Tutorial 5

Untargeted analysis of DIA datasets

In this tutorial, we will perform an untargeted analysis of a data-independent acquisition (DIA) dataset using the FragPipe computational tool collection. We will analyse a subset of samples from the published clear cell renal cell carcinoma (ccRCC) studies. that were originally described in the following publication: D. J. Clark et al. “Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma”, Cell 2019 179(4):964-983. doi: 10.1016/j.cell.2019.10.007 (https://pubmed.ncbi.nlm.nih.gov/31675502/). Briefly, in the original studies, researchers from the CPTAC (Clinical Proteomic Tumor Analysis Consortium) profiled tumor (T) samples, together with normal adjacent tissue (NAT) samples from each cancer patient, to understand the tumorigenesis of ccRCC. 110 tumor and 83 NAT samples were collected from patients and their proteomes were profiled via mass spectrometry. These samples were originally profiled using: i) tandem mass tag (TMT), and ii) data-independent acquisition (DIA). The DIA set was generated on an Orbitrap Lumos mass spectrometer with a variable window acquisition scheme.

Here, we will use just 10 DIA runs from 5 ccRCC patients, one tumor and one paired NAT sample for each patient. To make the data processing faster, we will use only data in two isolation windows (613 to 650 Th mass range) from each original mzML file.

We will use FragPipe for these analyses, which is a Java Graphical User Interface (GUI) for a suite of computational tools enabling comprehensive analysis of mass spectrometry-based proteomics data. It is powered by MSFragger, an ultrafast proteomic search engine suitable for both conventional and open (wide precursor mass tolerance) peptide identification. FragPipe includes the Philosopher toolkit for downstream statistical post-processing of MSFragger search results (PeptideProphet, iProphet, ProteinProphet), FDR filtering, label-based quantification, and multi-experiment summary report generation. The software is well documented (https://fragpipe.nesvilab.org/) and the original publication is Yu, F et al.. (2023). Analysis of DIA proteomics data using MSFragger-DIA and FragPipe computational platform.*Nature Communications*, *14*(1), 4154.

In this tutorial, we will combine the MSFragger module with DIANN for direct analysis of data independent acquisition (DIA) data. We will first process the data with MSFragger to identify multiple peptides in chimeric spectra, then statistically validate the identification results with Percolator, and finally perform peptide quantification with DIA-NN. Once we get the identification and quantification results from FragPipe, we will load them in FragPipe-PDV to visualize the identifications, and we will perform some downstream analysis using FragPipe-Analyst. Finally, we will learn how to load the raw data in Skyline to see the extracted ion chromatograms for each of the identified peptides.

Parametrization of FragPipe graphical user interfase

In this first part of the tutorial we will set up the graphical user interface of FragPipe and launch a library-free search combining MSFragger-DIA and DIA-NN. The end result will be the generation of a collection matrices with the quantification values at the precursor and protein levels, as well as a summary pdf file of the experiment.

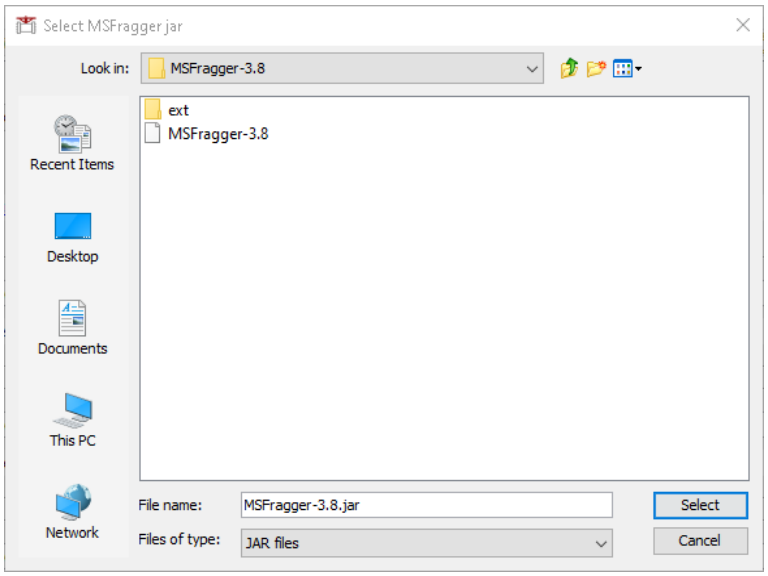
Note: This tutorial is based on FragPipe 20.1-build15.

- Go to Tutorial-5\Fragpipe\tools\Fragpipe-20.1-build15\fragpipe\bin
- Click in the fragpipe.exe icon to open the graphical user interface.

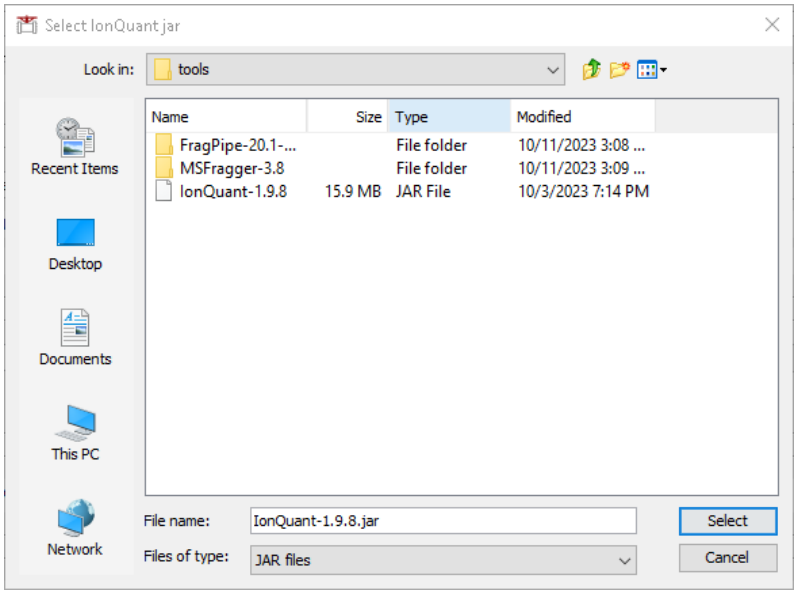
Parametrization of the *Config* section

In this section we need to make sure that all the different tools that are required by FragPipe are installed in the system and provide FragPipe with the path to the corresponding executables.

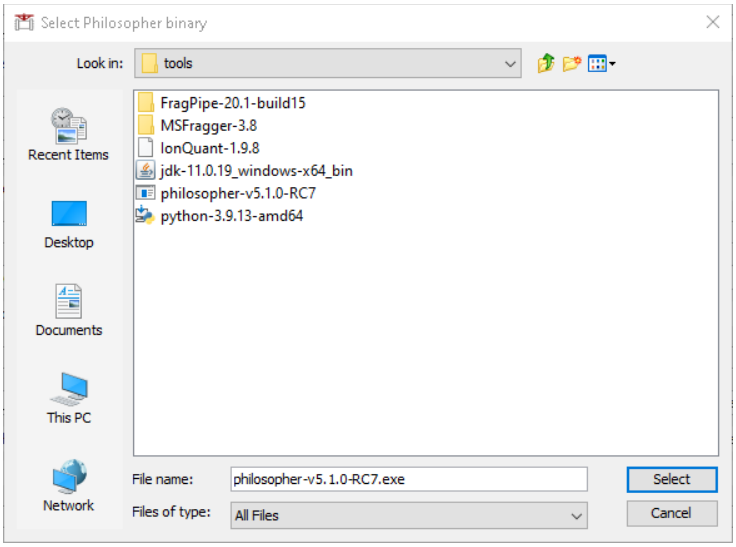
- Select the `Config` tab from the graphical user interfase of FragPipe.
- Go to the MSFragger section below and click “Browse”. Navigate to Tutorial-5\Fragpipe\tools\ MSFragger-3.8\MSFragger-3.8 and select the MSFragger-3.8.jar executable.



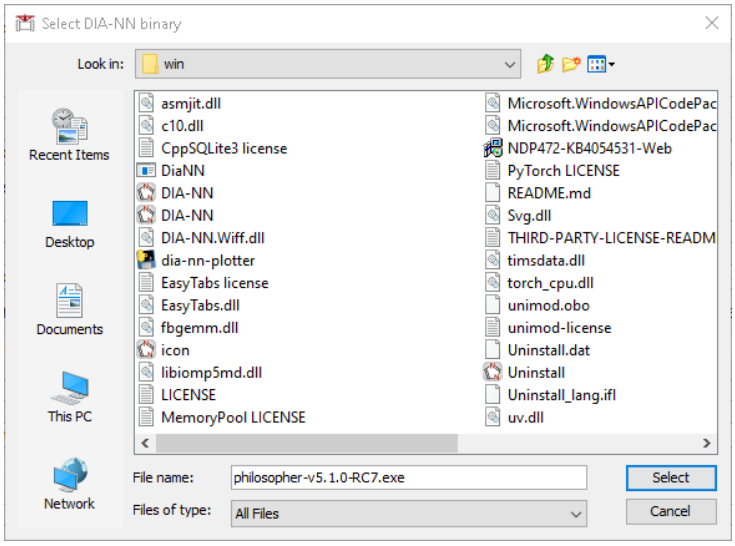
- Go to the IonQuant section below and click “Browse”. Navigate to Tutorial-5\Fragpipe\tools\ and select the IonQuant-1.9.8.jar executable.



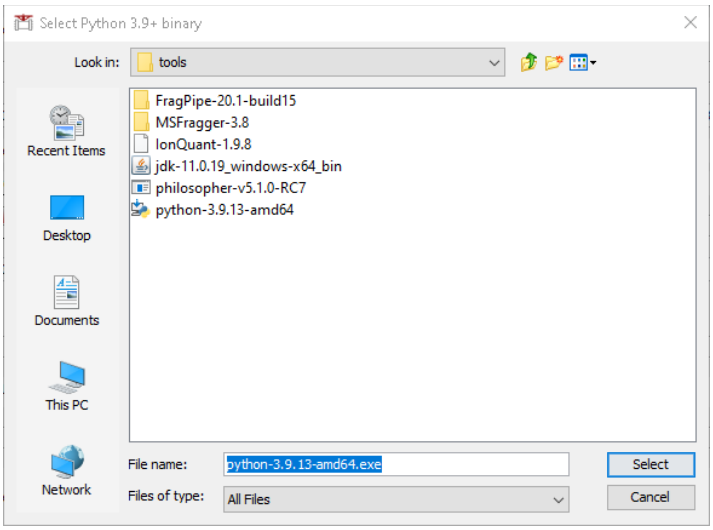
- Go to the Philosopher section below and click “Browse”. Navigate to Tutorial-5\Fragpipe\tools\ and select the philosopher-v5.1.0-RC7.exe executable.



- Go to the DIA-NN section below and click “Browse”. Navigate to Tutorial-5\Fragpipe\tools\ FragPipe-20.1-build15\fragpipe\tools\diann\1.8.2_beta_8\win and select the DIA-NN.exe executable.



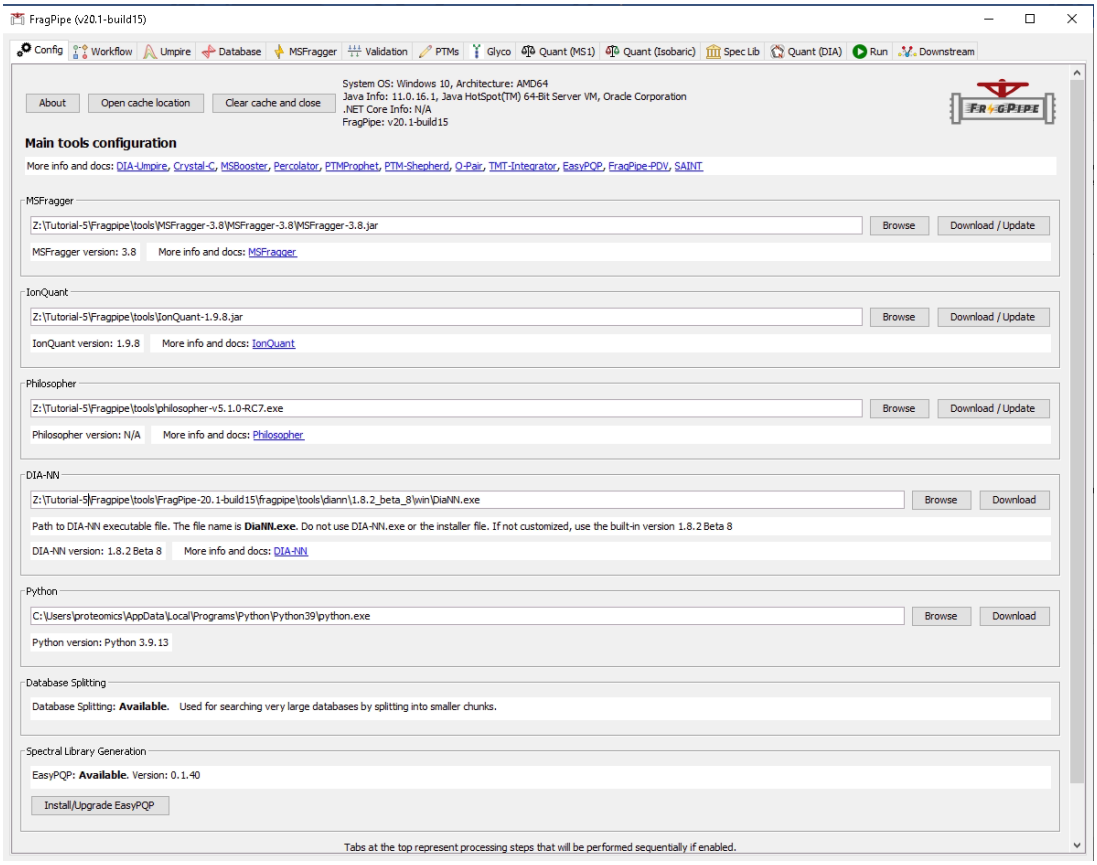
- Go to the Python section below and click “Browse”. Navigate to Tutorial-5\Fragpipe\tools\ and select the python-3.9.13-amd64 installer.



After the installer is finished installing Python, the path should be automatically updated to “C:\Users\[your user]\AppData\Local\Programs\Python\Python39\python.exe”. Otherwise, customize the path to python to your local installation.

- Go to the “Spectral Library Generation” section below and click “Install/Upgrade EasyPQP”. Wait until the installation of this python module is finished.

Your `Config` tab should look like this:



Parametrization of the *Workflow* section

FragPipe supports multiple proteomics workflows which can be customized, saved and shared with other users.

In the `Workflow` tab:

- Choose the workflow “DIA_SpecLib_Quant” workflows, which corresponds to the DIA spectral library generation and quantification using DIA-NN.
- Press “Load workflow” to load the parameters of the selected workflow.
- In Global settings, set the amount of RAM memory to zero. A RAM setting of 0 will allow FragPipe to automatically detect available memory and allocate a safe amount.
- In the “Parallelism” you can select the number of logical cores to use. Set this to the number of cores that your computer has minus one.

In “Input LC-MS Files” section we will load and annotated all the mzML files that contain the raw data acquired in the aforementioned experiment.

- Check “Regular MS”. Note that the option ‘IM-MS’ is meant only for Bruker timsTOF PASEF data whereas ‘Regular MS’ is meant for all other data types (including FAIMS).
- Click “Add files” and navigate to Tutorial-5\Fragpipe\mzml and select the 10 mzML files. Click “Select”.

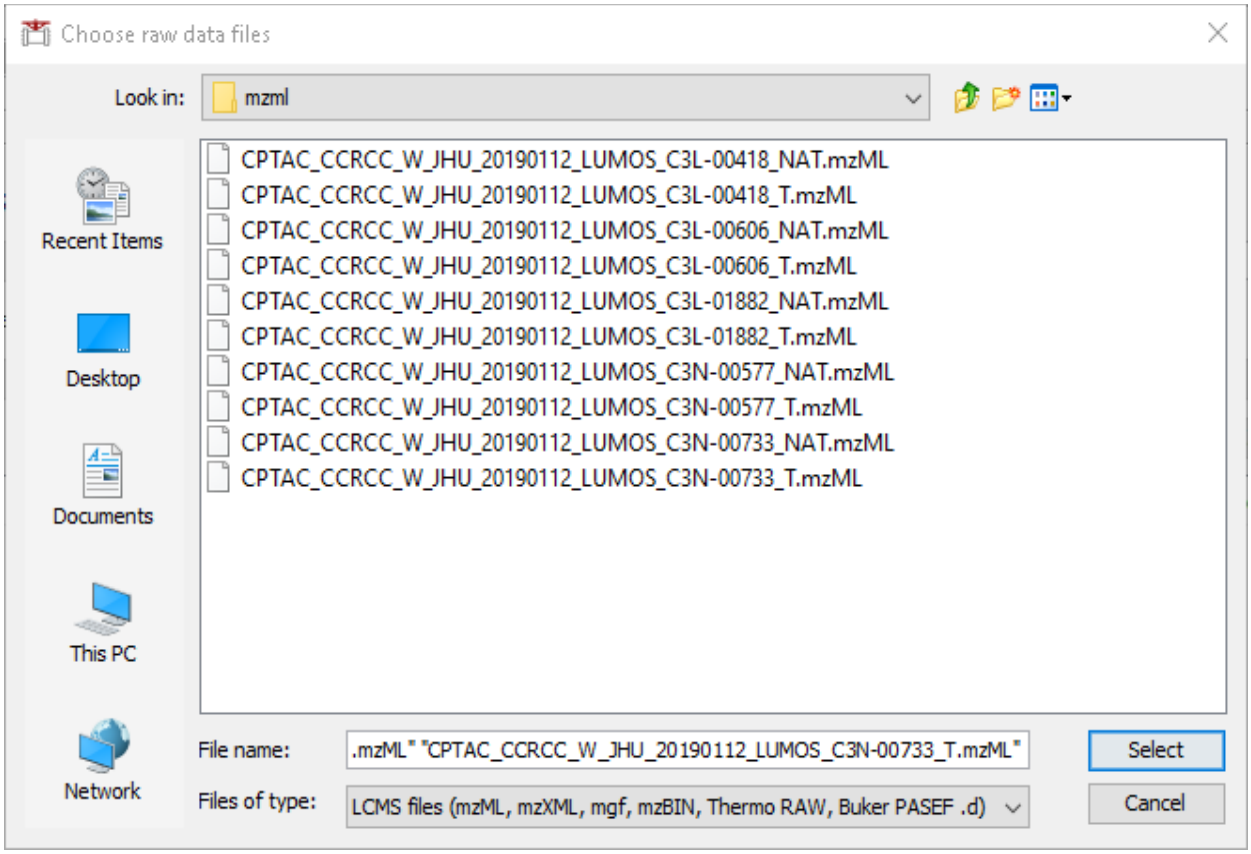
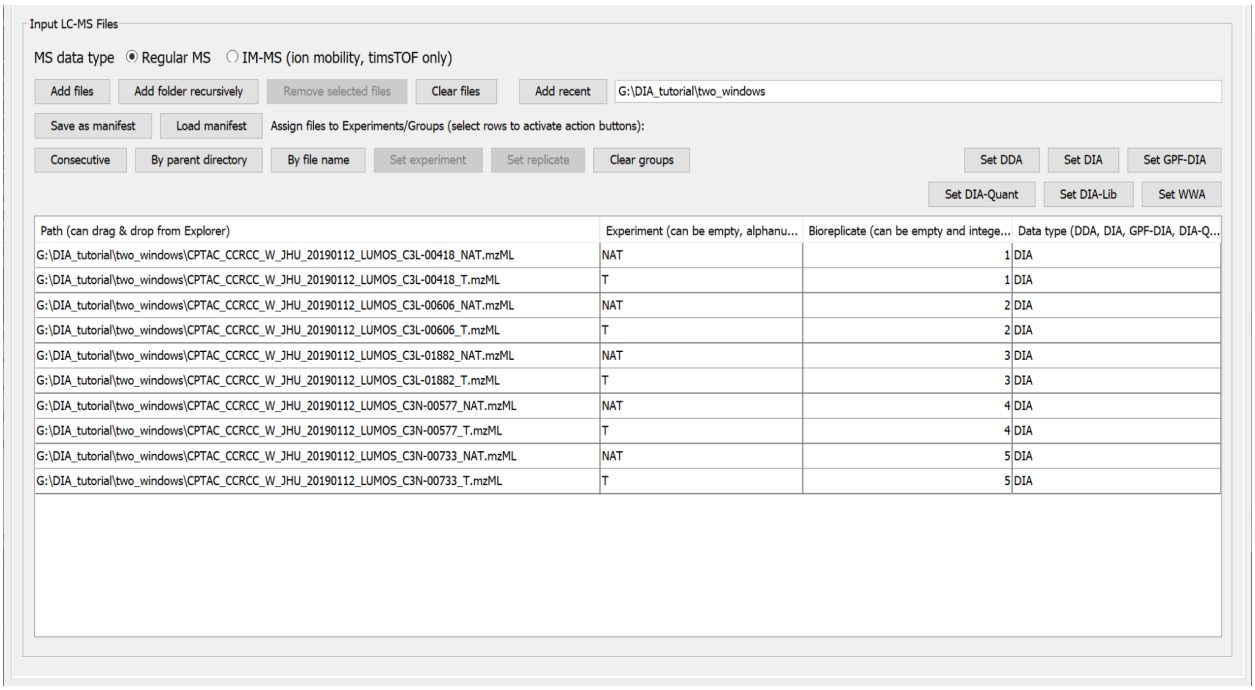


Table 1: File names and conditions

File Name	BioReplicate	Condition
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00418_NAT.mzML	1	NAT
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00418_T.mzML	1	T
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00606_NAT.mzML	2	NAT
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00606_T.mzML	2	T
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-01882_NAT.mzML	3	NAT
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-01882_T.mzML	3	T
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3N-00577_NAT.mzML	4	NAT
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3N-00577_T.mzML	4	T
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3N-00733_NAT.mzML	5	NAT
CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3N-00733_T.mzML	5	T

Now we need to annotated the Experiment and the Bioreplicate associated to each raw file according to the information provided in Table 1.

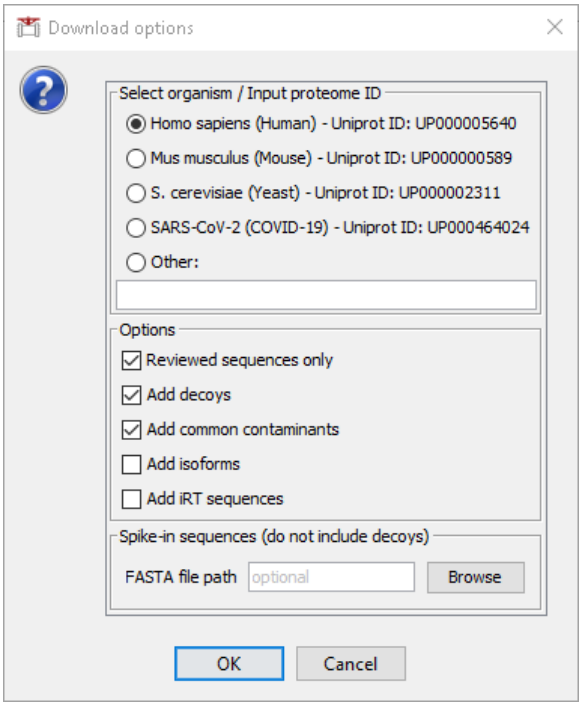
- For each file (row) select “Set experiment” and type the condition “NAT” or “T” according to Table 1. Note that one can select multiple rows with the “Control” key and annotate them simultaneously.
- For each file (row) select “Set Bioreplicate” and type the condition 1 to 5 according to Table 1. Note that the two conditions are always paired as they come from the same individual, and therefore, for each pair, we need to set the same bioreplicate number.



Parametrization of the *Database* section

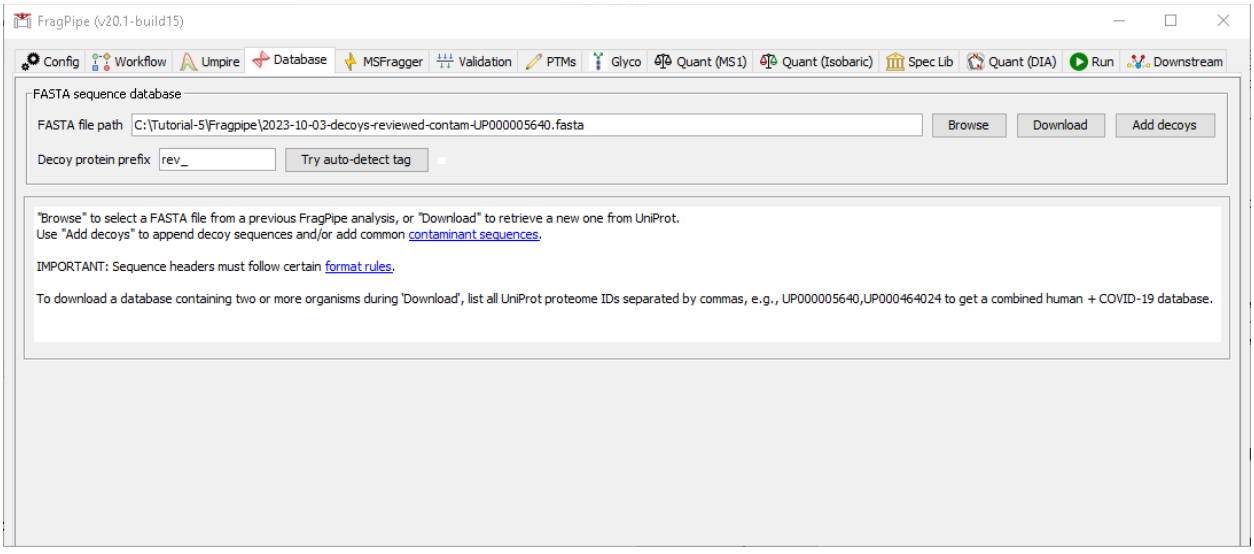
We will skip the `Umpire` tab as it is not meant to be executed in the selected workflow, and move directly to the `Database` tab.

- Click “Download” to retrieve a fresh UniProt human database including reviewed sequences only, plus contaminants and decoys.



- Save the fasta in the Tutorial-5 folder.

Note: Alternatively, one can also use the `fasta` file database provided in the “Tutorial-5\FragPipe” folder with the name `2023-10-03-decoys-reviewed-contam-UP000005640.fas`

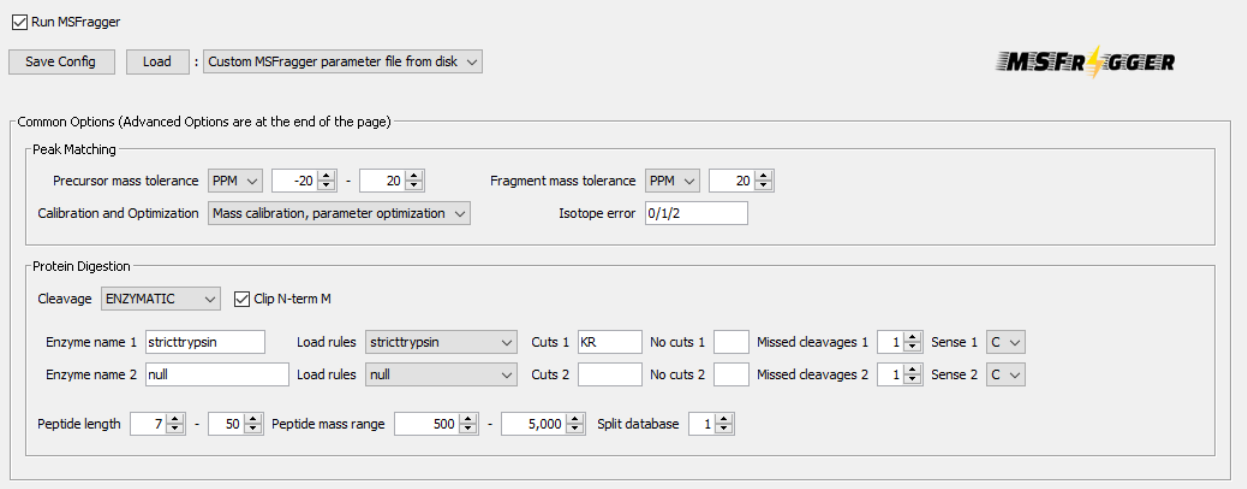


Parametrization of the *MSFragger* section

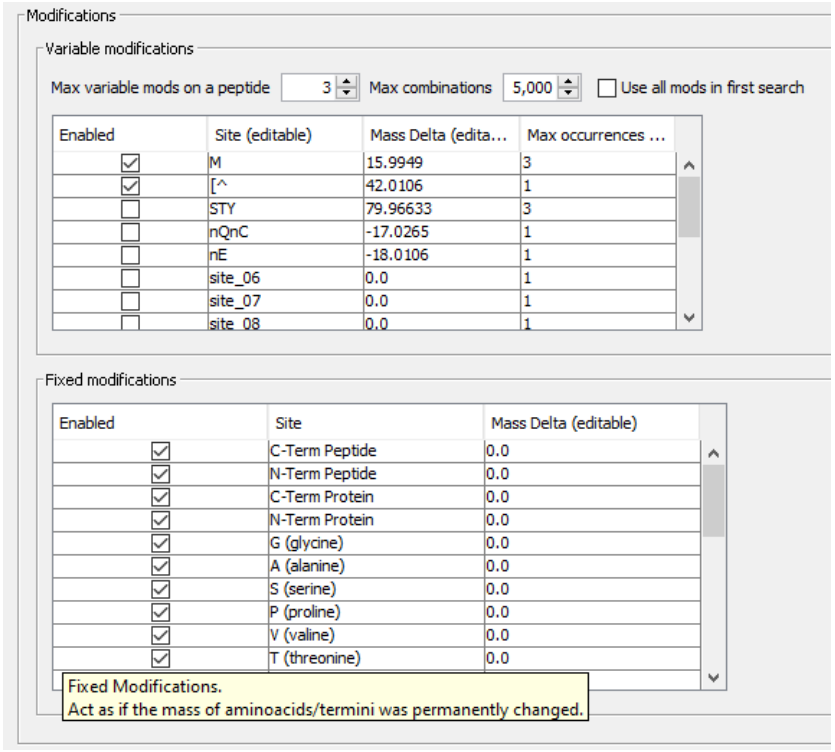
In the `MSFragger` tab you can check the search parameters that will be used to interpret the acquired spectra our analysis. The parameters have already been filled with the default values associated to the workflow selected. Let's review them.

- In **Peak Matching** the precursor and fragment mass tolerances are specified. In this case, it is set to 20 ppm, which is the standard in a so-called closed data search using data acquired in a high-resolution mass spectrometry analyzer. Options on whether there is the need for automatic mass calibration, parameter optimization and isotope peak selection correction are also present.
- In **Protein Digestion** we define that an enzymatic digestion was used to prepare the sample, and that trypsin was the enzyme used. The range of peptide length and mass are also specified. All these parameters are important when interpreting the spectra *in silico* because they define the set of potential peptides that can be present in the sample.

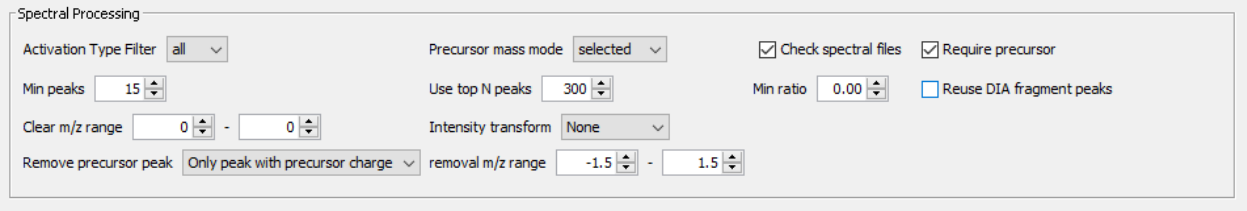
Note: *Calibration and Optimization* is set by default to "Mass Calibration, Parameter Optimization". This option will effectively perform multiple simplified MSFragger searches with different parameters to find the optimal settings for your data. In practice, it results in 5-10% improvement in the number of identified PSMs at the expense of increased analysis time. To save time, you can consider changing this option to "Mass Calibration" or even "None", especially if you already know your data (e.g. from previous searches of the same or similar files) and can adjust the corresponding MSFragger parameters (fragment tolerance, number of peaks used, intensity transformation) manually, if needed.

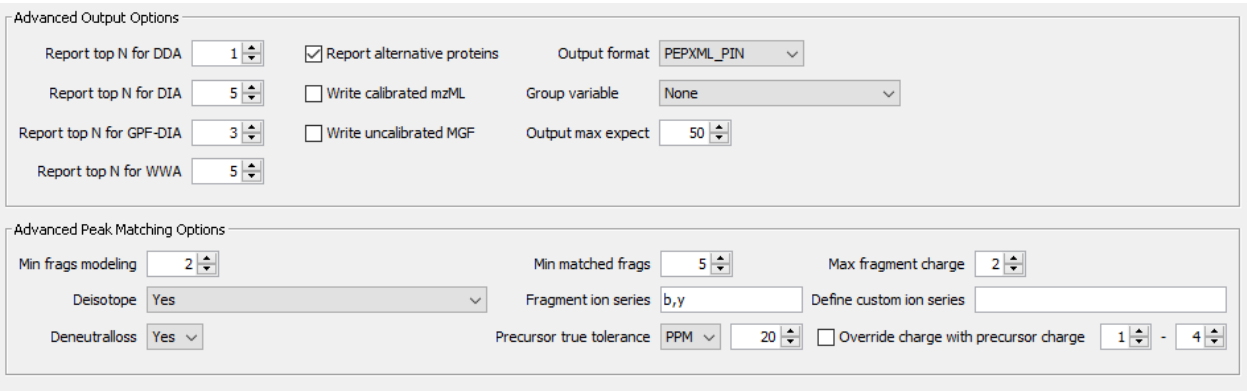


- In **Modifications** both variable and fixed modifications that can be found in the analysed peptides are specified, as well as the maximum number of allowed modifications per peptide and the maximum number of occurrences per single modification.



- Finally, there is the section of **Advanced Options**, which includes parameters for *Spectral Processing* that determine how many spectral peaks are taken into consideration. It also includes the *Advanced Output Options* and *Advances Peak Matching Options* that define the number of top N peptides to use for quantification, the output format, the fragment ion series, fragment charge range and minimum number of matched fragments to be considered during the search.



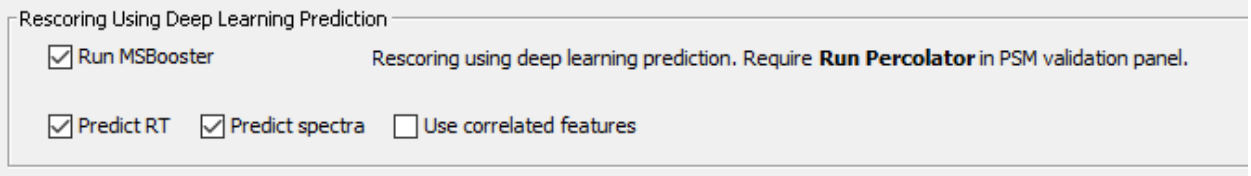


You can choose to save a customized parameter file to load for future use, or save the entire workflow (from either the 'Workflow' or the 'Run' tab).

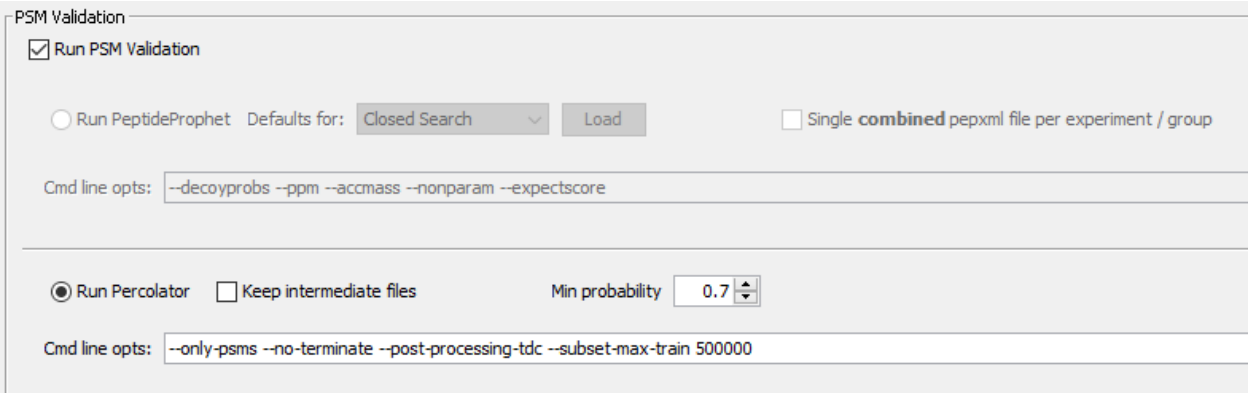
Parametrization of the *Validation* section

The `Validation` section will also be executed as part of the selected workflow. The search results obtained from MSFragger will be further analyzed by MSBooster, Percolator and ProteinProphet to get confident peptide identifications.

In this process, MSBooster will first use deep learning to predict additional features of the identified peptides including fragmentation spectra, retention time, and detectability (and ion mobility).



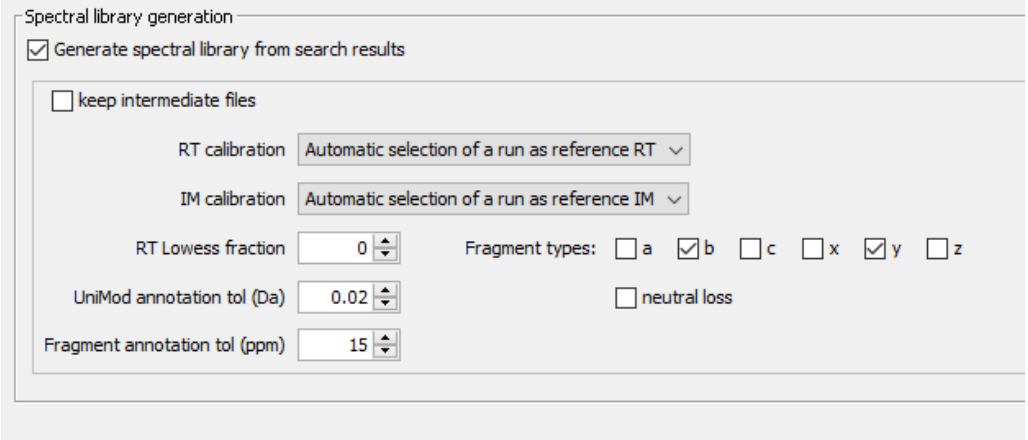
These features will be used to modify the initial identification scoring, and then Percolator will use them to improve its discrimination model to increase the number of confident identifications in the DIA dataset.



Finally, based on the identified peptides we will run the Protein Inference together with ProteinProphet to generate a confident list of protein groups identified in the sample at a maximum of 1% false discovery rate.

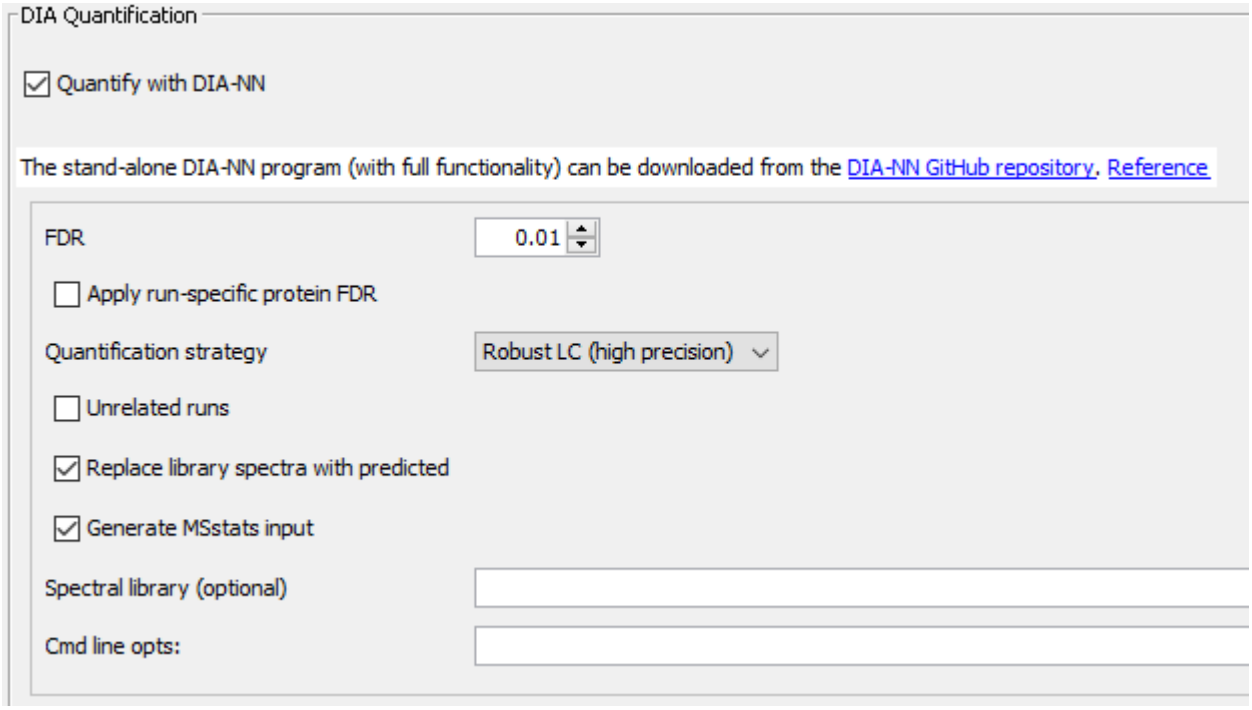
Parametrization of the *Spec Lib* section

Next, we will jump directly to the `Spec Lib` tab as the other ones (`PTMs`, `Glyco`, `Quant (MS1)`, and `Quant (isobaric)`) are not relevant for the selected workflow and will not be executed. In the Spec Lib section we will generate a spectral library from the search results, containing b and y fragment ions, and we will allow for an automatic selection of the runs that will be used as reference for the retention time.



Parametrization of the *Quant (DIA)* section

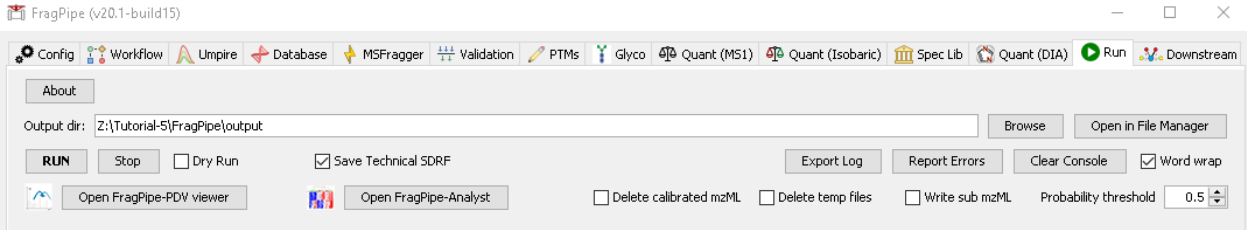
In the `Quant(DIA)` section we will set the quantification to be performed by DIA-NN with a maximum false discovery rate of 1%. In this section, we will also verify that the "Generate MSstats input" is checked.



Parametrization of the *Run* section

In this final section, we will indicate the output directory and run the analysis.

- Create a new folder in “Tutorial-5\FragPipe” called `output` and set is as the output directory of the results.
- Click “RUN”. The analysis will now be launched and it will take about 10-20 minutes. Once finished, do not close the FragPipe window. We will need it later to visualize the results.



Exploration of the FragPipe main results tables

In this first part of the tutorial we will go through the main results tables generated by FragPipe and some of its intermediate files.

Inspection of the FragPipe main output

- Go to Tutorial-5 and locate the “diann-output” folder that has been generated by FragPipe.
- Inside the “diann-output” folder locate the `report.pg_matrix.tsv` file and open it in Excel to inspect the protein-level output from the DIA-NN quantification module. You will see columns with the information such as protein group identifiers, gene names, and intensities from DIA runs calculated with the MaxLFQ algorithm embedded in DIA-NN.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Protein.Group	Protein.Ids	Protein.Names	Genes	First.Protein.Description	C:\esabid	C:\esabid	C:\esabid	C:\esabid	C:\esabid	C:\esabid	C:\esabid	C:\esabid	C:\esabid	C:\esabidc
2	A0A075B6H7	A0A075B6H7		IGKV3-7		1.15E+07		1.67E+07	5.23E+06	1.56E+06	3.31E+06	6.02E+06	582433	1.25E+06	9.46E+06
3	A0A075B6J2	A0A075B6J2		IGLV2-33		992891		852624	116486	129461		486764	108517	429645	127771
4	A0A075B6Q5	A0A075B6Q5		IGHV3-64		3.28E+06	3.00E+06	2.99E+06	1.58E+06	1.26E+06		3.64E+06	1.42E+06		1.01E+06
5	A0A075B6R9	A0A075B6R9		IGKV2D-24		7.77E+06	3.33E+06	8.29E+06	3.80E+06	2.57E+06	904343	6.36E+06	1.73E+06	3.85E+06	1.09E+06
6	A0A075B6S2	A0A075B6S2		IGKV2D-29		8.75E+06	310027	9.98E+06		375331		182868		379454	999943
7	A0A0A0MS15	A0A0A0MS15		IGHV3-49		1.79E+06	1.16E+06	3.40E+06	712559	1.43E+06	408955	1.35E+06		789723	1.37E+06
8	A0A0B4J1U7	A0A0B4J1U7		IGHV6-1		4.49E+06	217386	4.98E+06	220183	164504		351491	73166.3	244250	666500
9	A0A0B4J1V0	A0A0B4J1V0		IGHV3-15		2.93E+06	416617	2.74E+06	364616	289347	145960	697663	116222	285306	463471
10	A0A0B4J1V6	A0A0B4J1V6		IGHV3-73		1.73E+06	353681	1.90E+06	480621	450664	124681	644654		452981	950859
11	A0A0B4J1Y8	A0A0B4J1Y8		IGLV9-49		917628		556435	281035	485385					
12	A0A0B4J1Z2	A0A0B4J1Z2		IGKV1D-43		319835		245127							
13	A0A0C4DH24	A0A0C4DH24		IGKV6-21				314816						58471.5	392222
14	A0A0C4DH31	A0A0C4DH31		IGHV1-18		969456		1.43E+06							
15	A0A0C4DH36	A0A0C4DH36		IGHV3-38		1.23E+06		1.98E+06		516025	192168		181477	533340	583892
16	A0A1B0GUS4	A0A1B0GUS4		UBE2L5		223969	546748	350964	418114	190428	522785	818209	421558	320091	992621

- In the same folder, now open the `msstats.csv` file. This file contains the information required for MSstats at the fragment level. Note that the information related to “Experiment” and “Bioreplicate” annotated in FragPipe is provided now to MSstats as the “Condition” column and the “BioReplicate” column, respectively.

  Note: Msstats is an R package for statistical inference of proteomics data and can be accessed through the web at www.msstatsshiny.com. Kohler D, et al. MSstats Version 4.0: Statistical Analyses of Quantitative Mass Spectrometry-Based Proteomic Experiments with Chromatography-Based Quantification at Scale. J Proteome Res. 2023 May 5;22(5):1466-1482. doi: 10.1021/acs.jproteome.2c00834.

	A	B	C	D	E	F	G	H	I	J
1	ProteinName	PeptideSequence	PrecursorCharge	FragmentIon	ProductCharge	IsotopeLabelType	Condition	BioReplicate	Run	Intensity
2	Q86U42	(UniMod:1)AAAAAA	2	b4	1	L	NAT	4	CPTAC_	1821522
3	Q86U42	(UniMod:1)AAAAAA	2	y10	1	L	NAT	4	CPTAC_	856179
4	Q86U42	(UniMod:1)AAAAAA	2	y9	1	L	NAT	4	CPTAC_	741283.7
5	Q86U42	(UniMod:1)AAAAAA	2	y8	1	L	NAT	4	CPTAC_	876211.6
6	Q86U42	(UniMod:1)AAAAAA	2	y11	1	L	NAT	4	CPTAC_	816950.1
7	Q86U42	(UniMod:1)AAAAAA	2	y6	1	L	NAT	4	CPTAC_	654794.6
8	Q86U42	(UniMod:1)AAAAAA	2	y7	1	L	NAT	4	CPTAC_	420455.8
9	Q86U42	(UniMod:1)AAAAAA	2	b5	1	L	NAT	4	CPTAC_	1019006
10	Q86U42	(UniMod:1)AAAAAA	2	y12	1	L	NAT	4	CPTAC_	549599
11	Q86U42	(UniMod:1)AAAAAA	2	y13	1	L	NAT	4	CPTAC_	175193.2
12	Q86U42	(UniMod:1)AAAAAA	2	b6	1	L	NAT	4	CPTAC_	802748.4
13	Q86U42	(UniMod:1)AAAAAA	2	b4	1	L	NAT	1	CPTAC_	1975461
14	Q86U42	(UniMod:1)AAAAAA	2	y10	1	L	NAT	1	CPTAC_	1463101
15	Q86U42	(UniMod:1)AAAAAA	2	y9	1	L	NAT	1	CPTAC_	1288745
16	Q86U42	(UniMod:1)AAAAAA	2	y8	1	L	NAT	1	CPTAC_	1028672
17	Q86U42	(UniMod:1)AAAAAA	2	y11	1	L	NAT	1	CPTAC_	1430375

Inspection of intermediate FragPipe output files

If you are curious, you can explore FragPipe output files to get a better understanding of various FragPipe modules.

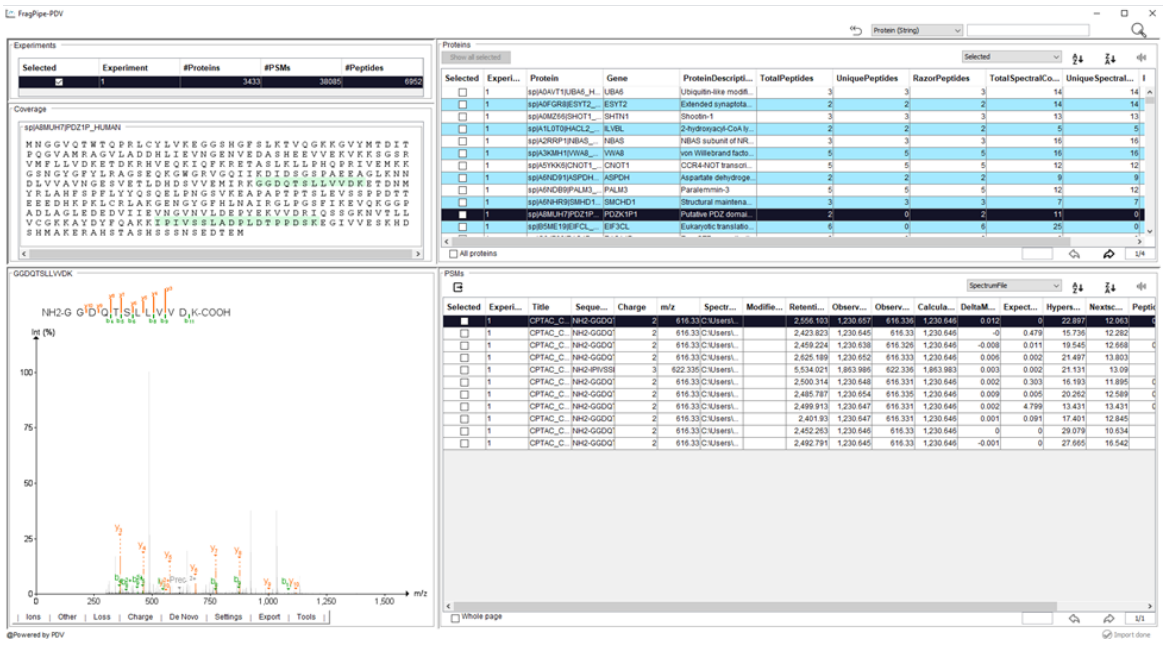
- Open the `psm.tsv` file with Excel and inspect the information that you have for each peptide-spectrum match. You will see the “SpectralSim” column, which indicates how well each PSM’s experimental fragment intensities match predicted intensities from the spectral prediction model; this is the ‘spectral entropy’ score, a value between 0 and 1, with 1 being a perfect match. You will also see the “RTScore”, which shows how much the experimental retention time of each PSM deviates from what is expected based on retention time predictions; the lower the value, the better.
- Open now the `.png` files inside *MSBooster_RTplots*. Each of these files corresponds to a different `mzML` file and shows the calibration curve fit between the predicted iRT scale and the experimental RT from this experiment’s chromatography setup.
- Open the `log` file with a text editor or your Notepad. In this file you will find all the commands that have been executed by the FragPipe workflow. Note the mass correction values printed at the mass calibration step of MSFragger. Inspect also the Percolator weights. The greater the magnitude of the weights, the more influence that variable has in Percolator rescoring.
- Open the `library.tsv` file with Excel. This is the library files built using EasyPQP from `PSM.tsv` and `mzML` files, and contains peptide ions passing 1% protein-level, peptide-level, and PSM-level FDR. For precursors identified from multiple PSMs (in the same or different runs), fragment ion intensities and retention time (after alignment to the reference run) of the best scoring PSM are used. This file is used as input to DIA-NN for extracting quantification.

Visualization of the FragPipe main results

Visualization of identification results in FragPipe-PDV

In this section we will visualize the identification results from FragPipe at different levels, including experiments, proteins, peptides and PSM information.

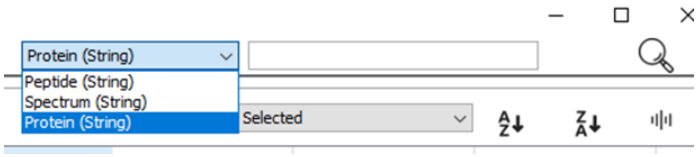
- Go to the Run tab in the graphical user interfase of FragPipe and open FragPipe-PDV by clicking on ‘**FragPipe-PDV viewer**’ to open the results.



A FragPipe-PDV viewer will open with five main panels including the information about the “Experiments”, “Protein coverage”, “Spectrum viewer with annotations”, “Table of identified proteins”, and the “Table with Peptide-Spectrum Matches (PSMs)”.

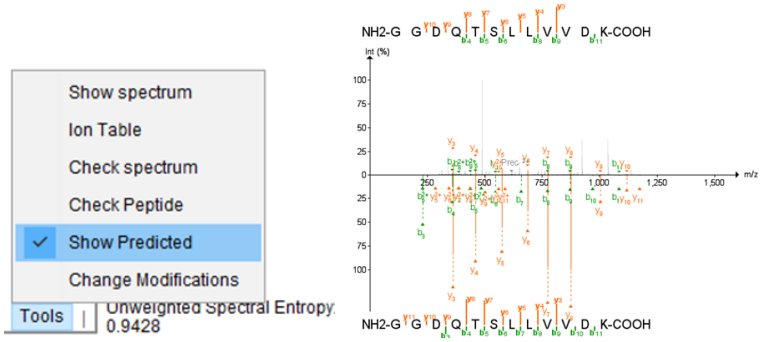
There are several functions embedded in FragPipe-PDV that we will explore. For example, one can look for certain peptide sequences or protein of interest.

- Search the protein “CTNA1”, using the searching function located on the top right corner. How many PSMs are associated to this protein? How many different unique peptide sequences have been identified for this protein? What are their PeptideProphetProbabilities



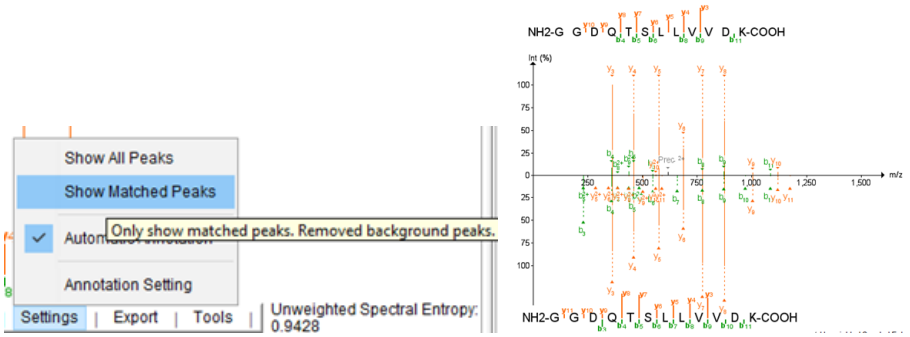
In FragPipe-PDV you can also see the annotated spectra in which peptides were identified. FragPipe-PDV has several options to configure the settings for peptide spectra visualization.

- Go to the “Tools” menu below the spectrum, click and select “Show Predicted” to show the predicted spectrum in a mirror spectra format.



Why do you think spectra are populated with so many different unmatched peaks? Are they good identifications?

- To clean the spectra, click “Show Matched Peaks” in the “Settings” menu to remove background peaks



Do the identifications look better now? Do you think that they are more credible?

Now we will see how different peptides can be identified in the same single MS2 spectrum. For this example, we will use one peptide SMEDSVDVSAPK from sp|Q8IVF2|AHNK2_HUMAN Protein. This is one of the ccRCC cancer biomarkers (overexpressed in tumor samples) that we will also use as an example later in this tutorial.

- Search for protein Q8IVF2 and find all peptides identified for this protein.
- Click on the peptide SMEDSVDVSAPK listed above to view its spectrum.
- Go to the Tutorial-5 folder and open the `PSM.tsv` file with Excel and look for the SMEDSVDVSAPK peptide. Note that the peptide has been identified twice, in two different spectra from two different raw files.
- Check the spectrum number for each of the identifications looking at the value of the first column.

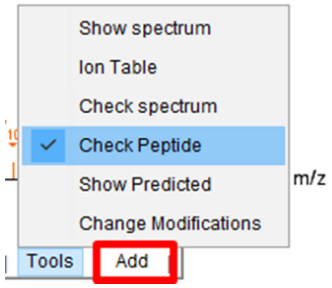
	A	B	C
1	Spectrum	Spectru	Peptide
4528	CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00418_T.01248.01248.0	C:\esabid	SMEDSVDVSAPK
27639	CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3N-00577_T.01224.01224.0	C:\esabid	SMEDSVDVSAPK

- Now filter the PSM.tsv file by the spectrum column containing the spectrum “CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00418_T.01248.01248.0”. Notice that there is another peptide, TDYM[+16]VGSYGPR, that was identified in that same MS2 scan.

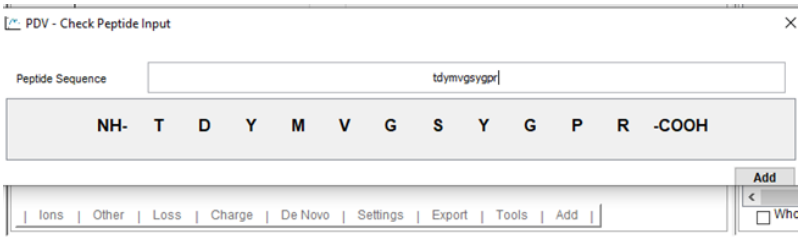
	A	B	C	D
1	Spectrum	Spectru	Peptide	Modified Peptide
4528	CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00418_T.01248.01248.0	C:\esabid	SMEDSVDVSAPK	
4529	CPTAC_CCRCC_W_JHU_20190112_LUMOS_C3L-00418_T.01248.01248.0	C:\esabid	TDYMVGSYGPR	TDYM[147]VGSYGPR

You can use the PDV viewer to visualize both peptides at the same time.

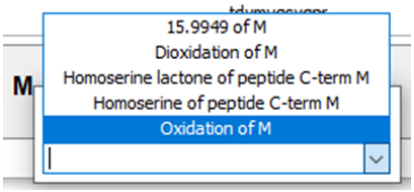
- Select “Check Peptide” function in the “Tools” menu to check different peptide matches on the current spectra.



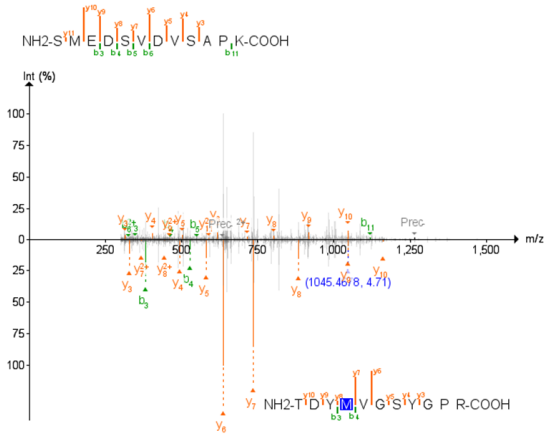
- Click “Add” and type the sequence of the peptide that you want to add into the visualization. Enter the peptide sequence without modifications.



- Click amino acid to add a modification on it.



Note: Remember than in “Settings” you can select to see either all peaks or only the matched peaks.

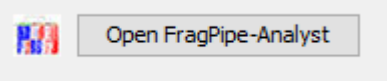


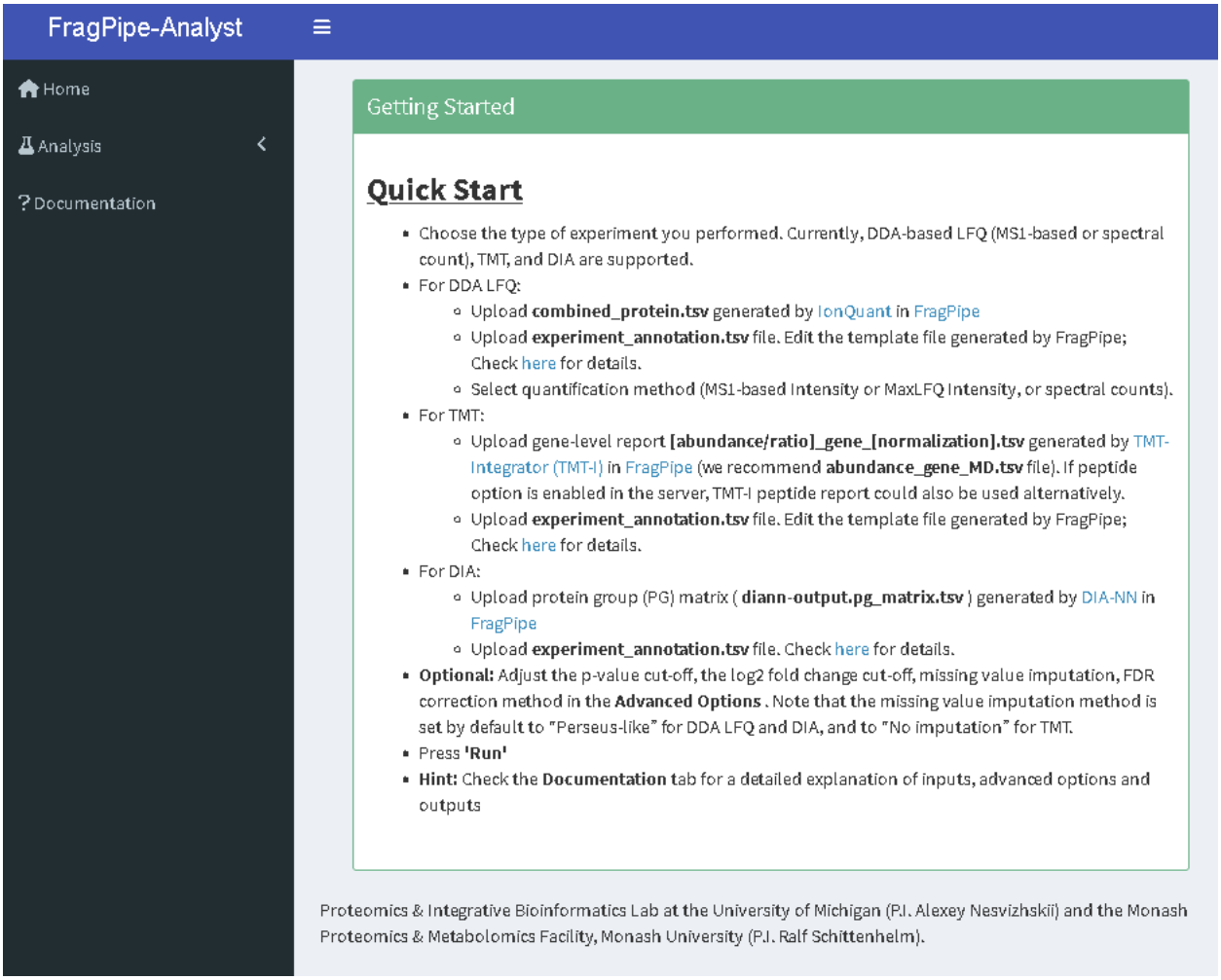
Downstream analysis of FragPipe main results

Downstream analysis using FragPipe-Analyst

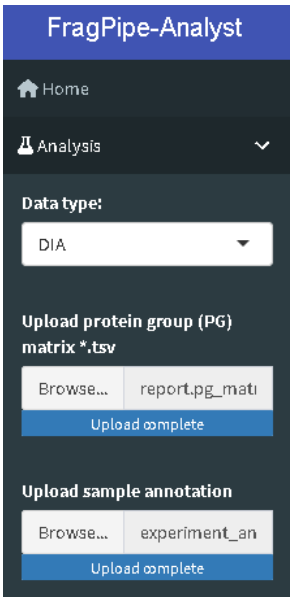
In this section we will do a downstream analysis and visualization of the quantitative results of the obtained results with FragPipe-Analyst and we will perform a principal components analysis (PCA) and a statistical assessment of protein abundance changes.

- Go to the "Run" tab of the graphical user interface ofFragPipe and click in the FragPipe-Analyst button. Alternatively, you can also access FragPipe-Analyst directly in your browser at http://fragpipe-analyst.nesvilab.org/



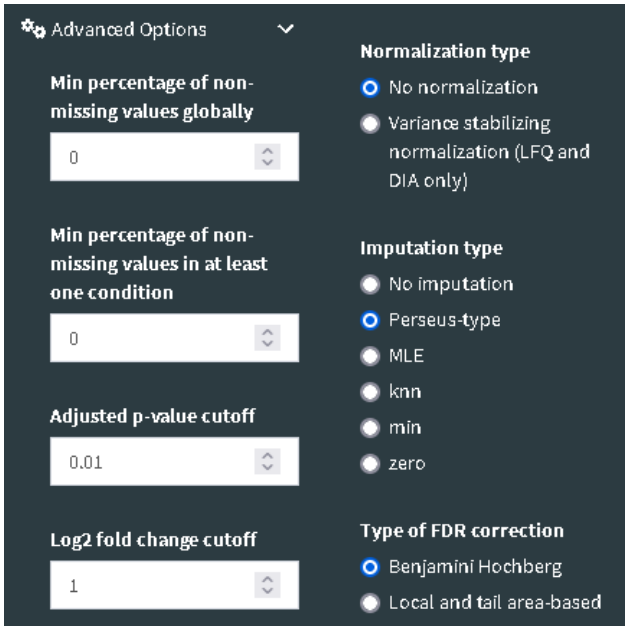


- Choose the Analysis option from the left-hand side menu and in the "Data type" dropdown menu, choose "DIA".
- Follow the instruction on the left-hand side menu to upload `report.pg_matrix.tsv` and `experiment_annotation.tsv`.

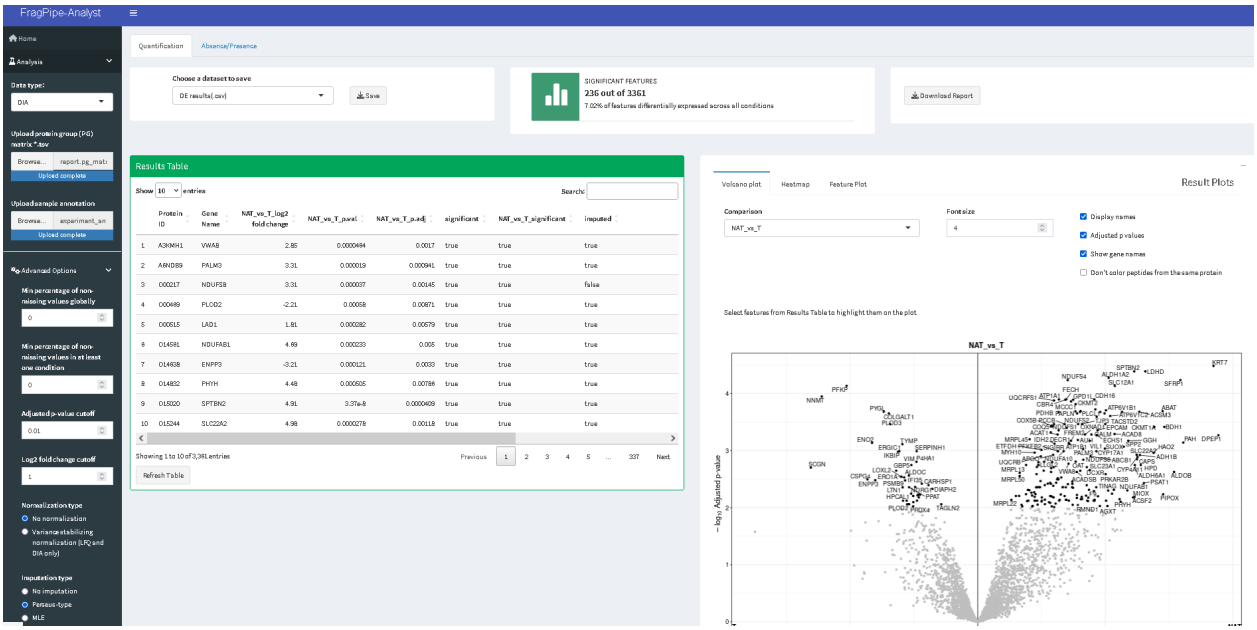


- Inspect the “Advanced Options” and review the values for the different sections.
  - Set the “Min percentage of non-missing values globally” to zero.
  - Set the “Min percentage of non-missing values in at least one condition“ to zero.
  - Set the “Adjusted p-value cutoff" to 0.01.
  - Set the “Log2 fold change cutoff” to 1.
  - Set the “Normalization type” to “No normalization”.
  - Set the “Imputation type” to Perseus-type
  - Set the “Type of FDR correction” to Benjamini Hochberg.

Note: In the FragPipe-Analyst, a Perseus-like imputation is used by default and the imputed matrix will be used to perform differential expression analysis via Limma. In this type of imputation, missing values are replaced by random numbers drawn from a normal distribution with a width of 0.3 and down shift of 1.8.

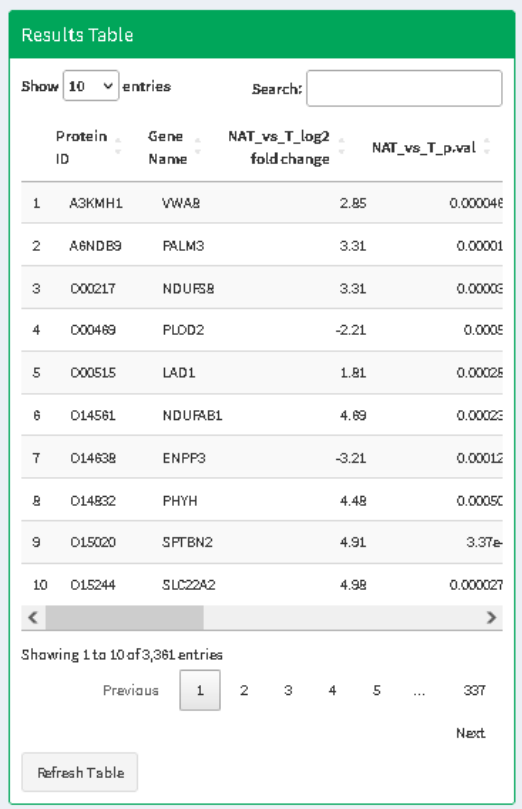


- Click the “Run” button located at the bottom of the page to start the downstream analysis. You should see your result shortly in the web interface.

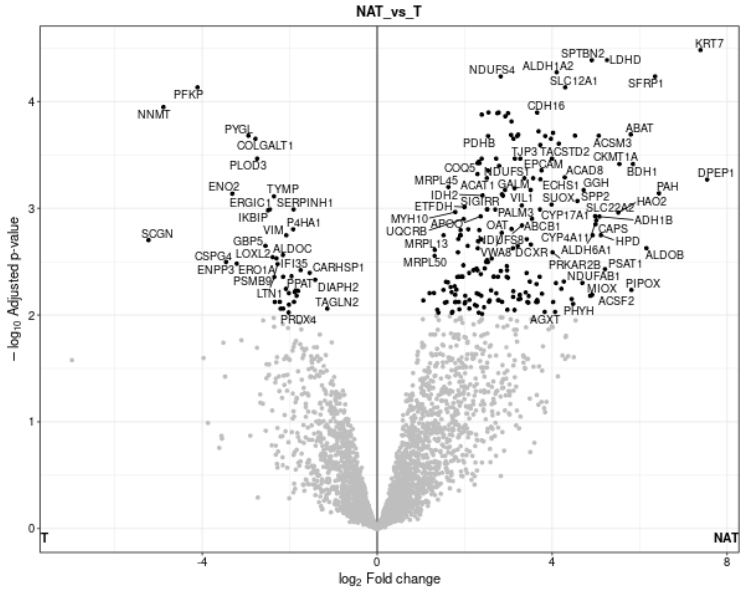


The results include:

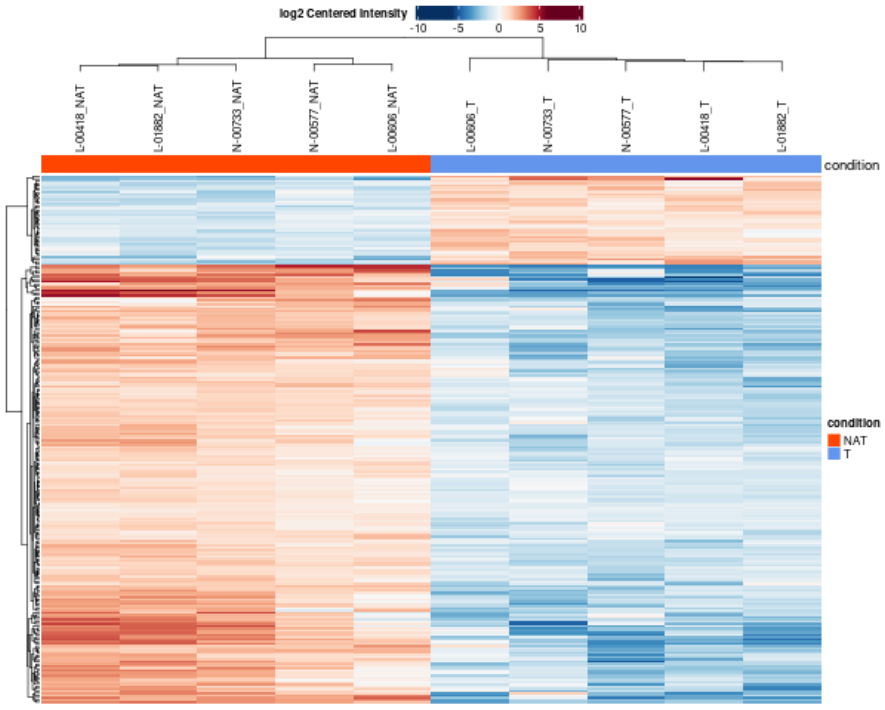
- “Results Table” with the statistical assessment of between the different conditions indicated in the experimental design described in the `experiment_annotation.tsv` file.



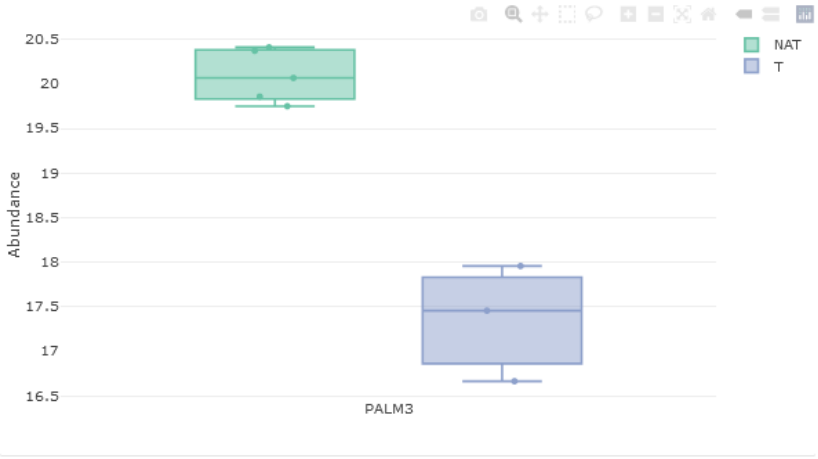
- “Volcano Plot” displaying the protein fold-changes and adjusted p-values for the different comparisons.



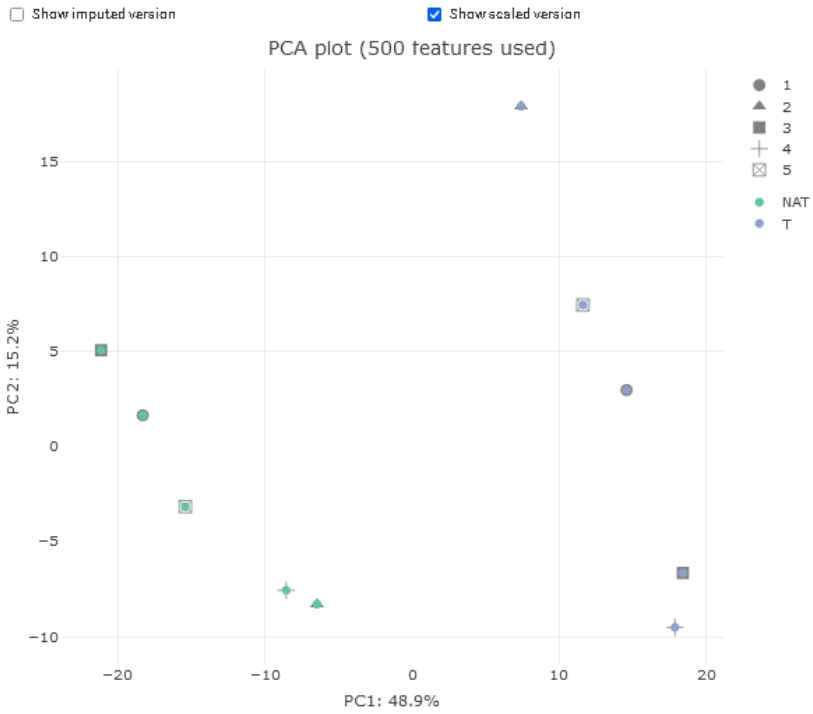
- “Heatmap” of protein abundances in each individual sample with hierarchical clustering of the different conditions.



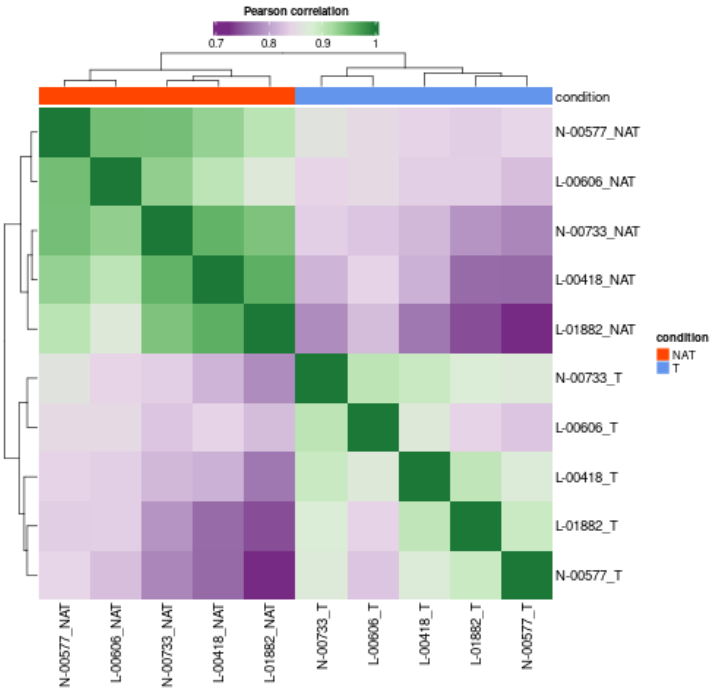
- “Feature Plot”, displaying boxplots or violin plots of your favourite (selected) proteins from the Results Table.



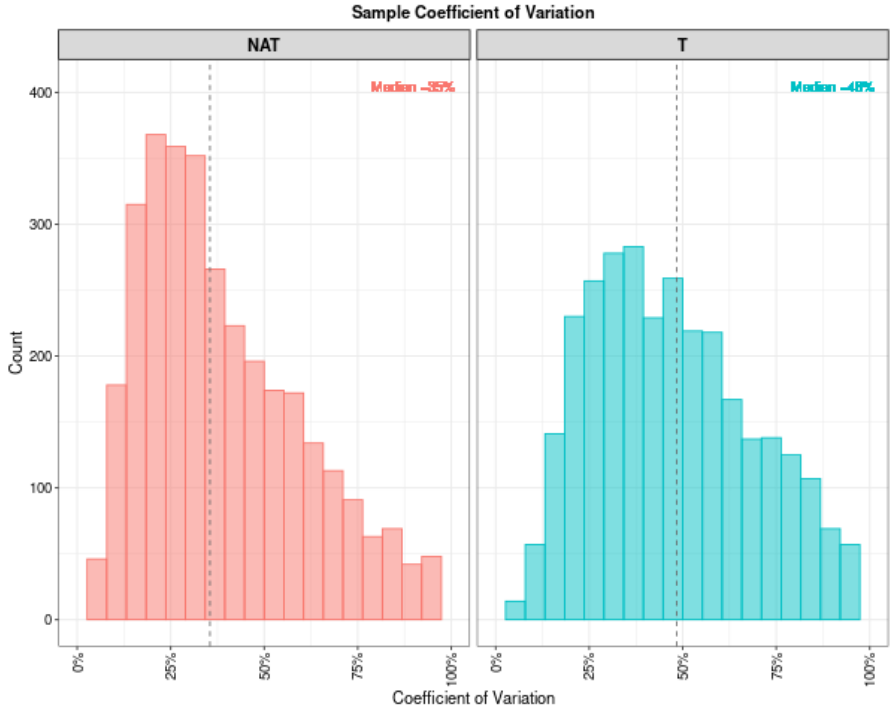
- "PCA Plot" showing the result of the principal components analysis.



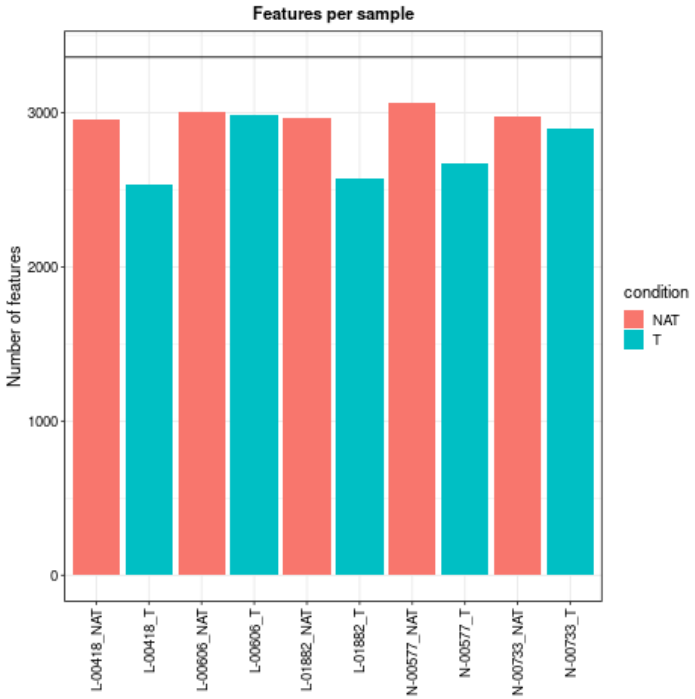
- "Sample correlation plot" showing the Pearson correlation among the protein abundances matrix of the different samples.



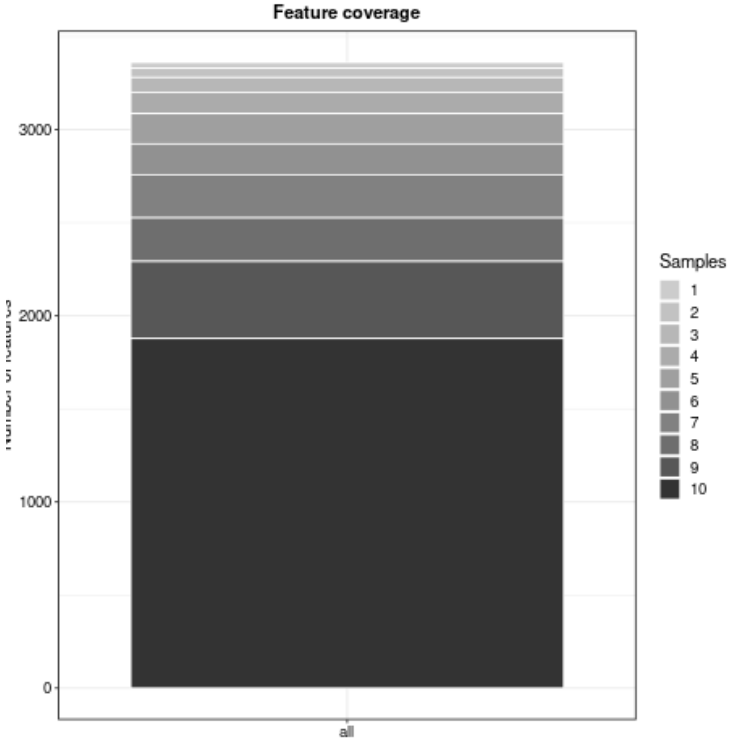
- "Sample CVs" shows the distribution of the coefficient of variation of the different proteins among the replicates of each biological condition.



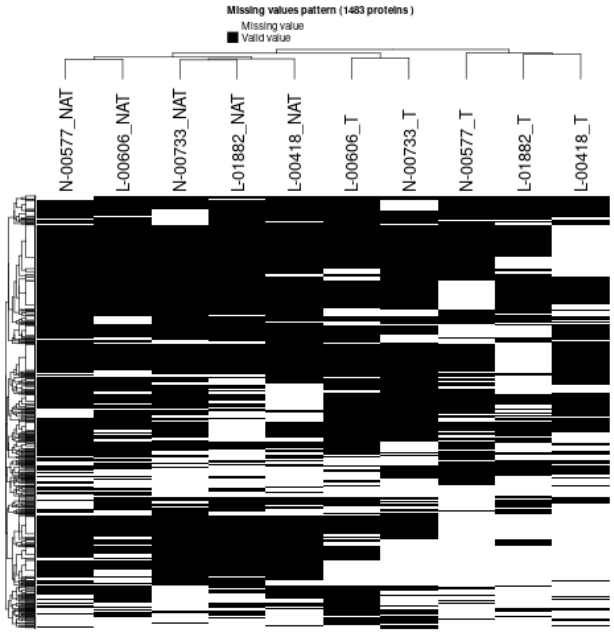
- "Feature Numbers" shows the number of proteins used for the quantification in each sample.



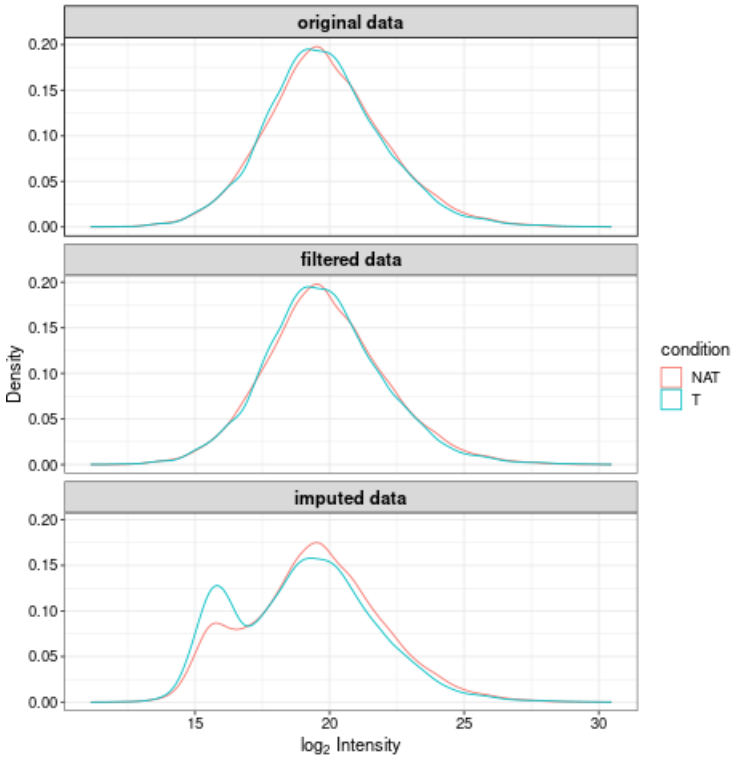
- "Sample coverage" shows the number of proteins that were found with valid quantitation values in all 10 samples, or only in 9 samples, 8, 7, etc.



- “Missing values - Heatmap” the distribution of missing values per protein and samples in the dataset.



- “Density plot” shows the distribution of protein abundances in the original data, in the filtered data, and in the set of proteins in which imputation was performed. In this case, the original data and the filtered data look the same as we did not force any filtering of the data in the “Advanced Options” of the Analysis section.



Normally, one can start with explorative analyses such as Principal Component Analysis (PCA) to see if the protein data exhibit tumor/normal difference. Following that, one can look for showing differential abundances in tumor samples compared to normal samples. Since the comparison is done for many proteins, multiple test correction is needed to control the false discovery rate.

- Take your time now to explore the results, data and plots in FragPipe-Analyst.
- Once you have explored the different sections, answer the following questions:

    - Do you think the proteome data exhibits any difference between tumor and normal? Inspect the PCA plot. What PC (principal component) captures the major differences between the protein expression profiles in tumor vs normal? How much of the total variance can be attributed to the difference between tumor and normal?

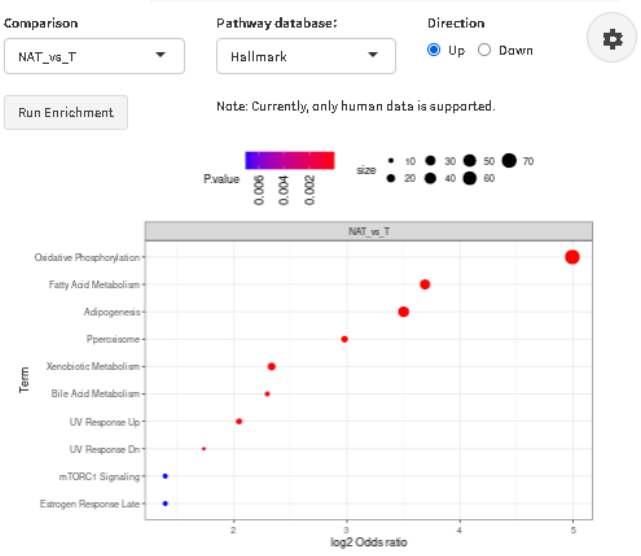
    - Inspect quality control (QC) plots to see if there are any issues with the data (e.g., too few proteins identified in one of the runs, consistent differences in protein abundance distributions between samples, etc.). e.g. inspect “Sample Correlation” plot to see if there are any outliers. Inspect “Density Plot” to see protein abundance distributions before imputation, and after missing value imputation.

    - Find and select a known cancer suppressor of kidney cancer, sFRP1. Find it on the volcano plot. Check its abundance levels across the tumor and normal samples in this dataset using “Feature Plot”. Select the protein in the “Results Table” to see the “Feature Plot”, and make sure to check the “Show imputed values” option.

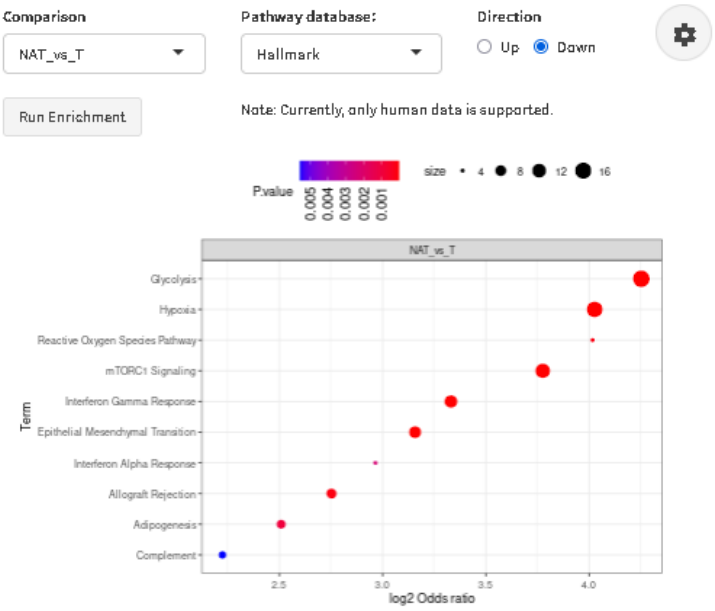
Note: When viewing volcano plots or doing enrichment analysis, pay special attention to which side represents which condition to correctly interpret the plots.

- Once the statistical analysis is conducted we get a list of proteins with abundance values altered in between tumor and healthy tisses. However, it is often difficult to make sense of individual genes, especially when there are many of them. Enrichment analysis enables us to aggregate the evidence to biological pathway (Pathway enrichment) or processes (Gene Ontology) to gain a higher-level insight of tumor features.

    - Go to the section “Pathway enrichment”. Select the “Hallmark” pathway database, check the “Up” direction, and click “Run Enrichment”. What are the most enrich pathways among the proteins in the “Up” direction?



- Repeat the analysis using direction “Down”. What are the most enrich pathways among the proteins in the “Down” direction?



Note: Currently the pathway enrichment can be done also with other databases like KEGG and Reactome, in addition to the Hallmark. However, at the moment the pathway enrichment analysis in FragPipe-Analysis only supports human data. In case you want to use any other external tool, you can download the results of the differential expression from FragPipe-Analyst by clicking on the “Save” button on the upper left corner and use in as input for other tools.

Note: To get better agreement with the published results, you can change the “Adjusted p-value cutoff” in the Analysis “Advanced Options” section to 0.05 (from 0.01).

Finally, take into account that we are only using a very small fraction of the global proteome data from the original paper. Therefore, it is likely that you will see discrepancies between the analysis in this tutorial and the final results of the publication, including the number of proteins quantified, the proteins identified as showing a significant change in abundance, and the enriched pathways. However, it is noteworthy to highlight that even this very small dataset is capable of recovering many of the observations in the paper.

Visualization of raw data in Skyline

In this section we will use Skyline to visualize the results in terms of extracted chromatograms generated by FragPipe during the library-free analysis of our dataset. We will use the built-in import wizard of Skyline to import the results and we will dedicate some time to review the raw data. Finally, we will define the experimental groups and perform the statistical inference for the group comparison.

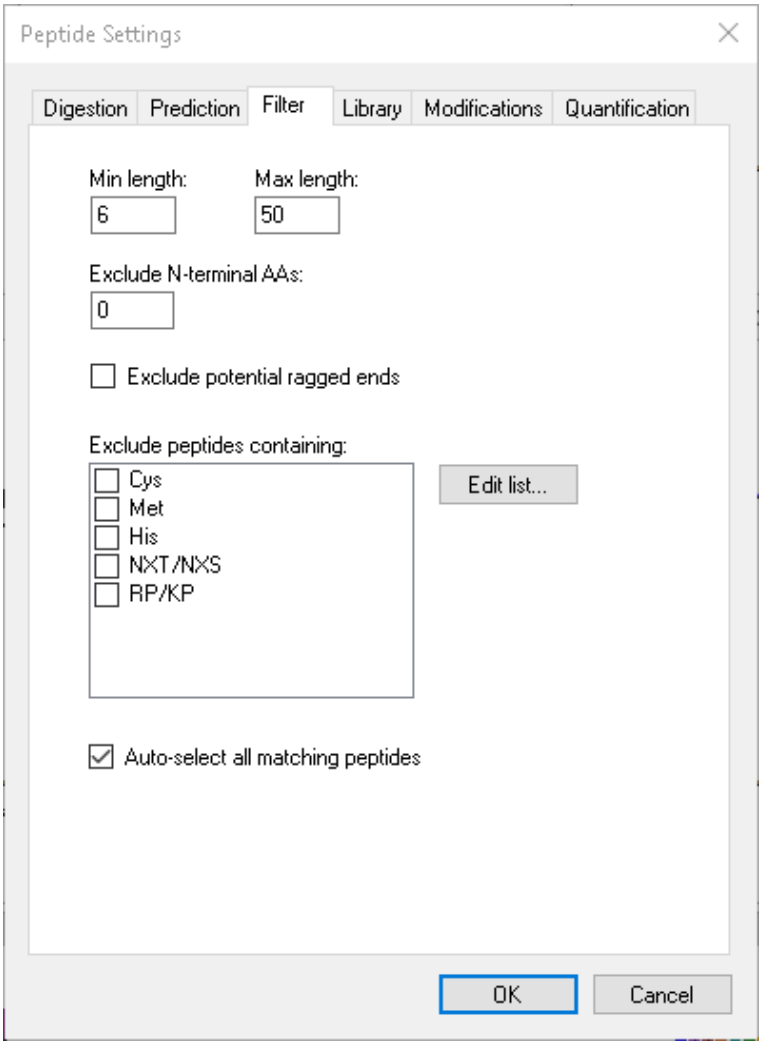
Note This part of the tutorial is based in Skyline-daily 23.1.1.268

- Open a “Blank document” in Skyline
- Go to Settings → Default.

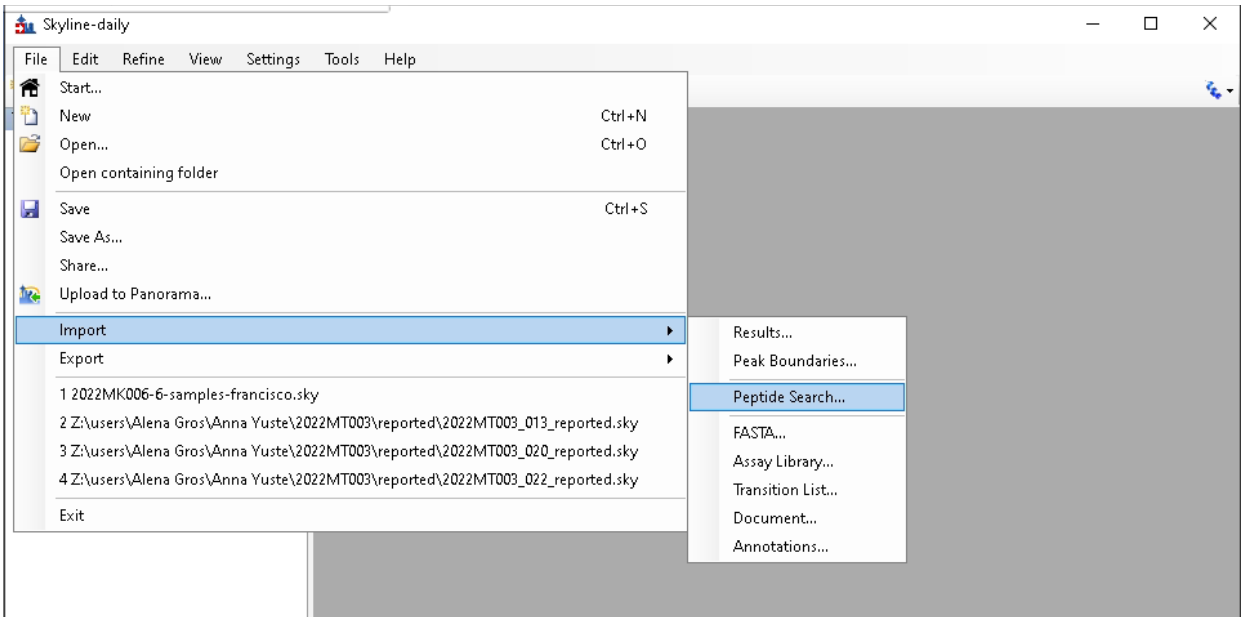
Save the document as `dia-fragpipe.sky` to the folder “Tutorial-5\FragPipe\output”.

Note: In order to avoid memory problems, please save your Skyline sessions in the computer’s C drive and not in any external drive or USB stick.

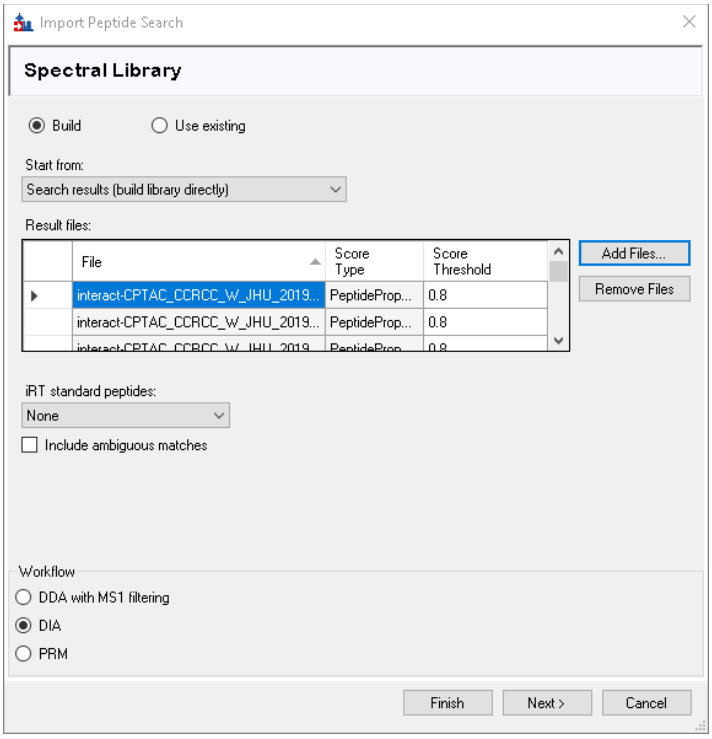
- First go to Settings → Peptide Settings and set the parameters as indicated



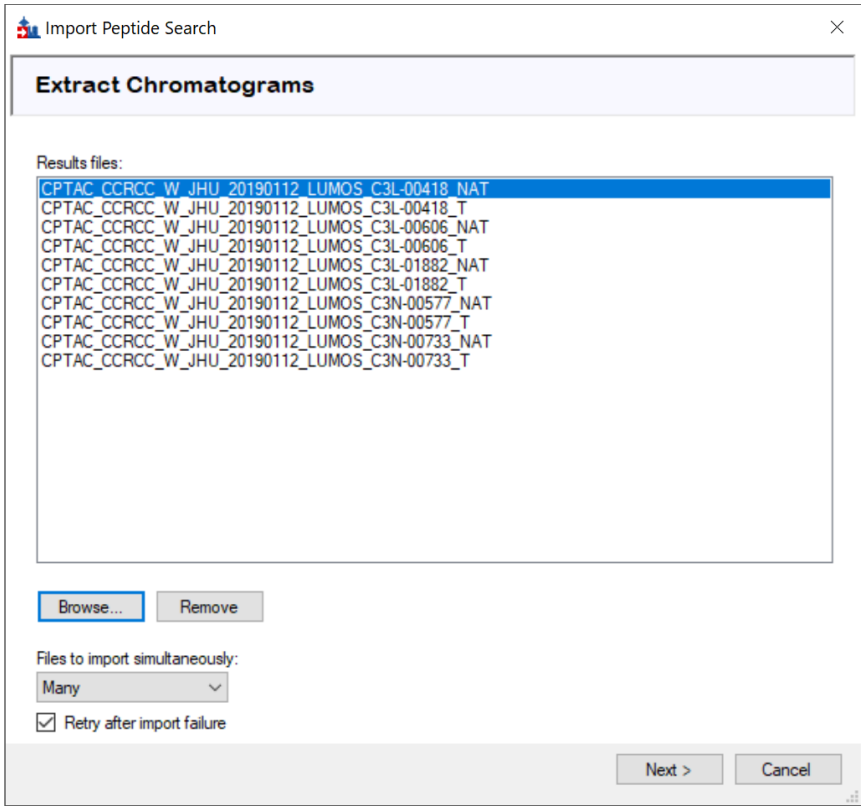
- Go to File → Import → Peptide Search…



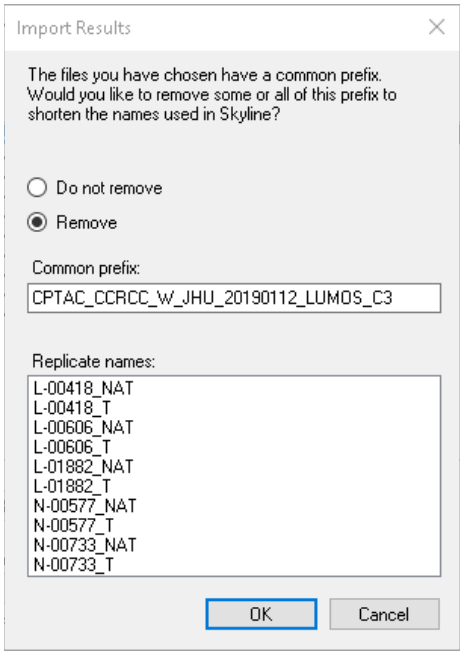
- In the Import Peptide Search window, click in “Add Files…”.
- Go to the Tutorial-5\Fragpipe\output and select all the `interact-*.pep.xml` files. Click “Open”.
- Set the “Score Threshold” to 0.8 which is the threshold corresponding to 1% FDR when FragPipe performs the search.
- Set Workflow to “DIA”. Then, click ‘Next’.



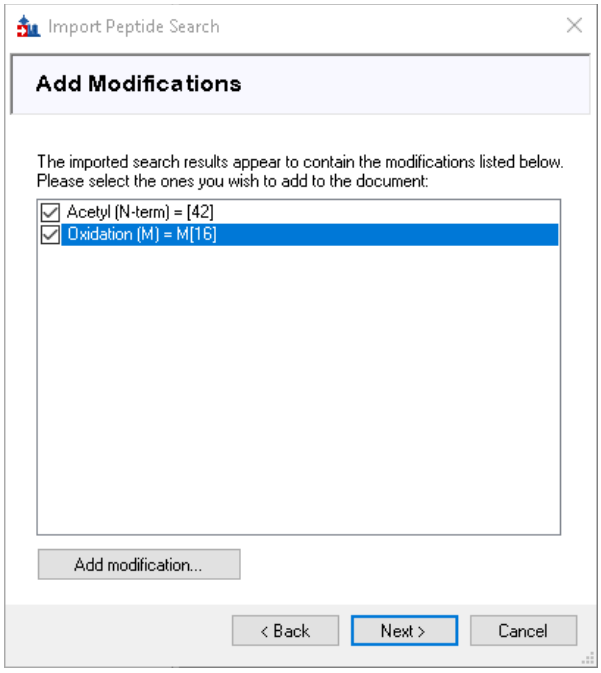
- Click “Browse…” and go to Tutorial-5\Fragpipe\mzml and select all `mzML` files as “Result files”, and click ‘Next’.



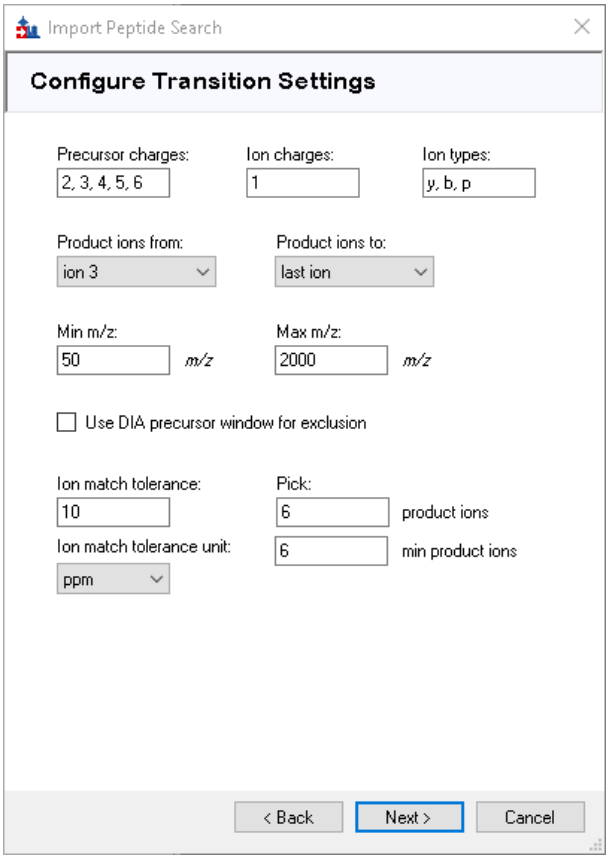
- Check the option to remove the Common prefix, and click “OK”.



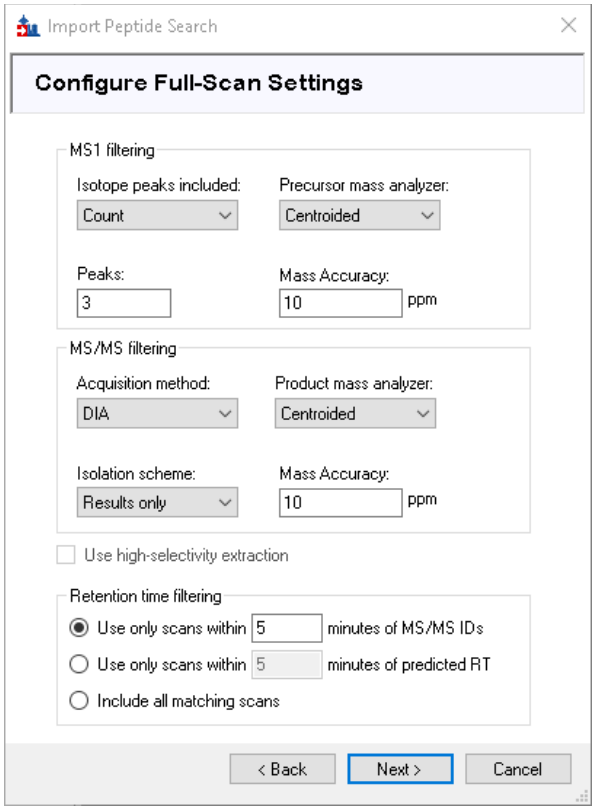
- Check the modifications corresponding to “Acetyl (N-term) = [42]” and “Oxidation (M) = M[16]”, and click “Next”.



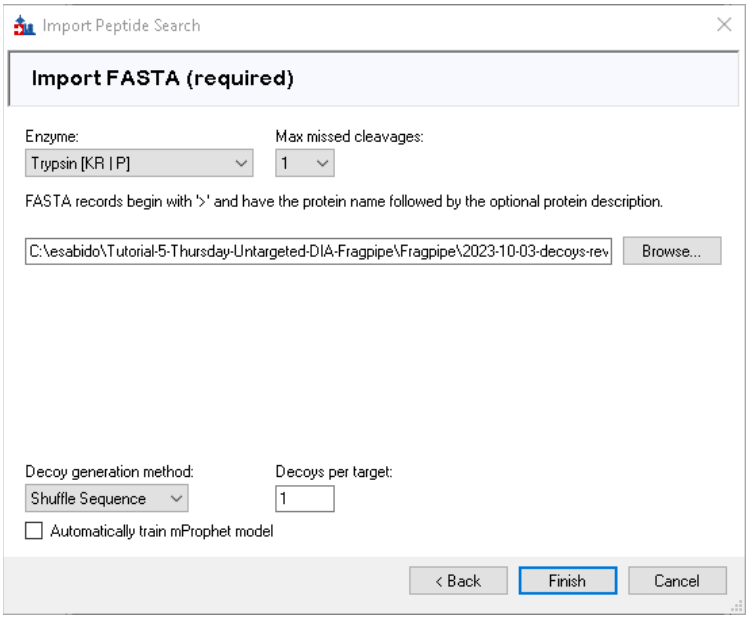
- Adjust the Transition Settings as depicted in the screenshot below, and click “Next”.



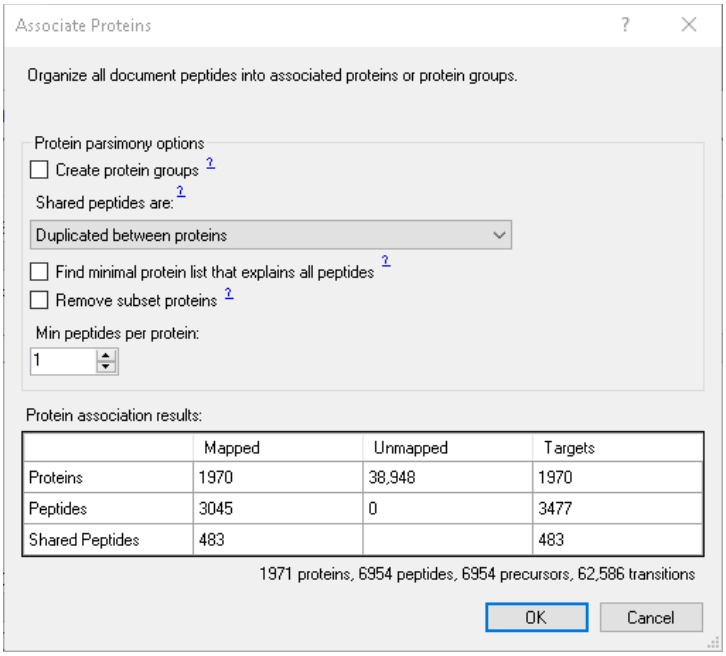
- Adjust the Full-scan settings as in the screenshot below. Note that we set a retention time tolerance of only 0.4 minutes. Then click “Next”.



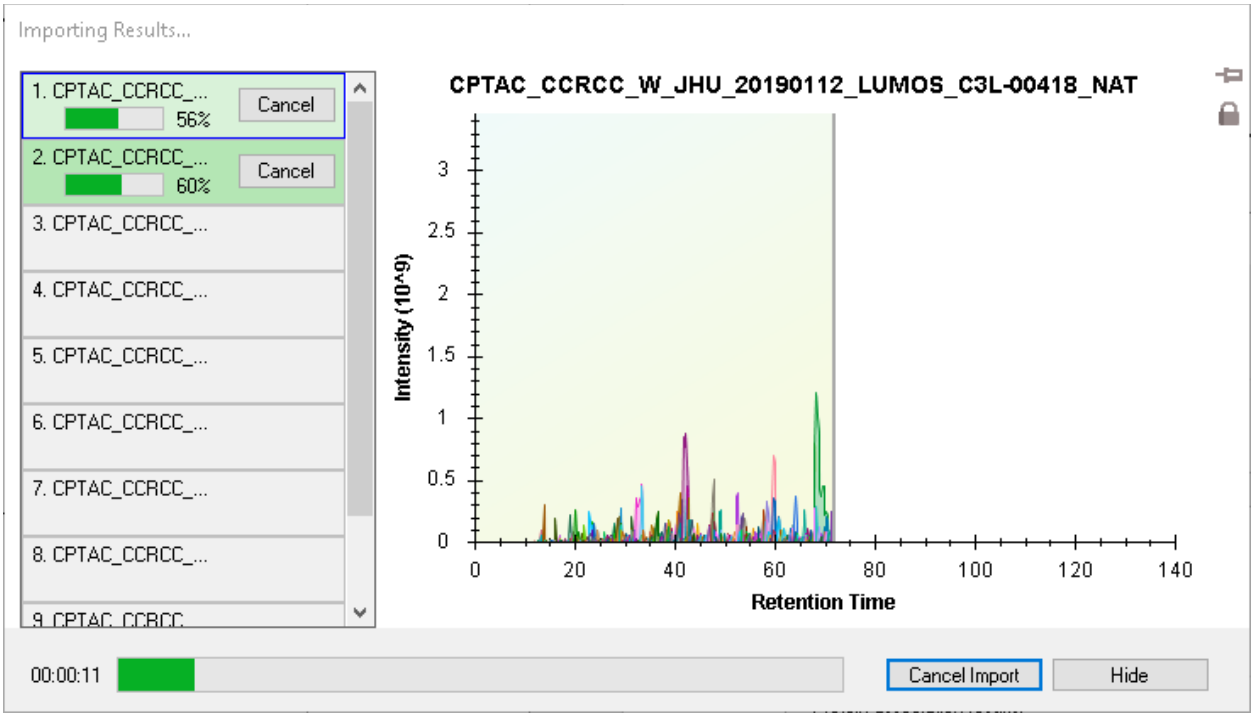
- Finally, in the “Import FASTA (required)” section, set the “Max missed cleavages to 1”, then click “Browse…” and go to Tutorial-5\Fragpipe and select the fasta file that you downloaded at the beginning of the tutorial when configuring the FragPipe analysis (`2023-10-03-decoys-reviewed-contam-UP000005640.fas`). Click “Finish”.



- Check that the Associate Proteins panel looks like the screenshot, and click “OK”.



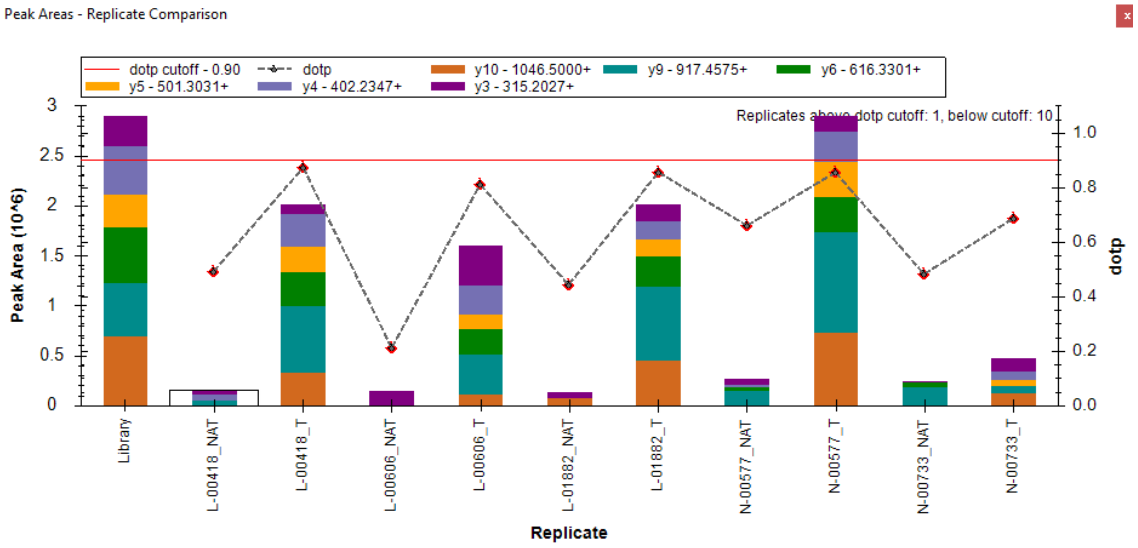
After clicking ‘OK’ in the next dialog window, Skyline will start to load the data.



Finally, we will explore the extracted chromatogram in Skyline to inspect the intensity of the peptide SMEDSVDVSAPK from protein sp|Q8IVF2|AHNK2_HUMAN, a known tumor biomarker of kidney cancer.

- Go to View ☾ Transitions ☾ Products to only show fragments
- Go to Edit ☾ Find… and search for the peptide SMEDSVDVSAPK
- In the 'View' menu, select 'Peak Areas' and then 'Replicate Comparison' to visualize the intensities among all samples, to confirm the upregulation of this peptide in tumor samples. Make sure that the option "Normalized To" is set to "Default (None). You can right click in the Peak Areas plot to check it.

How does the data look like? In which samples do you have an associated identification? Do the signals in these samples look better?



Now look for protein sFRP1 and inspect the different peptides that have been identified for this protein. How to they look like? Are the signals clearer in the healthy samples compared to the tumor samples?