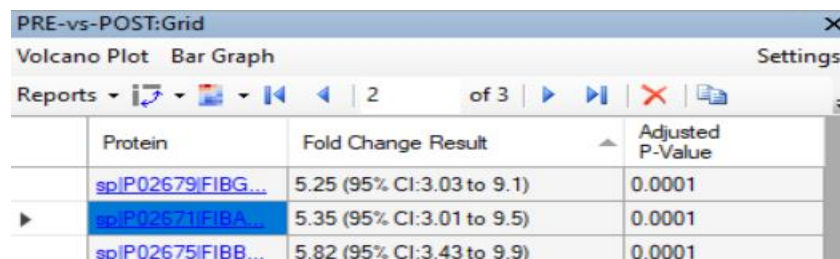


PIERRE WENSEL: PROTEOMICS PRACTICAL



Protein	Fold Change Result	Adjusted P-Value
sp P02679 FIBG...	5.25 (95% CI:3.03 to 9.1)	0.0001
sp P02671 FIBA...	5.35 (95% CI:3.01 to 9.5)	0.0001
sp P02675 FIBB...	5.82 (95% CI:3.43 to 9.9)	0.0001

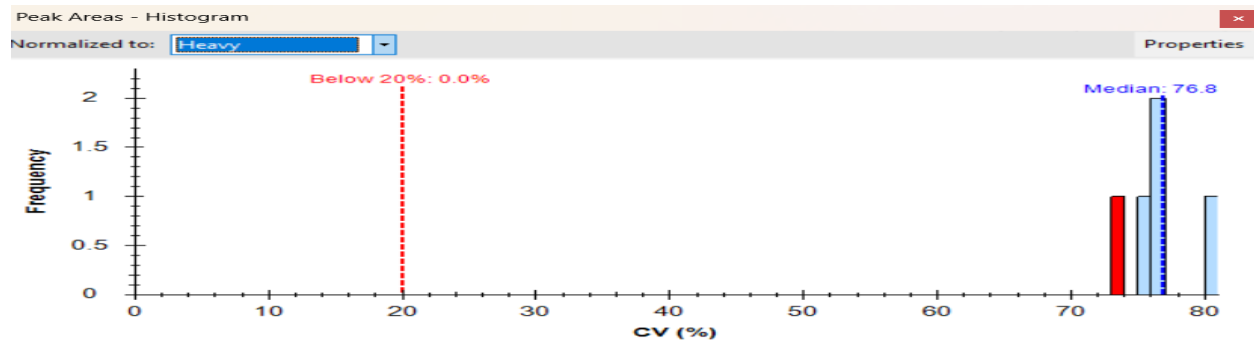
1. The effect of the experimental drug was to increase fibrinogen protein levels in patients by up to 5.82x. This was a statistically significant increase with adjusted p-value < 0.0001

2. Yes, I first used a library built with the neural network prediction tool PROSIT, which advantageously precludes the need to perform experiments to obtain the MSMS library which is useful when heavy peptides are not available as in large-scale DIA projects. Subsequently, only the precursors (with charge of 2 and 3) and transitions that have been identified in the library were displayed. I later can build an MS/MS spectral library from experimental data (search engine output file is in pep.xml format and the raw data in the standard mzXML format) obtained from a mixture of the target peptides of interest isotopically labelled (heavy peptides) which have been acquired in the mass spectrometer in DDA mode and have been searched against a protein database for identification. Spectra from both can be mirrored.

3. I used 90 transitions to quantify each 18 precursors for 5 peptides of 3 proteins. This quantification was enabled by activation of PROSIT spectral library. Only the precursors and transitions identified in the library are displayed.

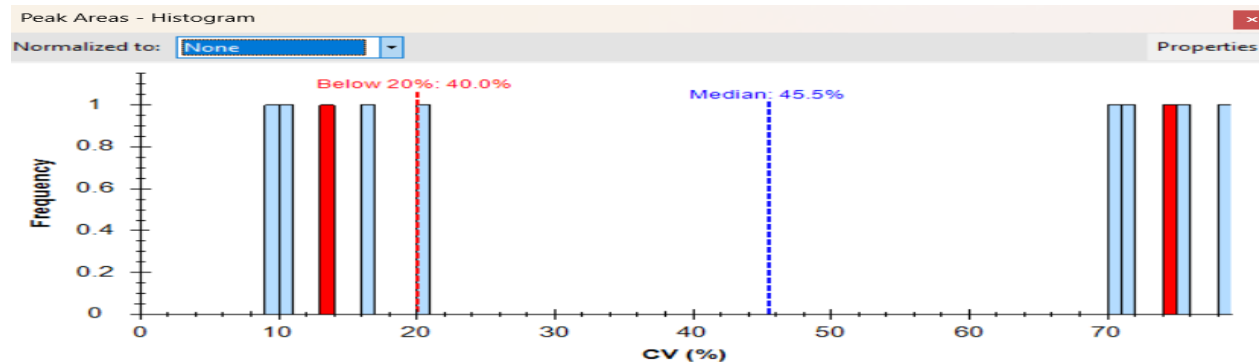
4. The coefficient of variation (CV) of the peak area for each peptide in each group indicates good reproducibility between replicates when it is at low values (<20%). Based on my histogram for "heavy" setting, the CV for peptide K.VAQLEA... was extremely high (81%). With "no normalization" setting, that of peptide R.HPDEAA... is well below 20% at 9% for one control PRE-condition vs. POST-condition.

5. We are targeting specific peptides with PRM (parallel reaction monitoring) whereas DIA collects data from wide, evenly-spaced precursor isolation windows. Parallel Reaction Monitoring enables qualitative and quantitative analysis through secondary full scans, exhibiting strong resistance to interference and high resolution in complex backgrounds. Synthetic standard peptides can be selectively incorporated as needed, saving experimental costs



Peak Areas - Replicate Comparison

Peak Areas - Histogram



Peak Areas - Replicate Comparison

Peak Areas - Histogram

Peptide	Protein	Replicate	Peptide Peak Found Ratio	Peptide Retention Time	Ratio To Standard	Quantification
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	POST_REP1	0.5	40.94	49.3823	493.8229 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	POST_REP2	0.5	41.17	34.8128	348.1282 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	POST_REP3	0.5	40.93	26.3942	263.9415 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	POST_REP4	0.5	41.05	29.8667	298.6667 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	POST_REP5	0.5	40.97	36.3135	363.135 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	PRE_REP1	0.5	41.31	3.8337	38.3373 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	PRE_REP2	0.5	41.77	3.1977	31.9772 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	PRE_REP3	0.5	41.53	15.0102	150.1016 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	PRE_REP4	0.5	41.55	7.5185	75.1846 fmol
HPDEAAFFDASTGK	sp P02671 FIBA_HUMAN	PRE_REP5	0.5	41.39	5.9531	59.5311 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	POST_REP1	0.5	21.04	705.1334	7051.3342 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	POST_REP2	0.5	21.33	662.3981	6623.9811 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	POST_REP3	0.5	21.23	385.3939	3853.9387 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	POST_REP4	0.5	21.36	568.0972	5680.9725 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	POST_REP5	0.5	21.36	748.4415	7484.4154 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	PRE_REP1	0.5	21.53	91.5872	915.8722 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	PRE_REP2	0.5	21.48	63.3751	633.7512 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	PRE_REP3	0.5	21.83	160.8562	1608.5624 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	PRE_REP4	0.5	21.38	139.3115	1393.115 fmol
ESSSHHPGIAEFPSR	sp P02671 FIBA_HUMAN	PRE_REP5	0.5	21.68	124.502	1245.0203 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	POST_REP1	1	59.31	46.9288	469.2882 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	POST_REP2	1	59.63	40.9065	409.0655 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	POST_REP3	1	59.44	50.0206	500.206 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	POST_REP4	1	59.39	42.318	423.1796 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	POST_REP5	1	59.27	43.0401	430.4006 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	PRE_REP1	1	59.86	5.6366	56.3661 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	PRE_REP2	1	59.78	4.4357	44.3573 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	PRE_REP3	1	59.64	16.2284	162.2838 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	PRE_REP4	1	59.69	9.8097	98.0968 fmol
HQLYIDETVNSNIPTNLR	sp P02675 FIBB_HUMAN	PRE_REP5	1	59.76	6.6938	66.9378 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	POST_REP1	0.5	37.31	664.3157	6643.1574 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	POST_REP2	0.5	37.64	452.0409	4520.4094 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	POST_REP3	0.5	37.59	350.5555	3505.5549 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	POST_REP4	0.5	37.6	419.3267	4193.2672 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	POST_REP5	0.5	37.6	450.0322	4500.3218 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	PRE_REP1	0.5	38.05	67.9395	679.3945 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	PRE_REP2	0.5	38.14	51.8583	518.583 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	PRE_REP3	0.5	38.29	175.4244	1754.2442 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	PRE_REP4	0.5	38.04	102.9552	1029.5516 fmol
YEASILTHDSSIR	sp P02679 FIBG_HUMAN	PRE_REP5	0.5	38.15	81.2699	812.6991 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	POST_REP1	0.5	22.98	615.4501	6154.5011 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	POST_REP2	0.5	23.32	400.5629	4005.6286 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	POST_REP3	0.5	23.34	265.6409	2656.4092 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	POST_REP4	0.5	23.25	338.828	3388.2803 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	POST_REP5	0.5	23.3	359.357	3593.5697 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	PRE_REP1	0.5	23.54	51.4211	514.2115 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	PRE_REP2	0.5	23.46	44.9138	449.1377 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	PRE_REP3	0.5	23.77	159.3392	1593.3919 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	PRE_REP4	0.5	23.5	87.6849	876.8491 fmol
VAQLEAQCQEPCK	sp P02679 FIBG_HUMAN	PRE_REP5	0.5	23.77	58.6816	586.8163 fmol