

Table1: Multiomic input files description

Input File	Description
ProtDataZip/ProtData	Zip file containing mzML file(s)
sampleIDs	List of Sample IDs mapping to the mzML files in ProtDataZip. One sample ID per line.
ref_proteome_fasta	Reference protein sequence fasta file
spectralLibFile	NIST spectral library file used for the spectral library search
pepSearchParams	The parameters used by the peptide search engines. Wings selects the peptide search engine based on the input parameter file type. For example: "ZhangMSGFPlus_Exact.params" selects "MSGFPlus" where as "ZhangMM_Exact.params" selects Myrimatch for peptide searches respectively
pepSpectralSearchParams	Peptome parameters for spectral library peptide search
pepConvertParams	Convert output files from all the peptide search(es) to pepXML for standardization
idpQonvertParams	idpQonvert parameter file to convert .pepXML to .idpDB format for idpAssembly processing
idpQonvertGeneParams	idpQonvert parameter file to embed gene data
condFile	Isobaric sample mapping (for iTRAQ data only)
protAssemblyParams	idpAssemble parameters for initial search (stringent)
protAssemblyParams_redone	idpAssemble parameters for secondary search (less stringent)
protConvertParams	idpQuery parameters to perform protein assembly by protein groups
protConvertParams_withGene	idpQuery parameters to perform protein assembly by gene groups
RNAData	Zip file containing fastq file(s)
RefFastaAnnot	customProDB annotation package bundle
cufflinksParams	cufflinks parameters
decoyParams	parameters to generate decoys and append to the proteins sequence database
fastqToBamParams	Tophat2 parameters file
genesAnnotFile	GTF format genes annotation file used for cufflinks
genomicsFASTA	Reference genomics sequence database
refFastaBundle	References files bundle used for Tophat2
refFastaBundleRSEM	Reference files bundle used for RSEM
rsemParams	RSEM parameters file
idpQonvertParams_Quant	idpQonvert parameter file to include quantitation data (for iTRAQ data only)
condFile_withQuantData	Isobaric sample mapping (for iTRAQ data only)

protAssemblyParams_withQuantData	idpAssemble parameters to add quantitation information (for iTRAQ data only)
protConvertParams_pepLevel	idpQuery parameters to perform protein assembly by peptides

Table2: Multiomic workflows output files description (intermediary files not included):

Output File	Description
ref_protConvertSpectra	Protein groups table with spectral counts (idpQuery output)
ref_protConvertSpectraWithGene	Gene groups table with spectral counts (idpQuery output)
ref_mergedPepFile	Zip file containing all the pepXML files associated with the analysis
ref_pepSpectralLibSearchLog	Log of the peptide spectral library search process
ref_protConvertLog	Log of the tabulating the results at protein group level (idpQuery log)
ref_protConvertLogWithGene	Log of the tabulating the results at gene group level (idpQuery log)
ref_pepSpectralSearchFinalParams	Parameters used for the peptide spectral library search
ref_searchLog	Log of the peptide search process
ref_searchParams	Parameters used for the peptide search
protassemblyLog	Protein assembly log at protein group level
protassemblyLog_redone	Protein assembly log at gene group level
alignedBamIndexFile	Log file pointing to the location of the aligned bam and associated bam index file
custom_mergedPepFile	Zip file containing all the pepXML files associated with the analysis (for custom protein sequence database search results)
custom_protassemblyLog_redone	Protein assembly log at gene group level (for custom protein sequence database search results)
custom_protassemblyLog	Protein assembly log at protein group level (for custom protein sequence database search results)
custom_protConvertLog_pepData	Log of the tabulating the results at peptide level (idpQuery log)
custom_protConvertLog_redone	Log of the tabulating the results at protein group level (idpQuery log)
custom_protConvertLogWithGene_redone	Log of the tabulating the results at gene group level (idpQuery log)
custom_protConvertSpectra_pepData	Peptide table with spectral counts (idpQuery output)
custom_protConvertSpectra_redone	Protein table with spectral counts (idpQuery)

	output)
custom_protConvertSpectraWithGene_redone	Gene groups table with spectral counts (idpQuery output)
custom_searchLog	Log of the peptide search process using custom protein sequence database
custom_searchParams	Parameters used for the peptide search using custom protein sequence database
deletionsBED	BED file containing genomic deletions only
FPKMFiles	Collection of FPKM measures files - generated by cufflinks. One file per sample is produced
outputIsoformsFPKM	Collection of FPKM measures for the isoforms - generated by cufflinks. One file per sample is produced
outputTranscriptsGTF	GTF format file for transcripts - generated by cufflinks. One file per sample is produced
ProteinSNVTable	Table of single nucleotide variants (SNVs) - generated by CustomProDB
rsemFile	Collection of RSEM measures files - generated by RSEM. One file per sample is produced
rsemIsoformExp	Collection of RSEM measures for the isoforms - generated by RSEM. One file per sample is produced
rsemLog	Log of the RSEM measures calculation process
rsemStat	Zip file of the additional files generated by RSEM
skippedGTF	GTF format file of the skipped transcripts by cufflinks
unmappedBamIndexFile	Log file pointing to the location of the unmapped/unaligned bam and associated bam index file
ref_mergedPepFile_withQuantData	Zip file containing all the pepXML files associated with the analysis after quantitation. Relevant to iTRAQ datasets only
ref_protassemblyLog_withQuantData	Protein assembly log at protein group level after quantitation
custom_mergedPepFile_withQuantData	Zip file containing all the pepXML files associated with the analysis after quantitation (for custom protein sequence database search results). Relevant to iTRAQ datasets only
custom_protassemblyLog_withQuantData	Protein assembly log at protein group level after quantitation (for custom protein sequence database search results).

Note: The input files, parameters and output files below may contain duplicate file names and/or descriptions to clarify their association with each of the meta workflows. Files associated with each workflow are separated by a blank gray row.

Table3: Meta-Analysis workflows input files description:

Input File	Description	Associated Workflow
OriginalProtFile	Protein groups table from the deposited data (idpQuery output)	MetaAnalysis_OriginalVsReanalysisFiles
ReanalysisProtFile	Protein groups table from the Stage 3 reanalysis data (idpQuery output)	MetaAnalysis_OriginalVsReanalysisFiles
ORSEMNormWideFile	RSEM table downloaded from the TCGA/GDC portal	MetaAnalysis_OriginalVsReanalysisFiles
ReRSEMNormWideFile	RSEM table generated for stage 3 reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
SampleIDs	List of Sample IDs mapping to the sample IDs in the <i>OriginalProtFile</i> and <i>ReanalysisProtFile</i> . One sample ID per line.	MetaAnalysis_OriginalVsReanalysisFiles
OSAAVFile	SAAV table from the deposited data (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
ReSAAVFile	SAAV table from the Stage 3 reanalysis data (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
OVariantPepFile	Variant peptide table from the deposited data (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
ReVariantPepFile	Variant peptide table from the Stage 3 reanalysis data (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
RNAProtPaired_SampleIDs	List of PAIRED Sample IDs mapping to the sample IDs in	MetaAnalysis_ParamSensitivityFiles

	the OSAAVFile, ReSAAVFile, OVariantPepFile, ReVariantPepFile and ReCustomProtFile. One sample ID per line.	
ReCustomProtFile	Protein groups table from the stage3 reanalysis custom protein sequence search (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
SampleIDs	List of Sample IDs mapping to the sample IDs in the <i>ProtFile1</i> , <i>ProtFile2</i> , <i>ProtFile3</i> and <i>ProtFile4</i> . One sample ID per line.	MetaAnalysis_ParamSensitivityFiles
MyrimatchProtFile1	Protein groups table from the first Myrimatch search (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
MyrimatchProtFile2	Protein groups table from the second Myrimatch search (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
MyrimatchPepFile1	Peptides table from the first Myrimatch search (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
MyrimatchPepFile2	Peptides table from the second Myrimatch search (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
ProtFile1	Protein groups table from the first search engine (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
ProtFile2	Protein groups table from the second search engine (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
ProtFile3	Protein groups table from the third search	MetaAnalysis_ParamSensitivityFiles

	engine (idpQuery output)	
ProtFile4	Protein groups table from the fourth search engine (idpQuery output)	MetaAnalysis_ParamSensitivityFiles
ProtFile1	Protein groups table from the first initial dataset (idpQuery output). In sample data, refers to CRC95	MetaAnalysis_AdditionalDataFiles
ProtFile2	Protein groups table from the second dataset. In this case, it refers to the initial CRC95 and additional 5 CRC samples. Total CRC100 samples data (idpQuery output)	MetaAnalysis_AdditionalDataFiles
ProtFile3	Protein groups table from the third dataset. In this case, it refers to the initial CRC95 and additional 10 CRC samples. Total CRC105 samples data (idpQuery output)	MetaAnalysis_AdditionalDataFiles
ProtFile4	Protein groups table from the fourth dataset. In this case, it refers to the initial CRC95 and additional 15 CRC samples. Total CRC110 samples data (idpQuery output)	MetaAnalysis_AdditionalDataFiles
ProtFile5	Protein groups table from the fifth dataset. In this case, it refers to the initial CRC95 and additional 20 CRC samples. Total CRC115 samples	MetaAnalysis_AdditionalDataFiles

	data (idpQuery output)	
SampleIDs1	Sample IDs mapping to first dataset. One sample ID per line. Refers to CRC95	MetaAnalysis_AdditionalDataFiles
SampleIDs2	Sample IDs mapping to second dataset data. One sample ID per line. Refers to the initial CRC95 + 5 new CRC samples. Total CRC100 samples	MetaAnalysis_AdditionalDataFiles
SampleIDs3	Sample IDs mapping to third dataset data. One sample ID per line. Refers to the initial CRC95 + 10 new CRC samples. Total CRC105 samples	MetaAnalysis_AdditionalDataFiles
SampleIDs4	Sample IDs mapping to fourth dataset data. One sample ID per line. Refers to the initial CRC95 + 15 new CRC samples. Total CRC110 samples	MetaAnalysis_AdditionalDataFiles
SampleIDs5	Sample IDs mapping to fifth dataset data. One sample ID per line. Refers to the initial CRC95 + 20 new CRC samples. Total CRC115 samples	MetaAnalysis_AdditionalDataFiles
sampleDupAnn1	Sample Annotation file mapping patient and sample ID to duplicates for first dataset (CRC95)	MetaAnalysis_AdditionalDataFiles
sampleDupAnn2	Sample Annotation file mapping patient and sample ID to duplicates for first	MetaAnalysis_AdditionalDataFiles

	dataset (CRC100)	
sampleDupAnn3	Sample Annotation file mapping patient and sample ID to duplicates for first dataset (CRC105)	MetaAnalysis_AdditionalDataFiles
sampleDupAnn4	Sample Annotation file mapping patient and sample ID to duplicates for first dataset (CRC110)	MetaAnalysis_AdditionalDataFiles
sampleDupAnn5	Sample Annotation file mapping patient and sample ID to duplicates for first dataset (CRC115)	MetaAnalysis_AdditionalDataFiles
batchesFile	Sample ID to Mapping data processing batch ID for CRC95, CRC100, CRC105, CRC110 and CRC115 data. Used for batch effect correction	MetaAnalysis_AdditionalDataFiles
dataSubtypeAnn	Subtype annotation file to map earlier discovered subtypes to sample IDs	MetaAnalysis_AdditionalDataFiles
ProtFile1	Protein groups table from the CRC95 data set (idpQuery output)	MetaAnalysis_NewDataFiles
ProtFile2	Protein groups table from the NCI60 dataset (idpQuery output)	MetaAnalysis_NewDataFiles
ProtFile3	Protein groups table from the OV dataset (idpQuery output)	MetaAnalysis_NewDataFiles
ProtFile4	Protein groups table from the BRCA dataset (idpQuery output)	MetaAnalysis_NewDataFiles
SAAVFile1	SAAV file for the CRC95 dataset	MetaAnalysis_NewDataFiles
SAAVFile2	SAAV file for the OV	MetaAnalysis_NewDataFiles

	dataset (assumes second dataset doesn't have SAAV information because of lack of SAAV information for the NCI60 dataset in figure 5). Workflow can be changed on request	
SAAVFile3	SAAV file for the BRCA dataset	MetaAnalysis_NewDataFiles
SampleIDs1	Sample IDs mapping to CRC95 dataset. One sample ID per line.	MetaAnalysis_NewDataFiles
SampleIDs2	Sample IDs mapping to NCI60 dataset. One sample ID per line.	MetaAnalysis_NewDataFiles
SampleIDs3	Sample IDs mapping to OV data. One sample ID per line.	MetaAnalysis_NewDataFiles
SampleIDs4	Sample IDs mapping to BRCA data. One sample ID per line.	MetaAnalysis_NewDataFiles

Table4: 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 - spectral counts were used as protein measures	MetaAnalysis_OriginalVsReanalysisFiles

	(Original analysis)	
OReProtDensityPlot	Density plot for protein correlations between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
OReProtRSEMByGeneSPlot	Scatter plot of mRNA-Protein correlations for original and reanalysis per gene	MetaAnalysis_OriginalVsReanalysisFiles
OReProtRSEMBySampleSPlot	Scatter plot of mRNA-Protein correlations for original and reanalysis per sample	MetaAnalysis_OriginalVsReanalysisFiles
OReProtsBarplot	Barplots of protein count per sample in original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
OReRSEMDensityPlot	Density plot for mRNA correlations between original and reanalysis	MetaAnalysis_OriginalVsReanalysisFiles
overlapOReProtIDs	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 current sample - spectral counts were used as	MetaAnalysis_OriginalVsReanalysisFiles

	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_ReCustomProt s	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
protPerSearchBarplot	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	MetaAnalysis_ParamSensitivityFiles

	and reanalysis	
vennPepMyrimatch	Venn diagram of peptides between two instance of the same search engine (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFiles
vennProtMyrimatch	Venn diagram of proteins between two instance of the same search engine (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFiles
widePepMyrimatchFile1	Matrix format file of peptides for the first search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFiles
widePepMyrimatchFile2	Matrix format file of peptides for the second search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFiles
wideSCMyrimatchFile1	Matrix format file of proteins for the first search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFiles
wideSCMyrimatchFile2	Matrix format file of proteins for the second search engine instance (search engine in this case is Myrimatch)	MetaAnalysis_ParamSensitivityFiles
wideSCFile1	Matrix format file of protein measures for the first search engine	MetaAnalysis_ParamSensitivityFiles
wideSCFile3	Matrix format file of	MetaAnalysis_ParamSensitivityFiles

	protein measures for the third search engine	
wideSCFile4	Matrix format file of protein measures for the fourth search engine	MetaAnalysis_ParamSensitivityFiles
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	MetaAnalysisCompare_AdditionalDataFiles

	for fifth dataset. In this case, it refers to the initial CRC95 and additional 20 CRC samples. Total CRC115 samples	
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 dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFiles
coreSamplesWithBE	Selected core samples based on	MetaAnalysisCompare_AdditionalDataFiles

	positive silhouette width for fifth dataset BEFORE batch correction (CRC115)	
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 (CRC100)	MetaAnalysisCompare_AdditionalDataFiles
heatmap3	Heatmap for the third dataset	MetaAnalysisCompare_AdditionalDataFiles

	(CRC105)	
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	MetaAnalysisCompare_AdditionalDataFiles

	clustering for third dataset (CRC105)	
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	MetaAnalysisCompare_AdditionalDataFiles

	dataset (CRC100)	
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	MetaAnalysisCompare_AdditionalDataFiles

	third dataset (CRC105)	
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 SAAVs were not generated for second i.e. NCI60	MetaAnalysis_NewDataFiles

	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