

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 ([0..1], 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.
Type		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 mono-isotopic 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. Note: This column can contain missing values (NaN).
Match time difference		When the option 'match between runs' is used in MaxQuant, 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_IolR		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'.
Experiment g1_PX1194_PCa3_3		Number of evidence entries for this 'Experiment'.

[illegible]

[illegible]

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 g1_PX419_human_18507		Number of evidence entries for this 'Experiment'.
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 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		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_Exp1		Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Exp2		Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-HU_Exp3		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'.
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 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 g1_GK1_Chromatin_hilR		
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 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		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 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 g1_KW9_120425		Normalized 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_120425		Coefficient of variability 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_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 g1_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 quantitation 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 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 variability [%] g1_PX1194_H4		Coefficient of variability 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_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 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 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 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		
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 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		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 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		
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 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 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		
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 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 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 quantitation 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 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 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 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 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 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		
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		
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 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 g1_PX309_HCC202-1		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-1		
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_HCC202-2		
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_HCC202-3		
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.

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 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_HMEC1-1		
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_HMEC1-2		
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_HMEC1-3		
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_HMEC2-1		
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_HMEC2-2		
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_HMEC2-3		
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_HMTS1-1		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		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_HMTS1-2		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_HMTS1-3		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-1		
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-2		
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 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_MFM223-1		
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_MFM223-2		
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_MFM223-3		
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		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		
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		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 [%] 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 [%] 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 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 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		
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.

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 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.
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		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 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 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		
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 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		
Ratio H/L g2_PX058_expC		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 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		
Ratio H/L g2_PX058_expD		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 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		
Ratio H/L g2_PX058_expE		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 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 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		
Ratio H/L g2_PX537_exp14 rep1 20h		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 variability [%] g2_PX537_exp14 rep1 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 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 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		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		
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 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		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 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		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.

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 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		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		
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 g3_PX328_Diff5_Exp1		The ratio between two medium and light label partners.

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 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 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		The ratio between two medium and light label partners.
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		The ratio between two medium and light label partners.
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		The ratio between two medium and light label partners.
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		The ratio between two medium and light label partners.
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 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 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		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 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 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 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		
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 naturally logarithmized ratios times 100.
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		
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-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 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/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 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		
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 Ion Current (XIC) of all isotopic clusters associated with the identified AA 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 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 which 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_IolR		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'.

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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_PX419_human_18507		Number of evidence entries for this 'Experiment'.
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 q3_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		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-roscs_s1		Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-roscs_s2		Number of evidence entries for this 'Experiment'.
Experiment g4_NCC-roscs_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'.
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 g1_GK1_Chromatin_hilR		
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 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		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 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 g1_KW9_120425		Normalized 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_120425		Coefficient of variability 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_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 g1_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 quantitation 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 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 variability [%] g1_PX1194_H4		Coefficient of variability 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_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 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 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 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		
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 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		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 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		
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 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 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		
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 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 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 quantitation 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 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 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 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 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 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		
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		

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 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 g1_PX309_HCC202-1		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-1		
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_HCC202-2		
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_HCC202-3		
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.
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 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_HMEC1-1		
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_HMEC1-2		
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_HMEC1-3		
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_HMEC2-1		
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_HMEC2-2		
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_HMEC2-3		
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_HMTS1-1		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		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_HMTS1-2		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_HMTS1-3		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-1		
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-2		
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 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_MFM223-1		
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_MFM223-2		
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_MFM223-3		
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		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		
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		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 [%] 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 [%] 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 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 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		
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.
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 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.

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		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 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 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		
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 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		

Ratio H/L g2_PX058_expC		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 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		
Ratio H/L g2_PX058_expD		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 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		
Ratio H/L g2_PX058_expE		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 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 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		
Ratio H/L g2_PX537_exp14 rep1 20h		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 variability [%] g2_PX537_exp14 rep1 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 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 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 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 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 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 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		
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.
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 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 [%] 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 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		
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 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 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 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 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		
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 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 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		
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 naturally logarithmized ratios times 100.
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		
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-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 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/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 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		
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.

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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 Ion Current (XIC) of all isotopic clusters associated with the identified 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 position 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_IolR		
Score diff g1_GK1_Chromatin_IolR		
PEP g1_GK1_Chromatin_IolR		
Score g1_GK1_Chromatin_IolR		
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		
Score diff g1_KW8_131126		
PEP g1_KW8_131126		
Score g1_KW8_131126		
Localization prob g1_KW8_140117		
Score diff g1_KW8_140117		
PEP g1_KW8_140117		
Score g1_KW8_140117		
Localization prob g1_KW9_120425		
Score diff g1_KW9_120425		
PEP g1_KW9_120425		
Score g1_KW9_120425		
Localization prob g1_KW9_120510		
Score diff g1_KW9_120510		
PEP g1_KW9_120510		
Score g1_KW9_120510		
Localization prob g1_PX1194_H1		
Score diff g1_PX1194_H1		
PEP g1_PX1194_H1		
Score g1_PX1194_H1		
Localization prob g1_PX1194_H10		
Score diff g1_PX1194_H10		
PEP g1_PX1194_H10		
Score g1_PX1194_H10		
Localization prob g1_PX1194_H11		
Score diff g1_PX1194_H11		
PEP g1_PX1194_H11		
Score g1_PX1194_H11		
Localization prob g1_PX1194_H12		
Score diff g1_PX1194_H12		
PEP g1_PX1194_H12		
Score g1_PX1194_H12		
Localization prob g1_PX1194_H2		
Score diff g1_PX1194_H2		
PEP g1_PX1194_H2		
Score g1_PX1194_H2		
Localization prob g1_PX1194_H3		
Score diff g1_PX1194_H3		
PEP g1_PX1194_H3		
Score g1_PX1194_H3		
Localization prob g1_PX1194_H4		
Score diff g1_PX1194_H4		
PEP g1_PX1194_H4		
Score g1_PX1194_H4		
Localization prob g1_PX1194_H5		
Score diff g1_PX1194_H5		
PEP g1_PX1194_H5		
Score g1_PX1194_H5		
Localization prob g1_PX1194_H6		
Score diff g1_PX1194_H6		
PEP g1_PX1194_H6		
Score g1_PX1194_H6		

Localization prob g1_PX1194_H7		
Score diff g1_PX1194_H7		
PEP g1_PX1194_H7		
Score g1_PX1194_H7		
Localization prob g1_PX1194_H8		
Score diff g1_PX1194_H8		
PEP g1_PX1194_H8		
Score g1_PX1194_H8		
Localization prob g1_PX1194_H9		
Score diff g1_PX1194_H9		
PEP g1_PX1194_H9		
Score g1_PX1194_H9		
Localization prob g1_PX1194_PCa1_1		
Score diff g1_PX1194_PCa1_1		
PEP g1_PX1194_PCa1_1		
Score g1_PX1194_PCa1_1		
Localization prob g1_PX1194_PCa1_2		
Score diff g1_PX1194_PCa1_2		
PEP g1_PX1194_PCa1_2		
Score g1_PX1194_PCa1_2		
Localization prob g1_PX1194_PCa2_1		
Score diff g1_PX1194_PCa2_1		
PEP g1_PX1194_PCa2_1		
Score g1_PX1194_PCa2_1		
Localization prob g1_PX1194_PCa2_2		
Score diff g1_PX1194_PCa2_2		
PEP g1_PX1194_PCa2_2		
Score g1_PX1194_PCa2_2		
Localization prob g1_PX1194_PCa2_3		
Score diff g1_PX1194_PCa2_3		
PEP g1_PX1194_PCa2_3		
Score g1_PX1194_PCa2_3		
Localization prob g1_PX1194_PCa3_1		
Score diff g1_PX1194_PCa3_1		
PEP g1_PX1194_PCa3_1		
Score g1_PX1194_PCa3_1		
Localization prob g1_PX1194_PCa3_2		
Score diff g1_PX1194_PCa3_2		
PEP g1_PX1194_PCa3_2		
Score g1_PX1194_PCa3_2		
Localization prob g1_PX1194_PCa3_3		
Score diff g1_PX1194_PCa3_3		
PEP g1_PX1194_PCa3_3		
Score g1_PX1194_PCa3_3		
Localization prob g1_PX1194_PCa4_1		
Score diff g1_PX1194_PCa4_1		
PEP g1_PX1194_PCa4_1		
Score g1_PX1194_PCa4_1		
Localization prob g1_PX1194_PCa4_2		
Score diff g1_PX1194_PCa4_2		
PEP g1_PX1194_PCa4_2		
Score g1_PX1194_PCa4_2		
Localization prob g1_PX1194_PCa4_3		
Score diff g1_PX1194_PCa4_3		
PEP g1_PX1194_PCa4_3		
Score g1_PX1194_PCa4_3		

Localization prob g1_PX1194_PCa5_1		
Score diff g1_PX1194_PCa5_1		
PEP g1_PX1194_PCa5_1		
Score g1_PX1194_PCa5_1		
Localization prob g1_PX1194_PCa5_2		
Score diff g1_PX1194_PCa5_2		
PEP g1_PX1194_PCa5_2		
Score g1_PX1194_PCa5_2		
Localization prob g1_PX1194_PCa5_3		
Score diff g1_PX1194_PCa5_3		
PEP g1_PX1194_PCa5_3		
Score g1_PX1194_PCa5_3		
Localization prob g1_PX1194_PCa6_1		
Score diff g1_PX1194_PCa6_1		
PEP g1_PX1194_PCa6_1		
Score g1_PX1194_PCa6_1		
Localization prob g1_PX1194_PCa7_1		
Score diff g1_PX1194_PCa7_1		
PEP g1_PX1194_PCa7_1		
Score g1_PX1194_PCa7_1		
Localization prob g1_PX1406_GM18486		
Score diff g1_PX1406_GM18486		
PEP g1_PX1406_GM18486		
Score g1_PX1406_GM18486		
Localization prob g1_PX1406_GM18498		
Score diff g1_PX1406_GM18498		
PEP g1_PX1406_GM18498		
Score g1_PX1406_GM18498		
Localization prob g1_PX1406_GM18499		
Score diff g1_PX1406_GM18499		
PEP g1_PX1406_GM18499		
Score g1_PX1406_GM18499		
Localization prob g1_PX1406_GM18501		
Score diff g1_PX1406_GM18501		
PEP g1_PX1406_GM18501		
Score g1_PX1406_GM18501		
Localization prob g1_PX1406_GM18502		
Score diff g1_PX1406_GM18502		
PEP g1_PX1406_GM18502		
Score g1_PX1406_GM18502		
Localization prob g1_PX1406_GM18504		
Score diff g1_PX1406_GM18504		
PEP g1_PX1406_GM18504		
Score g1_PX1406_GM18504		
Localization prob g1_PX1406_GM18505		
Score diff g1_PX1406_GM18505		
PEP g1_PX1406_GM18505		
Score g1_PX1406_GM18505		
Localization prob g1_PX1406_GM18507		
Score diff g1_PX1406_GM18507		
PEP g1_PX1406_GM18507		
Score g1_PX1406_GM18507		
Localization prob g1_PX1406_GM18508		
Score diff g1_PX1406_GM18508		

PEP g1_PX1406_GM18508		
Score g1_PX1406_GM18508		
Localization prob g1_PX1406_GM18510		
Score diff g1_PX1406_GM18510		
PEP g1_PX1406_GM18510		
Score g1_PX1406_GM18510		
Localization prob g1_PX1406_GM18511		
Score diff g1_PX1406_GM18511		
PEP g1_PX1406_GM18511		
Score g1_PX1406_GM18511		
Localization prob g1_PX1406_GM18516		
Score diff g1_PX1406_GM18516		
PEP g1_PX1406_GM18516		
Score g1_PX1406_GM18516		
Localization prob g1_PX1406_GM18517		
Score diff g1_PX1406_GM18517		
PEP g1_PX1406_GM18517		
Score g1_PX1406_GM18517		
Localization prob g1_PX1406_GM18519		
Score diff g1_PX1406_GM18519		
PEP g1_PX1406_GM18519		
Score g1_PX1406_GM18519		
Localization prob g1_PX1406_GM18520		
Score diff g1_PX1406_GM18520		
PEP g1_PX1406_GM18520		
Score g1_PX1406_GM18520		
Localization prob g1_PX1406_GM18522		
Score diff g1_PX1406_GM18522		
PEP g1_PX1406_GM18522		
Score g1_PX1406_GM18522		
Localization prob g1_PX1406_GM18523		
Score diff g1_PX1406_GM18523		
PEP g1_PX1406_GM18523		
Score g1_PX1406_GM18523		
Localization prob g1_PX1406_GM18852		
Score diff g1_PX1406_GM18852		
PEP g1_PX1406_GM18852		
Score g1_PX1406_GM18852		
Localization prob g1_PX1406_GM18855		
Score diff g1_PX1406_GM18855		
PEP g1_PX1406_GM18855		
Score g1_PX1406_GM18855		
Localization prob g1_PX1406_GM18858		
Score diff g1_PX1406_GM18858		
PEP g1_PX1406_GM18858		
Score g1_PX1406_GM18858		
Localization prob g1_PX1406_GM18861		
Score diff g1_PX1406_GM18861		
PEP g1_PX1406_GM18861		
Score g1_PX1406_GM18861		
Localization prob g1_PX1406_GM18862		
Score diff g1_PX1406_GM18862		
PEP g1_PX1406_GM18862		
Score g1_PX1406_GM18862		

Localization prob g1_PX1406_GM18870		
Score diff g1_PX1406_GM18870		
PEP g1_PX1406_GM18870		
Score g1_PX1406_GM18870		
Localization prob g1_PX1406_GM18871		
Score diff g1_PX1406_GM18871		
PEP g1_PX1406_GM18871		
Score g1_PX1406_GM18871		
Localization prob g1_PX1406_GM18907		
Score diff g1_PX1406_GM18907		
PEP g1_PX1406_GM18907		
Score g1_PX1406_GM18907		
Localization prob g1_PX1406_GM18909		
Score diff g1_PX1406_GM18909		
PEP g1_PX1406_GM18909		
Score g1_PX1406_GM18909		
Localization prob g1_PX1406_GM18912		
Score diff g1_PX1406_GM18912		
PEP g1_PX1406_GM18912		
Score g1_PX1406_GM18912		
Localization prob g1_PX1406_GM18913		
Score diff g1_PX1406_GM18913		
PEP g1_PX1406_GM18913		
Score g1_PX1406_GM18913		
Localization prob g1_PX1406_GM18916		
Score diff g1_PX1406_GM18916		
PEP g1_PX1406_GM18916		
Score g1_PX1406_GM18916		
Localization prob g1_PX1406_GM19092		
Score diff g1_PX1406_GM19092		
PEP g1_PX1406_GM19092		
Score g1_PX1406_GM19092		
Localization prob g1_PX1406_GM19093		
Score diff g1_PX1406_GM19093		
PEP g1_PX1406_GM19093		
Score g1_PX1406_GM19093		
Localization prob g1_PX1406_GM19098		
Score diff g1_PX1406_GM19098		
PEP g1_PX1406_GM19098		
Score g1_PX1406_GM19098		
Localization prob g1_PX1406_GM19099		
Score diff g1_PX1406_GM19099		
PEP g1_PX1406_GM19099		
Score g1_PX1406_GM19099		
Localization prob g1_PX1406_GM19101		
Score diff g1_PX1406_GM19101		
PEP g1_PX1406_GM19101		
Score g1_PX1406_GM19101		
Localization prob g1_PX1406_GM19102		
Score diff g1_PX1406_GM19102		
PEP g1_PX1406_GM19102		
Score g1_PX1406_GM19102		
Localization prob g1_PX1406_GM19108		
Score diff g1_PX1406_GM19108		

PEP g1_PX1406_GM19108		
Score g1_PX1406_GM19108		
Localization prob g1_PX1406_GM19114		
Score diff g1_PX1406_GM19114		
PEP g1_PX1406_GM19114		
Score g1_PX1406_GM19114		
Localization prob g1_PX1406_GM19116		
Score diff g1_PX1406_GM19116		
PEP g1_PX1406_GM19116		
Score g1_PX1406_GM19116		
Localization prob g1_PX1406_GM19119		
Score diff g1_PX1406_GM19119		
PEP g1_PX1406_GM19119		
Score g1_PX1406_GM19119		
Localization prob g1_PX1406_GM19127		
Score diff g1_PX1406_GM19127		
PEP g1_PX1406_GM19127		
Score g1_PX1406_GM19127		
Localization prob g1_PX1406_GM19128		
Score diff g1_PX1406_GM19128		
PEP g1_PX1406_GM19128		
Score g1_PX1406_GM19128		
Localization prob g1_PX1406_GM19130		
Score diff g1_PX1406_GM19130		
PEP g1_PX1406_GM19130		
Score g1_PX1406_GM19130		
Localization prob g1_PX1406_GM19131		
Score diff g1_PX1406_GM19131		
PEP g1_PX1406_GM19131		
Score g1_PX1406_GM19131		
Localization prob g1_PX1406_GM19137		
Score diff g1_PX1406_GM19137		
PEP g1_PX1406_GM19137		
Score g1_PX1406_GM19137		
Localization prob g1_PX1406_GM19138		
Score diff g1_PX1406_GM19138		
PEP g1_PX1406_GM19138		
Score g1_PX1406_GM19138		
Localization prob g1_PX1406_GM19140		
Score diff g1_PX1406_GM19140		
PEP g1_PX1406_GM19140		
Score g1_PX1406_GM19140		
Localization prob g1_PX1406_GM19143		
Score diff g1_PX1406_GM19143		
PEP g1_PX1406_GM19143		
Score g1_PX1406_GM19143		
Localization prob g1_PX1406_GM19144		
Score diff g1_PX1406_GM19144		
PEP g1_PX1406_GM19144		
Score g1_PX1406_GM19144		
Localization prob g1_PX1406_GM19147		
Score diff g1_PX1406_GM19147		
PEP g1_PX1406_GM19147		
Score g1_PX1406_GM19147		

Localization prob g1_PX1406_GM19152		
Score diff g1_PX1406_GM19152		
PEP g1_PX1406_GM19152		
Score g1_PX1406_GM19152		
Localization prob g1_PX1406_GM19153		
Score diff g1_PX1406_GM19153		
PEP g1_PX1406_GM19153		
Score g1_PX1406_GM19153		
Localization prob g1_PX1406_GM19160		
Score diff g1_PX1406_GM19160		
PEP g1_PX1406_GM19160		
Score g1_PX1406_GM19160		
Localization prob g1_PX1406_GM19172		
Score diff g1_PX1406_GM19172		
PEP g1_PX1406_GM19172		
Score g1_PX1406_GM19172		
Localization prob g1_PX1406_GM19192		
Score diff g1_PX1406_GM19192		
PEP g1_PX1406_GM19192		
Score g1_PX1406_GM19192		
Localization prob g1_PX1406_GM19193		
Score diff g1_PX1406_GM19193		
PEP g1_PX1406_GM19193		
Score g1_PX1406_GM19193		
Localization prob g1_PX1406_GM19200		
Score diff g1_PX1406_GM19200		
PEP g1_PX1406_GM19200		
Score g1_PX1406_GM19200		
Localization prob g1_PX1406_GM19203		
Score diff g1_PX1406_GM19203		
PEP g1_PX1406_GM19203		
Score g1_PX1406_GM19203		
Localization prob g1_PX1406_GM19204		
Score diff g1_PX1406_GM19204		
PEP g1_PX1406_GM19204		
Score g1_PX1406_GM19204		
Localization prob g1_PX1406_GM19207		
Score diff g1_PX1406_GM19207		
PEP g1_PX1406_GM19207		
Score g1_PX1406_GM19207		
Localization prob g1_PX1406_GM19209		
Score diff g1_PX1406_GM19209		
PEP g1_PX1406_GM19209		
Score g1_PX1406_GM19209		
Localization prob g1_PX1406_GM19222		
Score diff g1_PX1406_GM19222		
PEP g1_PX1406_GM19222		
Score g1_PX1406_GM19222		
Localization prob g1_PX1406_GM19257		
Score diff g1_PX1406_GM19257		
PEP g1_PX1406_GM19257		
Score g1_PX1406_GM19257		
Localization prob g1_PX151_Rep1		
Score diff g1_PX151_Rep1		
PEP g1_PX151_Rep1		

Score g1_PX151_Rep1		
Localization prob g1_PX151_Rep2		
Score diff g1_PX151_Rep2		
PEP g1_PX151_Rep2		
Score g1_PX151_Rep2		
Localization prob g1_PX151_Rep3		
Score diff g1_PX151_Rep3		
PEP g1_PX151_Rep3		
Score g1_PX151_Rep3		
Localization prob g1_PX309_HCC1143-1		
Score diff g1_PX309_HCC1143-1		
PEP g1_PX309_HCC1143-1		
Score g1_PX309_HCC1143-1		
Localization prob g1_PX309_HCC1143-2		
Score diff g1_PX309_HCC1143-2		
PEP g1_PX309_HCC1143-2		
Score g1_PX309_HCC1143-2		
Localization prob g1_PX309_HCC1143-3		
Score diff g1_PX309_HCC1143-3		
PEP g1_PX309_HCC1143-3		
Score g1_PX309_HCC1143-3		
Localization prob g1_PX309_HCC1599-1		
Score diff g1_PX309_HCC1599-1		
PEP g1_PX309_HCC1599-1		
Score g1_PX309_HCC1599-1		
Localization prob g1_PX309_HCC1599-2		
Score diff g1_PX309_HCC1599-2		
PEP g1_PX309_HCC1599-2		
Score g1_PX309_HCC1599-2		
Localization prob g1_PX309_HCC1599-3		
Score diff g1_PX309_HCC1599-3		
PEP g1_PX309_HCC1599-3		
Score g1_PX309_HCC1599-3		
Localization prob g1_PX309_HCC1937-1		
Score diff g1_PX309_HCC1937-1		
PEP g1_PX309_HCC1937-1		
Score g1_PX309_HCC1937-1		
Localization prob g1_PX309_HCC1937-2		
Score diff g1_PX309_HCC1937-2		
PEP g1_PX309_HCC1937-2		
Score g1_PX309_HCC1937-2		
Localization prob g1_PX309_HCC1937-3		
Score diff g1_PX309_HCC1937-3		
PEP g1_PX309_HCC1937-3		
Score g1_PX309_HCC1937-3		
Localization prob g1_PX309_HCC202-1		
Score diff g1_PX309_HCC202-1		
PEP g1_PX309_HCC202-1		
Score g1_PX309_HCC202-1		
Localization prob g1_PX309_HCC202-2		
Score diff g1_PX309_HCC202-2		
PEP g1_PX309_HCC202-2		
Score g1_PX309_HCC202-2		
Localization prob g1_PX309_HCC202-3		
Score diff g1_PX309_HCC202-3		
PEP g1_PX309_HCC202-3		

Score g1_PX309_HCC202-3		
Localization prob g1_PX309_HCC2218-1		
Score diff g1_PX309_HCC2218-1		
PEP g1_PX309_HCC2218-1		
Score g1_PX309_HCC2218-1		
Localization prob g1_PX309_HCC2218-2		
Score diff g1_PX309_HCC2218-2		
PEP g1_PX309_HCC2218-2		
Score g1_PX309_HCC2218-2		
Localization prob g1_PX309_HCC2218-3		
Score diff g1_PX309_HCC2218-3		
PEP g1_PX309_HCC2218-3		
Score g1_PX309_HCC2218-3		
Localization prob g1_PX309_HMEC1-1		
Score diff g1_PX309_HMEC1-1		
PEP g1_PX309_HMEC1-1		
Score g1_PX309_HMEC1-1		
Localization prob g1_PX309_HMEC1-2		
Score diff g1_PX309_HMEC1-2		
PEP g1_PX309_HMEC1-2		
Score g1_PX309_HMEC1-2		
Localization prob g1_PX309_HMEC1-3		
Score diff g1_PX309_HMEC1-3		
PEP g1_PX309_HMEC1-3		
Score g1_PX309_HMEC1-3		
Localization prob g1_PX309_HMEC2-1		
Score diff g1_PX309_HMEC2-1		
PEP g1_PX309_HMEC2-1		
Score g1_PX309_HMEC2-1		
Localization prob g1_PX309_HMEC2-2		
Score diff g1_PX309_HMEC2-2		
PEP g1_PX309_HMEC2-2		
Score g1_PX309_HMEC2-2		
Localization prob g1_PX309_HMEC2-3		
Score diff g1_PX309_HMEC2-3		
PEP g1_PX309_HMEC2-3		
Score g1_PX309_HMEC2-3		
Localization prob g1_PX309_HMTS1-1		
Score diff g1_PX309_HMTS1-1		
PEP g1_PX309_HMTS1-1		
Score g1_PX309_HMTS1-1		
Localization prob g1_PX309_HMTS1-2		
Score diff g1_PX309_HMTS1-2		
PEP g1_PX309_HMTS1-2		
Score g1_PX309_HMTS1-2		
Localization prob g1_PX309_HMTS1-3		
Score diff g1_PX309_HMTS1-3		
PEP g1_PX309_HMTS1-3		
Score g1_PX309_HMTS1-3		
Localization prob g1_PX309_MCF10a-1		
Score diff g1_PX309_MCF10a-1		
PEP g1_PX309_MCF10a-1		
Score g1_PX309_MCF10a-1		
Localization prob g1_PX309_MCF10a-2		

Score diff g1_PX309_MCF10a-2		
PEP g1_PX309_MCF10a-2		
Score g1_PX309_MCF10a-2		
Localization prob g1_PX309_MCF10a-3		
Score diff g1_PX309_MCF10a-3		
PEP g1_PX309_MCF10a-3		
Score g1_PX309_MCF10a-3		
Localization prob g1_PX309_MDAMB453-1		
Score diff g1_PX309_MDAMB453-1		
PEP g1_PX309_MDAMB453-1		
Score g1_PX309_MDAMB453-1		
Localization prob g1_PX309_MDAMB453-2		
Score diff g1_PX309_MDAMB453-2		
PEP g1_PX309_MDAMB453-2		
Score g1_PX309_MDAMB453-2		
Localization prob g1_PX309_MDAMB453-3		
Score diff g1_PX309_MDAMB453-3		
PEP g1_PX309_MDAMB453-3		
Score g1_PX309_MDAMB453-3		
Localization prob g1_PX309_MFM223-1		
Score diff g1_PX309_MFM223-1		
PEP g1_PX309_MFM223-1		
Score g1_PX309_MFM223-1		
Localization prob g1_PX309_MFM223-2		
Score diff g1_PX309_MFM223-2		
PEP g1_PX309_MFM223-2		
Score g1_PX309_MFM223-2		
Localization prob g1_PX309_MFM223-3		
Score diff g1_PX309_MFM223-3		
PEP g1_PX309_MFM223-3		
Score g1_PX309_MFM223-3		
Localization prob g1_PX359_0h_1		
Score diff g1_PX359_0h_1		
PEP g1_PX359_0h_1		
Score g1_PX359_0h_1		
Localization prob g1_PX359_0h_2		
Score diff g1_PX359_0h_2		
PEP g1_PX359_0h_2		
Score g1_PX359_0h_2		
Localization prob g1_PX359_0h_3		
Score diff g1_PX359_0h_3		
PEP g1_PX359_0h_3		
Score g1_PX359_0h_3		
Localization prob g1_PX359_BSA_1		
Score diff g1_PX359_BSA_1		
PEP g1_PX359_BSA_1		
Score g1_PX359_BSA_1		
Localization prob g1_PX359_BSA_2		
Score diff g1_PX359_BSA_2		
PEP g1_PX359_BSA_2		
Score g1_PX359_BSA_2		
Localization prob g1_PX359_BSA_3		
Score diff g1_PX359_BSA_3		
PEP g1_PX359_BSA_3		
Score g1_PX359_BSA_3		
Localization prob g1_PX359_FN_1		
Score diff g1_PX359_FN_1		

PEP g1_PX359_FN_1		
Score g1_PX359_FN_1		
Localization prob g1_PX359_FN_2		
Score diff g1_PX359_FN_2		
PEP g1_PX359_FN_2		
Score g1_PX359_FN_2		
Localization prob g1_PX359_FN_3		
Score diff g1_PX359_FN_3		
PEP g1_PX359_FN_3		
Score g1_PX359_FN_3		
Localization prob g1_PX359_GFR_1		
Score diff g1_PX359_GFR_1		
PEP g1_PX359_GFR_1		
Score g1_PX359_GFR_1		
Localization prob g1_PX359_GFR_2		
Score diff g1_PX359_GFR_2		
PEP g1_PX359_GFR_2		
Score g1_PX359_GFR_2		
Localization prob g1_PX359_GFR_3		
Score diff g1_PX359_GFR_3		
PEP g1_PX359_GFR_3		
Score g1_PX359_GFR_3		
Localization prob g1_PX359_LAM_1		
Score diff g1_PX359_LAM_1		
PEP g1_PX359_LAM_1		
Score g1_PX359_LAM_1		
Localization prob g1_PX359_LAM_2		
Score diff g1_PX359_LAM_2		
PEP g1_PX359_LAM_2		
Score g1_PX359_LAM_2		
Localization prob g1_PX359_LAM_3		
Score diff g1_PX359_LAM_3		
PEP g1_PX359_LAM_3		
Score g1_PX359_LAM_3		
Localization prob g1_PX359_Matr 12h_1		
Score diff g1_PX359_Matr 12h_1		
PEP g1_PX359_Matr 12h_1		
Score g1_PX359_Matr 12h_1		
Localization prob g1_PX359_Matr 12h_2		
Score diff g1_PX359_Matr 12h_2		
PEP g1_PX359_Matr 12h_2		
Score g1_PX359_Matr 12h_2		
Localization prob g1_PX359_Matr 12h_3		
Score diff g1_PX359_Matr 12h_3		
PEP g1_PX359_Matr 12h_3		
Score g1_PX359_Matr 12h_3		
Localization prob g1_PX359_Matr 24h_1		
Score diff g1_PX359_Matr 24h_1		
PEP g1_PX359_Matr 24h_1		
Score g1_PX359_Matr 24h_1		
Localization prob g1_PX359_Matr 24h_2		
Score diff g1_PX359_Matr 24h_2		
PEP g1_PX359_Matr 24h_2		
Score g1_PX359_Matr 24h_2		
Localization prob g1_PX359_Matr 24h_3		
Score diff g1_PX359_Matr 24h_3		

PEP g1_PX359_Matr 24h_3		
Score g1_PX359_Matr 24h_3		
Localization prob g1_PX359_Matr 30h_1		
Score diff g1_PX359_Matr 30h_1		
PEP g1_PX359_Matr 30h_1		
Score g1_PX359_Matr 30h_1		
Localization prob g1_PX359_Matr 30h_2		
Score diff g1_PX359_Matr 30h_2		
PEP g1_PX359_Matr 30h_2		
Score g1_PX359_Matr 30h_2		
Localization prob g1_PX359_Matr 30h_3		
Score diff g1_PX359_Matr 30h_3		
PEP g1_PX359_Matr 30h_3		
Score g1_PX359_Matr 30h_3		
Localization prob g1_PX359_Matr dil_1		
Score diff g1_PX359_Matr dil_1		
PEP g1_PX359_Matr dil_1		
Score g1_PX359_Matr dil_1		
Localization prob g1_PX359_Matr dil_2		
Score diff g1_PX359_Matr dil_2		
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		
Score g1_PX419_human_18507		
Localization prob g1_PX419_human_18516		
Score diff g1_PX419_human_18516		
PEP g1_PX419_human_18516		
Score g1_PX419_human_18516		
Localization prob g1_PX419_human_19193		
Score diff g1_PX419_human_19193		
PEP g1_PX419_human_19193		
Score g1_PX419_human_19193		
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		
Score g1_PX438_Xeno092		
Localization prob g1_PX438_Xeno441		
Score diff g1_PX438_Xeno441		
PEP g1_PX438_Xeno441		
Score g1_PX438_Xeno441		
Localization prob g1_PX438_Xeno561		
Score diff g1_PX438_Xeno561		
PEP g1_PX438_Xeno561		
Score g1_PX438_Xeno561		

Localization prob g1_PX438_Xeno691		
Score diff g1_PX438_Xeno691		
PEP g1_PX438_Xeno691		
Score g1_PX438_Xeno691		
Localization prob g2_PX058_expA		
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		
Score g2_PX089_Rep2		
Localization prob g2_PX537_exp14 rep1 20h		
Score diff g2_PX537_exp14 rep1 20h		
PEP g2_PX537_exp14 rep1 20h		
Score g2_PX537_exp14 rep1 20h		
Localization prob g2_PX537_exp14 rep1 6h		
Score diff g2_PX537_exp14 rep1 6h		
PEP g2_PX537_exp14 rep1 6h		
Score g2_PX537_exp14 rep1 6h		
Localization prob g2_PX537_exp14 rep2 20h		
Score diff g2_PX537_exp14 rep2 20h		
PEP g2_PX537_exp14 rep2 20h		
Score g2_PX537_exp14 rep2 20h		
Localization prob g2_PX537_exp14 rep2 6h		
Score diff g2_PX537_exp14 rep2 6h		
PEP g2_PX537_exp14 rep2 6h		
Score g2_PX537_exp14 rep2 6h		
Localization prob g2_PX537_exp14 rep3 20h		
Score diff g2_PX537_exp14 rep3 20h		
PEP g2_PX537_exp14 rep3 20h		
Score g2_PX537_exp14 rep3 20h		
Localization prob g2_PX537_exp14 rep3 6h		

Score diff g2_PX537_exp14 rep3 6h		
PEP g2_PX537_exp14 rep3 6h		
Score g2_PX537_exp14 rep3 6h		
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 g3_GK1_Chromatin_CC_2		
PEP g3_GK1_Chromatin_CC_2		
Score g3_GK1_Chromatin_CC_2		
Localization prob g3_GK1_Chromatin_EHT_1		
Score diff g3_GK1_Chromatin_EHT_1		
PEP g3_GK1_Chromatin_EHT_1		
Score g3_GK1_Chromatin_EHT_1		
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		

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		

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 g4_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		
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/L___1		The ratio between two heavy and light label partners.
Ratio H/L___2		The ratio between two heavy and light label partners.
Ratio H/L___3		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 normalized___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___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___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		
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_AL___1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_AL___2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_AL___3		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_AL___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_GK1_Chromatin_AL___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_AL___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. 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 g1_GK1_Chromatin_AL		
Occupancy L g1_GK1_Chromatin_AL		
Occupancy H g1_GK1_Chromatin_AL		
Ratio H/L g1_GK1_Chromatin_CPT		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CPT__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CPT__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CPT__3		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 normalized g1_GK1_Chromatin_CPT__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_GK1_Chromatin_CPT__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_CPT__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. g1_GK1_Chromatin_CPT		
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_Chromatin_CPT		
Ratio H/L g1_GK1_Chromatin_CR		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CR__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CR__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_CR__3		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_CR__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_GK1_Chromatin_CR__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_CR__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. g1_GK1_Chromatin_CR		
Ratio H/L localized g1_GK1_Chromatin_CR		
Ratio H/L nmods g1_GK1_Chromatin_CR		
Ratio H/L variability [%] g1_GK1_Chromatin_CR		
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		
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_HepHek__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_HepHek__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_HepHek__3		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_HepHek__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_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_HepHek__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. 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 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		
Occupancy L g1_GK1_Chromatin_HepHek		
Occupancy H g1_GK1_Chromatin_HepHek		
Ratio H/L g1_GK1_Chromatin_hilR		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_hilR__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_hilR__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_hilR__3		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_hilR__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_GK1_Chromatin_hilR__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_hilR__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. g1_GK1_Chromatin_hilR		
Ratio H/L localized g1_GK1_Chromatin_hilR		
Ratio H/L nmods g1_GK1_Chromatin_hilR		
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_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_hilR		
Occupancy L g1_GK1_Chromatin_hilR		
Occupancy H g1_GK1_Chromatin_hilR		
Ratio H/L g1_GK1_Chromatin_IolR		The ratio between two heavy and light label partners.

Ratio H/L g1_GK1_Chromatin_loIR__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_loIR__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_loIR__3		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_loIR__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_GK1_Chromatin_loIR__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_loIR__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. g1_GK1_Chromatin_loIR		
Ratio H/L localized g1_GK1_Chromatin_loIR		
Ratio H/L nmods g1_GK1_Chromatin_loIR		
Ratio H/L variability [%] g1_GK1_Chromatin_loIR		
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		
Occupancy L g1_GK1_Chromatin_loIR		
Occupancy H g1_GK1_Chromatin_loIR		
Ratio H/L g1_GK1_Chromatin_mH2A_1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_1__3		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 normalized g1_GK1_Chromatin_mH2A_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_GK1_Chromatin_mH2A_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 normalized g1_GK1_Chromatin_mH2A_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. 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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_2__3		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 normalized g1_GK1_Chromatin_mH2A_2__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_GK1_Chromatin_mH2A_2__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_mH2A_2__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. g1_GK1_Chromatin_mH2A_2		
Ratio H/L localized g1_GK1_Chromatin_mH2A_2		
Ratio H/L nmods g1_GK1_Chromatin_mH2A_2		
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_2		
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		
Occupancy L g1_GK1_Chromatin_mH2A_2		
Occupancy H 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 g1_GK1_Chromatin_mH2A_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_mH2A_3__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 normalized g1_GK1_Chromatin_mH2A_3__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_GK1_Chromatin_mH2A_3__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_mH2A_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. g1_GK1_Chromatin_mH2A_3		
Ratio H/L localized g1_GK1_Chromatin_mH2A_3		
Ratio H/L nmods g1_GK1_Chromatin_mH2A_3		
Ratio H/L variability [%] g1_GK1_Chromatin_mH2A_3		
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		
Occupancy L g1_GK1_Chromatin_mH2A_3		
Occupancy H 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 g1_GK1_Chromatin_TNFa_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_1__3		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 normalized g1_GK1_Chromatin_TNFa_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_GK1_Chromatin_TNFa_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 normalized g1_GK1_Chromatin_TNFa_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. 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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_2__3		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_2__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_GK1_Chromatin_TNFa_2__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_2__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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_GK1_Chromatin_TNFa_3__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 normalized g1_GK1_Chromatin_TNFa_3__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_GK1_Chromatin_TNFa_3__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_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. 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_110506__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_110506__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_110506__3		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_110506__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_KW10_110506__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_KW10_110506__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. 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_131126__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_131126__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_131126__3		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_131126__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_KW10_131126__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_KW10_131126__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. 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_140117__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_140117__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW10_140117__3		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_140117__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_KW10_140117__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_KW10_140117__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. 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_130125__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_130125__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_130125__3		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_130125__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_KW11_130125__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_130125__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. 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		
Ratio H/L g1_KW11_140104_nE		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_140104_nE__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_140104_nE__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_140104_nE__3		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_nE__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_KW11_140104_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 normalized g1_KW11_140104_nE__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. 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 g1_KW11_140104_wE__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_140104_wE__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW11_140104_wE__3		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_wE__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_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_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. g1_KW11_140104_wE		
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_130317__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_130317__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_130317__3		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_130317__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_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_130317__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. g1_KW12_130317		
Ratio H/L localized g1_KW12_130317		
Ratio H/L nmods g1_KW12_130317		
Ratio H/L variability [%] g1_KW12_130317		
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		
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_131223__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_131223__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW12_131223__3		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_131223__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_KW12_131223__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_131223__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. g1_KW12_131223		
Ratio H/L localized g1_KW12_131223		

Ratio H/L nmods g1_KW12_131223		
Ratio H/L variability [%] g1_KW12_131223		
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		
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_130328__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW13_130328__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW13_130328__3		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_130328__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_KW13_130328__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_KW13_130328__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. g1_KW13_130328		
Ratio H/L localized g1_KW13_130328		
Ratio H/L nmods g1_KW13_130328		
Ratio H/L variability [%] g1_KW13_130328		
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		
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_130317__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW14_130317__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW14_130317__3		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_130317__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_KW14_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_KW14_130317__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. 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_130317__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW15_130317__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW15_130317__3		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 normalized g1_KW15_130317__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_KW15_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_KW15_130317__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. 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 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		
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_130319__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW17_130319__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW17_130319__3		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 normalized g1_KW17_130319__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_KW17_130319__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_KW17_130319__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. 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		
Ratio H/L g1_KW8_120517		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_120517__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_120517__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_120517__3		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 g1_KW8_120517__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_KW8_120517__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_KW8_120517__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. g1_KW8_120517		
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 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		
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_131126__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_131126__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_131126__3		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_131126__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_KW8_131126__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_KW8_131126__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. g1_KW8_131126		
Ratio H/L localized g1_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		
Ratio H/L g1_KW8_140117		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_140117__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_140117__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW8_140117__3		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_140117__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_KW8_140117__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_KW8_140117__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. 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 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		
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_120425__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_120425__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_120425__3		The ratio between two heavy and light label partners.
Ratio H/L normalized g1_KW9_120425		Normalized 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_120425__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_KW9_120425__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_KW9_120425__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. g1_KW9_120425		
Ratio H/L localized g1_KW9_120425		
Ratio H/L nmods g1_KW9_120425		
Ratio H/L variability [%] g1_KW9_120425		
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 L 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_120510__1		The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_120510__2		The ratio between two heavy and light label partners.
Ratio H/L g1_KW9_120510__3		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_120510__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_KW9_120510__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_KW9_120510__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. 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		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H1__3		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 normalized g1_PX1194_H1__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_H1__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_H1__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. 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_H10__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H10__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H10__3		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_H10__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_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_H10__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. g1_PX1194_H10		
Ratio H/L localized g1_PX1194_H10		
Ratio H/L nmods g1_PX1194_H10		
Ratio H/L variability [%] g1_PX1194_H10		

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		
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_H11__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H11__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H11__3		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_H11__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_H11__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_H11__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. 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_H12__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H12__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H12__3		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_H12__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_H12__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_H12__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. 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_H2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H2__3		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_H2__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_H2__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_H2__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. 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		
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_H3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H3__3		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_H3__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_H3__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_H3__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. 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 heavy and light label partners.
Ratio H/L g1_PX1194_H4__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H4__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H4__3		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_H4__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_H4__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_H4__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. 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		
Ratio H/L g1_PX1194_H5		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H5__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H5__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H5__3		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 g1_PX1194_H5__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_H5__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_H5__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. 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_H6__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H6__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H6__3		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_H6__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_H6__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_H6__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. 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_H7__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H7__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H7__3		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_H7__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_H7__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_H7__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. 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_H8__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H8__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H8__3		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 normalized g1_PX1194_H8__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_H8__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_H8__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. g1_PX1194_H8		
Ratio H/L localized g1_PX1194_H8		
Ratio H/L nmods g1_PX1194_H8		
Ratio H/L variability [%] g1_PX1194_H8		
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_H9__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H9__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_H9__3		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_H9__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_H9__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_H9__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. 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 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		
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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_1__3		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_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_PCa1_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 normalized g1_PX1194_PCa1_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. 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_2_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_2_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa1_2_3		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_2_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_2_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_2_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. 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_1_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_1_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_1_3		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_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_PCa2_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 normalized g1_PX1194_PCa2_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. 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_2_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_2_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_2_3		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 normalized g1_PX1194_PCa2_2_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_2_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_PCa2_2_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. 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 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_3_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_3_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa2_3_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 normalized g1_PX1194_PCa2_3_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_3_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_PCa2_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. 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_1_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_1_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_1_3		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_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_PCa3_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 normalized g1_PX1194_PCa3_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. 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_2_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_2_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_2_3		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_2_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_2_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_2_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. g1_PX1194_PCa3_2		
Ratio H/L localized g1_PX1194_PCa3_2		
Ratio H/L nmods g1_PX1194_PCa3_2		
Ratio H/L variability [%] g1_PX1194_PCa3_2		
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		
Occupancy L g1_PX1194_PCa3_2		
Occupancy H g1_PX1194_PCa3_2		
Ratio H/L g1_PX1194_PCa3_3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_3_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_3_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa3_3_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 normalized g1_PX1194_PCa3_3_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_3_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_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. 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 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		
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_1_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_1_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_1_3		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 normalized g1_PX1194_PCa4_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_PCa4_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 normalized g1_PX1194_PCa4_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. 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 quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1194_PCa4_1		
Occupancy L g1_PX1194_PCa4_1		
Occupancy H g1_PX1194_PCa4_1		

Ratio H/L g1_PX1194_PCa4_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_2_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_2_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_2_3		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 normalized g1_PX1194_PCa4_2_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_PCa4_2_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_PCa4_2_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. 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_3_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_3_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa4_3_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 normalized g1_PX1194_PCa4_3_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_PCa4_3_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_PCa4_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. 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_1_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_1_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_1_3		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 normalized g1_PX1194_PCa5_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_PCa5_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 normalized g1_PX1194_PCa5_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. 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 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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_2__3		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_2__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_PCa5_2__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_2__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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa5_3__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 normalized g1_PX1194_PCa5_3__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_PCa5_3__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_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. 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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa6_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa6_1__3		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_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_PCa6_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 normalized g1_PX1194_PCa6_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. g1_PX1194_PCa6_1		
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 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		
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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa7_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1194_PCa7_1__3		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_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 normalized g1_PX1194_PCa7_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. 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_GM18486__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18486__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18486__3		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_GM18486__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_GM18486__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_GM18486__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. 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		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18498__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18498__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18498__3		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_GM18498__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_GM18498__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_GM18498__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. 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_GM18499__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18499__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18499__3		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_GM18499__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_GM18499__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_GM18499__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. 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_GM18501__1		The ratio between two heavy and light label partners.

Ratio H/L g1_PX1406_GM18501__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18501__3		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 normalized g1_PX1406_GM18501__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_GM18501__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_GM18501__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. 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_GM18502__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18502__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18502__3		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_GM18502__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_GM18502__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_GM18502__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. 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_GM18504__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18504__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18504__3		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_GM18504__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_GM18504__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_GM18504__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. 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_GM18505__3		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_GM18505__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_GM18505__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_GM18505__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. 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_GM18507__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18507__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18507__3		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_GM18507__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_GM18507__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_GM18507__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. 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 quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM18507		
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 g1_PX1406_GM18508__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18508__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18508__3		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_GM18508__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_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_GM18508__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. 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_GM18510__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18510__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18510__3		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_GM18510__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_GM18510__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_GM18510__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. 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_GM18511__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18511__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18511__3		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_GM18511__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_GM18511__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_GM18511__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. 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		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18516__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18516__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18516__3		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_GM18516__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_GM18516__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_GM18516__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. 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_GM18517__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18517__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18517__3		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 g1_PX1406_GM18517__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_GM18517__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_GM18517__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. 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_GM18519__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18519__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18519__3		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_GM18519__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_GM18519__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_GM18519__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. 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 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		
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_GM18520__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18520__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18520__3		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_GM18520__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_GM18520__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_GM18520__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. g1_PX1406_GM18520		
Ratio H/L localized g1_PX1406_GM18520		

Ratio H/L nmods g1_PX1406_GM18520		
Ratio H/L variability [%] g1_PX1406_GM18520		
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_GM18522__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18522__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18522__3		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_GM18522__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_GM18522__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_GM18522__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. 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.
Ratio H/L g1_PX1406_GM18523__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18523__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18523__3		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_GM18523__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_GM18523__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_GM18523__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. 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_GM18852__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18852__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18852__3		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_GM18852__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_GM18852__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_GM18852__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. g1_PX1406_GM18852		
Ratio H/L localized g1_PX1406_GM18852		
Ratio H/L nmods g1_PX1406_GM18852		
Ratio H/L variability [%] g1_PX1406_GM18852		
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_GM18855__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18855__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18855__3		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_GM18855__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_GM18855__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_GM18855__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. g1_PX1406_GM18855		
Ratio H/L localized g1_PX1406_GM18855		
Ratio H/L nmods g1_PX1406_GM18855		
Ratio H/L variability [%] g1_PX1406_GM18855		
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		
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_GM18858__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18858__2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX1406_GM18858__3		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_GM18858__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_GM18858__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. 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 g1_PX1406_GM18861__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18861__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18861__3		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 normalized g1_PX1406_GM18861__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_GM18861__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_GM18861__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. 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 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		
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_GM18862__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18862__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18862__3		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 g1_PX1406_GM18862__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_GM18862__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_GM18862__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. 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_GM18870__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18870__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18870__3		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_GM18870__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_GM18870__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_GM18870__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. 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_GM18871__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18871__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18871__3		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_GM18871__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_GM18871__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_GM18871__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. 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 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		
Occupancy L g1_PX1406_GM18871		
Occupancy H g1_PX1406_GM18871		
Ratio H/L g1_PX1406_GM18907		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18907__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18907__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18907__3		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_GM18907__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_GM18907__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_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. g1_PX1406_GM18907		
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 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		
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_GM18909__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18909__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18909__3		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 g1_PX1406_GM18909__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_GM18909__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_GM18909__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. 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.

Ratio H/L g1_PX1406_GM18912__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18912__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18912__3		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_GM18912__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_GM18912__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_GM18912__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. 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 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		
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_GM18913__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18913__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18913__3		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_GM18913__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_GM18913__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_GM18913__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. 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 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		
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_GM18916__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18916__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM18916__3		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 normalized g1_PX1406_GM18916__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_GM18916__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_GM18916__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. 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 g1_PX1406_GM18916		
Ratio H/L g1_PX1406_GM19092		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19092__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19092__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19092__3		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 normalized g1_PX1406_GM19092__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_GM19092__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_GM19092__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. 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 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		
Occupancy L g1_PX1406_GM19092		
Occupancy H g1_PX1406_GM19092		
Ratio H/L g1_PX1406_GM19093		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19093__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19093__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19093__3		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_GM19093__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_GM19093__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_GM19093__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. 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 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		
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 g1_PX1406_GM19098__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19098__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19098__3		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 normalized g1_PX1406_GM19098__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_GM19098__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_GM19098__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. 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_GM19099__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19099__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19099__3		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 normalized g1_PX1406_GM19099__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_GM19099__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_GM19099__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. 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 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		
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_GM19101__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19101__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19101__3		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_GM19101__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_GM19101__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_GM19101__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. 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_GM19102__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19102__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19102__3		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_GM19102__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_GM19102__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_GM19102__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. 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_GM19108__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19108__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19108__3		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_GM19108__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_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_GM19108__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. 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 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		
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_GM19114__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19114__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19114__3		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 g1_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_GM19114__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. 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 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		
Occupancy L g1_PX1406_GM19114		
Occupancy H g1_PX1406_GM19114		
Ratio H/L g1_PX1406_GM19116		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19116__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19116__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19116__3		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 normalized g1_PX1406_GM19116__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_GM19116__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_GM19116__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. 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 g1_PX1406_GM19119__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19119__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19119__3		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 normalized g1_PX1406_GM19119__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_GM19119__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_GM19119__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. g1_PX1406_GM19119		
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 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		
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_GM19127__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19127__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19127__3		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_GM19127__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_GM19127__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_GM19127__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. 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 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		
Occupancy L g1_PX1406_GM19127		
Occupancy H g1_PX1406_GM19127		
Ratio H/L g1_PX1406_GM19128		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19128__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19128__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19128__3		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_GM19128__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_GM19128__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_GM19128__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. 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_GM19130__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19130__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19130__3		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_GM19130__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_GM19130__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_GM19130__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. 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_GM19131__1		The ratio between two heavy and light label partners.

Ratio H/L g1_PX1406_GM19131__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19131__3		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 normalized g1_PX1406_GM19131__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_GM19131__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_GM19131__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. g1_PX1406_GM19131		
Ratio H/L localized g1_PX1406_GM19131		
Ratio H/L nmods g1_PX1406_GM19131		
Ratio H/L variability [%] g1_PX1406_GM19131		
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		
Occupancy L g1_PX1406_GM19131		
Occupancy H g1_PX1406_GM19131		
Ratio H/L g1_PX1406_GM19137		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19137__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19137__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19137__3		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 normalized g1_PX1406_GM19137__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_GM19137__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_GM19137__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. g1_PX1406_GM19137		
Ratio H/L localized g1_PX1406_GM19137		
Ratio H/L nmods g1_PX1406_GM19137		
Ratio H/L variability [%] g1_PX1406_GM19137		
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_GM19137		
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.
Ratio H/L g1_PX1406_GM19138__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19138__3		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 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 g1_PX1406_GM19138__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_GM19138__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. 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_GM19140__1		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_GM19140__3		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_GM19140__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_GM19140__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_GM19140__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. 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_GM19143__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19143__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19143__3		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_GM19143__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_GM19143__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_GM19143__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. 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		
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_GM19144__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19144__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19144__3		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_GM19144__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_GM19144__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_GM19144__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. 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_GM19147__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19147__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19147__3		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_GM19147__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_GM19147__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_GM19147__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. 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_GM19152__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19152__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19152__3		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 g1_PX1406_GM19152__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_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_GM19152__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. 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_GM19153__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19153__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19153__3		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_GM19153__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_GM19153__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_GM19153__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. 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_GM19160__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19160__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19160__3		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 g1_PX1406_GM19160__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_GM19160__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_GM19160__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. 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 quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX1406_GM19160		
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_GM19172__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19172__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19172__3		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 normalized g1_PX1406_GM19172__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_GM19172__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_GM19172__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. g1_PX1406_GM19172		
Ratio H/L localized g1_PX1406_GM19172		
Ratio H/L nmods 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_GM19192__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19192__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19192__3		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_GM19192__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_GM19192__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_GM19192__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. g1_PX1406_GM19192		
Ratio H/L localized g1_PX1406_GM19192		

Ratio H/L nmods g1_PX1406_GM19192		
Ratio H/L variability [%] g1_PX1406_GM19192		
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_GM19193__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19193__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19193__3		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_GM19193__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_GM19193__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_GM19193__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. 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_GM19200__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19200__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19200__3		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_GM19200__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_GM19200__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_GM19200__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. 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 g1_PX1406_GM19203__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19203__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19203__3		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 normalized g1_PX1406_GM19203__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_GM19203__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_GM19203__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. 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 g1_PX1406_GM19203		
Occupancy H g1_PX1406_GM19203		
Ratio H/L g1_PX1406_GM19204		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19204__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19204__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19204__3		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_GM19204__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_GM19204__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_GM19204__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. g1_PX1406_GM19204		
Ratio H/L localized g1_PX1406_GM19204		
Ratio H/L nmods g1_PX1406_GM19204		
Ratio H/L variability [%] g1_PX1406_GM19204		
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		
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_GM19207__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19207__2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX1406_GM19207__3		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_GM19207__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_GM19207__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. 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 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		
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_GM19209__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19209__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19209__3		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_GM19209__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. g1_PX1406_GM19209		
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 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		
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_GM19222__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19222__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX1406_GM19222__3		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_GM19222__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_GM19222__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_GM19222__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. 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_GM19257__1		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_GM19257__3		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_GM19257__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_GM19257__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_GM19257__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. 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_Rep1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep1__3		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 normalized g1_PX151_Rep1__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_PX151_Rep1__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_PX151_Rep1__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. 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_Rep2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep2__3		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 normalized g1_PX151_Rep2__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_PX151_Rep2__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_PX151_Rep2__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. 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		
Ratio H/L g1_PX151_Rep3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX151_Rep3__3		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 normalized g1_PX151_Rep3__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_PX151_Rep3__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_PX151_Rep3__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. 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_HCC1143-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143-1__3		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_HCC1143-1__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_PX309_HCC1143-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1143-1__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. g1_PX309_HCC1143-1		
Ratio H/L localized g1_PX309_HCC1143-1		

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_HCC1143-1		
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_HCC1143-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143-2__3		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_HCC1143-2__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_HCC1143-2__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_HCC1143-2__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. 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_HCC1143-2		
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_HCC1143-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1143-3__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 normalized g1_PX309_HCC1143-3__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_HCC1143-3__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_HCC1143-3__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. 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 L 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 partners.
Ratio H/L g1_PX309_HCC1599-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-1__3		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 normalized g1_PX309_HCC1599-1__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_PX309_HCC1599-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1599-1__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. g1_PX309_HCC1599-1		
Ratio H/L localized g1_PX309_HCC1599-1		
Ratio H/L nmods g1_PX309_HCC1599-1		
Ratio H/L variability [%] g1_PX309_HCC1599-1		
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		
Occupancy L g1_PX309_HCC1599-1		
Occupancy H g1_PX309_HCC1599-1		
Ratio H/L g1_PX309_HCC1599-2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-2__3		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 normalized g1_PX309_HCC1599-2__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_HCC1599-2__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_HCC1599-2__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. g1_PX309_HCC1599-2		
Ratio H/L localized g1_PX309_HCC1599-2		
Ratio H/L nmods g1_PX309_HCC1599-2		
Ratio H/L variability [%] g1_PX309_HCC1599-2		
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		
Occupancy L g1_PX309_HCC1599-2		
Occupancy H g1_PX309_HCC1599-2		
Ratio H/L g1_PX309_HCC1599-3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1599-3__2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX309_HCC1599-3__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 normalized g1_PX309_HCC1599-3__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_HCC1599-3__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_HCC1599-3__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. g1_PX309_HCC1599-3		
Ratio H/L localized g1_PX309_HCC1599-3		
Ratio H/L nmods g1_PX309_HCC1599-3		
Ratio H/L variability [%] g1_PX309_HCC1599-3		
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		
Occupancy L g1_PX309_HCC1599-3		
Occupancy H g1_PX309_HCC1599-3		
Ratio H/L g1_PX309_HCC1937-1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-1__3		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 normalized g1_PX309_HCC1937-1__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_PX309_HCC1937-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC1937-1__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. 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		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		
Occupancy L g1_PX309_HCC1937-1		
Occupancy H 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__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-2__3		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 normalized g1_PX309_HCC1937-2__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_HCC1937-2__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_HCC1937-2__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. 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_HCC1937-2		
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_HCC1937-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC1937-3__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 normalized g1_PX309_HCC1937-3__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_HCC1937-3__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_HCC1937-3__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. 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_HCC1937-3		
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_HCC202-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-1__3		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_HCC202-1__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_PX309_HCC202-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC202-1__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. g1_PX309_HCC202-1		
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 g1_PX309_HCC202-1		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count g1_PX309_HCC202-1		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-1		
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_HCC202-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-2__2		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_HCC202-2__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_HCC202-2__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_HCC202-2__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. 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_HCC202-2		
Occupancy L g1_PX309_HCC202-2		
Occupancy H g1_PX309_HCC202-2		
Ratio H/L g1_PX309_HCC202-3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC202-3__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 normalized g1_PX309_HCC202-3__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_HCC202-3__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_HCC202-3__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. 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_HCC202-3		
Ratio H/L g1_PX309_HCC2218-1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-1__1		The ratio between two heavy and light label partners.

Ratio H/L g1_PX309_HCC2218-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-1__3		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 normalized g1_PX309_HCC2218-1__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_PX309_HCC2218-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HCC2218-1__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. g1_PX309_HCC2218-1		
Ratio H/L localized g1_PX309_HCC2218-1		
Ratio H/L nmods g1_PX309_HCC2218-1		
Ratio H/L variability [%] g1_PX309_HCC2218-1		
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		
Occupancy L g1_PX309_HCC2218-1		
Occupancy H g1_PX309_HCC2218-1		
Ratio H/L g1_PX309_HCC2218-2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-2__3		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 normalized g1_PX309_HCC2218-2__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_HCC2218-2__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_HCC2218-2__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. g1_PX309_HCC2218-2		
Ratio H/L localized g1_PX309_HCC2218-2		
Ratio H/L nmods g1_PX309_HCC2218-2		
Ratio H/L variability [%] g1_PX309_HCC2218-2		
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		
Occupancy L g1_PX309_HCC2218-2		
Occupancy H 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__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HCC2218-3__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 normalized g1_PX309_HCC2218-3__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_HCC2218-3__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_HCC2218-3__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. 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_HCC2218-3		
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_HMEC1-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-1__3		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_HMEC1-1__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_PX309_HMEC1-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L 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. g1_PX309_HMEC1-1		
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_HMEC1-1		
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_HMEC1-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-2__3		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_HMEC1-2__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_HMEC1-2__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_HMEC1-2__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. 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		
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_HMEC1-2		
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_HMEC1-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC1-3__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 normalized g1_PX309_HMEC1-3__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_HMEC1-3__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_HMEC1-3__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. 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_HMEC1-3		
Occupancy L g1_PX309_HMEC1-3		
Occupancy H g1_PX309_HMEC1-3		
Ratio H/L g1_PX309_HMEC2-1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-1__3		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_HMEC2-1__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_PX309_HMEC2-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMEC2-1__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. 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_HMEC2-1		
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_HMEC2-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-2__3		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 normalized g1_PX309_HMEC2-2__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_HMEC2-2__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_HMEC2-2__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. g1_PX309_HMEC2-2		
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 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_HMEC2-2		
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_HMEC2-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMEC2-3__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 normalized g1_PX309_HMEC2-3__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_HMEC2-3__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_HMEC2-3__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. 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_HMEC2-3		
Occupancy L g1_PX309_HMEC2-3		
Occupancy H g1_PX309_HMEC2-3		
Ratio H/L g1_PX309_HMTS1-1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-1__3		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_HMTS1-1__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_PX309_HMTS1-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_HMTS1-1__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. g1_PX309_HMTS1-1		
Ratio H/L localized g1_PX309_HMTS1-1		

Ratio H/L nmods g1_PX309_HMTS1-1		
Ratio H/L variability [%] g1_PX309_HMTS1-1		
Ratio H/L count g1_PX309_HMTS1-1		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_HMTS1-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-2__3		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_HMTS1-2__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_HMTS1-2__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_HMTS1-2__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. 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_HMTS1-2		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		
Ratio H/L g1_PX309_HMTS1-3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_HMTS1-3__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 normalized g1_PX309_HMTS1-3__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_HMTS1-3__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_HMTS1-3__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. 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_HMTS1-3		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-1__1		The ratio between two heavy and light label partners.

Ratio H/L g1_PX309_MCF10a-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a-1__3		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 normalized g1_PX309_MCF10a-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_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 normalized g1_PX309_MCF10a-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. g1_PX309_MCF10a-1		
Ratio H/L localized g1_PX309_MCF10a-1		
Ratio H/L nmods g1_PX309_MCF10a-1		
Ratio H/L variability [%] g1_PX309_MCF10a-1		
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-1		
Occupancy L g1_PX309_MCF10a-1		
Occupancy H g1_PX309_MCF10a-1		
Ratio H/L g1_PX309_MCF10a-2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a-2__3		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 normalized g1_PX309_MCF10a-2__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-2__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_MCF10a-2__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. g1_PX309_MCF10a-2		
Ratio H/L localized g1_PX309_MCF10a-2		
Ratio H/L nmods g1_PX309_MCF10a-2		
Ratio H/L variability [%] g1_PX309_MCF10a-2		
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-2		
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.
Ratio H/L g1_PX309_MCF10a-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MCF10a-3__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 normalized g1_PX309_MCF10a-3__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__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_MCF10a-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. 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-3		
Occupancy L g1_PX309_MCF10a-3		
Occupancy H g1_PX309_MCF10a-3		
Ratio H/L g1_PX309_MDAMB453-1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-1__3		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_MDAMB453-1__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_PX309_MDAMB453-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MDAMB453-1__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. 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_MDAMB453-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-2__3		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_MDAMB453-2__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_MDAMB453-2__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_MDAMB453-2__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. 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 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_MDAMB453-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MDAMB453-3__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 normalized g1_PX309_MDAMB453-3__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_MDAMB453-3__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_MDAMB453-3__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. 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_MFM223-1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-1__3		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_MFM223-1__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_PX309_MFM223-1__2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L normalized g1_PX309_MFM223-1__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. 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_MFM223-1		
Occupancy L g1_PX309_MFM223-1		
Occupancy H g1_PX309_MFM223-1		
Ratio H/L g1_PX309_MFM223-2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX309_MFM223-2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-2__3		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_MFM223-2__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_MFM223-2__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_MFM223-2__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. 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_MFM223-2		
Occupancy H g1_PX309_MFM223-2		
Ratio H/L g1_PX309_MFM223-3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX309_MFM223-3__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 normalized g1_PX309_MFM223-3__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_MFM223-3__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_MFM223-3__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. 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_MFM223-3		
Ratio H/L g1_PX359_0h_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_1__3		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 normalized g1_PX359_0h_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_PX359_0h_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 normalized g1_PX359_0h_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. 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		
Ratio H/L g1_PX359_0h_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_2__3		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 normalized g1_PX359_0h_2__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_0h_2__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_0h_2__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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_0h_3__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 normalized g1_PX359_0h_3__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_0h_3__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_0h_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. 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		
Ratio H/L g1_PX359_BSA_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_1__3		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 normalized g1_PX359_BSA_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_PX359_BSA_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 normalized g1_PX359_BSA_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. g1_PX359_BSA_1		
Ratio H/L localized g1_PX359_BSA_1		
Ratio H/L nmods g1_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 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		
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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_2__3		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_2__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_BSA_2__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_2__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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_BSA_3__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 normalized g1_PX359_BSA_3__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_BSA_3__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_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. 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		
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		
Occupancy L g1_PX359_BSA_3		
Occupancy H g1_PX359_BSA_3		

Ratio H/L g1_PX359_FN_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_1__3		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 normalized g1_PX359_FN_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_PX359_FN_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 normalized g1_PX359_FN_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. 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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_2__3		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 normalized g1_PX359_FN_2__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_FN_2__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_FN_2__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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_FN_3__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 normalized g1_PX359_FN_3__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_FN_3__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_FN_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. 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		

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		
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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_1__3		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_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_PX359_GFR_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 normalized g1_PX359_GFR_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. 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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_2__3		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_2__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_2__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_2__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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_GFR_3__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 normalized g1_PX359_GFR_3__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_3__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_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. 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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_1__3		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_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_PX359_LAM_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 normalized g1_PX359_LAM_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. g1_PX359_LAM_1		
Ratio H/L localized g1_PX359_LAM_1		
Ratio H/L nmods g1_PX359_LAM_1		
Ratio H/L variability [%] g1_PX359_LAM_1		
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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_2__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_2__3		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 normalized g1_PX359_LAM_2__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_2__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_LAM_2__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. 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		
Ratio H/L g1_PX359_LAM_3		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_LAM_3__2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX359_LAM_3__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 normalized g1_PX359_LAM_3__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_3__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_LAM_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. 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 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		
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 12h_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h_1__3		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 normalized g1_PX359_Matr 12h_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_PX359_Matr 12h_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 normalized g1_PX359_Matr 12h_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. 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 [%] g1_PX359_Matr 12h_1		
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		
Occupancy L g1_PX359_Matr 12h_1		
Occupancy H 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 g1_PX359_Matr 12h_2__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 12h_2__2		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_2__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 12h_2__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_2__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. 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		
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_3__1		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_3__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 12h_3__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_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. 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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_1__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_1__3		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_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_PX359_Matr 24h_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 normalized g1_PX359_Matr 24h_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. 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 24h_1		
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 24h_2_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_2_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_2_3		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_2_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_2_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_2_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. 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_3_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_3_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 24h_3_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 normalized g1_PX359_Matr 24h_3_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_3_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_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. 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_1_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_1_2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX359_Matr 30h_1__3		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_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_PX359_Matr 30h_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 normalized g1_PX359_Matr 30h_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. 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_2__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_2__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_2__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. 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 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		
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 30h_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr 30h_3__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 normalized g1_PX359_Matr 30h_3__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_3__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_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. 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_1_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_1_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_1_3		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_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_PX359_Matr dil_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 normalized g1_PX359_Matr dil_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. 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_2_1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_2_2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_2_3		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_2_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_2_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_2_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. 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_3__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_3__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX359_Matr dil_3__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 normalized g1_PX359_Matr dil_3__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_3__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_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. 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 g1_PX419_human_18507__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_18507__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_18507__3		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 normalized g1_PX419_human_18507__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_PX419_human_18507__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_PX419_human_18507__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. 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 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		
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_18516__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_18516__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_18516__3		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 normalized g1_PX419_human_18516__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_PX419_human_18516__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_PX419_human_18516__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. 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_19193__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_19193__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_19193__3		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_19193__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_PX419_human_19193__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_PX419_human_19193__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. 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 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		
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.
Ratio H/L g1_PX419_human_19204__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_19204__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX419_human_19204__3		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_19204__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_PX419_human_19204__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_PX419_human_19204__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. g1_PX419_human_19204		

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_Xeno092__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno092__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno092__3		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 g1_PX438_Xeno092__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_PX438_Xeno092__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. 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_Xeno441__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno441__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno441__3		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 normalized g1_PX438_Xeno441__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_Xeno441__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_PX438_Xeno441__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. 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_Xeno561__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno561__2		The ratio between two heavy and light label partners.

Ratio H/L g1_PX438_Xeno561__3		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_Xeno561__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_Xeno561__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_PX438_Xeno561__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. 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 g1_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_Xeno691__1		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno691__2		The ratio between two heavy and light label partners.
Ratio H/L g1_PX438_Xeno691__3		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_Xeno691__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_PX438_Xeno691__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. g1_PX438_Xeno691		
Ratio H/L localized g1_PX438_Xeno691		
Ratio H/L nmods g1_PX438_Xeno691		
Ratio H/L variability [%] g1_PX438_Xeno691		
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_expA__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expA__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expA__3		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 normalized g2_PX058_expA__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 g2_PX058_expA__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 g2_PX058_expA__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. 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_expB__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expB__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expB__3		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_expB__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 g2_PX058_expB__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 g2_PX058_expB__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. 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_expC__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expC__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expC__3		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_expC__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 g2_PX058_expC__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 g2_PX058_expC__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. 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 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		
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_expD__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expD__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expD__3		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_expD__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 g2_PX058_expD__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 g2_PX058_expD__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. g2_PX058_expD		
Ratio H/L localized g2_PX058_expD		
Ratio H/L nmods g2_PX058_expD		

Ratio H/L variability [%] g2_PX058_expD		
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_expE___1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expE___2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expE___3		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_expE___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 g2_PX058_expE___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 g2_PX058_expE___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. 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_expF___1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expF___2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX058_expF___3		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_expF___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 g2_PX058_expF___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 g2_PX058_expF___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. 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_Rep1___1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep1___2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep1___3		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_Rep1___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 g2_PX089_Rep1___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 g2_PX089_Rep1___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. 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 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		
Ratio H/L g2_PX089_Rep2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep2__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep2__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX089_Rep2__3		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_Rep2__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 g2_PX089_Rep2__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 g2_PX089_Rep2__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. 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 20h		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 20h__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 20h__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep1 20h__3		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 20h__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 g2_PX537_exp14 rep1 20h__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 g2_PX537_exp14 rep1 20h__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. 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 6h__2		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 6h__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 g2_PX537_exp14 rep1 6h__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 g2_PX537_exp14 rep1 6h__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. 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 20h__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 20h__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 20h__3		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 20h__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 g2_PX537_exp14 rep2 20h__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 g2_PX537_exp14 rep2 20h__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. 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		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 6h__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 6h__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep2 6h__3		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 normalized g2_PX537_exp14 rep2 6h__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 g2_PX537_exp14 rep2 6h__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 g2_PX537_exp14 rep2 6h__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. 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 20h__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 20h__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 20h__3		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 20h__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 g2_PX537_exp14 rep3 20h__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 g2_PX537_exp14 rep3 20h__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. 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 6h__1		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 6h__2		The ratio between two heavy and light label partners.
Ratio H/L g2_PX537_exp14 rep3 6h__3		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 6h__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 g2_PX537_exp14 rep3 6h__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 g2_PX537_exp14 rep3 6h__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. 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		
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_1__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_1__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_1__3		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_1__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_1__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_A_TSA_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_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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_1__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_1__3		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_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 g3_GK1_Chromatin_A_TSA_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 normalized g3_GK1_Chromatin_A_TSA_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. 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_1__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_1__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_1__3		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_1__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_1__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_1__3		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_2__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_2__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_A_TSA_2__3		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 normalized g3_GK1_Chromatin_A_TSA_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_A_TSA_2__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_A_TSA_2__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_A_TSA_2		
Ratio M/L localized g3_GK1_Chromatin_A_TSA_2		
Ratio M/L nmods g3_GK1_Chromatin_A_TSA_2		
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 g3_GK1_Chromatin_A_TSA_2__1		The ratio between two heavy and light label partners.

Ratio H/L g3_GK1_Chromatin_A_TSA_2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_A_TSA_2__3		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_2__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_2__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_2__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_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_2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_A_TSA_2__3		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_2__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_2__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_2__3		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 g3_GK1_Chromatin_A_TSA_2		
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		
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_1__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_1__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_CC_1__3		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_1__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_1__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_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		
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 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 g3_GK1_Chromatin_CC_1__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_1__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_1__3		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 normalized g3_GK1_Chromatin_CC_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 g3_GK1_Chromatin_CC_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 normalized g3_GK1_Chromatin_CC_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. 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 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 g3_GK1_Chromatin_CC_1__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_CC_1__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_CC_1__3		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 normalized g3_GK1_Chromatin_CC_1__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_CC_1__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_1__3		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_2__1		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_2__3		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_2__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__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_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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_CC_2__3		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_2__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_CC_2__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_2__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_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_2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_CC_2__2		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_2__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_CC_2__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_2__3		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_1__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_1__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_1__3		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_1__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_1__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_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_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_1__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_1__2		The ratio between two heavy and light label partners.

Ratio H/L g3_GK1_Chromatin_EHT_1___3		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_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 g3_GK1_Chromatin_EHT_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 normalized g3_GK1_Chromatin_EHT_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. 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_1___1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_1___2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_1___3		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_1___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_1___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_1___3		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_2___1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_2___2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_2___3		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_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_EHT_2_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_2_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_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_2_1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_2_2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_2_3		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_2_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_2_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_2_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_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_2_1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_2_2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_2_3		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_2_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_2_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_2_3		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 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		
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_3__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_3__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_3__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 normalized g3_GK1_Chromatin_EHT_3__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_3__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_3__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_EHT_3		
Ratio M/L localized g3_GK1_Chromatin_EHT_3		
Ratio M/L nmods g3_GK1_Chromatin_EHT_3		
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 g3_GK1_Chromatin_EHT_3__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_3__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_3__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 normalized g3_GK1_Chromatin_EHT_3__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_3__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_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_3__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_3__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_3__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 normalized g3_GK1_Chromatin_EHT_3__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_3__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_3__3		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_4__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_4__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_4__3		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_4__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_4__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_4__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_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		
Ratio H/L g3_GK1_Chromatin_EHT_4		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_4__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_4__2		The ratio between two heavy and light label partners.

Ratio H/L g3_GK1_Chromatin_EHT_4__3		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 g3_GK1_Chromatin_EHT_4__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_4__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_4__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_4		
Ratio H/L localized g3_GK1_Chromatin_EHT_4		
Ratio H/L nmods g3_GK1_Chromatin_EHT_4		
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 g3_GK1_Chromatin_EHT_4__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_4__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_4__3		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 normalized g3_GK1_Chromatin_EHT_4__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_4__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_4__3		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.
Ratio M/L g3_GK1_Chromatin_EHT_5__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_5__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_5__3		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 normalized g3_GK1_Chromatin_EHT_5__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_5__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_5__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_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_5__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_5__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_5__3		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_5__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_5__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_5__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_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_5__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_5__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_5__3		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_5__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_5__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_5__3		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_6__1		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_6__2		The ratio between two medium and light label partners.
Ratio M/L g3_GK1_Chromatin_EHT_6__3		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_6__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_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 g3_GK1_Chromatin_EHT_6__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_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		
Ratio H/L g3_GK1_Chromatin_EHT_6		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_6__1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_6__2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_EHT_6__3		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 normalized g3_GK1_Chromatin_EHT_6__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_6__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_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_6__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_6__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_EHT_6__3		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_6__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_6__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_6__3		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__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_mH2A_4_5__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_mH2A_4_5__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_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		

Ratio H/L g3_GK1_Chromatin_mH2A_4_5		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_mH2A_4_5___ 1		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_mH2A_4_5___ 2		The ratio between two heavy and light label partners.
Ratio H/L g3_GK1_Chromatin_mH2A_4_5___ 3		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 normalized g3_GK1_Chromatin_mH2A_4_5___ 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_mH2A_4_5___ 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_mH2A_4_5___ 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_mH2A_4_5		
Ratio H/L localized g3_GK1_Chromatin_mH2A_4_5		
Ratio H/L nmods g3_GK1_Chromatin_mH2A_4_5		
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 g3_GK1_Chromatin_mH2A_4_5___ 1		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_mH2A_4_5___ 2		The ratio between two heavy and medium label partners.
Ratio H/M g3_GK1_Chromatin_mH2A_4_5___ 3		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 normalized g3_GK1_Chromatin_mH2A_4_5___ 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_mH2A_4_5___ 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_mH2A_4_5___ 3		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_mH2A_4_5		
Ratio H/M localized g3_GK1_Chromatin_mH2A_4_5		
Ratio H/M nmods g3_GK1_Chromatin_mH2A_4_5		
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		
Occupancy L g3_GK1_Chromatin_mH2A_4_5		
Occupancy M g3_GK1_Chromatin_mH2A_4_5		

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_ET__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET__3		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_ET__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_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__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_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_ET__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET__2		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET__3		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 normalized g3_KW35_ET__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_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__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_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_ET__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET__3		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_ET__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_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__3		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 quantitation that are quantified with the re-quantify method.
Ratio H/M type g3_KW35_ET		
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_2__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET_2__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_ET_2__3		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_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_KW35_ET_2__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_2__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_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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET_2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_ET_2__3		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_2__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_KW35_ET_2__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_2__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_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_2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET_2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_ET_2__3		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_2__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_KW35_ET_2__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_2__3		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_nE__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE__3		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_nE__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_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__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_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_nE__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE__2		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE__3		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_nE__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_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 normalized g3_KW35_nE__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_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_nE__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE__3		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_nE__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_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__3		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		
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_2__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE_2__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_nE_2__3		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_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_KW35_nE_2__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_2__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_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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE_2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_nE_2__3		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 normalized g3_KW35_nE_2__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_KW35_nE_2__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_nE_2__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_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_2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE_2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_nE_2__3		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_2__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_KW35_nE_2__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_2__3		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_ET__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_rot_ET__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_rot_ET__3		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_ET__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_KW35_rot_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_rot_ET__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_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_ET__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_rot_ET__2		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_rot_ET__3		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_ET__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_KW35_rot_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_rot_ET__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_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 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 g3_KW35_rot_ET__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_rot_ET__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_rot_ET__3		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_ET__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_KW35_rot_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_rot_ET__3		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_wE__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE__3		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_wE__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_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__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_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_wE__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE__2		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE__3		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_wE__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_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__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_KW35_wE		
Ratio H/L localized g3_KW35_wE		
Ratio H/L nmods g3_KW35_wE		
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_wE__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE__3		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_wE__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_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__3		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_2__1		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE_2__2		The ratio between two medium and light label partners.
Ratio M/L g3_KW35_wE_2__3		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 normalized g3_KW35_wE_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_KW35_wE_2__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_2__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_KW35_wE_2		
Ratio M/L localized g3_KW35_wE_2		
Ratio M/L nmods g3_KW35_wE_2		
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_2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_KW35_wE_2__2		The ratio between two heavy and light label partners.

Ratio H/L g3_KW35_wE_2__3		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_2__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_KW35_wE_2__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_2__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_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_2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE_2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_KW35_wE_2__3		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_2__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_KW35_wE_2__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_2__3		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_Exp1__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp1__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp1__3		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_Exp1__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_PX328_Diff3_Exp1__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_PX328_Diff3_Exp1__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_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 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 g3_PX328_Diff3_Exp1___1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp1___2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp1___3		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_Exp1___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_PX328_Diff3_Exp1___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_PX328_Diff3_Exp1___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_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_Exp1___1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp1___2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp1___3		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_Exp1___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_PX328_Diff3_Exp1___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_PX328_Diff3_Exp1___3		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_Exp2__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp2__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff3_Exp2__3		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_Exp2__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_PX328_Diff3_Exp2__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_PX328_Diff3_Exp2__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_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_Exp2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff3_Exp2__3		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_Exp2__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_PX328_Diff3_Exp2__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_PX328_Diff3_Exp2__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_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_Exp2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff3_Exp2__3		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_Exp2__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_PX328_Diff3_Exp2___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_PX328_Diff3_Exp2___3		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_Exp1___1		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp1___2		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp1___3		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_Exp1___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_PX328_Diff4_Exp1___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_PX328_Diff4_Exp1___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_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_Exp1___1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp1___2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp1___3		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_Exp1___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_PX328_Diff4_Exp1___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_PX328_Diff4_Exp1___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_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		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff4_Exp1__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff4_Exp1__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff4_Exp1__3		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_Exp1__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_PX328_Diff4_Exp1__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_PX328_Diff4_Exp1__3		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.
Ratio M/L g3_PX328_Diff4_Exp2__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp2__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff4_Exp2__3		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_Exp2__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_PX328_Diff4_Exp2__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_PX328_Diff4_Exp2__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_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.

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 g3_PX328_Diff4_Exp2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff4_Exp2__3		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 normalized g3_PX328_Diff4_Exp2__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_PX328_Diff4_Exp2__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_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 H/L unmod. pep. g3_PX328_Diff4_Exp2		
Ratio H/L localized g3_PX328_Diff4_Exp2		
Ratio H/L nmods g3_PX328_Diff4_Exp2		
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 g3_PX328_Diff4_Exp2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff4_Exp2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff4_Exp2__3		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 normalized g3_PX328_Diff4_Exp2__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_PX328_Diff4_Exp2__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_PX328_Diff4_Exp2__3		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_Exp2		
Ratio H/M localized g3_PX328_Diff4_Exp2		
Ratio H/M nmods g3_PX328_Diff4_Exp2		
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		
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 g3_PX328_Diff5_Exp1__1		The ratio between two medium and light label partners.

Ratio M/L g3_PX328_Diff5_Exp1__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff5_Exp1__3		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 normalized g3_PX328_Diff5_Exp1__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_PX328_Diff5_Exp1__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_PX328_Diff5_Exp1__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_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_Exp1__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp1__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp1__3		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_Exp1__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_PX328_Diff5_Exp1__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_PX328_Diff5_Exp1__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_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_Exp1__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp1__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp1__3		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_Exp1__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_PX328_Diff5_Exp1__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_PX328_Diff5_Exp1__3		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_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_Exp2__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff5_Exp2__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX328_Diff5_Exp2__3		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_Exp2__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_PX328_Diff5_Exp2__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_PX328_Diff5_Exp2__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_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_Exp2__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp2__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX328_Diff5_Exp2__3		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_Exp2__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_PX328_Diff5_Exp2__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_PX328_Diff5_Exp2__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_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 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 g3_PX328_Diff5_Exp2__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp2__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX328_Diff5_Exp2__3		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_Exp2__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_PX328_Diff5_Exp2__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_PX328_Diff5_Exp2__3		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_Spr__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A1_Spr__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A1_Spr__3		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_Spr__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_PX597_A1_Spr__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_PX597_A1_Spr__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_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_Spr__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A1_Spr__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A1_Spr__3		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 normalized g3_PX597_A1_Spr__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_PX597_A1_Spr__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_PX597_A1_Spr__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_PX597_A1_Spr		
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_Spr__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A1_Spr__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A1_Spr__3		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_Spr__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_PX597_A1_Spr__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_PX597_A1_Spr__3		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_Spr__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A2_Spr__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A2_Spr__3		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_Spr__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_PX597_A2_Spr__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_PX597_A2_Spr__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_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		
Ratio H/L g3_PX597_A2_Spr		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A2_Spr__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A2_Spr__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A2_Spr__3		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 g3_PX597_A2_Spr__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_PX597_A2_Spr__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_PX597_A2_Spr__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_PX597_A2_Spr		
Ratio H/L localized g3_PX597_A2_Spr		
Ratio H/L nmods g3_PX597_A2_Spr		
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_Spr__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A2_Spr__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A2_Spr__3		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_Spr__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_PX597_A2_Spr__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_PX597_A2_Spr__3		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		
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_Spr__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A3_Spr__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_A3_Spr__3		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 normalized g3_PX597_A3_Spr__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_PX597_A3_Spr__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_PX597_A3_Spr__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_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_Spr__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A3_Spr__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_A3_Spr__3		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_Spr__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_PX597_A3_Spr__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_PX597_A3_Spr__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_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_Spr__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A3_Spr__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_A3_Spr__3		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_Spr__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_PX597_A3_Spr__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_PX597_A3_Spr__3		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		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B1_Spr__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B1_Spr__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B1_Spr__3		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 normalized g3_PX597_B1_Spr__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_PX597_B1_Spr__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_PX597_B1_Spr__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_PX597_B1_Spr		
Ratio M/L localized g3_PX597_B1_Spr		
Ratio M/L nmods g3_PX597_B1_Spr		
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 g3_PX597_B1_Spr__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B1_Spr__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B1_Spr__3		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 normalized g3_PX597_B1_Spr__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_PX597_B1_Spr__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_PX597_B1_Spr__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_PX597_B1_Spr		
Ratio H/L localized g3_PX597_B1_Spr		
Ratio H/L nmods g3_PX597_B1_Spr		
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 g3_PX597_B1_Spr__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B1_Spr__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B1_Spr__3		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 normalized g3_PX597_B1_Spr__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_PX597_B1_Spr__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_PX597_B1_Spr__3		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_B1_Spr		
Ratio H/M localized g3_PX597_B1_Spr		
Ratio H/M nmods 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_Spr__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B2_Spr__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B2_Spr__3		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_Spr__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_PX597_B2_Spr__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_PX597_B2_Spr__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_PX597_B2_Spr		
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 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 g3_PX597_B2_Spr__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B2_Spr__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B2_Spr__3		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 normalized g3_PX597_B2_Spr__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_PX597_B2_Spr__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_PX597_B2_Spr__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_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_Spr__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B2_Spr__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B2_Spr__3		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 normalized g3_PX597_B2_Spr__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_PX597_B2_Spr__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_PX597_B2_Spr__3		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		
Ratio M/L g3_PX597_B3_Spr		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B3_Spr__1		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B3_Spr__2		The ratio between two medium and light label partners.
Ratio M/L g3_PX597_B3_Spr__3		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 normalized g3_PX597_B3_Spr__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_PX597_B3_Spr__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_PX597_B3_Spr__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_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_Spr__1		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B3_Spr__2		The ratio between two heavy and light label partners.
Ratio H/L g3_PX597_B3_Spr__3		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_Spr__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_PX597_B3_Spr__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_PX597_B3_Spr__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_PX597_B3_Spr		
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_Spr__1		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B3_Spr__2		The ratio between two heavy and medium label partners.
Ratio H/M g3_PX597_B3_Spr__3		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 normalized g3_PX597_B3_Spr__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_PX597_B3_Spr__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_PX597_B3_Spr__3		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_A__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_A__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_A__3		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_A__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_A__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_A__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_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_B__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_B__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_B__3		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_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_NCC_B__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_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_NCC_B		
Ratio H/L localized g4_NCC_B		
Ratio H/L nmods g4_NCC_B		
Ratio H/L variability [%] g4_NCC_B		

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		
Occupancy L g4_NCC_B		
Occupancy H g4_NCC_B		
Ratio H/L g4_NCC_C		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_C__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_C__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC_C__3		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 normalized g4_NCC_C__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_C__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_C__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_NCC_C		
Ratio H/L localized g4_NCC_C		
Ratio H/L nmods g4_NCC_C		
Ratio H/L variability [%] g4_NCC_C		
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		
Occupancy L g4_NCC_C		
Occupancy H 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__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s1__2		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		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_s1__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_s1__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-CPT_s1__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_NCC-CPT_s1		
Ratio H/L localized g4_NCC-CPT_s1		
Ratio H/L nmods g4_NCC-CPT_s1		
Ratio H/L variability [%] g4_NCC-CPT_s1		
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		
Occupancy L g4_NCC-CPT_s1		
Occupancy H g4_NCC-CPT_s1		
Ratio H/L g4_NCC-CPT_s2		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		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_s2__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_s2__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-CPT_s2__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_NCC-CPT_s2		

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_s3__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s3__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-CPT_s3__3		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_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-CPT_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-CPT_s3__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_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_Ex1__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex1__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex1__3		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_Ex1__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-HU_Ex1__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-HU_Ex1__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_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_Ex2__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex2__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex2__3		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_Ex2__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-HU_Ex2__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-HU_Ex2__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_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_Ex3__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex3__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-HU_Ex3__3		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_Ex3__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-HU_Ex3__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-HU_Ex3__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_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_s1__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s1__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-rosco_s1__3		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_s1__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_s1__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_s1__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_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_s2__1		The ratio between two heavy and light label partners.

Ratio H/L g4_NCC-roscos2_2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-roscos2_3		The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-roscos2		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-roscos2_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-roscos2_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-roscos2_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_NCC-roscos2		
Ratio H/L localized g4_NCC-roscos2		
Ratio H/L nmods g4_NCC-roscos2		
Ratio H/L variability [%] g4_NCC-roscos2		
Ratio H/L count g4_NCC-roscos2		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-roscos2		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-roscos2		
Occupancy L g4_NCC-roscos2		
Occupancy H g4_NCC-roscos2		
Ratio H/L g4_NCC-roscos3		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-roscos3_1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-roscos3_2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-roscos3_3		The ratio between two heavy and light label partners.
Ratio H/L normalized g4_NCC-roscos3		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-roscos3_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-roscos3_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-roscos3_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_NCC-roscos3		
Ratio H/L localized g4_NCC-roscos3		
Ratio H/L nmods g4_NCC-roscos3		
Ratio H/L variability [%] g4_NCC-roscos3		
Ratio H/L count g4_NCC-roscos3		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count g4_NCC-roscos3		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g4_NCC-roscos3		
Occupancy L g4_NCC-roscos3		
Occupancy H g4_NCC-roscos3		
Ratio H/L g4_NCC-TSA_Exp1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp1_1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp1_2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp1_3		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_Exp1_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-TSA_Exp1_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-TSA_Exp1_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_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.

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		
Occupancy L g4_NCC-TSA_Exp1		
Occupancy H g4_NCC-TSA_Exp1		
Ratio H/L g4_NCC-TSA_Exp2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp2__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp2__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp2__3		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 normalized g4_NCC-TSA_Exp2__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-TSA_Exp2__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-TSA_Exp2__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_NCC-TSA_Exp2		
Ratio H/L localized g4_NCC-TSA_Exp2		
Ratio H/L nmods g4_NCC-TSA_Exp2		
Ratio H/L variability [%] g4_NCC-TSA_Exp2		
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		
Occupancy L g4_NCC-TSA_Exp2		
Occupancy H g4_NCC-TSA_Exp2		
Ratio H/L g4_NCC-TSA_Exp3		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp3__1		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp3__2		The ratio between two heavy and light label partners.
Ratio H/L g4_NCC-TSA_Exp3__3		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 normalized g4_NCC-TSA_Exp3__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-TSA_Exp3__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-TSA_Exp3__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_NCC-TSA_Exp3		
Ratio H/L localized g4_NCC-TSA_Exp3		
Ratio H/L nmods g4_NCC-TSA_Exp3		
Ratio H/L variability [%] g4_NCC-TSA_Exp3		
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		
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__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_A__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_A__3		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 normalized g4_PX183_A__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_A__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_PX183_A__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_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_B__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_B__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_B__3		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 g4_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_B__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_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		
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_C__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_C__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_C__3		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_C__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_C__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_PX183_C__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_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_D__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_D__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_D__3		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_D__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_D__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_PX183_D__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_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_E__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_E__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX183_E__3		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_E__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_E__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_PX183_E__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_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_E1__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E1__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E1__3		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_E1__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_PX441_E1__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_E1__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_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.
Ratio H/L type g4_PX441_E1		
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.
Ratio H/L g4_PX441_E2__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E2__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E2__3		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_E2__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_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_E2__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_PX441_E2		
Ratio H/L localized g4_PX441_E2		
Ratio H/L nmods g4_PX441_E2		
Ratio H/L variability [%] g4_PX441_E2		
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_E3__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E3__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E3__3		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_E3__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_PX441_E3__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_E3__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_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_E4__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E4__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E4__3		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_E4__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_PX441_E4__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_E4__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_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_E5__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E5__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_E5__3		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 normalized g4_PX441_E5__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_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_E5__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_PX441_E5		
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 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_PX441_F1__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F1__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F1__3		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_F1__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_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 g4_PX441_F1__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_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_F2__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F2__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F2__3		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_F2__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_PX441_F2__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_F2__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_PX441_F2		
Ratio H/L localized g4_PX441_F2		
Ratio H/L nmods g4_PX441_F2		
Ratio H/L variability [%] g4_PX441_F2		
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		

Occupancy L g4_PX441_F2		
Occupancy H g4_PX441_F2		
Ratio H/L g4_PX441_F3		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F3__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F3__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F3__3		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 normalized g4_PX441_F3__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_PX441_F3__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_F3__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_PX441_F3		
Ratio H/L localized g4_PX441_F3		
Ratio H/L nmods g4_PX441_F3		
Ratio H/L variability [%] g4_PX441_F3		
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		
Occupancy L g4_PX441_F3		
Occupancy H g4_PX441_F3		
Ratio H/L g4_PX441_F4		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F4__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F4__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F4__3		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 normalized g4_PX441_F4__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_PX441_F4__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_F4__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_PX441_F4		
Ratio H/L localized g4_PX441_F4		
Ratio H/L nmods g4_PX441_F4		
Ratio H/L variability [%] g4_PX441_F4		
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		
Occupancy L g4_PX441_F4		
Occupancy H g4_PX441_F4		
Ratio H/L g4_PX441_F5		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F5__1		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F5__2		The ratio between two heavy and light label partners.
Ratio H/L g4_PX441_F5__3		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 normalized g4_PX441_F5__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_PX441_F5__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_F5__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_PX441_F5		
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_hilR		
Ratio mod/base H g1_GK1_Chromatin_hilR		

Intensity g1_GK1_Chromatin_IolR		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA 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_IolR		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_GK1_Chromatin_IolR		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g1_GK1_Chromatin_IolR		
Ratio mod/base H g1_GK1_Chromatin_IolR		
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 g1_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 g1_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		
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		

[illegible]

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 associated with the identified AA 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 associated with the identified AA 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		
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 g1_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 g1_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 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.
Ratio mod/base L g1_PX1406_GM18510		
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 g1_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 associated with the identified AA 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 associated with the identified AA 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 g1_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		
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 g1_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 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.
Ratio mod/base L g1_PX1406_GM19108		
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 g1_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 g1_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 g1_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 g1_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 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.
Ratio mod/base L g1_PX1406_GM19147		
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 g1_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 g1_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 g1_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 g1_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 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.
Ratio mod/base L g1_PX309_HMEC1-2		
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 g1_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_MDAMB453-1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-1		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_MDAMB453-2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-2		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_MDAMB453-3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H g1_PX309_MDAMB453-3		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		
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 12h_1		
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.
Ratio mod/base L g1_PX359_Matr 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 dil_1		
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 dil_2		
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		

[illegible]

Intensity H g2_PX537_exp14 rep1 20h		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		
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		

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 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.
Ratio mod/base L g3_GK1_Chromatin_A_TSA_2		
Ratio mod/base M g3_GK1_Chromatin_A_TSA_2		
Ratio mod/base H g3_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.

Intensity H g3_GK1_Chromatin_mH2A_4_5		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Ratio mod/base L g3_GK1_Chromatin_mH2A_4_5		
Ratio mod/base M g3_GK1_Chromatin_mH2A_4_5		
Ratio mod/base H g3_GK1_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 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.
Ratio mod/base L g3_KW35_ET		
Ratio mod/base M g3_KW35_ET		
Ratio mod/base H g3_KW35_ET		
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.
Ratio mod/base L g3_KW35_ET_2		
Ratio mod/base M g3_KW35_ET_2		
Ratio mod/base H g3_KW35_ET_2		
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.
Ratio mod/base L g3_KW35_nE		
Ratio mod/base M g3_KW35_nE		
Ratio mod/base H g3_KW35_nE		
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		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.
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.
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.
Ratio mod/base L g3_KW35_rot_ET		
Ratio mod/base M g3_KW35_rot_ET		
Ratio mod/base H g3_KW35_rot_ET		

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		
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 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.
Ratio mod/base L g3_PX328_Diff4_Exp2		
Ratio mod/base M g3_PX328_Diff4_Exp2		
Ratio mod/base H g3_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		
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 associated with the identified 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 g3_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 M g3_PX597_A2_Spr		
Ratio mod/base H g3_PX597_A2_Spr		

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		
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.
Ratio mod/base L g3_PX597_B1_Spr		
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		
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		
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		
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 associated with the identified 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 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, occurring 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, occurring 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, occurring 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 column '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 g1_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 g1_KW14_130317
Peptides g1_KW15_130317		Number of peptides (distinct peptide sequences) in experiment g1_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 g1_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 g1_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

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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 g1_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 g1_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 g2_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

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 g3_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 g3_GK1_Chromatin_EHT_5		Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_5
Peptides g3_GK1_Chromatin_EHT_6		Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_EHT_6
Peptides g3_GK1_Chromatin_mH2A_4_5		Number of peptides (distinct peptide sequences) in experiment g3_GK1_Chromatin_mH2A_4_5
Peptides g3_KW35_ET		Number of peptides (distinct peptide sequences) in experiment g3_KW35_ET
Peptides g3_KW35_ET_2		Number of peptides (distinct peptide sequences) in experiment g3_KW35_ET_2
Peptides g3_KW35_nE		Number of peptides (distinct peptide sequences) in experiment g3_KW35_nE
Peptides g3_KW35_nE_2		Number of peptides (distinct peptide sequences) in experiment g3_KW35_nE_2
Peptides g3_KW35_rot_ET		Number of peptides (distinct peptide sequences) in experiment g3_KW35_rot_ET
Peptides g3_KW35_wE		Number of peptides (distinct peptide sequences) in experiment g3_KW35_wE
Peptides g3_KW35_wE_2		Number of peptides (distinct peptide sequences) in experiment g3_KW35_wE_2
Peptides g3_PX328_Diff3_Exp1		Number of peptides (distinct peptide sequences) in experiment g3_PX328_Diff3_Exp1
Peptides g3_PX328_Diff3_Exp2		Number of peptides (distinct peptide sequences) in experiment g3_PX328_Diff3_Exp2
Peptides g3_PX328_Diff4_Exp1		Number of peptides (distinct peptide sequences) in experiment g3_PX328_Diff4_Exp1
Peptides g3_PX328_Diff4_Exp2		Number of peptides (distinct peptide sequences) in experiment g3_PX328_Diff4_Exp2
Peptides g3_PX328_Diff5_Exp1		Number of peptides (distinct peptide sequences) in experiment g3_PX328_Diff5_Exp1
Peptides g3_PX328_Diff5_Exp2		Number of peptides (distinct peptide sequences) in experiment g3_PX328_Diff5_Exp2
Peptides g3_PX597_A1_Spr		Number of peptides (distinct peptide sequences) in experiment g3_PX597_A1_Spr
Peptides g3_PX597_A2_Spr		Number of peptides (distinct peptide sequences) in experiment g3_PX597_A2_Spr
Peptides g3_PX597_A3_Spr		Number of peptides (distinct peptide sequences) in experiment g3_PX597_A3_Spr
Peptides g3_PX597_B1_Spr		Number of peptides (distinct peptide sequences) in experiment g3_PX597_B1_Spr
Peptides g3_PX597_B2_Spr		Number of peptides (distinct peptide sequences) in experiment g3_PX597_B2_Spr
Peptides g3_PX597_B3_Spr		Number of peptides (distinct peptide sequences) in experiment g3_PX597_B3_Spr
Peptides g4_NCC_A		Number of peptides (distinct peptide sequences) in experiment g4_NCC_A
Peptides g4_NCC_B		Number of peptides (distinct peptide sequences) in experiment g4_NCC_B
Peptides g4_NCC_C		Number of peptides (distinct peptide sequences) in experiment g4_NCC_C
Peptides g4_NCC-CPT_s1		Number of peptides (distinct peptide sequences) in experiment g4_NCC-CPT_s1
Peptides g4_NCC-CPT_s2		Number of peptides (distinct peptide sequences) in experiment g4_NCC-CPT_s2
Peptides g4_NCC-CPT_s3		Number of peptides (distinct peptide sequences) in experiment g4_NCC-CPT_s3
Peptides g4_NCC-HU_Ex1		Number of peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex1
Peptides g4_NCC-HU_Ex2		Number of peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex2
Peptides g4_NCC-HU_Ex3		Number of peptides (distinct peptide sequences) in experiment g4_NCC-HU_Ex3
Peptides g4_NCC-rosco_s1		Number of peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s1
Peptides g4_NCC-rosco_s2		Number of peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s2

Peptides g4_NCC-rosco_s3		Number of peptides (distinct peptide sequences) in experiment g4_NCC-rosco_s3
Peptides g4_NCC-TSA_Exp1		Number of peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp1
Peptides g4_NCC-TSA_Exp2		Number of peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp2
Peptides g4_NCC-TSA_Exp3		Number of peptides (distinct peptide sequences) in experiment g4_NCC-TSA_Exp3
Peptides g4_PX183_A		Number of peptides (distinct peptide sequences) in experiment g4_PX183_A
Peptides g4_PX183_B		Number of peptides (distinct peptide sequences) in experiment g4_PX183_B
Peptides g4_PX183_C		Number of peptides (distinct peptide sequences) in experiment g4_PX183_C
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_PX441_E1
Peptides g4_PX441_E2		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_E4
Peptides g4_PX441_E5		Number of peptides (distinct peptide sequences) in experiment g4_PX441_E5
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_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_F4
Peptides g4_PX441_F5		Number of peptides (distinct peptide sequences) in experiment g4_PX441_F5
Razor + unique peptides g1_GK1_Chromatin_AL		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_AL
Razor + unique peptides g1_GK1_Chromatin_CPT		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CPT
Razor + unique peptides g1_GK1_Chromatin_CR		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_CR
Razor + unique peptides g1_GK1_Chromatin_HepHek		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_HepHek
Razor + unique peptides g1_GK1_Chromatin_hilR		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_hilR
Razor + unique peptides g1_GK1_Chromatin_lolR		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_lolR
Razor + unique peptides g1_GK1_Chromatin_mH2A_1		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_1
Razor + unique peptides g1_GK1_Chromatin_mH2A_2		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_2
Razor + unique peptides g1_GK1_Chromatin_mH2A_3		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_mH2A_3
Razor + unique peptides g1_GK1_Chromatin_TNFA_1		Number of razor + unique peptides (distinct peptide sequences) in experiment 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_GK1_Chromatin_TNFA_3		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_GK1_Chromatin_TNFA_3
Razor + unique peptides g1_KW10_110506		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW10_110506
Razor + unique peptides g1_KW10_131126		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW10_131126
Razor + unique peptides g1_KW10_140117		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW10_140117
Razor + unique peptides g1_KW11_130125		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW11_130125
Razor + unique peptides g1_KW11_140104_nE		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW11_140104_nE
Razor + unique peptides g1_KW11_140104_wE		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW11_140104_wE
Razor + unique peptides g1_KW12_130317		Number of razor + unique peptides (distinct peptide sequences) in experiment g1_KW12_130317

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Unique peptides g4_PX183_A		Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_A
Unique peptides g4_PX183_B		Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_B
Unique peptides g4_PX183_C		Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_C
Unique peptides g4_PX183_D		Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_D
Unique peptides g4_PX183_E		Number of unique peptides (distinct peptide sequences) in experiment g4_PX183_E
Unique peptides g4_PX441_E1		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_E1
Unique peptides g4_PX441_E2		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_E2
Unique peptides g4_PX441_E3		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_E3
Unique peptides g4_PX441_E4		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_E4
Unique peptides g4_PX441_E5		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_E5
Unique peptides g4_PX441_F1		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F1
Unique peptides g4_PX441_F2		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F2
Unique peptides g4_PX441_F3		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F3
Unique peptides g4_PX441_F4		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F4
Unique peptides g4_PX441_F5		Number of unique peptides (distinct peptide sequences) in experiment g4_PX441_F5
Sequence coverage [%]		Percentage of the sequence that is covered by the identified peptides of the best protein sequence contained in the group.
Unique + razor sequence coverage [%]		Percentage of the sequence that is covered by the identified unique and razor peptides of the best protein sequence contained in the group.
Unique sequence coverage [%]		Percentage of the sequence that is covered by the identified unique peptides of the best protein sequence contained in the group.
Mol. weight [kDa]		Molecular weight of the leading protein sequence contained in the protein group.
Sequence length		The length of the leading protein sequence contained in the group.
Sequence lengths		The length of all sequences of the proteins contained in the group.
Q-value		This is the ratio of reverse to forward protein groups.
Score		Protein score which is derived from peptide posterior error probabilities.
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 g1_GK1_Chromatin_hilR		
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 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		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 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 g1_KW9_120425		Normalized 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_120425		Coefficient of variability 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_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 g1_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 quantitation 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 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 variability [%] g1_PX1194_H4		Coefficient of variability 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_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 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 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 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		
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 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		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 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		
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 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 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		
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 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 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 quantitation 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 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 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 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 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 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		
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		
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 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 g1_PX309_HCC202-1		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type g1_PX309_HCC202-1		
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_HCC202-2		
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_HCC202-3		
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.

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 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_HMEC1-1		
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_HMEC1-2		
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_HMEC1-3		
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_HMEC2-1		
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_HMEC2-2		
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_HMEC2-3		
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_HMTS1-1		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		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_HMTS1-2		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_HMTS1-3		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-1		
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-2		
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 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_MFM223-1		
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_MFM223-2		
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_MFM223-3		
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		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		
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		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 [%] 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 [%] 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 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 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		
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.

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 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.
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		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 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 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		
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 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		
Ratio H/L g2_PX058_expC		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 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		
Ratio H/L g2_PX058_expD		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 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		
Ratio H/L g2_PX058_expE		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 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 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		
Ratio H/L g2_PX537_exp14 rep1 20h		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 variability [%] g2_PX537_exp14 rep1 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 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 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 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 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 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 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		
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.

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 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 [%] 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 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		

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 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 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 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 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		
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 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 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		
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 naturally logarithmized ratios times 100.
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		
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-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 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/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 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		
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.

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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-roscsco_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-roscsco_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-roscsco_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.

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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.
Type		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. $m*a+b - \text{round}(m*a+b)$ 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 second of chromatography.
Multiplets / s		The average number of labeling multiplets detected per second of 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.
Type		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 the 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 scan number 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 ([0..1], 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.
Type		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 the MS spectrum.
Precursor Full ScanNumber		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.
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.