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-CPT_s3	
Ratio H/L g4_NCC-HU_Ex1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU_Ex1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- HU_Ex1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-HU_Ex1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex1	
Ratio H/L g4_NCC-HU_Ex2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- HU Ex2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- HU_Ex2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the
Ratio H/L count g4_NCC-HU_Ex2	naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU Ex2	Number of redundant peptides (MS1 features) used for guantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex2	The second secon
Ratio H/L g4_NCC-HU_Ex3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-HU_Ex3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-HU_Ex3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-HU_Ex3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- HU_Ex3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-HU_Ex3	
Ratio H/L g4_NCC-rosco_s1	The ratio between two heavy and light label partners.

Ratio H/L normalized g4_NCC-	Normalized ratio between two medium and light label partners.
rosco_s1	The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-rosco_s1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-rosco_s1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s1	
Ratio H/L g4_NCC-rosco_s2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- rosco s2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-rosco_s2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-rosco_s2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s2	
Ratio H/L g4_NCC-rosco_s3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-rosco_s3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-rosco_s3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-rosco_s3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-rosco_s3	
Ratio H/L g4_NCC-TSA_Exp1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- TSA_Exp1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC- TSA_Exp1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp1	
Ratio H/L g4_NCC-TSA_Exp2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-TSA_Exp2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-TSA_Exp2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp2	
Ratio H/L g4_NCC-TSA_Exp3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC- TSA_Exp3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_NCC-TSA_Exp3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_NCC-TSA_Exp3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC- TSA_Exp3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-TSA_Exp3	
Ratio H/L g4_PX183_A	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX183_A	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX183_A	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX183_A	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H.V. and p.Y.183_B Ratio H.V. and p.Y.183_C Ratio H.V. and p.V. and p.V	Ratio H/L type g4_PX183_A	
Ratio H/L normalized g4_PX183_B Ratio H/L variability (%) get px183_B Ratio H/L variability (%) get px183_B Ratio H/L count g4_PX183_B Ratio H/L count g4_PX183_B Ratio H/L so-count g4_PX183_C Ratio H/L variability (%) get px183_C Ratio H/L count g4_PX183_C Ratio H/L variability (%) get px183_C Ratio H/L variability (%) get px183_C Ratio H/L count g4_PX183_C Ratio H/L variability (%) get px183_C Ratio H/L variability (%) get px183_C Ratio H/L count g4_PX183_C Ratio H/L so-count g4_PX183_D Ratio H/L so-count g4_PX183_E Ratio H/L so-count g4		The ratio between two heavy and light label partners.
peptides, it is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX183_B Ratio H/L count g4_PX183_B Ratio H/L count g4_PX183_B Ratio H/L variability (%) peptides, H/S count g4_PX183_C Ratio H/L variability (%) Ratio H/L variability (%) peptides, H/S count g4_PX183_C Ratio H/L yariability (%) pertides (MS1 features) used for quantitation that are quantified with the re-quantity method. Ratio H/L variability (%) peptides, H/S count g4_PX183_C Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) pertides (MS1 features) used for quantitation. Ratio H/L variability (%) peptides. H/S calculated as the standard deviation of the naturally forgarithmized ratio between two medium and light label partners. Ratio H/L variability (MS1) peptides. H/S calculated as the standard deviation of the naturally forgarithmized ratio between two medium and light label partners. Ratio H/L variability (MS1) peptides. H/S calculated as the standard deviation of the naturally forgarithmized ratio between two medium and light label partners. Ratio H/L so-count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L count g4_PX183_E Ratio H/L so-count g4_PX183_E Ratio H/L so-count g4_PX441_E1 Ratio H/L so-count g4_PX441_E1 R	<u> </u>	Normalized ratio between two medium and light label partners.
Ratio H/L Iso-count g4_PX183_B Ratio H/L Iso-count g4_PX183_B Ratio H/L Iyop g4_PX183_B Ratio H/L Iyop g4_PX183_B Ratio H/L Iyop g4_PX183_C Ratio H/L p4_PX183_C Ratio H/L service in the service i		peptides. It is calculated as the standard deviation of the
Ratio H/L type g4_PX183_B Ratio H/L type g4_PX183_C Ratio H/L normalized g4_PX183_C Ratio H/L variability [%] g4_PX183_C Ratio H/L so-count g4_PX183_C Ratio H/L type g4_PX183_D The ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L type g4_PX183_D The ratio between two heavy and light label partners. Ratio H/L variability (%) g4_PX183_D Ratio H/L so-count g4_PX183_E Ratio H/L variability (%) g4_PX183_E The ratio between two heavy and light label partners. Ratio H/L variability (%) g4_PX183_E Ratio H/L variability	Ratio H/L count g4_PX183_B	
Ratio H/L pd_PX183_C Ratio H/L variability [%] Ratio H/L count g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L so-count g4_PX183_D Ratio H/L variability [%] Ratio H/L variability [%] Ratio H/L variability [%] Ratio H/L count g4_PX183_D Ratio H/L so-count g4_PX183_D Ratio H/L variability (%) Ratio H/L varia	Ratio H/L iso-count g4_PX183_B	
Ratio H/L normalized g4_PX183_C Ratio H/L variability [%] g4_PX183_C Ratio H/L variability [%] g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L sio-count g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L variability [%] g4_PX183_D Ratio H/L sio-count g4_PX183_D Ratio H/L variability [%] g4_PX183_B Ratio H/L variability [%] g4_PX183_E Ratio H/L variability [%] g4_PX184_E1 Ratio H/L variability [%] g4_PX184_E2 Ratio H/L variability [%] g4_PX184_E2 Ratio H/L variability	Ratio H/L type g4_PX183_B	
The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g/4_PX183_C Ratio H/L count g4_PX183_C Ratio H/L sise-count g4_PX183_C Ratio H/L sise-count g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_C Ratio H/L type g4_PX183_D Ratio H/L sise-count g4_PX183_D Ratio H/L variability [%] g/4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L sise-count g4_PX183_D Ra	Ratio H/L g4_PX183_C	The ratio between two heavy and light label partners.
peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX183_C Ratio H/L iso-count g4_PX183_C Ratio H/L ype g4_PX183_C Ratio H/L ype g4_PX183_C Ratio H/L variability [%] g4_PX183_D Ratio H/L variability [%] g4_PX183_D Ratio H/L variability [%] g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L so-count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L count g4_PX183_D Ratio H/L ype g4_PX183_E Ratio H/L variability [%] g4_PX183_E Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E1 Ratio H/L count g4_PX184_E3 Ratio H/L count g4_PX184_E3 Ratio H/L count g4_PX184_E3 Ratio H/L count g4_PX184_E3 Ratio	Ratio H/L normalized g4_PX183_C	
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quantitation that are quantified with the re-quantify method. Ratio H/L type g4_PX441_E2 Ratio H/L normalized g4_PX441_E2 Ratio H/L variability [%] g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L variability [%] g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L type g4_PX441_E3 Ratio H/L variability [%] Ratio H/L variability [%] Ratio H/L type g4_PX441_E3 Ratio H/L ormalized g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L count g4_PX441_E1	
Ratio H/L g4_PX441_E2 Ratio H/L normalized g4_PX441_E2 Ratio H/L variability [%] g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L type g4_PX441_E3 Ratio H/L normalized g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L ratio between two heavy and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L iso-count g4_PX441_E2 Ratio H/L so-count g4_PX441_E2 Ratio H/L ratio between two heavy and light label partners. Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3	Ratio H/L iso-count g4_PX441_E1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L normalized g4_PX441_E2 Ratio H/L variability [%] g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L type g4_PX441_E3 Ratio H/L normalized g4_PX441_E3 Ratio H/L count g4_PX441_E3 Ratio H/L count g4_PX441_E3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for quantitation. Ratio H/L type g4_PX441_E2 Ratio H/L g4_PX441_E3 The ratio between two heavy and light label partners. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L type g4_PX441_E1	
The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L type g4_PX441_E3 Ratio H/L normalized g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 The ratio between two heavy and light label partners. Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for quantifable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Number of redundant peptides (MS1 features) used for	Ratio H/L g4_PX441_E2	The ratio between two heavy and light label partners.
g4_PX441_E2 peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Number of redundant peptides (MS1 features) used for quantitation. Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Ratio H/L type g4_PX441_E2 Ratio H/L g4_PX441_E3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L normalized g4_PX441_E2	
Ratio H/L count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L iso-count g4_PX441_E2 Ratio H/L type g4_PX441_E2 Ratio H/L g4_PX441_E3 Ratio H/L normalized g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L variability [%] g4_PX441_E3 Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method. Normalized ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		peptides. It is calculated as the standard deviation of the
quantitation that are quantified with the re-quantify method. Ratio H/L type g4_PX441_E2 Ratio H/L q4_PX441_E3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L count g4_PX441_E2	Number of redundant peptides (MS1 features) used for
Ratio H/L g4_PX441_E3 The ratio between two heavy and light label partners. Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L iso-count g4_PX441_E2	
Ratio H/L normalized g4_PX441_E3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for	Ratio H/L type g4_PX441_E2	
Ratio H/L normalized g4_PX441_E3 Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1. Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		The ratio between two heavy and light label partners.
Ratio H/L variability [%] g4_PX441_E3 Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100. Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		Normalized ratio between two medium and light label partners.
Ratio H/L count g4_PX441_E3 Number of redundant peptides (MS1 features) used for		peptides. It is calculated as the standard deviation of the
	Ratio H/L count g4_PX441_E3	Number of redundant peptides (MS1 features) used for

Ratio H/L iso-count g4_PX441_E3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E3	quantitation that are quantitied with the re-quantity mentur.
Ratio H/L g4_PX441_E4	The ratio between two heavy and light label partners.
Ratio H/L g4_FX441_E4 Ratio H/L normalized g4_PX441_E4	Normalized ratio between two medium and light label partners.
Ratio H/L variability [%]	The median of the total ratio population was shifted to 1. Coefficient of variability over all redundant quantifiable
g4_PX441_E4	peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E4	
Ratio H/L g4_PX441_E5	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_E5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_E5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_E5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_E5	
Ratio H/L g4_PX441_F1	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F1	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F1	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F1	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F1	
Ratio H/L g4_PX441_F2	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F2	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F2	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F2	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F2	
Ratio H/L g4_PX441_F3	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F3	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F3	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F3	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F3	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F3	
Ratio H/L g4_PX441_F4	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F4	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F4	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F4	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F4	
Ratio H/L g4_PX441_F5	The ratio between two heavy and light label partners.
Ratio H/L normalized g4_PX441_F5	Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] g4_PX441_F5	Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_PX441_F5	Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_PX441_F5	
Sequence coverage g1_GK1_Chromatin_AL [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_CPT [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_CR [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_HepHek [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_hilR [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_loIR [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_mH2A_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_mH2A_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_mH2A_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_TNFa_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_TNFa_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_GK1_Chromatin_TNFa_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW10_110506 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW10_131126 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW10_140117 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW11_130125 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW11_140104_nE [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW11_140104_wE [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW12_130317 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW12_131223 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW13_130328 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW14_130317 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW15_130317 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW17_130319 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW8_120517 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence

Sequence coverage g1_KW8_131126 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence
91_1000_101120[70]	contained within the group.
Sequence coverage g1_KW8_140117 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW9_120425 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_KW9_120510 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H10 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H11 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H12 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H4 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H5 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H6 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H7 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H8 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_H9 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa1_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa1_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa2_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa2_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa2_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa3_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa3_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa3_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa4_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa4_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa4_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g1_PX1194_PCa5_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence
91_1 X1104_1 Odo_1 [70]	contained within the group.
Sequence coverage g1_PX1194_PCa5_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa5_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa6_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1194_PCa7_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18486 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18498 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18499 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18501 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18502 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18504 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18505 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18507 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18508 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18510 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18511 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18516 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18517 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18519 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18520 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18522 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18523 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18852 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18855 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18858 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18861 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18862 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g1_PX1406_GM18870 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18871 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18907 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18909 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18912 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18913 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM18916 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19092 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19093 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19098 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19099 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19101 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19102 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19108 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19114 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19116 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19119 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19127 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19128 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19130 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19131 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19137 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19138 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19140 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19143 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19144 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19147 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g1_PX1406_GM19152 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19153 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19160 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19172 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19192 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19193 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19200 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19203 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19204 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19207 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19209 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19222 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX1406_GM19257 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX151_Rep1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX151_Rep2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX151_Rep3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1143-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1143-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1143-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1599-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1599-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1599-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1937-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1937-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC1937-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC202-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC202-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g1_PX309_HCC202-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC2218-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC2218-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HCC2218-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMEC1-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMEC1-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMEC1-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMEC2-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMEC2-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMEC2-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMTS1-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMTS1-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_HMTS1-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MCF10a-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MCF10a-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MCF10a-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MDAMB453-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MDAMB453-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MDAMB453-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MFM223-1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MFM223-2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX309_MFM223-3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_0h_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_0h_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_0h_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_BSA_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_BSA_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g1_PX359_BSA_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_FN_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_FN_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_FN_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_GFR_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_GFR_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_GFR_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_LAM_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_LAM_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_LAM_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 12h_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 12h_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 12h_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 24h_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 24h_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 24h_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 30h_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 30h_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr 30h_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr dil_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr dil_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX359_Matr dil_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX419_human_18507 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX419_human_18516 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX419_human_19193 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX419_human_19204 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX438_Xeno092 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g1_PX438_Xeno441 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence
91_1	contained within the group.
Sequence coverage g1_PX438_Xeno561 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g1_PX438_Xeno691 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX058_expA [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX058_expB [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX058_expC [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX058_expD [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX058_expE [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX058_expF [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX089_Rep1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX089_Rep2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX537_exp14 rep1 20h [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX537_exp14 rep1 6h [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX537_exp14 rep2 20h [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX537_exp14 rep2 6h [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX537_exp14 rep3 20h [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g2_PX537_exp14 rep3 6h [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_A_TSA_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_A_TSA_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_CC_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_CC_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_EHT_1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_EHT_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_EHT_3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_EHT_4 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_EHT_5 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_GK1_Chromatin_EHT_6 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g3_GK1_Chromatin_mH2A_4_5 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_ET [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_ET_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_nE [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_nE_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_rot_ET [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_wE [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_KW35_wE_2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX328_Diff3_Exp1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX328_Diff3_Exp2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX328_Diff4_Exp1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX328_Diff4_Exp2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX328_Diff5_Exp1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX328_Diff5_Exp2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX597_A1_Spr [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX597_A2_Spr [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX597_A3_Spr [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX597_B1_Spr [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX597_B2_Spr [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g3_PX597_B3_Spr [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC_A [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC_B [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC_C [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-CPT_s1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-CPT_s2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC- CPT_s3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC- HU_Ex1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage g4_NCC-HU_Ex2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-HU_Ex3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-rosco_s1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-rosco_s2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-rosco_s3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-TSA_Exp1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-TSA_Exp2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_NCC-TSA_Exp3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX183_A [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX183_B [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX183_C [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX183_D [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX183_E [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_E1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_E2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_E3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_E4 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_E5 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_F1 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_F2 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_F3 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_F4 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage g4_PX441_F5 [%]	Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Intensity	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_GK1_Chromatin_AL	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
, -	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity H g1_GK1_Chromatin_AL	linked to the heavy label partner.
Intensity g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CPT	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_CR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_HepHek	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_hiIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_hilR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_loIR	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_mH2A_3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_mH2A_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
g1_GK1_Chromatin_TNFa_2 Intensity H	linked to the light label partner. Summed up eXtracted Ion Current (XIC) of the isotopic cluster
g1_GK1_Chromatin_TNFa_2	linked to the heavy label partner.
Intensity g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_TNFa_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_110506	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW10_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_130125	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW11_140104_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW12_131223	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW13_130328	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW14_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW15_130317	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW17_130319	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_120517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_131126	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW8_140117	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120425	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_KW9_120510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H10	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H11	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H12	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H7	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H8	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_H9	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa1_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa1_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa2_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa3_3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa3_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa4_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa5_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa6_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa6_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1194_PCa7_1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1194_PCa7_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18486	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18498	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18498	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18498	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18499	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18499	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

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Intensity L g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18501	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18502	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18504	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18505	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18508	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18508	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18510	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18511	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18516	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18516	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18516	Summed up extracted lon Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18517	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18517	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18519	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18520	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18520	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18522	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18523	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18523	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18852	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18852	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18855	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18855	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18855	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18858	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18858	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18861	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18862	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18862	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18862	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18870	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18870	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18871	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18907	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18909	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18912	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18913	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM18916	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19093	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19098	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19099	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19101	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19102	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19108	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19114	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19116	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19119	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19127	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19128	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19130	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19130	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19131	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19131	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19137	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19138	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19138	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19140	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19143	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19144	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19147	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19147	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19152	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19153	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19160	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19160	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19160	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19172	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19172	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19192	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

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Intensity L g1_PX1406_GM19192	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19192	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19200	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19200	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19203	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19207	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19207	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19209	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19209	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19222	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX1406_GM19257	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX1406_GM19257	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX1406_GM19257	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX151_Rep3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX151_Rep3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1143-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1599-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC1937-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC202-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HCC2218-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HCC2218-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC1-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

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Intensity L g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMEC2-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_HMTS1-3	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_HMTS1-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_HMTS1-3	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MCF10a-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

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Intensity L g1_PX309_MDAMB453- 2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MDAMB453-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MFM223-2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MFM223-3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_0h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_BSA_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_FN_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_GFR_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_2	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_LAM_3	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_LAM_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 12h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 24h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr 30h_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
, ,	linked to the light label partner.
Intensity H g1_PX359_Matr dil_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX359_Matr dil_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18507	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_18516	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19193	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX419_human_19204	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX419_human_19204	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno092	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno441	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno561	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno561	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno561	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g1_PX438_Xeno691	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g1_PX438_Xeno691	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX438_Xeno691	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expA	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expA	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expB	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expC	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expD	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX058_expF	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX089_Rep1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX089_Rep2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep1 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep1 6h	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep1 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.

Intensity L g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep2 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep2 6h	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep2 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep3 20h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g2_PX537_exp14 rep3 6h	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_A_TSA_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_A_TSA_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_CC_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic
	patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
	Summed up eXtracted Ion Current (XIC) of the isotopic cluster

Intensity g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3 GK1 Chromatin EHT 3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_4	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_EHT_6	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_GK1_Chromatin_mH2A_4_5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_ET	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_ET	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_ET_2	Summed up eXtracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_ET_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
	Summed up eXtracted Ion Current (XIC) of the isotopic cluster
Intensity M g3_KW35_ET_2	linked to the medium label partner.

Intensity g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_nE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_nE_2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_nE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_rot_ET	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_rot_ET	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_KW35_wE_2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_KW35_wE_2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff3_Exp1	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp1	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff3_Exp2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff3_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff4_Exp1	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff4_Exp2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff4_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX328_Diff5_Exp2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX328_Diff5_Exp2	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX328_Diff5_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A1_Spr	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A2_Spr	Summed up extracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_A3_Spr	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_A3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B1_Spr	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B1_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g3_PX597_B2_Spr	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B2_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H g3_PX597_B3_Spr	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_B	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC_C	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-CPT_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-HU_Ex2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-HU_Ex3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g4_NCC-HU_Ex3	Summed up extracted Ion Current (XIC) of the isotopic cluster
Intensity g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experient this is the total intensity of all the isotopic
Intensity L g4_NCC-rosco_s1	patterns in the label cluster. Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s2	Summed up extracted lon Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-rosco_s3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp1	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp2	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_NCC-TSA_Exp3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_A	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_A	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_B	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_B	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_C	Summed up extracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_C	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_D	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_D	Summed up eXtracted lon Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g4_PX183_D	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX183_E	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX183_E	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_E5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F1	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F2	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F3	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.

Intensity H g4_PX441_F4	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g4_PX441_F5	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Only identified by site	When marked with '+', this particular protein group was identified only by a modification site.
Reverse	When marked with '+', this particular protein group contains no protein, made up of at least 50% of the peptides of the leading protein, with a peptide derived from the reversed part of the decoy database. These should be removed for further data analysis. The 50% rule is in place to prevent spurious protein hits to erroneously flag the protein group as reverse.
Potential contaminant	When marked with '+', this particular protein group was found to be a commonly occurring contaminant. These should be removed for further data analysis.
id	A unique (consecutive) identifier for each row in the proteinGroups table, which is used to cross-link the information in this file with the information stored in the other files.
Peptide IDs	Identifier(s) of the associated peptide sequence(s) summary, which can be found in the file 'peptides.txt'.
Peptide is razor	Indicates for each peptide ID if it is a razor or group unique peptide (true) or a non unique non razor peptide (false).
Mod. peptide IDs	
Evidence IDs	
MS/MS IDs	
Best MS/MS	The identifier of the best (in terms of quality) MS/MS scans identifying the peptides of this protein, referenced against the msms table.
Oxidation (M) site IDs	Identifier(s) for site(s) associated with the protein group, which show(s) evidence of the modification, referenced against the appropriate modification site file.
Oxidation (M) site positions	Positions of the sites in the leading protein of this group.

All peptides

Name	Separator	Description
Raw file		Name of the raw file the spectral data was extracted from.
Туре		The type of detection for the peptide. SILAC – A SILAC pair was detected. ISO – An isotope pattern was detected.
Charge		The charge state of the peptide.
m/z		The mass divided by the charge of the charged peptide.
Mass		The mass of the neutral peptide ((m/z-proton) * charge).
Uncalibrated m/z		m/z before recalibrations have been applied.
Resolution		The resolution of the peak detected for the peptide measured in Full Width at Half Maximum (FWHM).
Number of data points		The number of data points (peak centroids) collected for this peptide feature.
Number of scans		The number of MS scans that the 3d peaks of this peptide feature are overlapping with.
Number of isotopic peaks		The number of isotopic peaks contained in this peptide feature.
PIF		Short for Parent Ion Fraction; indicates the fraction the target peak makes up of the total intensity in the inclusion window.
Mass fractional part		The values after the radix point (ie value - floor(value)).
Mass deficit		Empirically derived deviation measure to the next nearest integer scaled to center around 0. Can be used to visually detect contaminants in a plot setting Mass against this value.
		m*a+b – round(m*a+b) m: the peptide mass a: 0.999555 b: -0.10
Mass precision [ppm]		The precision of the mass detection of the peptide in parts-per- million.
Max intensity m/z 0		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Max intensity m/z 1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Max intensity m/z 2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Retention time		The retention time of the peak detected for the peptide measured in minutes.
Retention Length		The total retention time width of the peak (last timepoint – first timepoint) in seconds.
Retention Length (FWHM)		The full width at half maximum value retention time width of the peak in seconds.
Min scan number		The first scan-number at which the peak was encountered.
Max scan number		The last scan-number at which the peak was encountered.
Identified		When marked with '+' this particular MS/MS scan was identified as a peptide; when marked with '-' no identification was made.
MS/MS IDs		Unique identifier linking this identification to the MS/MS scans.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column "Sequence".
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to 'unmodified'.
		Note: This column only set when this MS/MS spectrum has been identified.
Modified sequence		Sequence representation of the peptide including location(s) of modified AAs.
		Note: This column only set when this MS/MS spectrum has been identified.
Proteins		Identifiers of proteins this peptide is associated with.
		Note: This column only set when this MS/MS spectrum has been identified.

Score	The score of the identification (higher is better).
	Note: This column only set when this MS/MS spectrum has been identified.
Lys Count	The number of instances of Lys contained within the sequence. The value for this can reliably be determined in the case of SILAC partners, based on the distance between the partners. These counts are used to solidify the peptide identification process.
Arg Count	The number of instances of Arg contained within the sequence. The value for this can reliably be determined in the case of SILAC partners, based on the distance between the partners. These counts are used to solidify the peptide identification process.
Ratio M/L	The ratio between two medium and light multiplet members.
Ratio M/L normalized	Normalized ratio between two medium and light multiplet members. The median of the total ratio population was shifted to 1.
Ratio H/L	The ratio between two heavy and light multiplet members.
Ratio H/L normalized	Normalized ratio between two heavy and light multiplet members. The median of the total ratio population was shifted to 1.
Ratio H/M	The ratio between two heavy and medium multiplet members.
Ratio H/M normalized	Normalized ratio between two heavy and medium multiplet members. The median of the total ratio population was shifted to 1.
Intensity	Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity M	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the medium label partner.
Intensity H	Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensities L	The intensity values of the light SILAC partner isotopes.
Intensities M	The intensity values of the medium SILAC partner isotopes.
Intensities H	The intensity values of the heavy SILAC partner isotopes.
MS/MS Count	The number of MS/MS spectra recorded for the peptide.
MSMS Scan Numbers	The scan numbers where the MS/MS spectra were recorded.
MSMS SILAC States	The SILAC partner detected for the peptide. The value 0 is always the light partner. In the case of double SILAC labeling 1 is the heavy partner. In the case of triple SILAC labeling 1 is the medium and 2 the heavy partner.
MSMS Isotope Indices	Indices of the isotopic peaks that the MS/MS spectra reside on. A value of 0 corresponds to the monoisotopic peak.

MS scans

The msScans table contains information about the full scans, which can be used to verify data quality and generated useful statistics about the interaction between the samples and LC.

Name	Separator	Description
Raw file		The name of the RAW-file the mass spectral data originates from.
Scan number		The scan number (defined in the raw-file) at which the full scan was made.
Scan index		The consecutive index of this full scan.
Retention time		The retention time at which the full scan was made.
Cycle time		The total time (full scan including the tandem MS scans) this full scan has taken up.
Ion injection time		The total injection time that was required to capture the specified amount of ions. This value is limited by a maximum, which can be used to determine whether the time has maxed out (indicative of a bad acquisition).
Base peak intensity		The intensity of the most intense ion in the spectrum.
Total ion current		The total intensity acquired in the full scan.
MS/MS count		The number of tandem MS scans that were made based on this full scan (e.g. a top 10 method selects the top 10 most intense ions in the scan and fragments those).
Mass calibration		The applied mass correction in Th to the full scan.
Experiment		
Peak length		The average time between the start and the end of the peaks detected in the full scan.
Isotope pattern length		The average time between the start and the end of the isotope patterns detected in the full scan.
Multiplet length		The average time between the start and the end of the isotope patterns of the labeling multiplets detected in the full scan.
Peaks / s		The average number of peaks detected per second of chromatography.
Single peaks / s		The average number of single peaks detected per second of chromatography.
Isotope patterns / s		The average number of isotope patterns detected per second of chromatography.
Single isotope patterns / s		The average number of single isotope patterns detected per of second chromatography.
Multiplets / s		The average number of labeling multiplets detected per of second chromatography.
Identified multiplets / s		The percentage of labeling multiplets actually identified.
Multiplet identification rate [%]		The percentage of the detected labeling multiplets that were identified.
MS/MS / s		The average number of MS/MS events per second of chromatography.
Identified MS/MS / s		The average number of identified MS/MS events per second of chromatography.
MS/MS identification rate [%]		The percentage of tandem MS scans that were identified.
Intens Comp Factor		Taken from the Thermo RAW file.
CTCD Comp		Taken from the Thermo RAW file.
RawOvFtT		For Thermo Fisher only. TIC estimation done with the orbitrap cell.
AGC Fill		Taken from the Thermo RAW file.

MZ range

Name	Separator	Description
Raw file		The name of the RAW-file the mass spectral data was derived from.
m/z		The mass-over-charge value.
Peaks / Da		The average number of peaks detected per Dalton.
Single peaks / Da		The average number of single peaks detected per Dalton.
Isotope patterns / Da		The average number of isotope patterns detected per Dalton.
Single isotope patterns / Da		The average number of single isotope patterns detected per Dalton.
SILAC pairs / Da		The average number of SILAC pairs detected per Dalton.
Identified SILAC pairs / Da		The percentage of SILAC pairs actually identified.
SILAC identification rate [%]		The percentage of the detected SILAC pairs that were identified.
MS/MS / Da		The average number of MS/MS events per Dalton.
Identified MS/MS / Da		The average number of identified MS/MS events per Dalton.
Identification rate [%]		The percentage of tandem MS scans that were identified.

MS/MS scans

Name	Separator	Description
Raw file		Name of the RAW file the spectral MS/MS data was extracted
		from.
Scan number		RAW file derived scan number for the MS/MS spectrum.
Retention time		Time point along the elution profile at which the MS/MS data was recorded.
Ion injection time		The ion inject time for the MS/MS scan. This can be used to determine if this time equals to the maximum ion inject time, general indicative of a lower quality spectrum.
Total ion current		The total ion current of the MS/MS scan. For Thermo data this value is calculated by summing all the intensity values found in the mass spectral data, which is different from the Xcalibur reported TIC (Xcalibur TIC is about 25% of the value reported here).
Collision energy		The collision energy used for the fragmentation that resulted in this MS/MS scan.
Summations		For time of flight instruments only.
Base peak intensity		The intensity of the most intense ion in the spectrum.
Elapsed time		The time the MS/MS scan took to complete.
Identified		When marked with '+' this particular MS/MS scan was identified as a peptide; when marked with '-' no identification was made.
MS/MS IDs		Unique identifier linking this identification to the MS/MS scans.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column "Sequence".
Filtered peaks		Number of peaks after the 'top X per 100 Da' filtering.
m/z		Recalibrated m/z of the precursor ion.
Mass		Charge corrected mass of the precursor ion.
Charge		Charge state of the precursor ion.
Туре		The type of precursor ion as identified by MaxQuant. ISO – isotopic cluster. PEAK – single peak. MULTI – labeling cluster.
Fragmentation		The type of fragmentation used to create the MS/MS spectrum. CID – Collision Induced Dissociation. HCD – High energy Collision induced Dissociation. ETD – Electron Transfer Dissociation.
Mass analyzer		The mass analyzer used to record the MS/MS spectrum. ITMS – Ion trap. FTMS – Fourier transform ICR or orbitrap cell. TOF – Time of flight.
Parent intensity fraction		The percentage the parent ion intensity makes up of the total intensity in the selection window.
Fraction of total spectrum		The percentage the parent ion intensity makes up of the total intensity of the whole MS spectrum.
Base peak fraction		The percentage the parent ion intensity in comparison to the highest peak in he MS spectrum.
Precursor full scan number		The full scan number where the precursor ion was selected for fragmentation.
Precursor intensity		The intensity of the precursor ion at the scannumber it was selected.
Precursor apex fraction		The fraction the intensity of the precursor ion makes up of the peak (apex) intensity.
Precursor apex offset		How many full scans the precursor ion is offset from the peak (apex) position.
Precursor apex offset time		How much time the precursor ion is offset from the peak (apex) position.
Scan event number		This number indicates which MS/MS scan this one is in the consecutive order of the MS/MS scans that are acquired after an MS scan.
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to 'unmodified'.
		Note: This column only set when this MS/MS spectrum has been identified.
Modified sequence		Sequence representation of the peptide including location(s) of modified AAs.
		Note: This column only set when this MS/MS spectrum has been identified.

Proteins	Identifiers of proteins this peptide is associated with.
	Note: This column only set when this MS/MS spectrum has been identified.
Score	The score of the identification (higher is better).
	Note: This column only set when this MS/MS spectrum has been identified.
Experiment	
Intens Comp Factor	Taken from the Thermo RAW file.
CTCD Comp	Taken from the Thermo RAW file.
RawOvFtT	For Thermo Fisher only. TIC estimation done with the orbitrap cell.
AGC Fill	Taken from the Thermo RAW file.
Scan index	Consecutive index of the MS/MS spectrum.
MS scan index	Consecutive index of the MS spectrum prior to this MS/MS spectrum.
MS scan number	Scan number of the MS spectrum prior to this MS/MS spectrum.

MS/MS

Name	Separator	Description
Raw file		The name of the RAW file the mass spectral data was read from.
Scan number		The RAW-file derived scan number of the MS/MS spectrum.
Scan index		The consecutive index of the MS/MS spectrum.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column "Sequence".
Missed cleavages		Number of missed enzymatic cleavages.
Modifications		Post-translational modifications contained within the identified peptide sequence.
Modified sequence		Sequence representation including the post-translational modifications (abbreviation of the modification in brackets before the modified AA). The sequence is always surrounded by underscore characters ('_').
Oxidation (M) Probabilities		Sequence representation of the peptide including PTM positioning probabilities ([01], where 1 is best match) for 'Oxidation (M)'.
Oxidation (M) Score Diffs		
Acetyl (Protein N-term)		
Oxidation (M)		
Proteins		The identifiers of the proteins the identified peptide is associated with.
Gene Names		Names of genes the identified peptide is associated with.
Protein Names		Descriptions of the proteins the identified peptide is associated with.
Charge		The charge state of the precursor ion.
Fragmentation		The type of fragmentation used to create the MS/MS spectrum. CID – Collision Induced Dissociation. HCD – High energy Collision induced Dissociation. ETD – Electron Transfer Dissociation.
Mass analyzer		The mass analyzer used to record the MS/MS spectrum. ITMS – Ion trap. FTMS – Fourier transform ICR or orbitrap cell. TOF – Time of flight.
Туре		The type of precursor ion as identified by MaxQuant. ISO – isotopic cluster. PEAK – single peak. MULTI – labeling cluster.
Scan event number		
Isotope index		
m/z		The mass-over-charge of the precursor ion.
Mass		The charge corrected mass of the precursor ion.
Mass Error [ppm]		Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence.
Simple Mass Error [ppm]		
Retention time		The uncalibrated retention time in minutes where the MS/MS spectrum has been acquired.
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
Score		Andromeda score for the best associated MS/MS spectrum.
Delta score		Score difference to the second best identified peptide with a different amino acid sequence.
Score diff		Score difference to the second best positioning of modifications identified peptide with the same amino acid sequence.
Localization prob		
Combinatorics		Number of possible distributions of the modifications over the peptide sequence.
Labeling State		Labeling state of the precursor isotope pattern used to identify the peptide.
PIF		Short for Parent Ion Fraction; indicates the fraction the target peak makes up of the total intensity in the inclusion window.
Fraction of total spectrum		The percentage the parent ion intensity makes up of the total intensity of the whole spectrum.
Base peak fraction		The percentage the parent ion intensity in comparison to the highest peak in he MS spectrum.
Precursor Full ScanNumber		The full scannumber where the precursor ion was selected for fragmentation.

Precursor Intensity	The intensity of the precursor ion at the scannumber it was selected.
Precursor Apex Fraction	The fraction the intensity of the precursor ion makes up of the peak (apex) intensity.
Precursor Apex Offset	How many full scans the precursor ion is offset from the peak (apex) position.
Precursor Apex Offset Time	How much time the precursor ion is offset from the peak (apex) position.
Matches	The species of the peaks in the fragmentation spectrum after TopN filtering.
Intensities	The intensities of the peaks in the fragmentation spectrum after TopN filtering.
Mass Deviations [Da]	The mass deviation of each peak in the fragmentation spectrum in absolute mass units.
Mass Deviations [ppm]	The mass deviation of each peak in the fragmentation spectrum in parts per million.
Masses	The masses-over-charge of the peaks in the fragmentation spectrum.
Number of Matches	The number of peaks matching to the predicted fragmentation spectrum.
Intensity coverage	The fraction of intensity in the MS/MS spectrum that is annotated.
Peak coverage	The fraction of peaks in the MS/MS spectrum that are annotated.
Neutral loss level	How many neutral losses were applied to each fragment in the Andromeda scoring.
ETD identification type	For ETD spectra several different combinations of ion series are scored. Here the highest scoring combination is indicated
Reverse	When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.
All scores	
All sequences	
All modified sequences	
id	A unique (consecutive) identifier for each row in the msms table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs	The identifier of the protein-group this redundant peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple id's can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Peptide ID	The identifier of the non-redundant peptide sequence.
Mod. peptide ID	Identifier of the associated modification summary stored in the file 'modificationSpecificPeptides.txt'.
Evidence ID	Identifier of the associated evidence stored in the file 'evidence.txt'.
Oxidation (M) site IDs	Identifier of the oxidation summary stored in the file 'Oxidation (M)Sites.txt'.

AIF MS/MS

Name	Separator	Description
id		A unique (consecutive) identifier for each row in the AIF MS/MS table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs		The identifier of the protein group this redundant peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple id's can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Peptide ID		The identifier of the non-redundant peptide sequence.
Mod. peptide ID		Identifier of the associated modification summary stored in the file 'modificationSpecificPeptides.txt'.
Evidence ID		Identifier for analyzed peptide evidence associated with the protein group referenced against the evidences table.
Oxidation (M) site IDs		
Raw file		Name of the RAW file the spectral data was extracted from, which led to the identification of this peptide.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column "Sequence".
Missed Cleavages		Number of missed enzymatic cleavages.
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to 'unmodified'. Note: This column only set when this MS/MS spectrum has been identified.
Modified Sequence		Sequence representation of the peptide including location(s) of modified AAs. Note: This column only set when this MS/MS spectrum has been identified.
Oxidation (M) Probabilities		
Oxidation (M) Score Diffs		
Acetyl (Protein N-term)		
Oxidation (M)		
Proteins		The IPI identifiers of the proteins the identified peptide is associated with.
Charge		The charge of the precursor ion.
m/z		The mass-over-charge of the precursor ion.
Mass		The charge corrected mass of the precursor ion.
Retention time		The uncalibrated retention time in minutes in the elution profile of the precursor ion.
Precursor intensity		The intensity of the precursor ion.
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
Score		Andromeda identification score for the MS/MS spectrum.
Delta score		Score difference to the second best identified peptide.
Combinatorics		Number of possible distributions of the modifications over the peptide sequence.
Matches		
Intensities		The intensities of the peaks in the fragmentation spectrum after top-N filtering.
Mass Deviations		The search engine allowed mass deviations of the peaks in the fragmentation spectrum.
Masses		The masses-over-charge of the peaks in the fragmentation spectrum.
Charges		
Correlations		
Number of Matches		
Reverse		When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.