

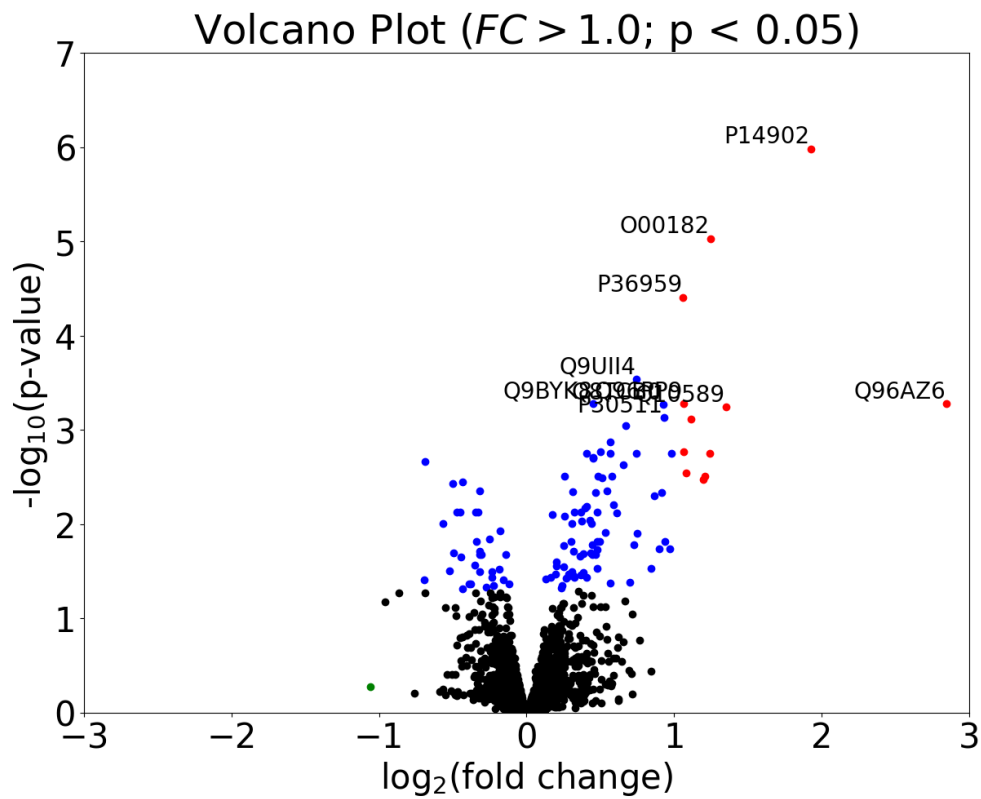
# QCQuan report: Test3

## 1 Differential Expression Analysis

Reference condition: **Untreated**

### 1.1 Minimal expression

**INFB:**



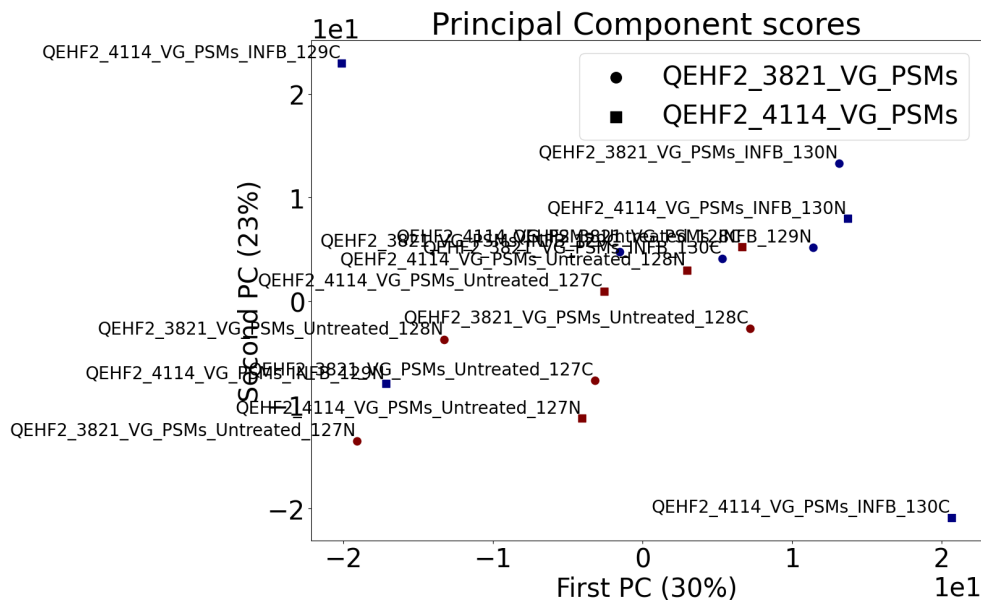
protein description	log2 fold change (INFB)	adjusted p-value (INFB)	#peptides (INFB)	#peptides (Untreated)
P14902	1.926372	0.000001	28	28
O00182	1.248225	0.000009	16	16
P36959	1.062272	0.000039	12	12
Q9UII4	0.746718	0.000287	16	16
Q96AZ6	2.847470	0.000527	4	4
Q9BYK8	0.453692	0.000527	36	36
Q96PP9	1.065580	0.000527	16	16
Q8TCB0	0.926452	0.000542	8	8
Q10589	1.350176	0.000573	16	16
P30511	0.931567	0.000741	4	4

## 2 Quality control

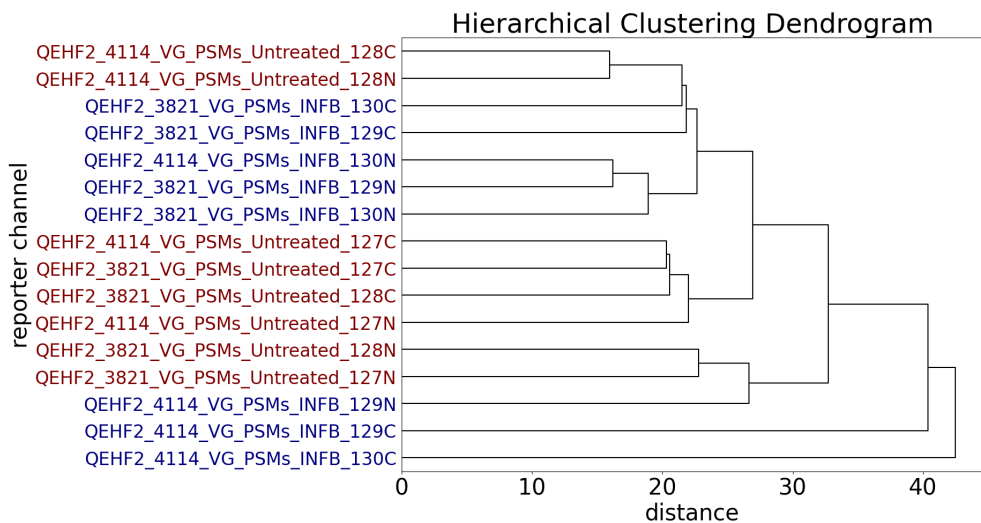
### 2.1 Experimental setup schema

MS run	INFB	Untreated
QEHF2_3821_VG_PSMs	['QEHF2_3821_VG_PSMs_INFB_129N',	['QEHF2_3821_VG_PSMs_U
	'QEHF2_3821_VG_PSMs_INFB_129C',	'QEHF2_3821_VG_PSMs_U
	'QEHF2_3821_VG_PSMs_INFB_130N',	'QEHF2_3821_VG_PSMs_U
	'QEHF2_3821_VG_PSMs_INFB_130C']	'QEHF2_3821_VG_PSMs_U
QEHF2_4114_VG_PSMs	['QEHF2_4114_VG_PSMs_INFB_129N',	['QEHF2_4114_VG_PSMs_U
	'QEHF2_4114_VG_PSMs_INFB_129C',	'QEHF2_4114_VG_PSMs_U
	'QEHF2_4114_VG_PSMs_INFB_130N',	'QEHF2_4114_VG_PSMs_U
	'QEHF2_4114_VG_PSMs_INFB_130C']	'QEHF2_4114_VG_PSMs_U

### 2.2 Principal components analysis plot

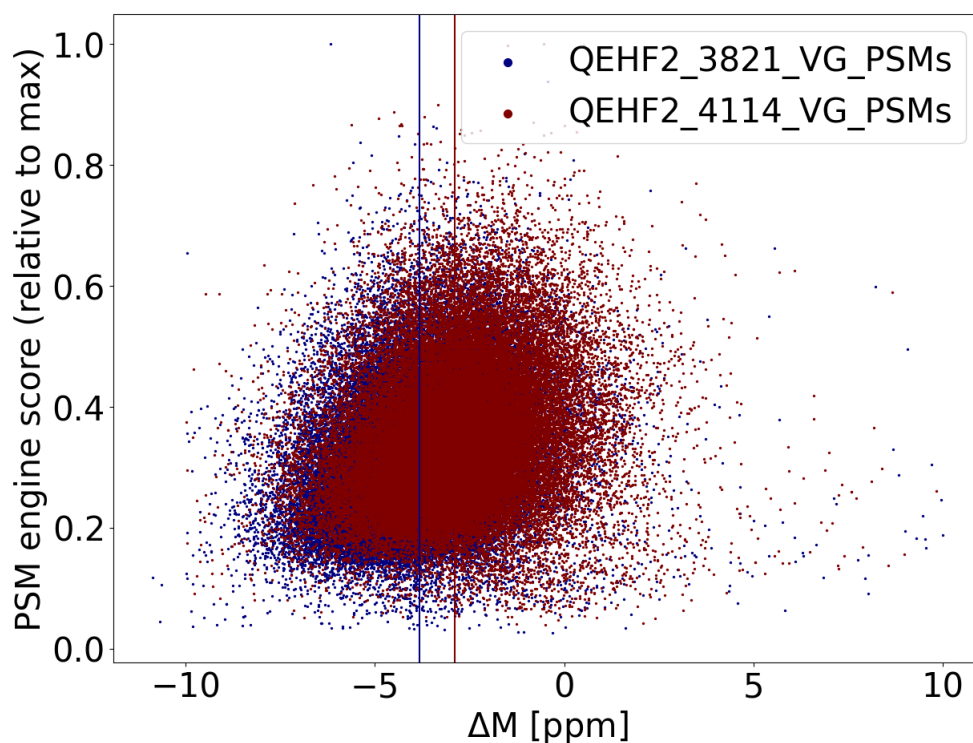


### 2.3 Hierarchical clustering dendrogram



## 2.3 Miscellaneous

### 2.3.1 MS1 calibration plot



### 2.3.2 MS1 Intensity histogram

(No MS1 Intensity information available)

### 2.3.3 Other QC info

peptides(\*) means non-redundant, possibly modified peptides

- Total number of peptides(\*) found = 34158
- Total number of unique (after protein grouping) peptides(\*) found = 31723
- Number of peptides(\*) found in all MS runs = 16419
- Number of peptides(\*) not found in all MS runs = 17739
- Number of proteins in the minimal expression result = 4928
- Number of PSMs detected and effectively used (i.e. after cleaning and removing PSM Engine redundancy):

	detected	used
<b>QEHF2_3821_VG_PSMs</b>	56867	45068
<b>QEHF2_4114_VG_PSMs</b>	50160	39293

- Percentage of PSMs with too high Isolation interference (>30.0%):

<b>QEHF2_3821_VG_PSMs</b>	<b>QEHF2_4114_VG_PSMs</b>
20.4224	21.3904

- Injection time information:

	max num	max num below
<b>QEHF2_3821_VG_PSMs</b>	110 6231	38837
<b>QEHF2_4114_VG_PSMs</b>	110 7519	31774

- DeltaM [ppm] statistics:

	<b>max</b>	<b>mean</b>	<b>std</b>
<b>QEHF2_3821_VG_PSMs</b>	9.53	-3.80334	1.57187
<b>QEHF2_4114_VG_PSMs</b>	9.82	-2.8783	1.76881

- MS2 intensity statistics:
  - QEHF2\_3821\_VG\_PSMs

	<b>max</b>	<b>mean</b>	<b>std</b>
<b>QEHF2_3821_VG_PSMs_INFB_129N</b>	4892.0	372.169929	298.927023
<b>QEHF2_3821_VG_PSMs_INFB_129C</b>	4627.5	351.893872	276.193856
<b>QEHF2_3821_VG_PSMs_INFB_130N</b>	4121.1	368.277904	294.891101
<b>QEHF2_3821_VG_PSMs_INFB_130C</b>	5675.6	321.620365	265.142201
<b>QEHF2_3821_VG_PSMs_Untreated_127N</b>	3464.0	317.535763	251.717542
<b>QEHF2_3821_VG_PSMs_Untreated_127C</b>	4784.6	377.509936	309.444871
<b>QEHF2_3821_VG_PSMs_Untreated_128N</b>	4652.6	341.934543	277.595271
<b>QEHF2_3821_VG_PSMs_Untreated_128C</b>	4764.4	427.261306	327.249858

- QEHF2\_4114\_VG\_PSMs

	<b>max</b>	<b>mean</b>	<b>std</b>
<b>QEHF2_4114_VG_PSMs_INFB_129N</b>	5082.0	243.380171	207.942294
<b>QEHF2_4114_VG_PSMs_INFB_129C</b>	3799.6	242.924792	207.954209
<b>QEHF2_4114_VG_PSMs_INFB_130N</b>	4018.6	236.017569	204.176522
<b>QEHF2_4114_VG_PSMs_INFB_130C</b>	2927.8	224.651112	179.703780
<b>QEHF2_4114_VG_PSMs_Untreated_127N</b>	4898.1	235.473661	193.931393
<b>QEHF2_4114_VG_PSMs_Untreated_127C</b>	3456.8	226.352696	186.853533
<b>QEHF2_4114_VG_PSMs_Untreated_128N</b>	4543.0	253.046798	201.418506
<b>QEHF2_4114_VG_PSMs_Untreated_128C</b>	4012.5	264.926095	206.254875

### 3 Log

- QCQuan version = 0.10.2
- date = 2023-12-08 14:19:59
- job duration = 178s

INFO:root:Starting processing of MSRun 'QEHF2\_3821\_VG\_PSMs' of job 'Test3' at 2023-12-08 14:20:37

WARNING:root:Column 'Intensity' was not found. Not gathering MS1 intensity QC info.

WARNING:root:Some PSMs have been removed from the workflow due to missing values: see removedData['missing'].

WARNING:root:Not all necessary columns found (see below); Adding 'Protein Descriptions' column with all empty strings.

Missing: Protein Descriptions

WARNING:root:Column 'Intensity' was not found. Not gathering MS1 intensity QC info.

WARNING:root:No PTM aggregation done.

INFO:root:Finished processing of MSRun 'QEHF2\_3821\_VG\_PSMs' of job 'Test3' at 2023-12-08 14:21:21

INFO:root:Starting processing of MSRun 'QEHF2\_4114\_VG\_PSMs' of job 'Test3' at 2023-12-08 14:21:21

WARNING:root:Column 'Intensity' was not found. Not gathering MS1 intensity QC info.

WARNING:root:Some PSMs have been removed from the workflow due to missing values: see removedData['missing'].

WARNING:root:Not all necessary columns found (see below); Adding 'Protein Descriptions' column with all empty strings.

Missing: Protein Descriptions

WARNING:root:Column 'Intensity' was not found. Not gathering MS1 intensity QC info.

WARNING:root:No PTM aggregation done.

INFO:root:Finished processing of MSRun 'QEHF2\_4114\_VG\_PSMs' of job 'Test3' at 2023-12-08 14:21:59

INFO:root:Starting analysis of job: Test3 at 2023-12-08 14:21:59

WARNING:root:Entry 'MS1Intensities\_PSMs\_all' was not found for MSRun QEHF2\_3821\_VG\_PSMs. Not gathering ANY MS1 intensity QC info.

WARNING:root:Entry 'MS1Intensities\_PSMs\_all' was not found for MSRun QEHF2\_4114\_VG\_PSMs. Not gathering ANY MS1 intensity QC info.

INFO:root:Finished analysis of job: Test3 at 2023-12-08 14:23:27

INFO:root:Starting visualization and report generation of job: Test3 at 2023-12-08 14:23:27

WARNING:matplotlib.axes.\_axes:'c' argument looks like a single numeric RGB or RGBA sequence, which should be avoided as value-mapping will have precedence in case its length matches with 'x' & 'y'. Please use a 2-D array with a single row if you really want to specify the same RGB or RGBA value for all points.

WARNING:matplotlib.axes.\_axes:'c' argument looks like a single numeric RGB or RGBA sequence, which should be avoided as value-mapping will have precedence in case its length matches with 'x' & 'y'. Please use a 2-D array with a single row if you really want to specify the same RGB or RGBA value for all points.

WARNING:root:QC entry 'MS1Intensities\_PSMs\_all' was not found. Not producing MS1IntensityHist.