Table1: Meta-Analysis workflows parameters description:

Parameter Name	Description	Associated workflow:
OReDatasetsStr	*String* - Comma separated string for two datasets. For the current comparison -"Original,Reanalysis" or "Deposited,Stage3" are used.	MetaAnalysis_OriginalVsReanalysisFiles
ODatasetName	*String* - Original dataset name. Should match the string before comma in the parameter "OReDatasetsStr"	MetaAnalysis_OriginalVsReanalysisFiles
OProtRSEMCorrByGeneColname	*String* - Column name to use for the values with correlation between mRNA and protein measures calculated per gene (For original dataset)	MetaAnalysis_OriginalVsReanalysisFiles
OProtRSEMCorrBySampleColname	*String* - Column name to use for the values with correlation between mRNA and protein measures calculated per sample (For original dataset)	MetaAnalysis_OriginalVsReanalysisFiles
ReProtRSEMCorrByGeneColname	*String* - Column name to use for the values with correlation between mRNA and protein measures calculated per gene (For reanalysis dataset)	MetaAnalysis_OriginalVsReanalysisFiles
ReProtRSEMCorrBySampleColname	*String* - Column name to use for the values with correlation between mRNA and protein measures calculated per sample (For reanalysis dataset)	MetaAnalysis_OriginalVsReanalysisFiles
ReDatasetName	*String* - Reanalysis dataset name. Should match the string after	MetaAnalysis_OriginalVsReanalysisFiles

	comma in the parameter "OReDatasetsStr"	
OReProtRSEMByGeneSplot	*String* - Scatterplot name between original and reanalysis for correlation values between mRNA and Protein per gene	MetaAnalysis_OriginalVsReanalysisFiles
OReProtRSEMBySampleSplot	*String* - Scatterplot name between original and reanalysis for correlation values between mRNA and Protein per sample	MetaAnalysis_OriginalVsReanalysisFiles
OReProtCorrColname	*String* - Column name to use for the correlation values between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
OReProtDPlotTitle	*String* - Density plot name of protein correlations between original and reanalysis. Ideally, use the same as "OReProtCorrColname" parameter	MetaAnalysis_OriginalVsReanalysisFiles
OReRSEMCorrColname	*String* - Column name to use for the correlation values between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
OReRSEMDPlotTitle	*String* - Density plot name of mRNA correlations between original and reanalysis. Ideally, use the same as "OReRSEMCorrColname" parameter	MetaAnalysis_OriginalVsReanalysisFiles
vennTitle_Proteins	Title for Venn diagram for protein groups.	MetaAnalysis_OriginalVsReanalysisFiles
Myrimatch_DatasetsStr	*String* - Comma separated string for two	MetaAnalysis_ParamSensitivityFlles

	datasets. For the current workflow -"Myrimatch1,Myrimatch2".	
OReDatasetStr	*String* - Comma separated string for two datasets. For the current workflow -"Original,Reanalysis" or "Deposited,Stage3" are used.	MetaAnalysis_ParamSensitivityFll es
ReRefCustomMMDplot	*String* - Density plot name for correlations of overlapping between standard vs custom protein sequence databases for the same dataset	MetaAnalysis_ParamSensitivityFll es
SAAVColname	*String* - Column name for SAAV IDs	MetaAnalysis_ParamSensitivityFll es
VariantPeptideColname	*String* - Column name for variant peptide IDs	MetaAnalysis_ParamSensitivityFll es
datasetName1	*String* - Name of the first search dataset	MetaAnalysis_ParamSensitivityFll es
datasetName2	*String* - Name of the second search dataset	MetaAnalysis_ParamSensitivityFll es
datasetName3	*String* - Name of the third search dataset	MetaAnalysis_ParamSensitivityFll es
datasetName4	*String* - Name of the fourth search dataset	MetaAnalysis_ParamSensitivityFll es
datasetNameMyrimatch1	*String* - Name of the first instance of search engine dataset. Myrimatch was used for analysis. The workflow is agnostic to search engine as long as the file format is maintained.	MetaAnalysis_ParamSensitivityFll es
datasetNameMyrimatch2	*String* - Name of the second instance of search engine dataset (with only one parameter different from "datasetNameMyrimatc	MetaAnalysis_ParamSensitivityFll es

	h1"). Myrimatch was used for analysis. The workflow is agnostic to search engine as long as the file format is maintained.	
datasetNameOProteogenomic	*String* - Name of the first custom protein sequence database search dataset with original data	MetaAnalysis_ParamSensitivityFll es
datasetNameReProteogenomic	*String* - Name of the first custom protein sequence database search dataset with reanalysis data	MetaAnalysis_ParamSensitivityFll es
pepseqColname	Peptide sequence column name	MetaAnalysis_ParamSensitivityFll es
protAccessionsColname	Protein accessions column name in the peptide file	MetaAnalysis_ParamSensitivityFll es
vennTitle_PepMyrimatch	Title for peptides venn diagram	MetaAnalysis_ParamSensitivityFll es
vennTitle_ProtMyrimatch	Title for protein groups venn diagram	MetaAnalysis_ParamSensitivityFll es
vennTitle_SAAVs	Title for SAAVs venn diagram	MetaAnalysis_ParamSensitivityFll es
vennTitle_VariantPeptides		MetaAnalysis_ParamSensitivityFll es
addDatasetName1	*String* - Name of first (CRC95) dataset	MetaAnalysis_AdditionalDataFiles
addDatasetName2	*String* - Name of second (CRC100) dataset	MetaAnalysis_AdditionalDataFiles
addDatasetName3	*String* - Name of third (CRC105) dataset	MetaAnalysis_AdditionalDataFiles
addDatasetName4	*String* - Name of fourth (CRC110) dataset	MetaAnalysis_AdditionalDataFiles
addDatasetName5	*String* - Name of fifth (CRC115) dataset	MetaAnalysis_AdditionalDataFiles
SAAVDatasetsStr	*String* - Comma separated string for the SAAV results datasets. For the current	MetaAnalysis_NewDataFiles

	workflow -"CRC95,OV,BRCA". Should match the names provided under parameters - "newDatasetName1", "newDatasetName3" and "newDatasetName4"	
SAAVColname	Column name containing SAAV measures	MetaAnalysis_NewDataFiles
newDatasetName1	*String* - Name of first dataset. Should match the first name provided under "SAAVDatasetsStr"	MetaAnalysis_NewDataFiles
newDatasetName2	*String* - Name of second dataset	MetaAnalysis_NewDataFiles
newDatasetName3	*String* - Name of third dataset. Should match the second name provided under "SAAVDatasetsStr"	MetaAnalysis_NewDataFiles
newDatasetName4	*String* - Name of fourth dataset. Should match the third name provided under "SAAVDatasetsStr"	MetaAnalysis_NewDataFiles

Table5: Meta-Analysis workflows output files description (intermediary files not included):

Output file prefix	Description	Associated workflow:
OLog2qnormMtx	Matrix with log 2 - quantile normalized values of the protein measures (Original analysis)	MetaAnalysis_OriginalVsReanalysisFiles
OLongLog2qnorm	Long format file with log 2 - quantile normalized values of the protein measures (Original analysis)	MetaAnalysis_OriginalVsReanalysisFiles
OProtSCMatrix	Matrix with protein measures. In current sample -	MetaAnalysis_OriginalVsReanalysisFiles

	spectral counts were used as protein measures (Original analysis)	
ORePProtDensityPlot	Density plot for protein correlations between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
ORePProtRSEMByGeneSPlot	Scatter plot of mRNA-Protein correlations for original and reanalysis per gene	MetaAnalysis_OriginalVsReanalysisFiles
ORePProtRSEMBySampleSPlot	Scatter plot of mRNA-Protein correlations for original and reanalysis per sample	MetaAnalysis_OriginalVsReanalysisFiles
ORePProtsBarplot	Barplots of protein count per sample in original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
OReRSEMDensityPlot	Density plot for mRNA correlations between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
overlapORePProtIDs	List of overlapping proteins between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
ReLog2qnormMtx	Matrix with log 2 - quantile normalized values of the protein measures (Reanalysis analysis)	MetaAnalysis_OriginalVsReanalysisFiles
ReLongLog2qnorm	Long format file with log 2 - quantile normalized values of the protein measures (Reanalysis analysis)	MetaAnalysis_OriginalVsReanalysisFiles
ReProtSCMatrix	Matrix with protein measures. In	MetaAnalysis_OriginalVsReanalysisFiles

	current sample - spectral counts were used as protein measures (Reanalysis analysis)	
vennProtIDs	Venn Diagram of proteins between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
densityPlot	Density Plot of protein correlations for overlapping proteins between Reference and custom protein sequence databases	MetaAnalysis_ParamSensitivityFIles
longLog2qnorm_Myrimatch	Long format file with log 2 - quantile normalized values of the protein measures (Reference protein sequence analysis)	MetaAnalysis_ParamSensitivityFIles
longLog2qnorm_ReCustomProts	Long format file with log 2 - quantile normalized values of the protein measures (Custom protein sequence analysis)	MetaAnalysis_ParamSensitivityFIles
longReCustomProtFile	Long format file with protein measures (Custom protein sequence analysis)	MetaAnalysis_ParamSensitivityFIles
protsPerSearchBarplot	Barplot of count of proteins identified across number of search engines	MetaAnalysis_ParamSensitivityFIles
vennOReSAAVs	Venn diagram of SAAVS between original and reanalysis	MetaAnalysis_ParamSensitivityFIles

vennOReVariantPeptides	Venn diagram of variant peptides between original and reanalysis	MetaAnalysis_ParamSensitivityFlles
vennPepMyrimatch	Venn diagram of peptides between two instance of the same search engine (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFlles
vennProtMyrimatch	Venn diagram of proteins between two instance of the same search engine (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFlles
widePepMyrimatchFile1	Matrix format file of peptides for the first search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFlles
widePepMyrimatchFile2	Matrix format file of peptides for the second search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFlles
wideSCMyrimatchFile1	Matrix format file of proteins for the first search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFlles
wideSCMyrimatchFile2	Matrix format file of proteins for the second search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFlles
wideSCFile1	Matrix format file of protein measures	MetaAnalysis_ParamSensitivityFlles

	for the first search engine	
wideSCFile3	Matrix format file of protein measures for the third search engine	MetaAnalysis_ParamSensitivityFlles
wideSCFile4	Matrix format file of protein measures for the fourth search engine	MetaAnalysis_ParamSensitivityFlles
ccResults1	Zip file containing consensus clustering results for initial dataset. CRC95 in this case	MetaAnalysisCompare_AdditionalDataFiles
ccResults2	Zip file containing consensus clustering results for second dataset. In this case, it refers to the initial CRC95 and additional 5 CRC samples. Total CRC100 samples	MetaAnalysisCompare_AdditionalDataFiles
ccResults3	Zip file containing consensus clustering results for third dataset. In this case, it refers to the initial CRC95 and additional 10 CRC samples. Total CRC105 samples	MetaAnalysisCompare_AdditionalDataFiles
ccResults4	Zip file containing consensus clustering results for fourth dataset. In this case, it refers to the initial CRC95 and additional 15 CRC samples. Total CRC110 samples	MetaAnalysisCompare_AdditionalDataFiles

ccResults5	Zip file containing consensus clustering results for fifth dataset. In this case, it refers to the initial CRC95 and additional 20 CRC samples. Total CRC115 samples	MetaAnalysisCompare_AdditionalDataFiles
ccResultsWithBE	Zip file containing consensus clustering results for fifth dataset BEFORE batch effect correction. In this case, it refers to the initial CRC95 and additional 20 CRC samples. Total CRC115 samples.	MetaAnalysisCompare_AdditionalDataFiles
coreSamples1	Selected core samples based on positive silhouette width for first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
coreSamples2	Selected core samples based on positive silhouette width for second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
coreSamples3	Selected core samples based on positive silhouette width for third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
coreSamples4	Selected core samples based on positive silhouette width for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
coreSamples5	Selected core samples based on positive silhouette width for fifth	MetaAnalysisCompare_AdditionalDataFiles

	dataset (CRC115)	
coreSamplesWithBE	Selected core samples based on positive silhouette width for fifth dataset BEFORE batch correction (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
coreSampleswithAnn1	Selected core samples annotated with earlier subtypes for first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
coreSampleswithAnn2	Selected core samples annotated with earlier subtypes for second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
coreSampleswithAnn3	Selected core samples annotated with earlier subtypes for third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
coreSampleswithAnn4	Selected core samples annotated with earlier subtypes for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
coreSampleswithAnn5	Selected core samples annotated with earlier subtypes for fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
coreSampleswithAnnWithBE	Selected core samples annotated with earlier subtypes for fifth dataset BEFORE batch correction (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
heatmap1	Heatmap for the first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
heatmap2	Heatmap for the second dataset	MetaAnalysisCompare_AdditionalDataFiles

	(CRC100)	
heatmap3	Heatmap for the third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
heatmap4	Heatmap for the fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
heatmap5	Heatmap for the fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
heatmapWithBE	Heatmap for the fifth dataset BEFORE batch correction (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
heatmapInputMatrix1	Matrix used as input for the first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
heatmapInputMatrix2	Matrix used as input for the second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
heatmapInputMatrix3	Matrix used as input for the third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
heatmapInputMatrix4	Matrix used as input for the fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
heatmapInputMatrix5	Matrix used as input for the fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
heatmapInputMatrixWithBE	Matrix used as input for the fifth dataset BEFORE batch correction (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
normDataForClustering1	Normalized protein data used for consensus clustering for first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
normDataForClustering2	Normalized protein data used for consensus clustering for second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles

normDataForClustering3	Normalized protein data used for consensus clustering for third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
normDataForClustering4	Normalized protein data used for consensus clustering for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
normDataForClustering5	Normalized protein data used for consensus clustering for fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
normDataForClusteringWithBE	Normalized protein data used for consensus clustering for fifth dataset BEFORE batch correction (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
protSCFiltMatrix1	Filtered protein measures matrix for first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
protSCFiltMatrix2	Filtered protein measures matrix for second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
protSCFiltMatrix3	Filtered protein measures matrix for third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
protSCFiltMatrix4	Filtered protein measures matrix for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
protSCFiltMatrix5	Filtered protein measures matrix for fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
longLog2qnorm1	Long format file for quantile normalized values for first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles

longLog2qnorm2	Long format file for quantile normalized values for second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
longLog2qnorm3	Long format file for quantile normalized values for third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
longLog2qnorm4	Long format file for quantile normalized values for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
longLog2qnorm5	Long format file for quantile normalized values for fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
silhouettePlot1	Silhouette plot for the first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
silhouettePlot2	Silhouette plot for the second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
silhouettePlot3	Silhouette plot for the third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
silhouettePlot4	Silhouette plot for the fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
silhouettePlot5	Silhouette plot for the fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
silhouettePlotWithBE	Silhouette plot for the fifth dataset BEFORE batch effect correction(CRC115)	MetaAnalysisCompare_AdditionalDataFiles
subtypeSampleMapping1	File with samples mapped to subtypes for the first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFiles
subtypeSampleMapping2	File with samples mapped to subtypes for the second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFiles

subtypeSampleMapping3	File with samples mapped to subtypes for the third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFiles
subtypeSampleMapping4	File with samples mapped to subtypes for the fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFiles
subtypeSampleMapping5	File with samples mapped to subtypes for the fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
subtypeSampleMappingWithBE	File with samples mapped to subtypes for the fifth dataset BEFORE batch effect correction (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
upsetFormatFile	File with protein data used as input for UpSet file	MetaAnalysisCompare_AdditionalDataFiles
upsetPlot	UpSet plot for protein intersections across first, second, third, fourth and fifth datasets (CRC95, CRC100, CRC105, CRC110, CRC115)	MetaAnalysisCompare_AdditionalDataFiles
barplotProtsPerDataset	Barplot of protein counts for each dataset	MetaAnalysis_NewDataFiles
barplotSAAVsPerDataset	Barplot of SAAV counts for each dataset	MetaAnalysis_NewDataFiles
vennSAAVs	Venn Diagram of SAAVS for the first, third and fourth dataset (CRC95, OV, BRCA). Primarily because	MetaAnalysis_NewDataFiles

	SAAVs were not generated for second i.e. NCI60 dataset Can be changed to include all datasets on request	
wideSCFile1	Matrix format file of protein measures for the first dataset (CRC95 spectral counts)	MetaAnalysis_NewDataFiles
wideSCFile2	Matrix format file of protein measures for the first dataset (NCI60 spectral counts)	MetaAnalysis_NewDataFiles
wideSCFile3	Matrix format file of protein measures for the first dataset (OV spectral counts)	MetaAnalysis_NewDataFiles
wideSCFile4	Matrix format file of protein measures for the first dataset (BRCA spectral counts)	MetaAnalysis_NewDataFiles