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_OriginalVsReanalys isFiles
ODatasetName	String - Original dataset name. Should match the string before comma in the parameter "OReDatasetsStr"	MetaAnalysis_OriginalVsReanalys isFiles
OProtRSEMCorrByGeneColna me	String - Column name to use for the values with correlation between mRNA and protein measures calculated per gene (For original dataset)	MetaAnalysis_OriginalVsReanalys isFiles
OProtRSEMCorrBySampleColn ame	String - Column name to use for the values with correlation between mRNA and protein measures calculated per sample (For original dataset)	MetaAnalysis_OriginalVsReanalys isFiles
ReProtRSEMCorrByGeneColn ame	String - Column name to use for the values with correlation between mRNA and protein measures calculated per gene (For reanalysis dataset)	MetaAnalysis_OriginalVsReanalys isFiles
ReProtRSEMCorrBySampleCol name	String - Column name to use for the values with correlation between mRNA and protein measures calculated per sample (For reanalysis dataset)	MetaAnalysis_OriginalVsReanalys isFiles
ReDatasetName	String - Reanalysis dataset name. Should match the string after	MetaAnalysis_OriginalVsReanalys isFiles

	comma in the	
	parameter	
	"OReDatasetsStr"	MetaAnalysis OriginalVsReanalys
	String - Scatterplot name between original	isFiles
	and reanalysis for	131 1163
	correlation values	
	between mRNA and	
OReProtRSEMByGeneSplot	Protein per gene	
	String - Scatterplot	MetaAnalysis_OriginalVsReanalys
	name between original	isFiles
	and reanalysis for	
	correlation values	
ODoDrotDSEMBySampleSplot	between mRNA and	
OReProtRSEMBySampleSplot	Protein per sample String - Column name	MetaAnalysis OriginalVsReanalys
	to use for the	isFiles
	correlation values	
	between original and	
OReProtCorrColname	reanalysis	
	String - Density plot	MetaAnalysis_OriginalVsReanalys
	name of protein	isFiles
	correlations between	
	original and reanalysis.	
	Ideally, use the same	
	"OReProtCorrColname"	
OReProtDPlotTitle	parameter	
	String - Column name	MetaAnalysis OriginalVsReanalys
	to use for the	isFiles
	correlation values	
	between original and	
OReRSEMCorrColname	reanalysis	
	String - Density plot	MetaAnalysis_OriginalVsReanalys
	name of mRNA correlations between	isFiles
	original and reanalysis.	
	Ideally, use the same	
	as	
	"OReRSEMCorrColna	
OReRSEMDPlotTitle	me" parameter	
	Title for Venn diagram	MetaAnalysis_OriginalVsReanalys
vennTitle_Proteins	for protein groups.	isFiles
M. wigo otale Data a sta Ctiv	Chuina Consus	Mata Analysia Davana Canalitinis Ell
Myrimatch_DatasetsStr	String - Comma	MetaAnalysis_ParamSensitivityFII
	separated string for two	es

	data a da Esculas	
	datasets. For the	
	current workflow	
	-"Myrimatch1,Myrimatc	
	h2".	
	String - Comma	MetaAnalysis_ParamSensitivityFll
	separated string for two	es
	datasets. For the	
	current workflow	
	-"Original,Reanalysis"	
	or "Deposited,Stage3"	
OReDatasetStr	are used.	
	String - Density plot	MetaAnalysis_ParamSensitivityFll
	name for correlations of	es
	overlapping between	
	standard vs custom	
	protein sequence	
	databases for the same	
ReRefCustomMMDplot	dataset	
	String - Column name	MetaAnalysis_ParamSensitivityFll
SAAVColname	for SAAV IDs	es
	String - Column name	MetaAnalysis_ParamSensitivityFll
VariantPeptideColname	for variant peptide IDs	es
	String - Name of the	MetaAnalysis_ParamSensitivityFll
datasetName1	first search dataset	es
	String - Name of the	MetaAnalysis_ParamSensitivityFll
datasetName2	second search dataset	es
	String - Name of the	MetaAnalysis_ParamSensitivityFll
datasetName3	third search dataset	es
	String - Name of the	MetaAnalysis_ParamSensitivityFll
datasetName4	fourth search dataset	es
	String - Name of the	MetaAnalysis_ParamSensitivityFll
	first instance of search	es
	engine dataset.	
	Myrimatch was used for	
	analysis. The workflow	
	is agnostic to search	
	engine as long as the	
	file format is	
datasetNameMyrimatch1	maintained.	
datasetNameMyrimatch2	String - Name of the	MetaAnalysis_ParamSensitivityFll
	second instance of	es
	search engine dataset	
	(with only one	
	parameter different	
	from	
	"datasetNameMyrimatc	

	1	<u> </u>
	h1"). Myrimatch was	
	used for analysis. The	
	workflow is agnostic to	
	search engine as long	
	as the file format is	
	maintained.	Mata Analysia Dayana Canaitiyity Ell
	String - Name of the first custom protein	MetaAnalysis_ParamSensitivityFll
	•	es
	sequence database search dataset with	
datacatNamaODratagganamia		
datasetNameOProteogenomic	original data	Moto Analysis Daram Consitivity Ell
	String - Name of the	MetaAnalysis_ParamSensitivityFII
	first custom protein	es
	sequence database search dataset with	
datasetNameReProteogenomic	reanalysis data	
addoctivation to the objectivities	Peptide sequence	MetaAnalysis_ParamSensitivityFII
pepseqColname	column name	es
poposequentante	Protein accessions	MetaAnalysis ParamSensitivityFII
	column name in the	es
protAccessionsColname	peptide file	
probaccessions comaine	Title for peptides venn	MetaAnalysis ParamSensitivityFII
vennTitle PepMyrimatch	diagram	es
· spiniyimiacon	Title for protein groups	MetaAnalysis_ParamSensitivityFII
vennTitle_ProtMyrimatch	venn diagram	es
	Title for SAAVs venn	MetaAnalysis_ParamSensitivityFll
vennTitle SAAVs	diagram	es
_		MetaAnalysis ParamSensitivityFII
vennTitle_VariantPeptides		es
	String - Name of first	MetaAnalysis_AdditionalDataFiles
addDatasetName1	(CRC95) dataset	
	String - Name of	MetaAnalysis_AdditionalDataFiles
	second (CRC100)	
addDatasetName2	dataset	
	String - Name of third	MetaAnalysis_AdditionalDataFiles
addDatasetName3	(CRC105) dataset	
	String - Name of fourth	MetaAnalysis_AdditionalDataFiles
addDatasetName4	(CRC110) dataset	
	String - Name of fifth	MetaAnalysis_AdditionalDataFiles
addDatasetName5	(CRC115) dataset	
CAAV/Data acts City	Christs Courses	Mata Arabasia Na Data 5'las
SAAVDatasetsStr	String - Comma	MetaAnalysis_NewDataFiles
	separated string for the	
	SAAV results datasets. For the current	
	I OF THE CHIPPENT	1

	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
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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

	apactral accepts	
	spectral counts	
	were used as	
	protein measures	
	(Original analysis)	Mata Analysia - Osisia al VaDana - Laia 71
	Density plot for	MetaAnalysis_OriginalVsReanalysisFiles
OReProtDensityPlot	protein correlations	
,	between original	
	and reanalysis	
	Scatter plot of	MetaAnalysis_OriginalVsReanalysisFiles
	mRNA-Protein	
OReProtRSEMByGeneSPlot	correlations for	
	original and	
	reanalysis per gene	
	Scatter plot of	MetaAnalysis_OriginalVsReanalysisFiles
	mRNA-Protein	
OReProtRSEMBySampleSPlot	correlations for	
	original and	
	reanalysis per	
	sample	
	Barplots of protein	MetaAnalysis_OriginalVsReanalysisFiles
OReProtsBarplot	count per sample in	
- 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	original and	
	reanalysis	
	Density plot for	MetaAnalysis_OriginalVsReanalysisFiles
OReRSEMDensityPlot	mRNA correlations	
	between original	
	and reanalysis	
	List of overlapping	MetaAnalysis_OriginalVsReanalysisFiles
overlapOReProtIDs	proteins between	
	original and	
	reanalysis	
	Matrix with log 2 -	MetaAnalysis_OriginalVsReanalysisFiles
	quantile normalized	
ReLog2qnormMtx	values of the	
	protein measures	
	(Reanalysis	
	analysis)	
	Long format file	MetaAnalysis_OriginalVsReanalysisFiles
	with log 2 - quantile	
	normalized values	
ReLongLog2qnorm	of the protein	
	measures	
	(Reanalysis	
	analysis)	
ReProtSCMatrix	Matrix with protein	MetaAnalysis_OriginalVsReanalysisFiles
I .	measures. In	

	T	
	current sample -	
	spectral counts	
	were used as	
	protein measures	
	(Reanalysis	
	`	
	analysis)	14 . 4 . 1 0
	Venn Diagram of	MetaAnalysis_OriginalVsReanalysisFiles
vennProtIDs	proteins between	
Verilli Totibs	original and	
	reanalysis	
densityPlot	Density Plot of	MetaAnalysis ParamSensitivityFlles
	protein correlations	, _ ,
	for overlapping	
	proteins between	
	ļ ·	
	Reference and	
	custom protein	
	sequence	
	databases	
longLog2qnorm_Myrimatch	Long format file	MetaAnalysis_ParamSensitivityFlles
	with log 2 - quantile	
	normalized values	
	of the protein	
	measures	
	(Reference protein	
	sequence analysis)	
longlog2gnorm DoCustomDrot	 	Mota Analysis Daram Consitivity Ellos
longLog2qnorm_ReCustomProt	Long format file	MetaAnalysis_ParamSensitivityFlles
S	with log 2 - quantile	
	normalized values	
	of the protein	
	measures (Custom	
	protein sequence	
	analysis)	
IongReCustomProtFile	Long format file	MetaAnalysis_ParamSensitivityFlles
J	with protein	
	measures (Custom	
	protein sequence	
protoDorCocrobDorniet	analysis)	Moto Analysia Baram Canaiti it III.
protsPerSearchBarplot	Barplot of count of	MetaAnalysis_ParamSensitivityFlles
	proteins identified	
	across number of	
	search engines	
vennOReSAAVs	Venn diagram of	MetaAnalysis_ParamSensitivityFlles
	SAAVS between	
	original and	
	reanalysis	
	Touridiyoio	

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
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ccResults1	Zip file containing consensus clustering results for initial dataset. CRC95 in this case	MetaAnalysisCompare_AdditionalDataFile s
CCRESUISI	Zip file containing consensus clustering results for second dataset. In this case, it refers to the initial CRC95 and additional 5 CRC samples. Total	MetaAnalysisCompare_AdditionalDataFile s
ccResults2	CRC100 samples	
	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	MetaAnalysisCompare_AdditionalDataFile s
ccResults3	samples	Moto Analygia Compara, Additional Data File
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_AdditionalDataFile s

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_AdditionalDataFile s
	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	MetaAnalysisCompare_AdditionalDataFile s
ccResultsWithBE	samples. Selected core samples based on positive silhouette width for first	MetaAnalysisCompare_AdditionalDataFile s
coreSamples1 coreSamples2	dataset (CRC95) Selected core samples based on positive silhouette width for second dataset (CRC100)	MetaAnalysisCompare_AdditionalDataFile s
coreSamples3	Selected core samples based on positive silhouette width for third dataset (CRC105)	MetaAnalysisCompare_AdditionalDataFile s
coreSamples4	Selected core samples based on positive silhouette width for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFile s
coreSamples5	Selected core samples based on positive silhouette width for fifth	MetaAnalysisCompare_AdditionalDataFile s

	dataset (CRC115)	
	Selected core samples based on positive silhouette	MetaAnalysisCompare_AdditionalDataFile s
	width for fifth dataset BEFORE batch correction	
coreSamplesWithBE	(CRC115)	
coreSampleswithAnn1	Selected core samples annotated with earlier subtypes for first dataset (CRC95)	MetaAnalysisCompare_AdditionalDataFile s
	Selected core samples annotated with earlier subtypes for second dataset	MetaAnalysisCompare_AdditionalDataFile s
coreSampleswithAnn2	(CRC100)	Add Add Add a Common Add I'll and Data E'll
	Selected core samples annotated with earlier subtypes for third	MetaAnalysisCompare_AdditionalDataFile s
coreSampleswithAnn3	dataset (CRC105) Selected core	Moto Analysis Compare, Additional Data File
coreSampleswithAnn4	samples annotated with earlier subtypes for fourth dataset (CRC110)	MetaAnalysisCompare_AdditionalDataFile s
coreSampleswithAnn5	Selected core samples annotated with earlier subtypes for fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFile s
	Selected core samples annotated with earlier subtypes for fifth dataset BEFORE batch correction	MetaAnalysisCompare_AdditionalDataFile s
coreSampleswithAnnWithBE	(CRC115) Heatmap for the first dataset	MetaAnalysisCompare_AdditionalDataFile s
heatmap1	(CRC95)	
heatmap2	Heatmap for the second dataset	MetaAnalysisCompare_AdditionalDataFile s

	(CRC100)	
	+ ` '	Mota Analysis Compare Additional Data File
	Heatmap for the third dataset	MetaAnalysisCompare_AdditionalDataFile
hootman?		S
heatmap3	(CRC105)	Marta Anal air Onnana Antilitin and Data Eile
	Heatmap for the	MetaAnalysisCompare_AdditionalDataFile
	fourth dataset	S
heatmap4	(CRC110)	
	Heatmap for the	MetaAnalysisCompare_AdditionalDataFile
	fifth dataset	S
heatmap5	(CRC115)	
	Heatmap for the	MetaAnalysisCompare_AdditionalDataFile
	fifth dataset	S
	BEFORE batch	
	correction	
heatmapWithBE	(CRC115)	
	Matrix used as	MetaAnalysisCompare_AdditionalDataFile
	input for the first	S
heatmapInputMatrix1	dataset (CRC95)	3
поантарттрациантя	Matrix used as	MetaAnalysisCompare_AdditionalDataFile
	input for the second	S
hootmanlanutMatriy2		5
heatmapInputMatrix2	dataset (CRC100)	Moto Analysis Compare Additional Data File
	Matrix used as	MetaAnalysisCompare_AdditionalDataFile
	input for the third	S
heatmapInputMatrix3	dataset (CRC105)	
	Matrix used as	MetaAnalysisCompare_AdditionalDataFile
	input for the fourth	S
heatmapInputMatrix4	dataset (CRC110)	
	Matrix used as	MetaAnalysisCompare_AdditionalDataFile
	input for the fifth	S
heatmapInputMatrix5	dataset (CRC115)	
	Matrix used as	MetaAnalysisCompare_AdditionalDataFile
	input for the fifth	s
	dataset BEFORE	
	batch correction	
heatmapInputMatrixWithBE	(CRC115)	
	Normalized protein	MetaAnalysisCompare_AdditionalDataFile
	data used for	S
	consensus	
	clustering for first	
normDataForClustering1	dataset (CRC95)	
Hombalai di Ciustellily1	Normalized protein	Mota Analysis Compare Additional Data File
	· '	MetaAnalysisCompare_AdditionalDataFile
	data used for	S
	consensus	
	clustering for	
	second dataset	
normDataForClustering2	(CRC100)	

	Normalized protein	MetaAnalysisCompare_AdditionalDataFile
	data used for	S
	consensus	
	clustering for third	
normDataForClustering3	dataset (CRC105)	
	Normalized protein	MetaAnalysisCompare_AdditionalDataFile
	data used for	S
	consensus	
	clustering for fourth	
normDataForClustering4	dataset (CRC110)	
	Normalized protein	MetaAnalysisCompare_AdditionalDataFile
	data used for	S
	consensus	
	clustering for fifth	
normDataForClustering5	dataset (CRC115)	
	Normalized protein	MetaAnalysisCompare_AdditionalDataFile
	data used for	S
	consensus	
	clustering for fifth	
	dataset BEFORE	
	batch correction	
normDataForClusteringWithBE	(CRC115)	
	Filtered protein	MetaAnalysisCompare_AdditionalDataFile
	measures matrix for	s
	first dataset	
protSCFiltMatrix1	(CRC95)	
	Filtered protein	MetaAnalysisCompare_AdditionalDataFile
	measures matrix for	s
	second dataset	
protSCFiltMatrix2	(CRC100)	
•	Filtered protein	MetaAnalysisCompare AdditionalDataFile
	measures matrix for	s
	third dataset	
protSCFiltMatrix3	(CRC105)	
•	Filtered protein	MetaAnalysisCompare_AdditionalDataFile
	measures matrix for	S
	fourth dataset	
protSCFiltMatrix4	(CRC110)	
•	Filtered protein	MetaAnalysisCompare AdditionalDataFile
	measures matrix for	S
	fifth dataset	
protSCFiltMatrix5	(CRC115)	
	Long format file for	MetaAnalysisCompare AdditionalDataFile
	quantile normalized	S
	values for first	
longLog2qnorm1	dataset (CRC95)	
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	Long format file for	MetaAnalysisCompare AdditionalDataFile
	quantile normalized	S
	values for second	
longLog2qnorm2	dataset (CRC100)	
	Long format file for	MetaAnalysisCompare AdditionalDataFile
	quantile normalized	S
	values for third	
longLog2qnorm3	dataset (CRC105)	
	Long format file for	MetaAnalysisCompare AdditionalDataFile
	quantile normalized	S
	values for fourth	
longLog2qnorm4	dataset (CRC110)	
	Long format file for	MetaAnalysisCompare AdditionalDataFile
	quantile normalized	s
	values for fifth	
longLog2qnorm5	dataset (CRC115)	
	Silhouette plot for	MetaAnalysisCompare AdditionalDataFile
	the first dataset	S
silhouettePlot1	(CRC95)	
	Silhouette plot for	MetaAnalysisCompare_AdditionalDataFile
	the second dataset	S
silhouettePlot2	(CRC100)	
	Silhouette plot for	MetaAnalysisCompare AdditionalDataFile
	the third dataset	S
silhouettePlot3	(CRC105)	
	Silhouette plot for	MetaAnalysisCompare AdditionalDataFile
	the fourth dataset	s
silhouettePlot4	(CRC110)	
	Silhouette plot for	MetaAnalysisCompare_AdditionalDataFile
	the fifth dataset	S
silhouettePlot5	(CRC115)	
	Silhouette plot for	MetaAnalysisCompare_AdditionalDataFile
	the fifth dataset	S
	BEFORE batch	
	effect	
silhouettePlotWithBE	correction(CRC115)	
	File with samples	MetaAnalysisCompare_AdditionalDataFile
	mapped to	S
	subtypes for the	
	first dataset	
subtypeSampleMapping1	(CRC95)	
	File with samples	MetaAnalysisCompare_AdditionalDataFile
	mapped to	S
	subtypes for the	
	second dataset	
subtypeSampleMapping2	(CRC100)	

subtypeSampleMapping3	File with samples mapped to subtypes for the third dataset (CRC105) File with samples	MetaAnalysisCompare_AdditionalDataFile s MetaAnalysisCompare_AdditionalDataFile
subtypeSampleMapping4	mapped to subtypes for the fourth dataset (CRC110)	S
subtypeSampleMapping5	File with samples mapped to subtypes for the fifth dataset (CRC115)	MetaAnalysisCompare_AdditionalDataFile s
subtypeSampleMappingWithBE	File with samples mapped to subtypes for the fifth dataset BEFORE batch effect correction (CRC115)	MetaAnalysisCompare_AdditionalDataFile s
upsetFormatFile	File with protein data used as input for UpSet file	MetaAnalysisCompare_AdditionalDataFile s
	UpSet plot for protein intersections across first, second, third, fourth and fifth datasets (CRC95, CRC100, CRC105,	MetaAnalysisCompare_AdditionalDataFile s
upsetPlot	CRC110, CRC115)	
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