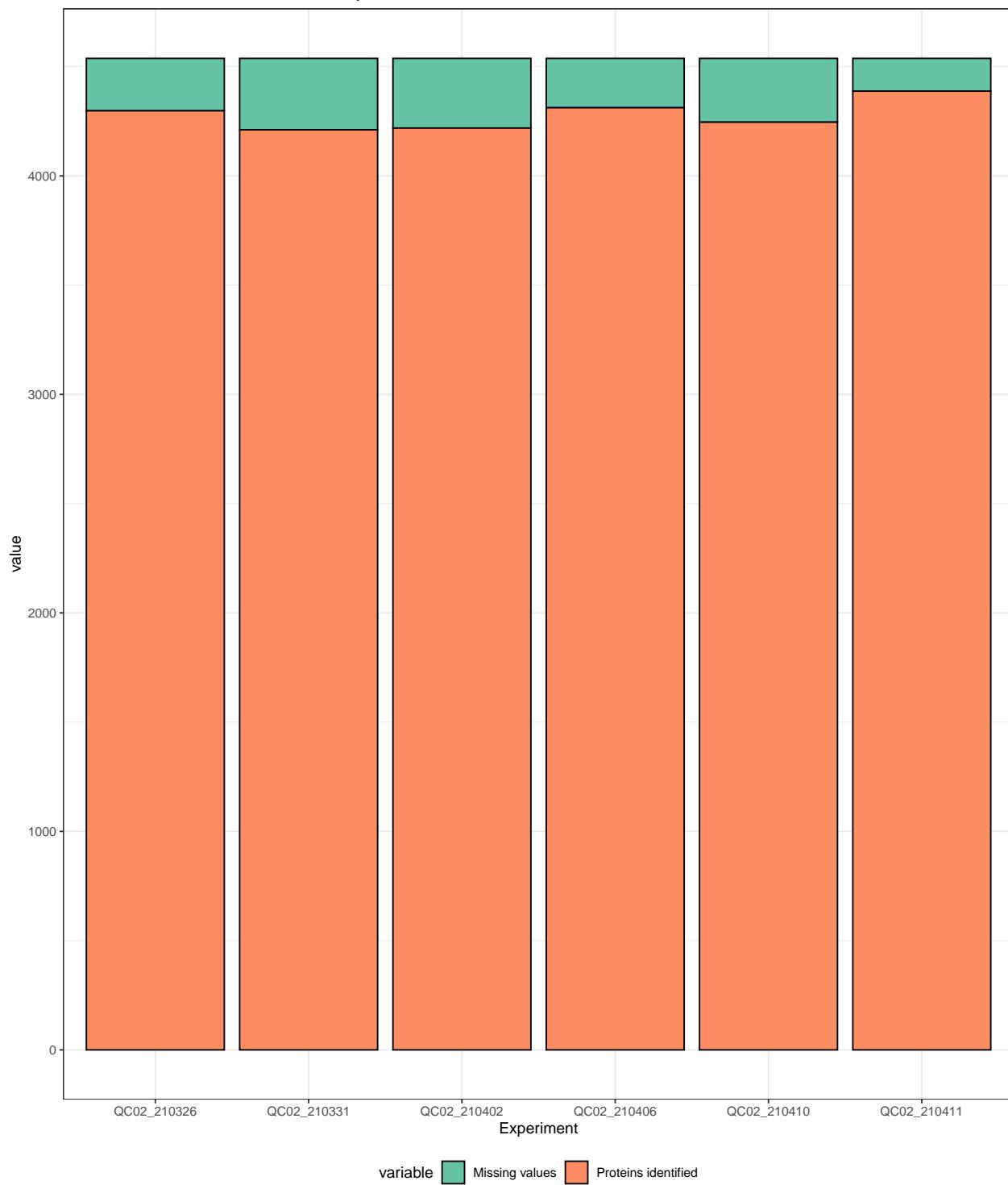


MQmetrics Report

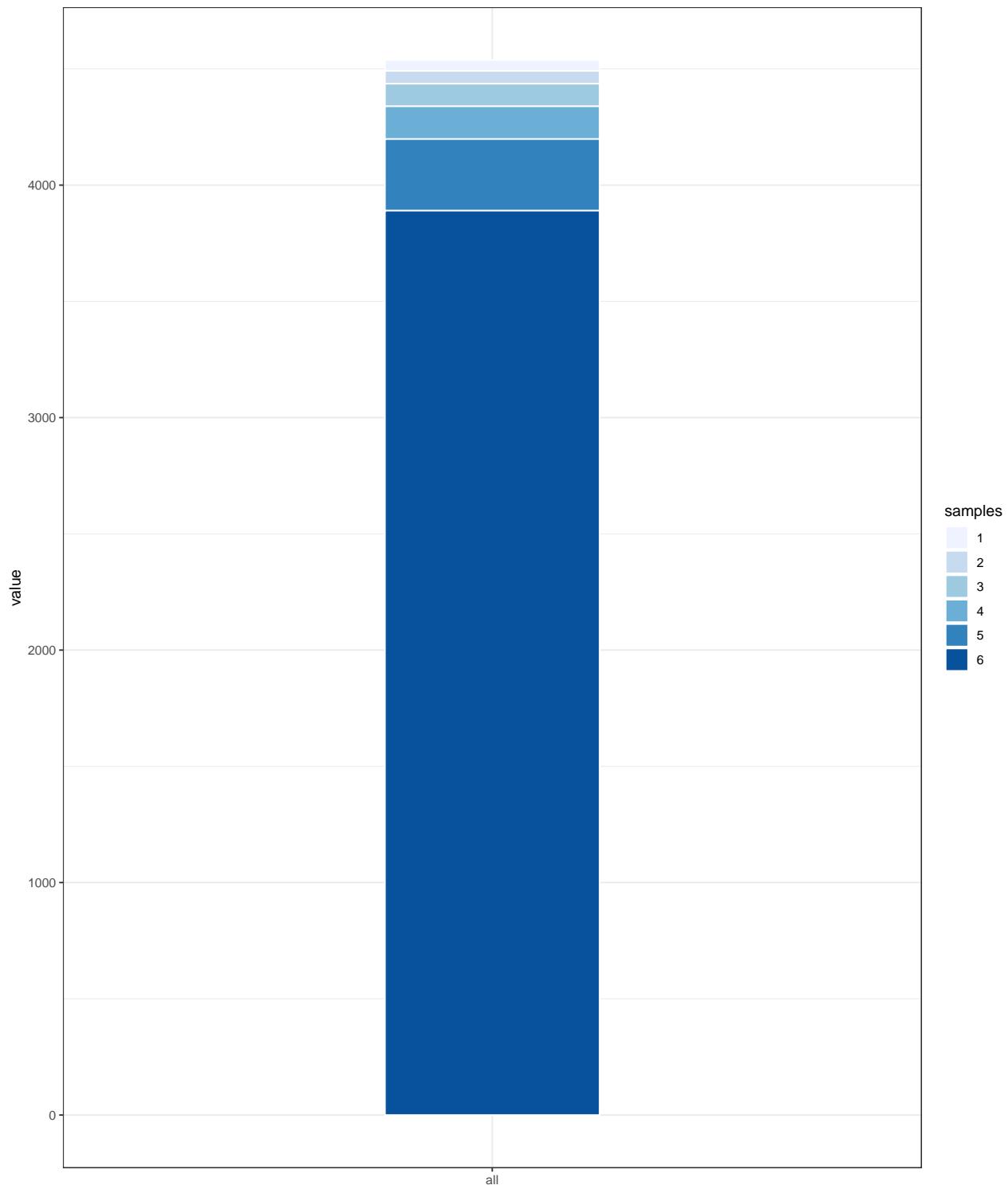
20 April, 2021

```
## [1] "The MaxQuant output directory is: /home/alvaro/R/x86_64-pc-linux-gnu-library/4.0/MQmetrics/extd
## [1] "The experiment started the day: 16/04/2021 at the time: 18:07:23."
## [1] "The whole experiment lasted: 02:15 (hours:minutes)."
## [1] "The MaxQuant version used was: 1.6.17.0"
## [1] "The user was: thomas.stehrer"
## [1] "The machine name was: FGU045PC004"
## [1] "The PSM FDR was: 0.01"
## [1] "The protein FDR was: 0.01"
## [1] "The match between runs was: True"
## [1] "The fasta file used was: C:\\MaxQuant_Databases\\iRT_peptides_Biognosys_irtfusion.fasta;C:\\Max
## [1] "The iBAQ presence is: False"
## [1] "The PTM selected is/are: Oxidation (M);Acetyl (Protein N-term)"
```

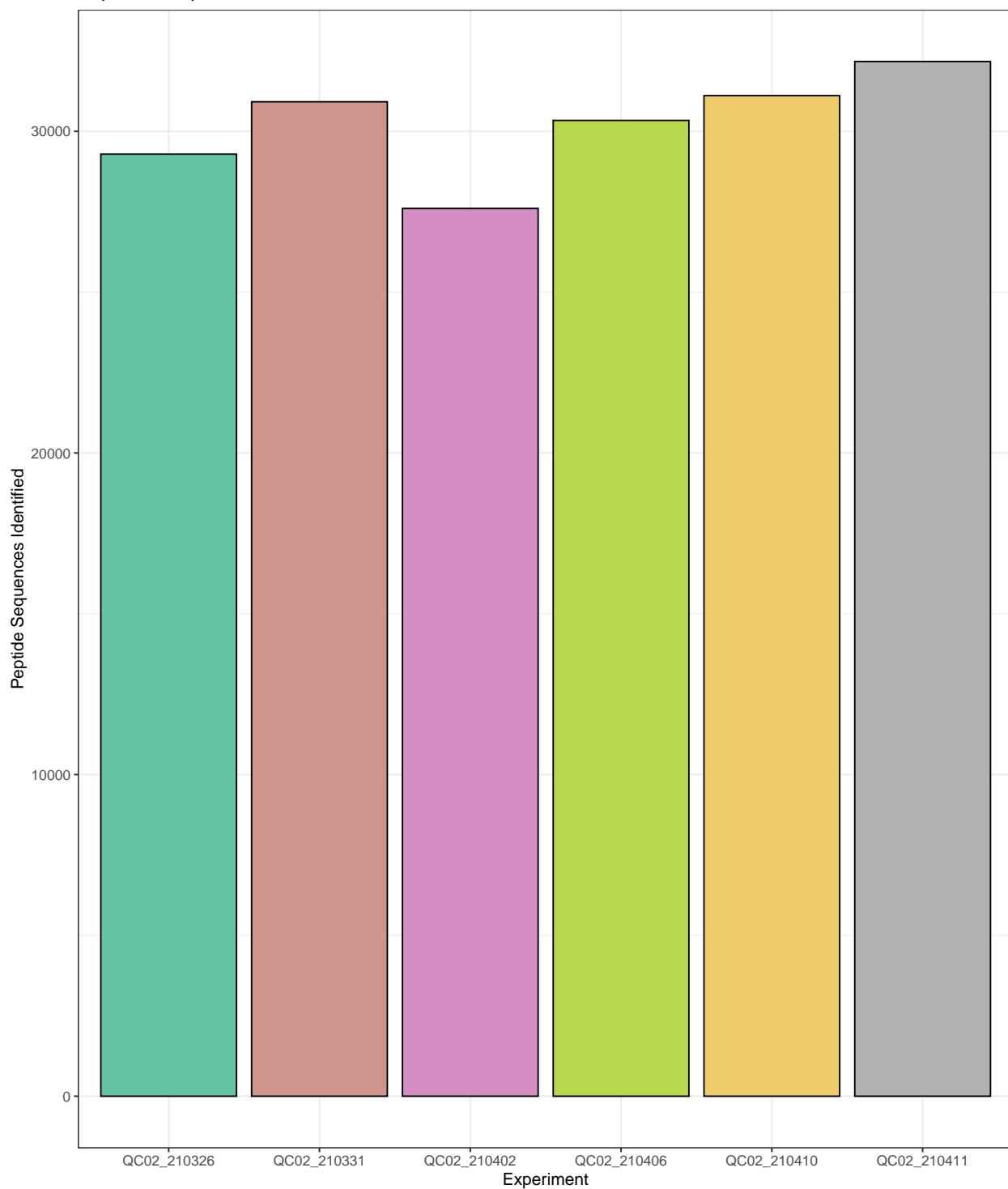
Proteins Identified based on Intensity



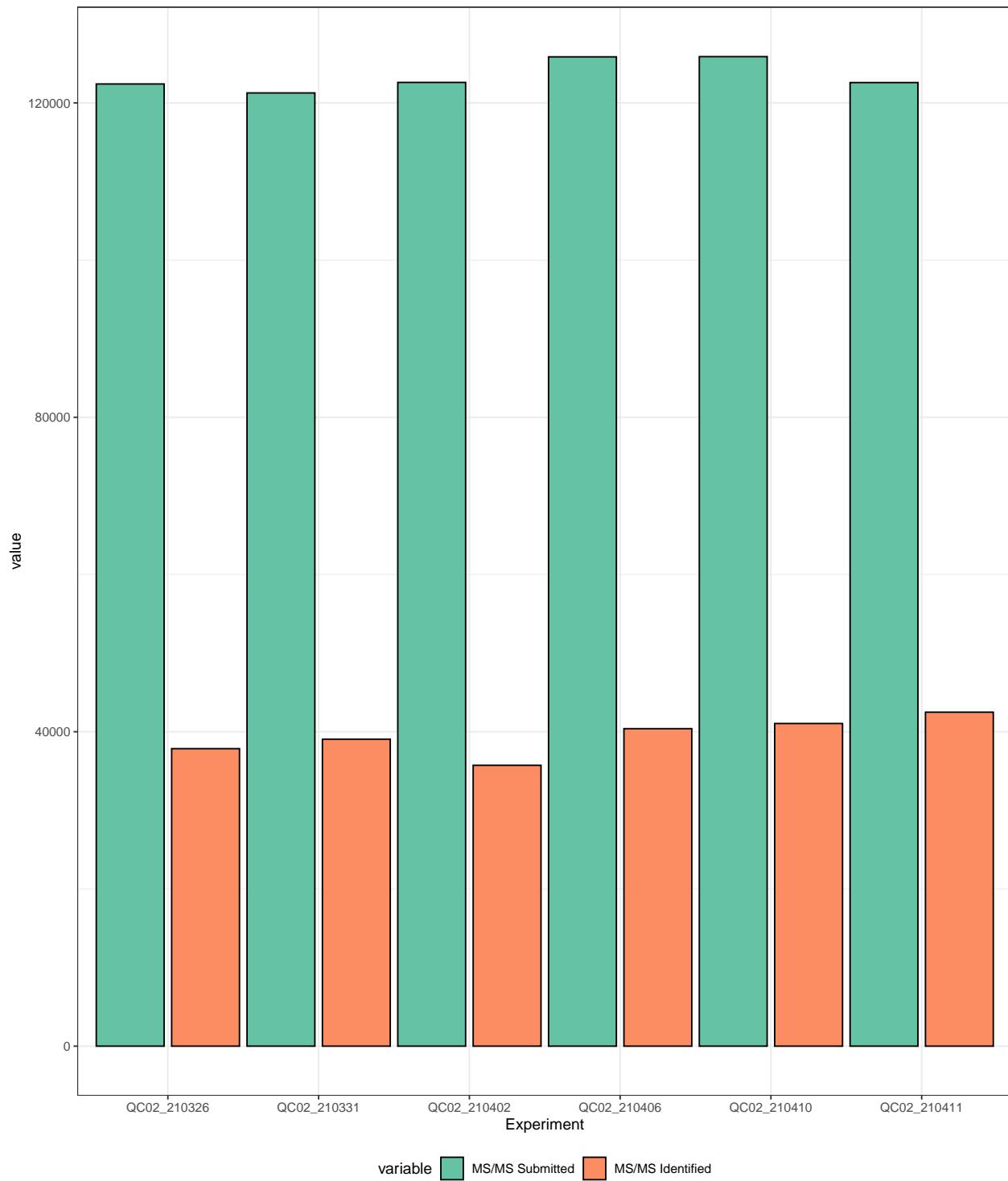
Protein Coverage of all samples



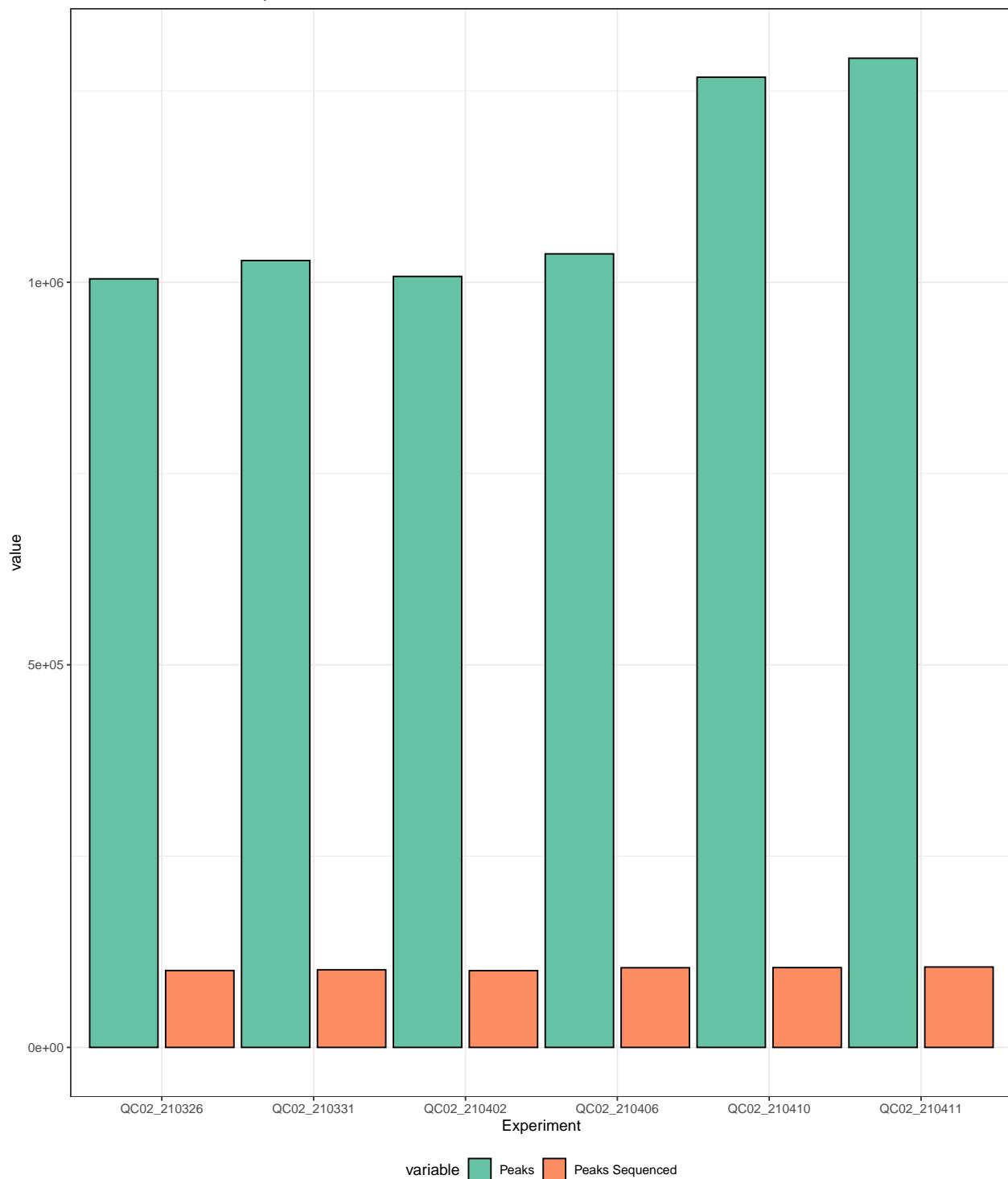
Peptides Sequences Identified



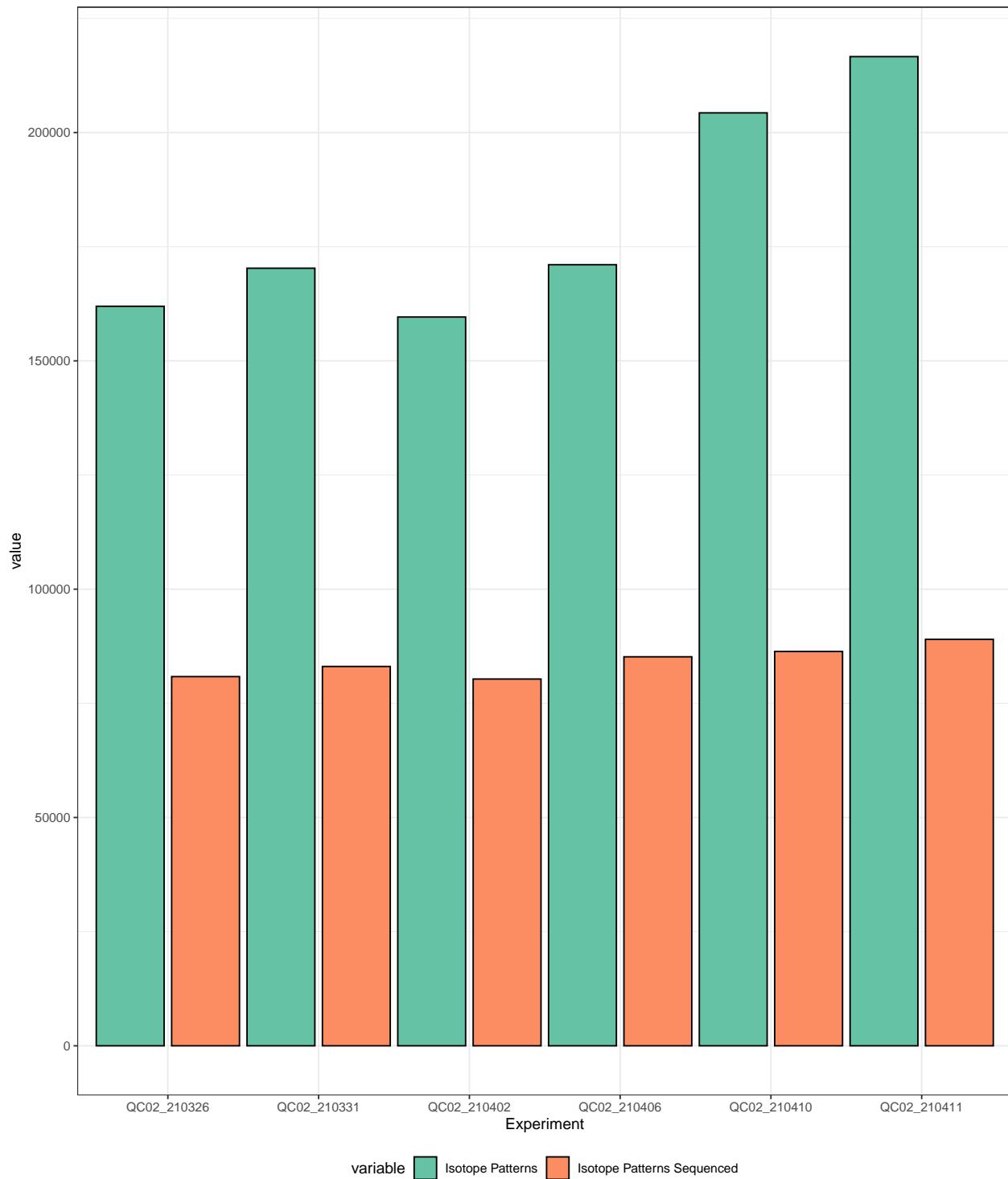
MS/MS Submitted and Identified



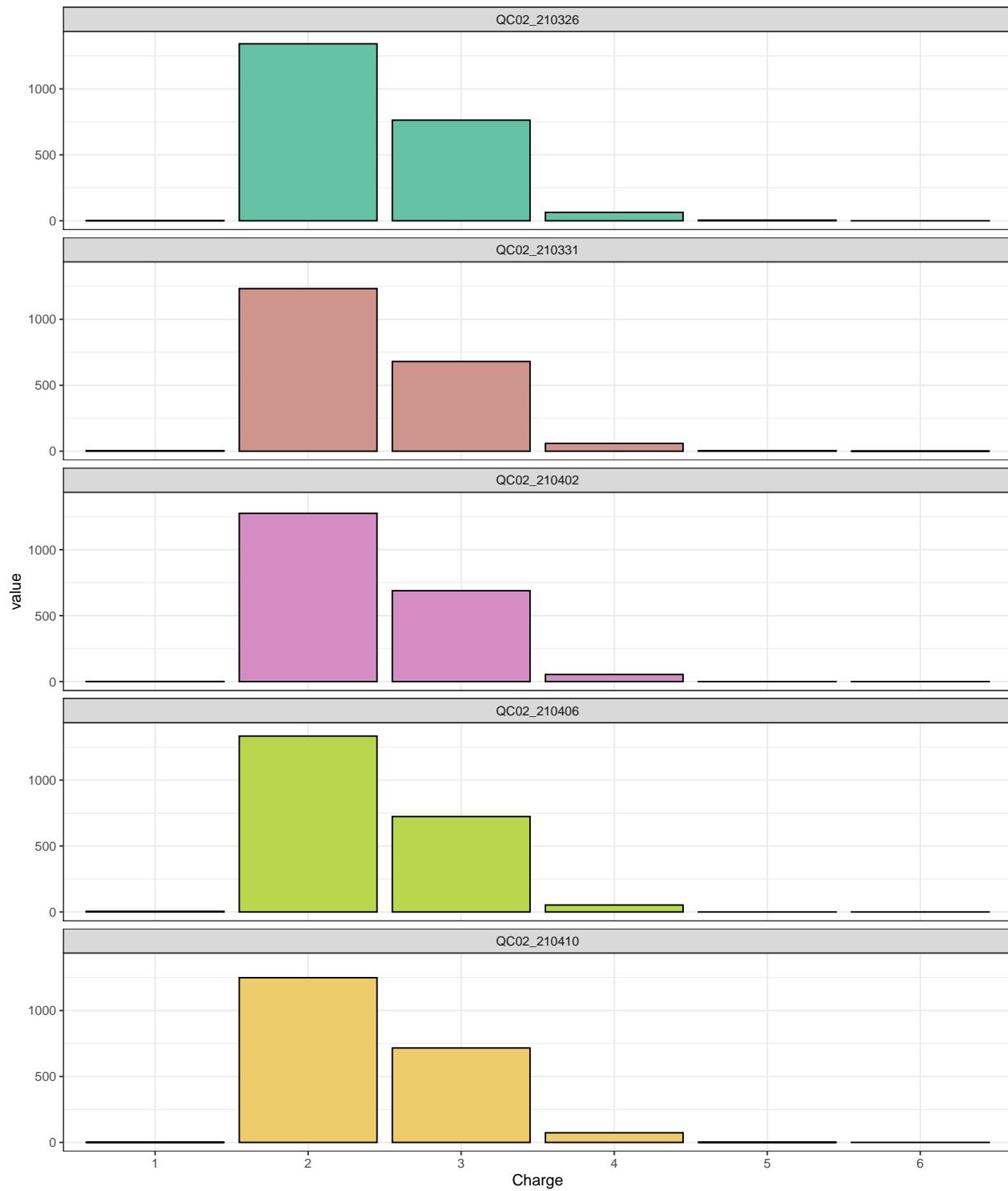
Peaks detected and sequenced in the full scans



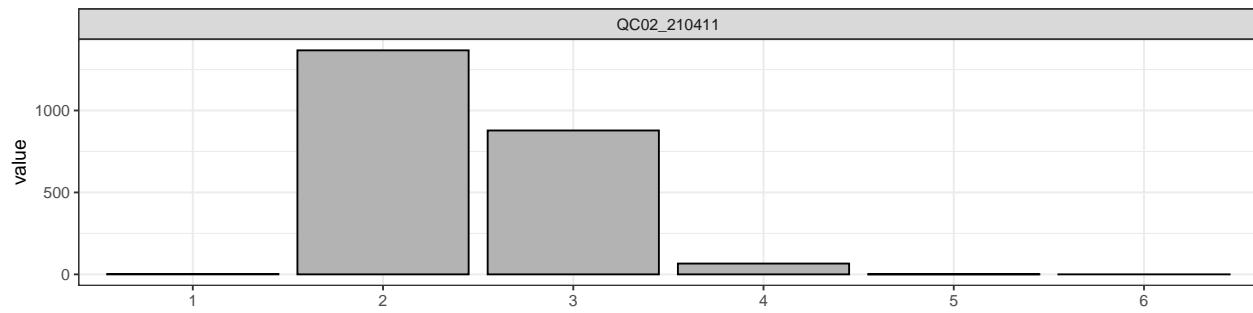
Isotope Patterns detected and sequenced



The charge-state of the precursor ion.



The charge-state of the precursor ion.

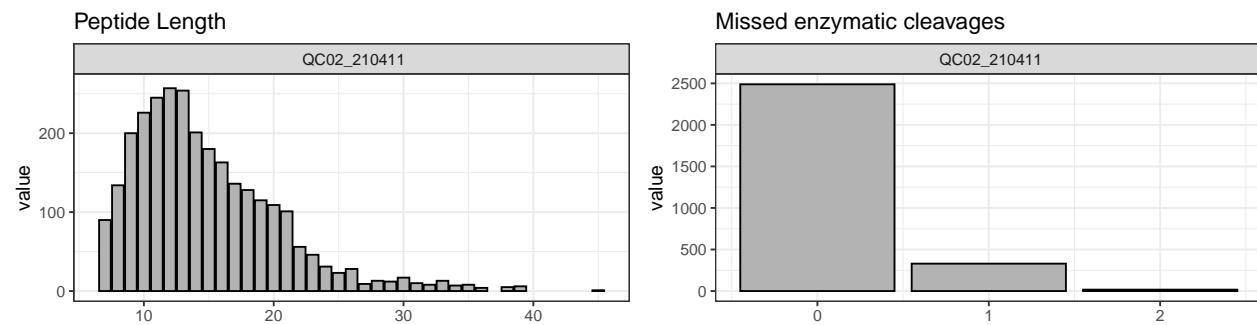


Charge

Protease Specificity



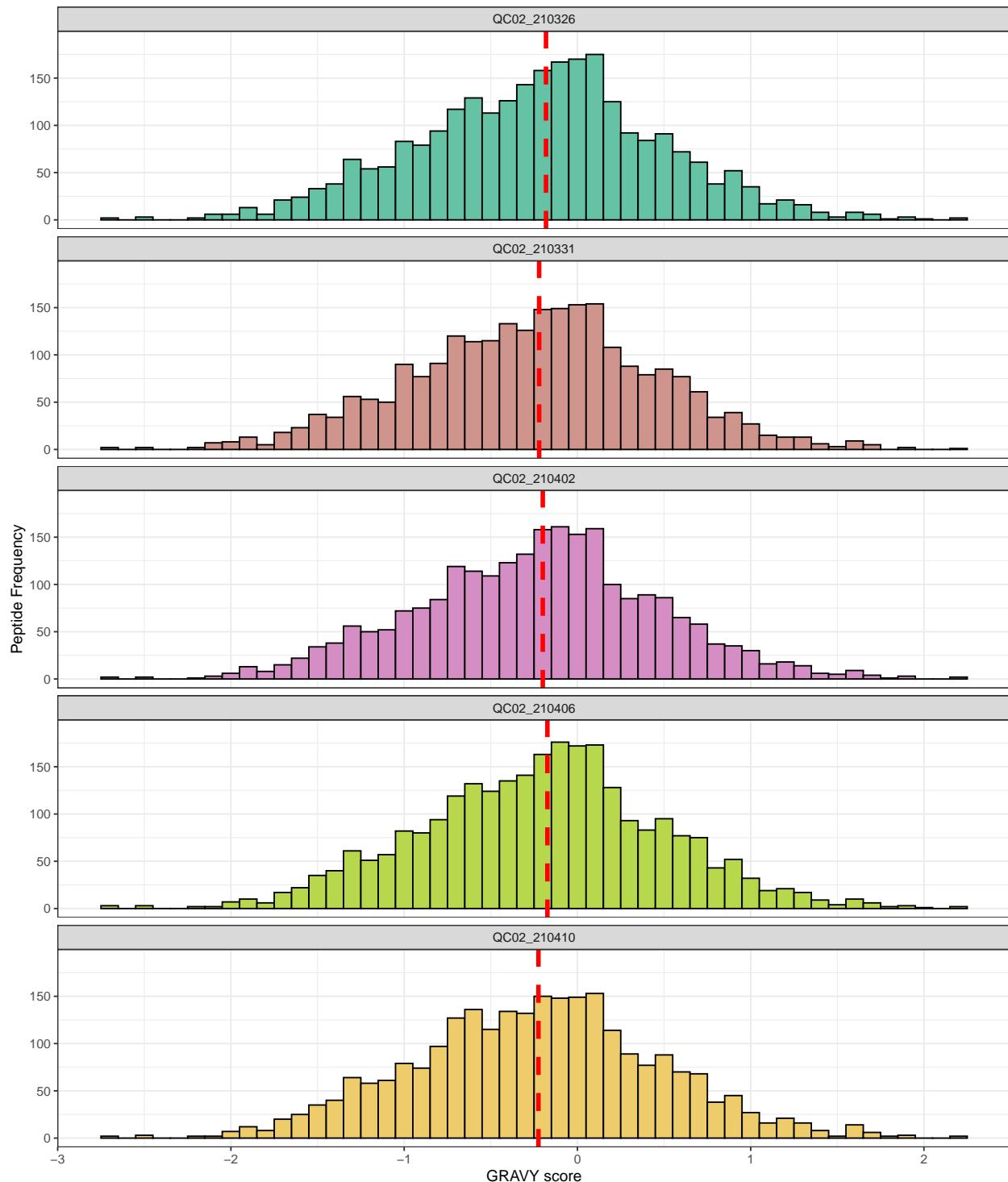
Protease Specificity



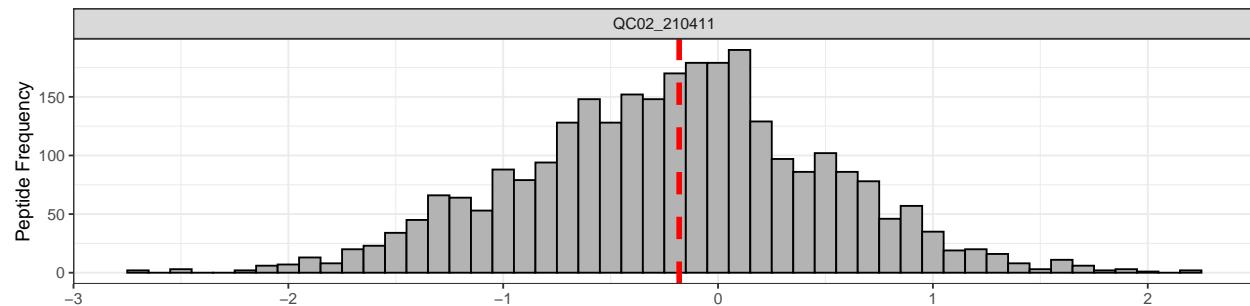
Peptide length

Missed Cleavages

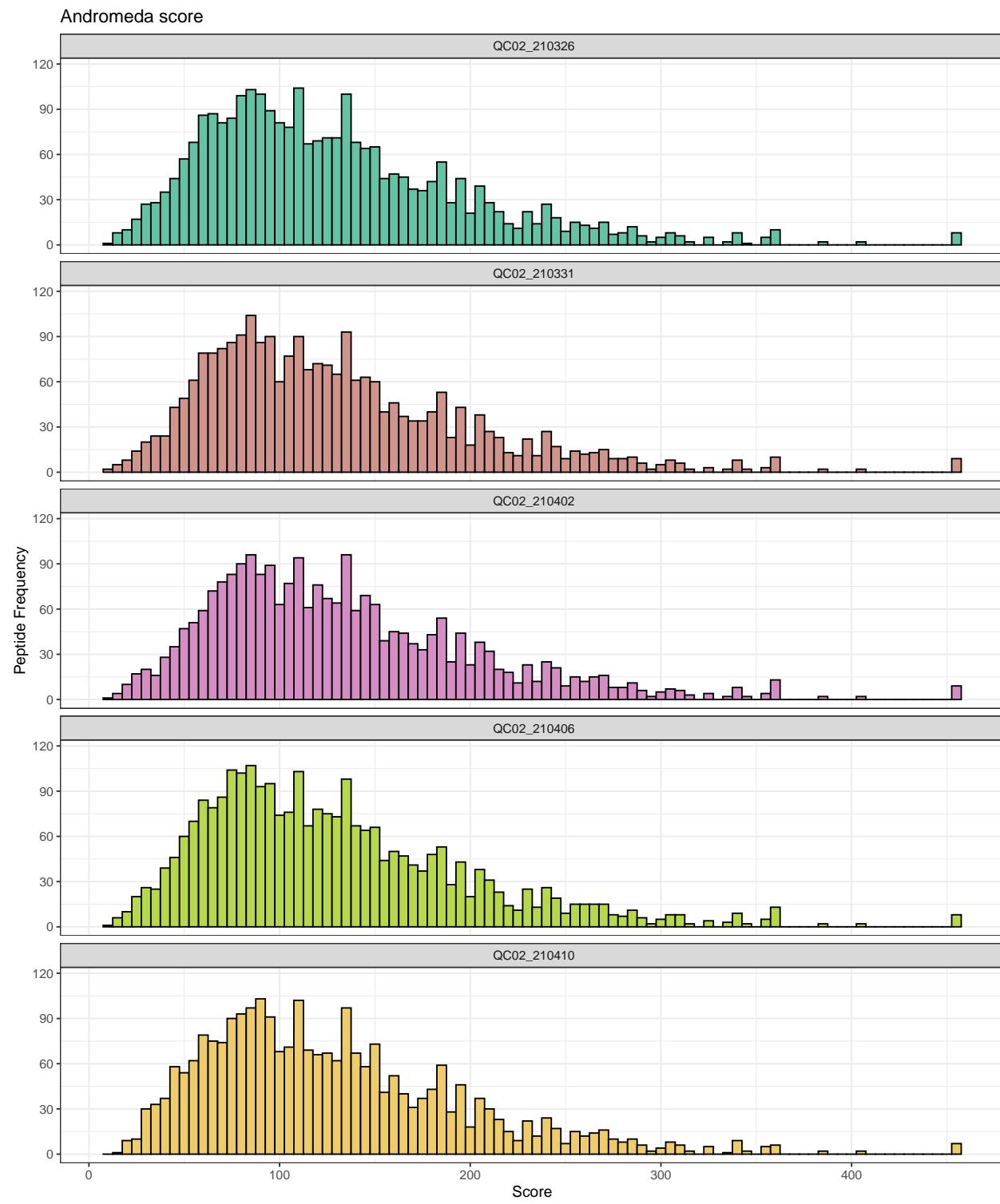
Peptide hydrophathy distribution

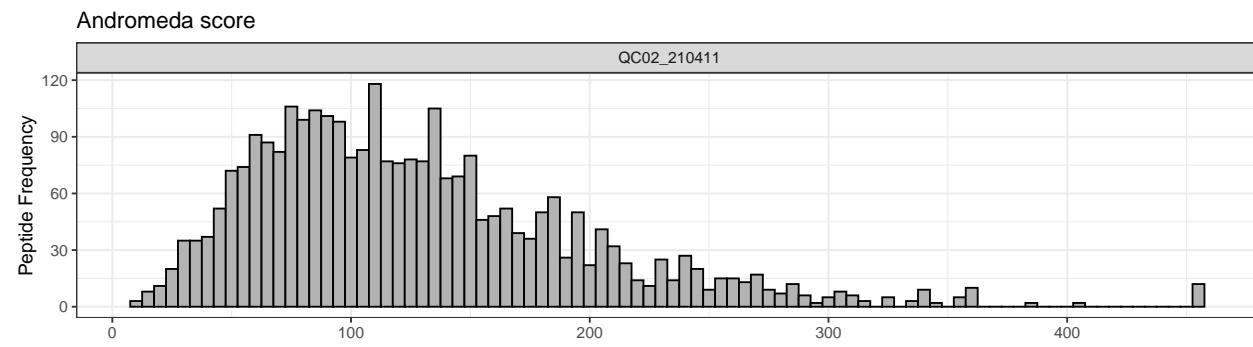


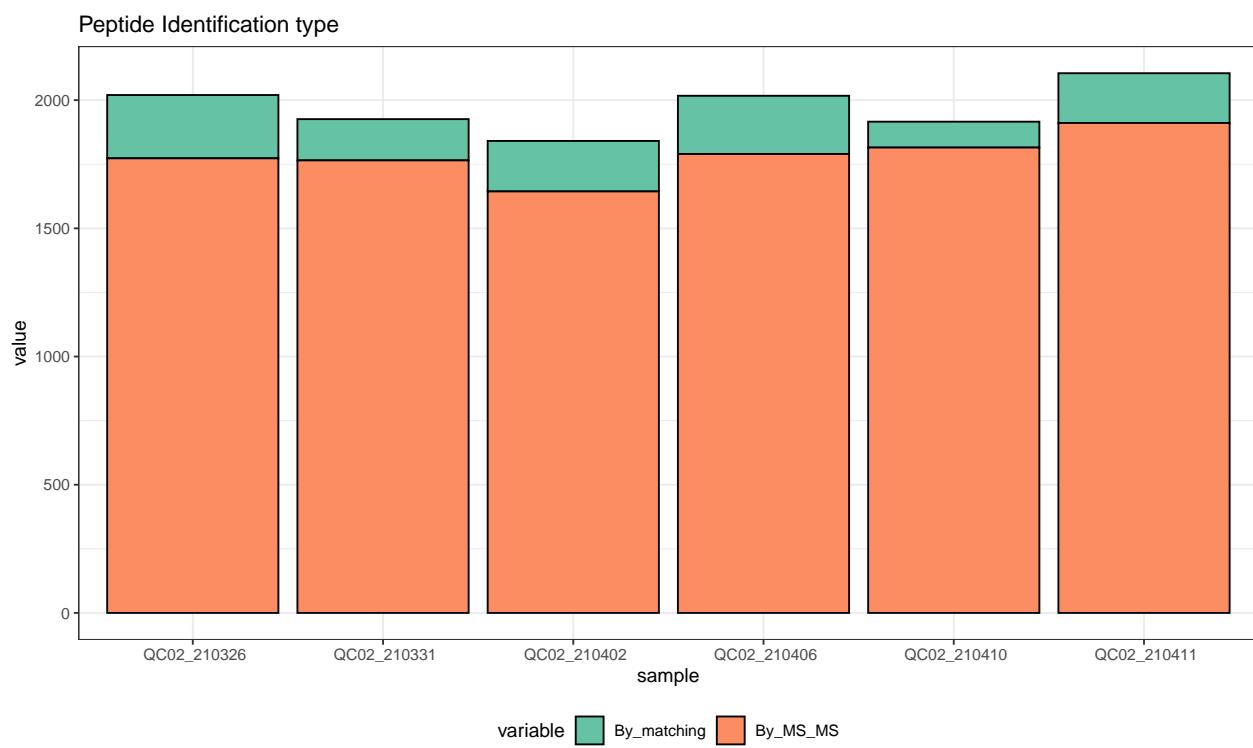
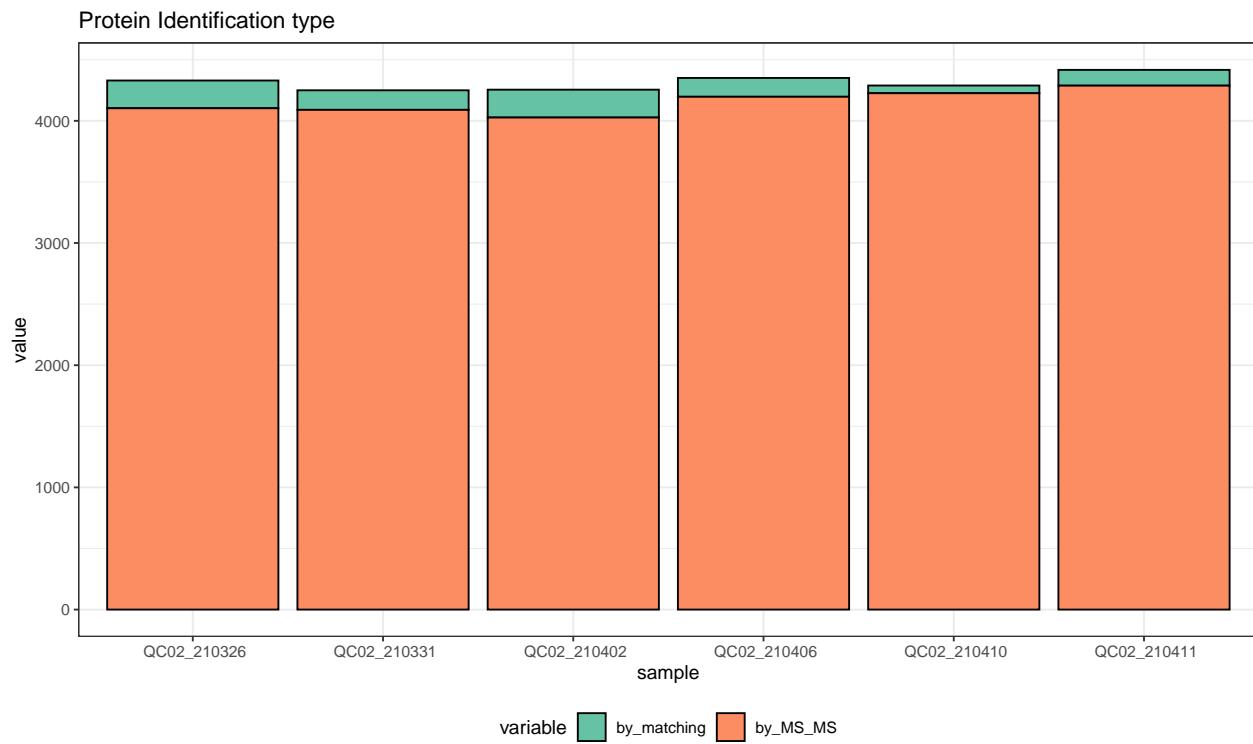
Peptide hydrophathy distribution



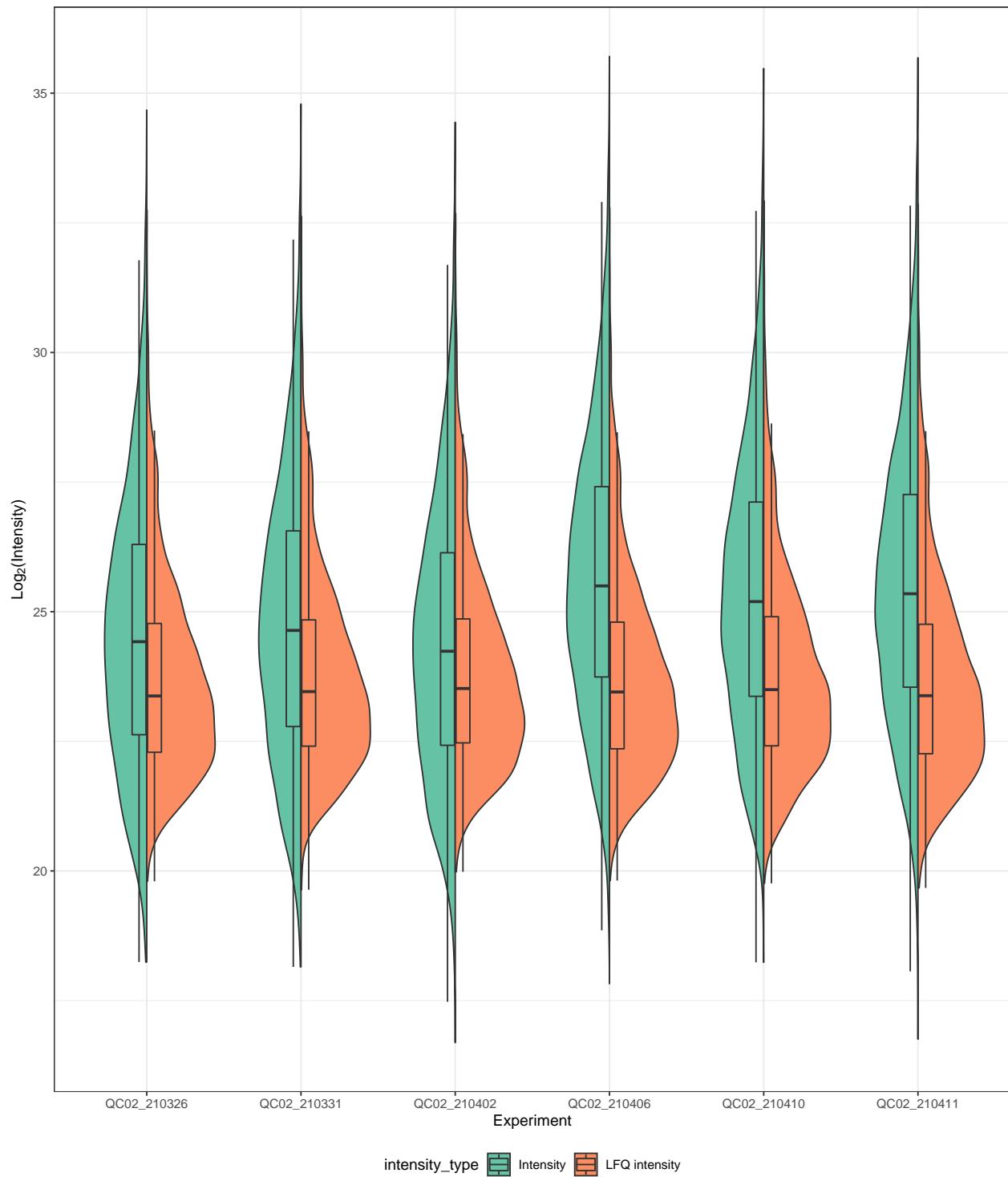
GRAVY score

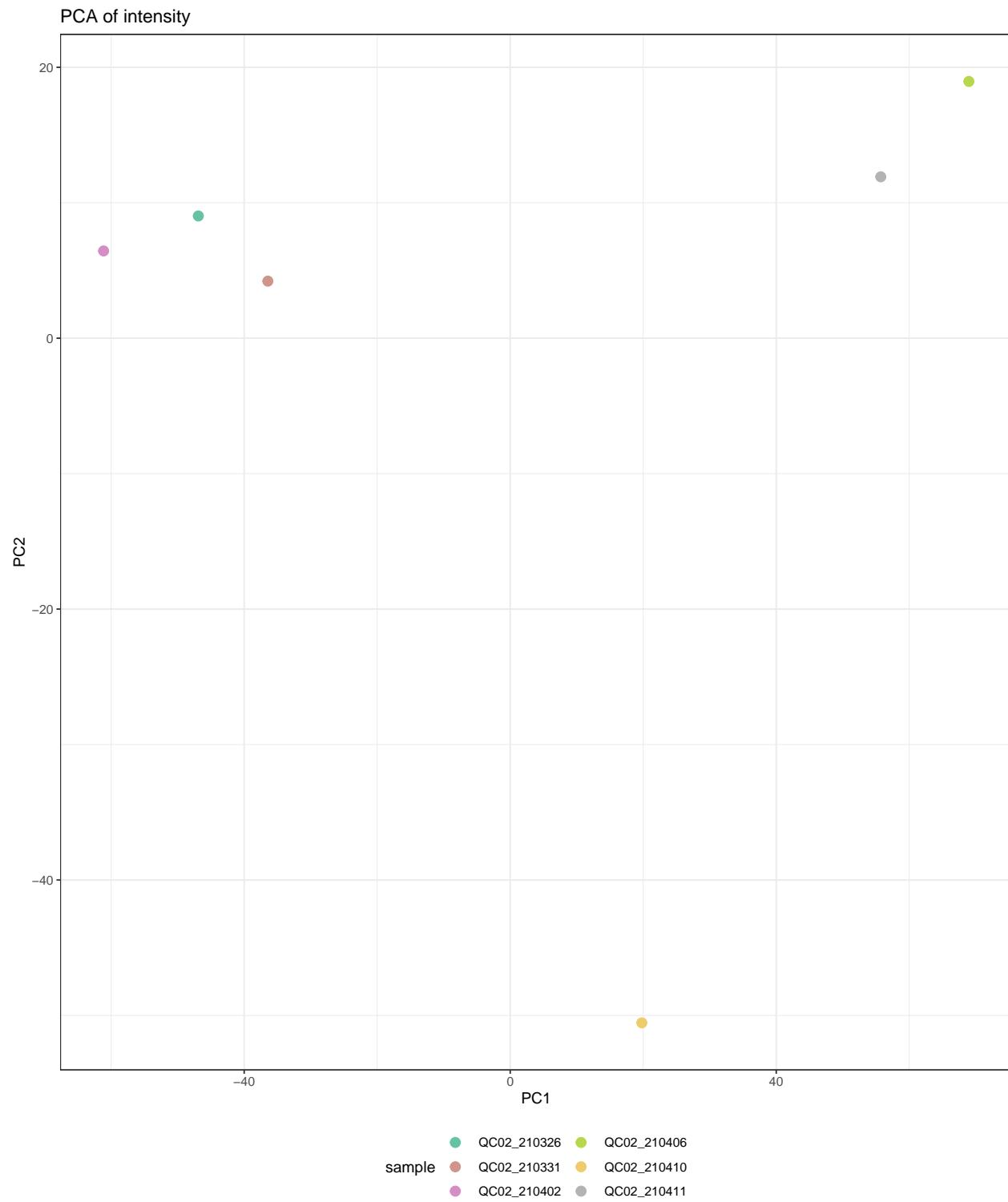




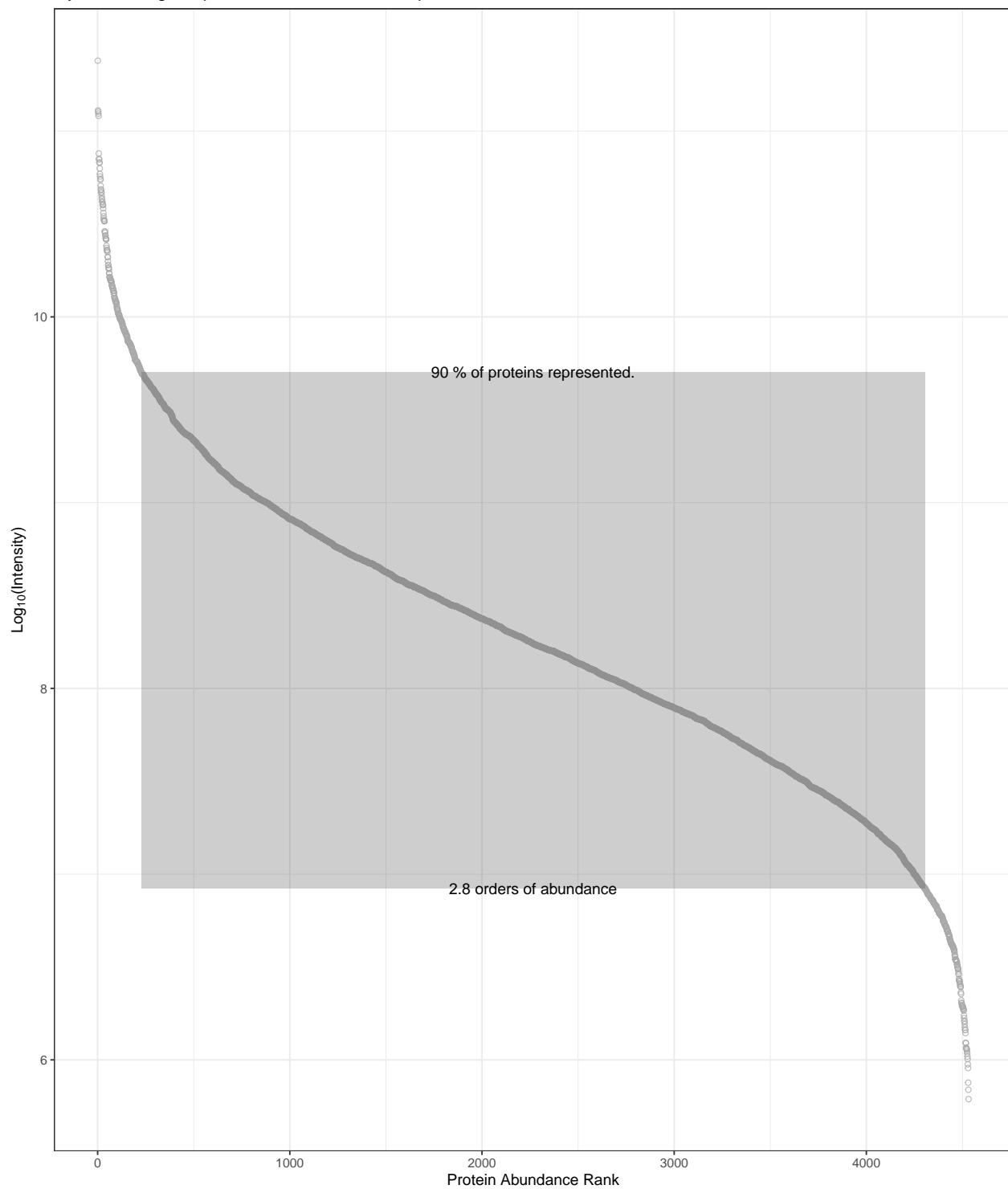


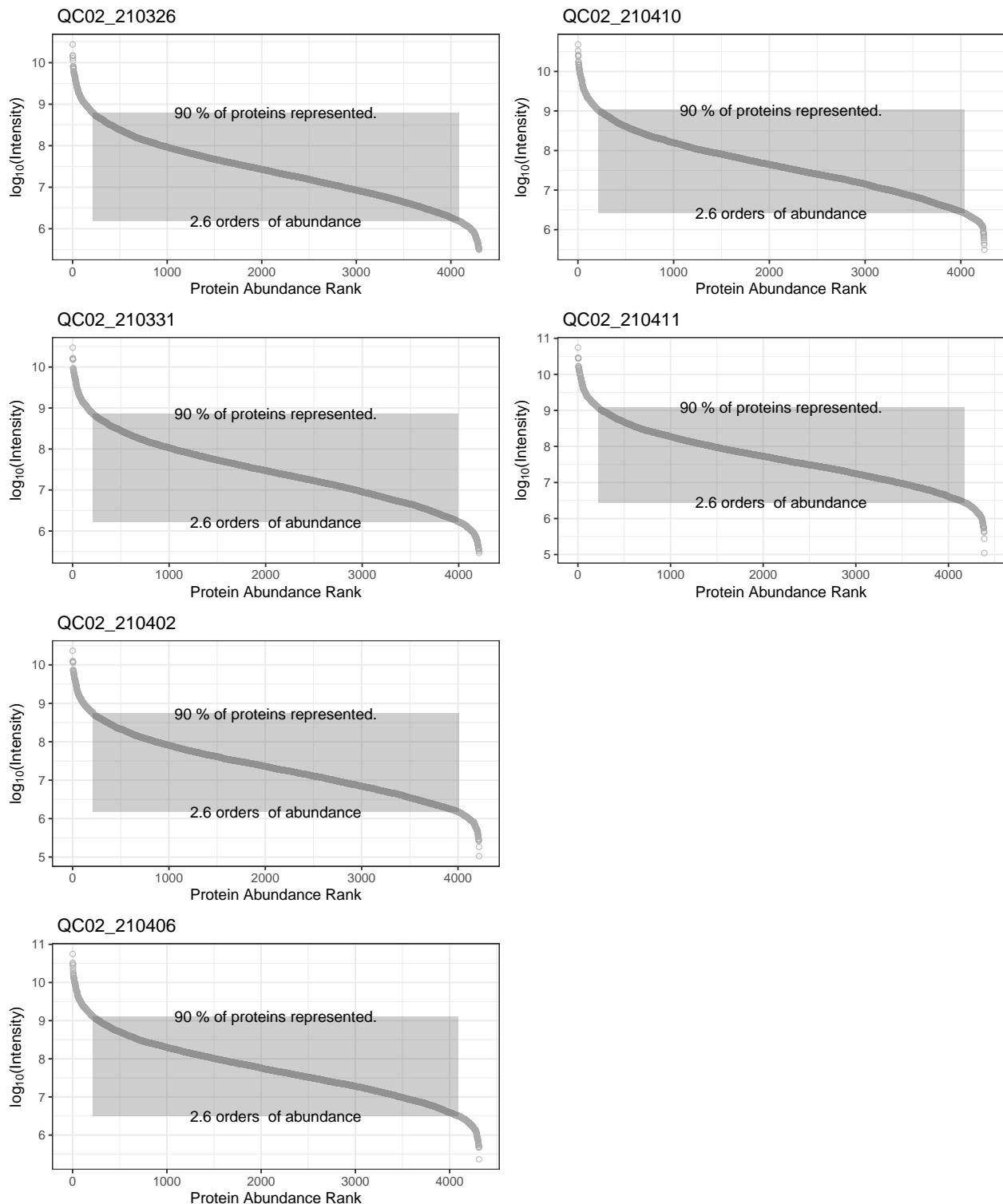
Protein Intensity & LFQ intensity





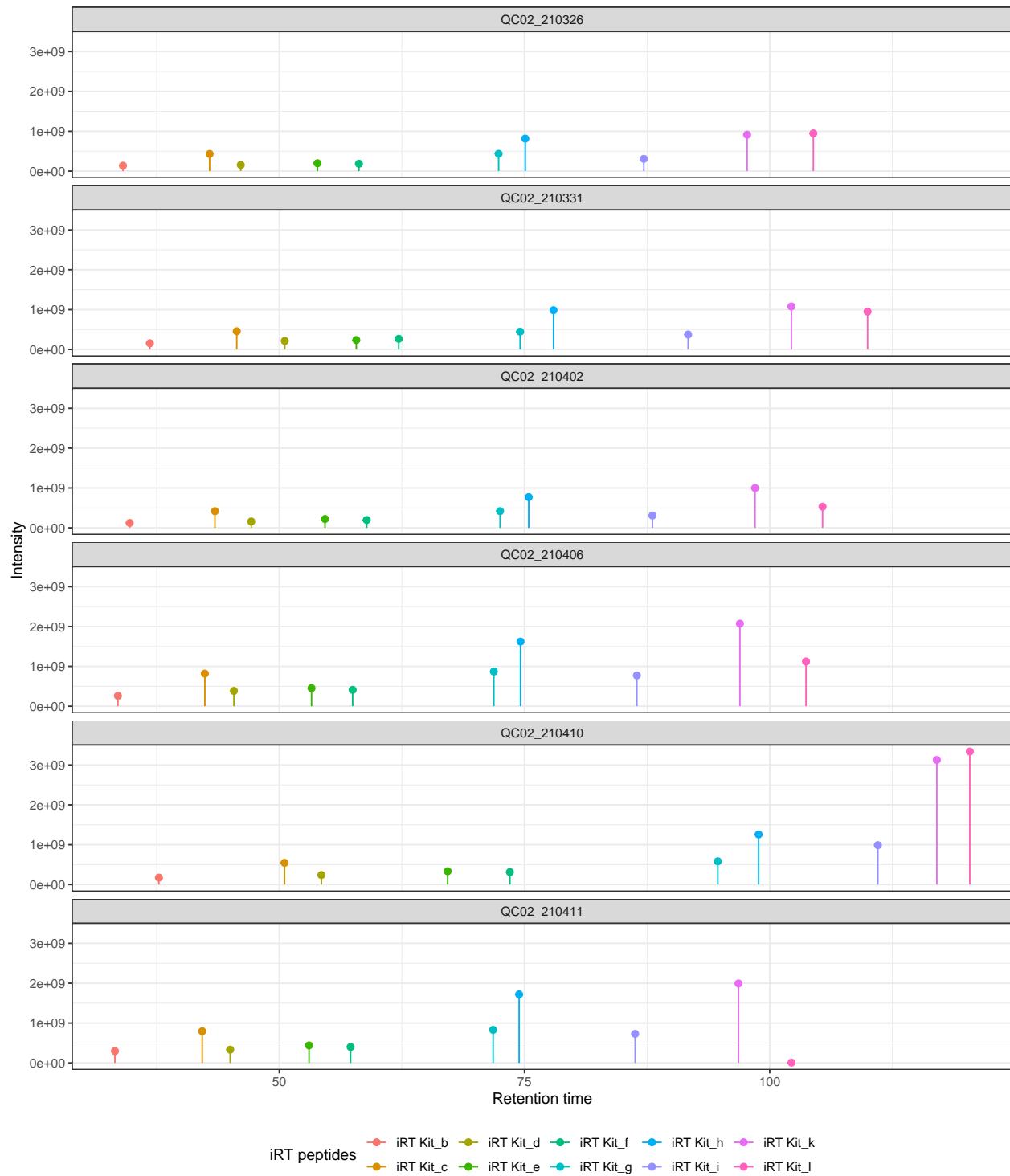
Dynamic range of protein abundance all samples



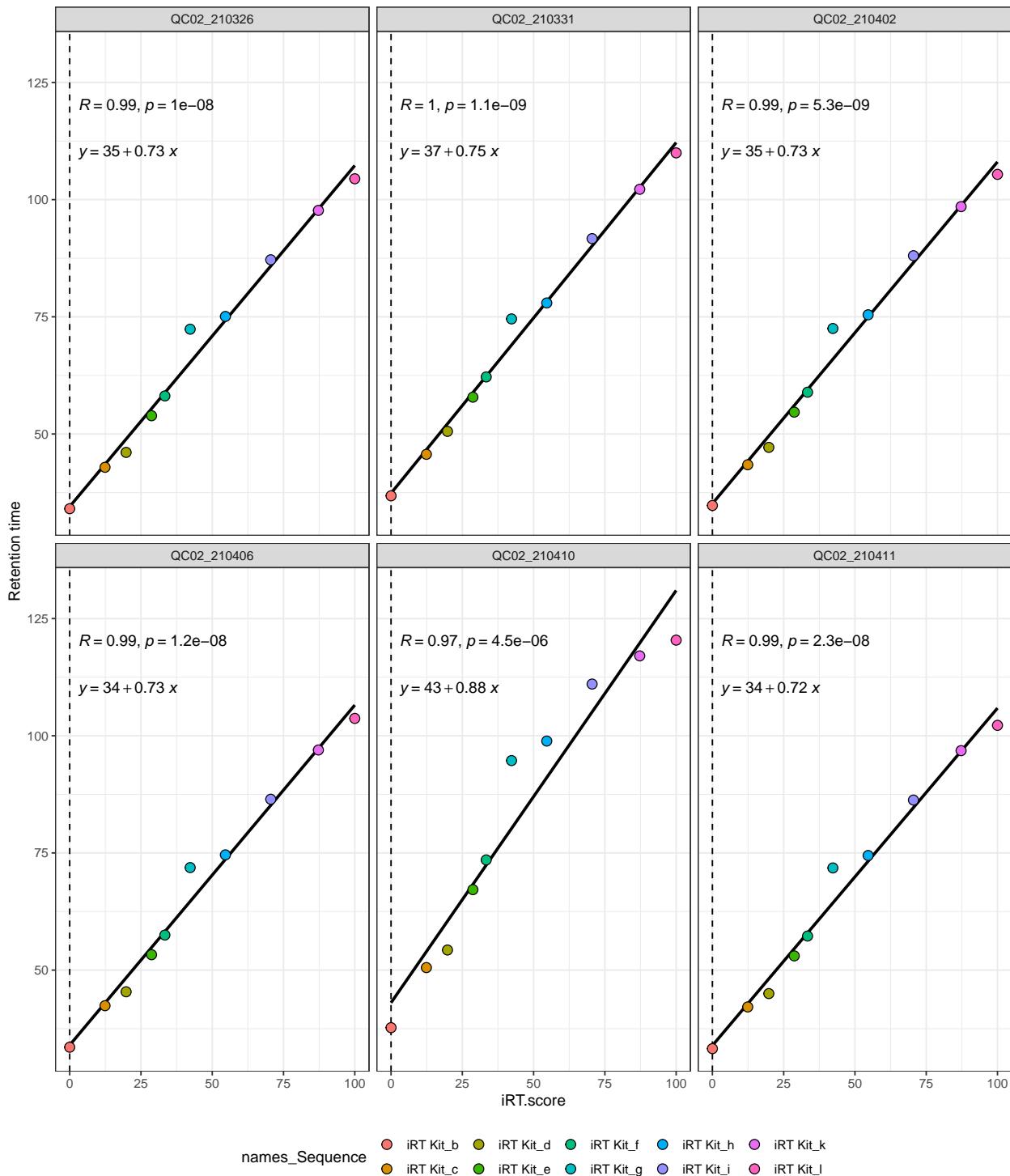


```
## [1] "No UniprotID provided."
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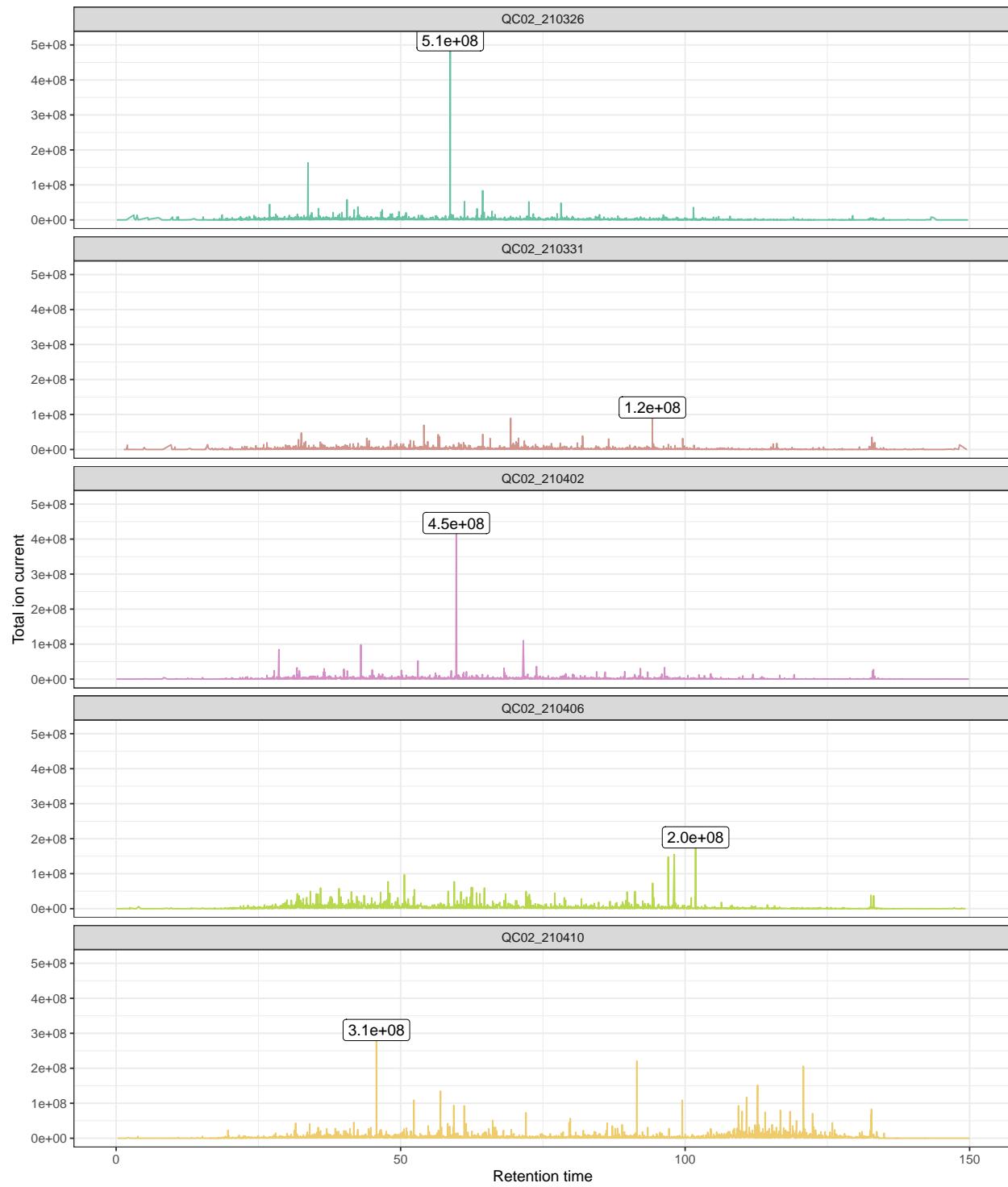
Biognosys iRT peptides in each sample.



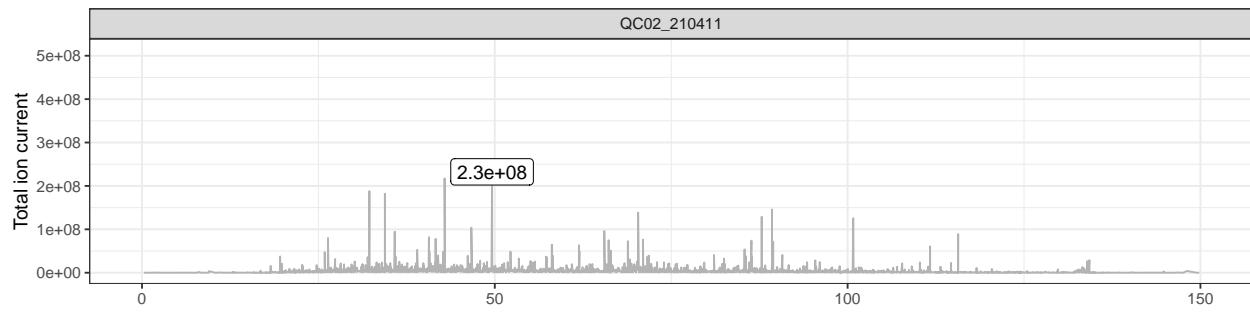
Retention time of the Biognosys iRT peptides.



Total Ion Current

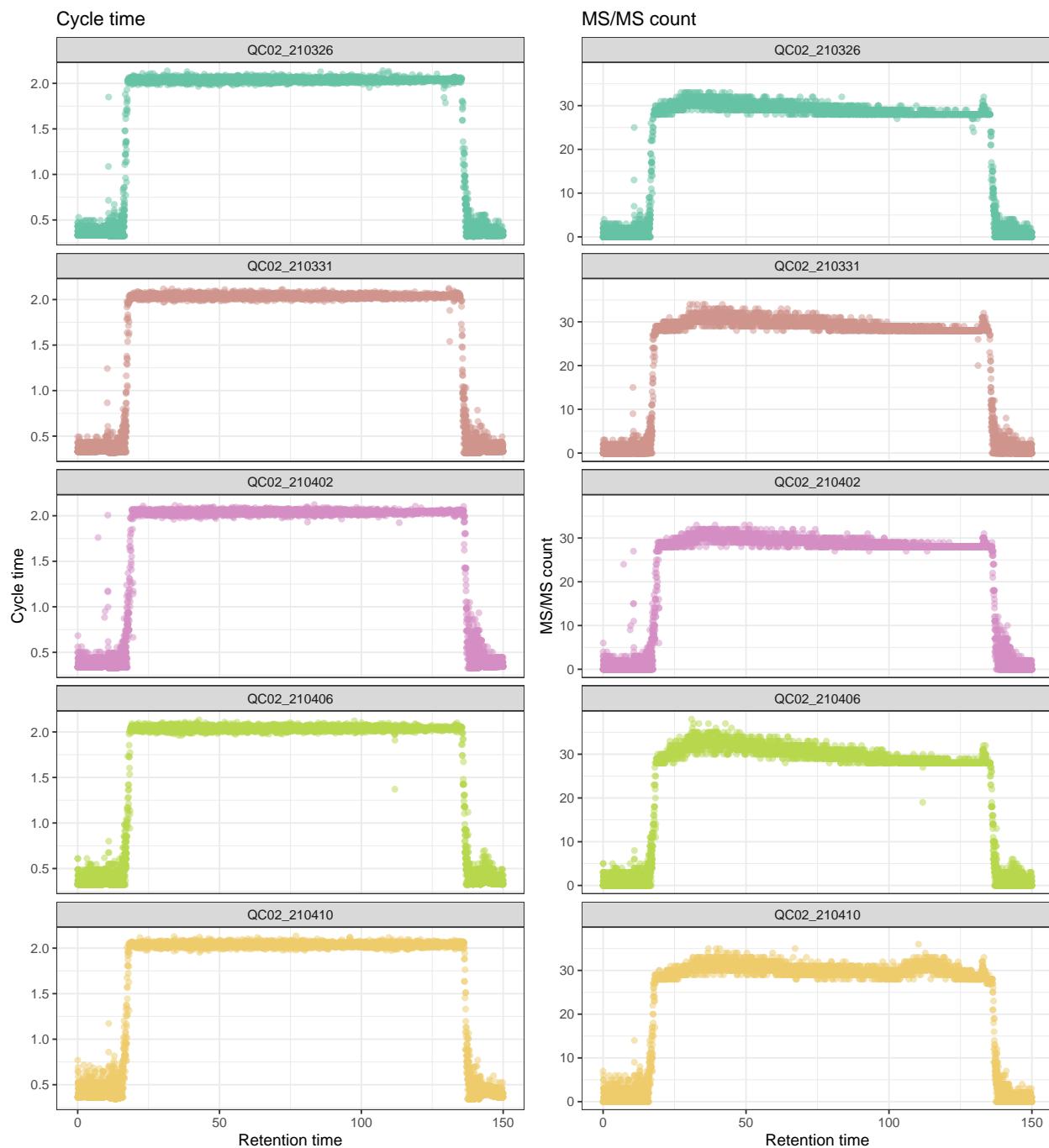


Total Ion Current

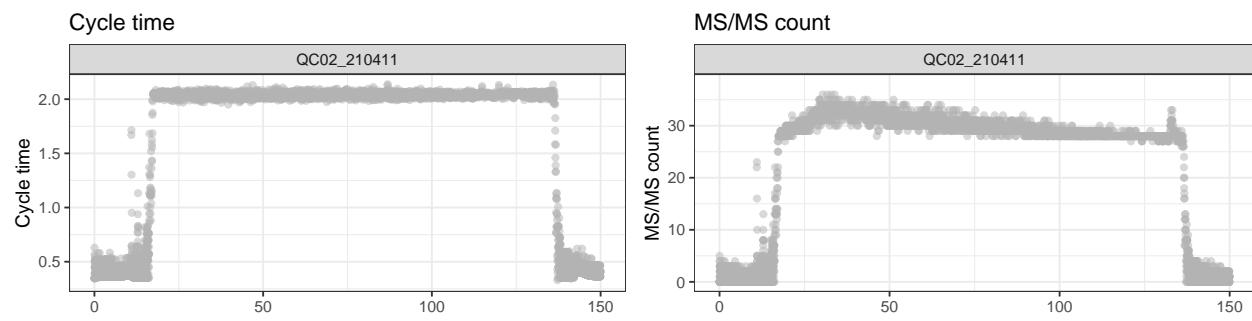


Retention time

Acquisition Cycle



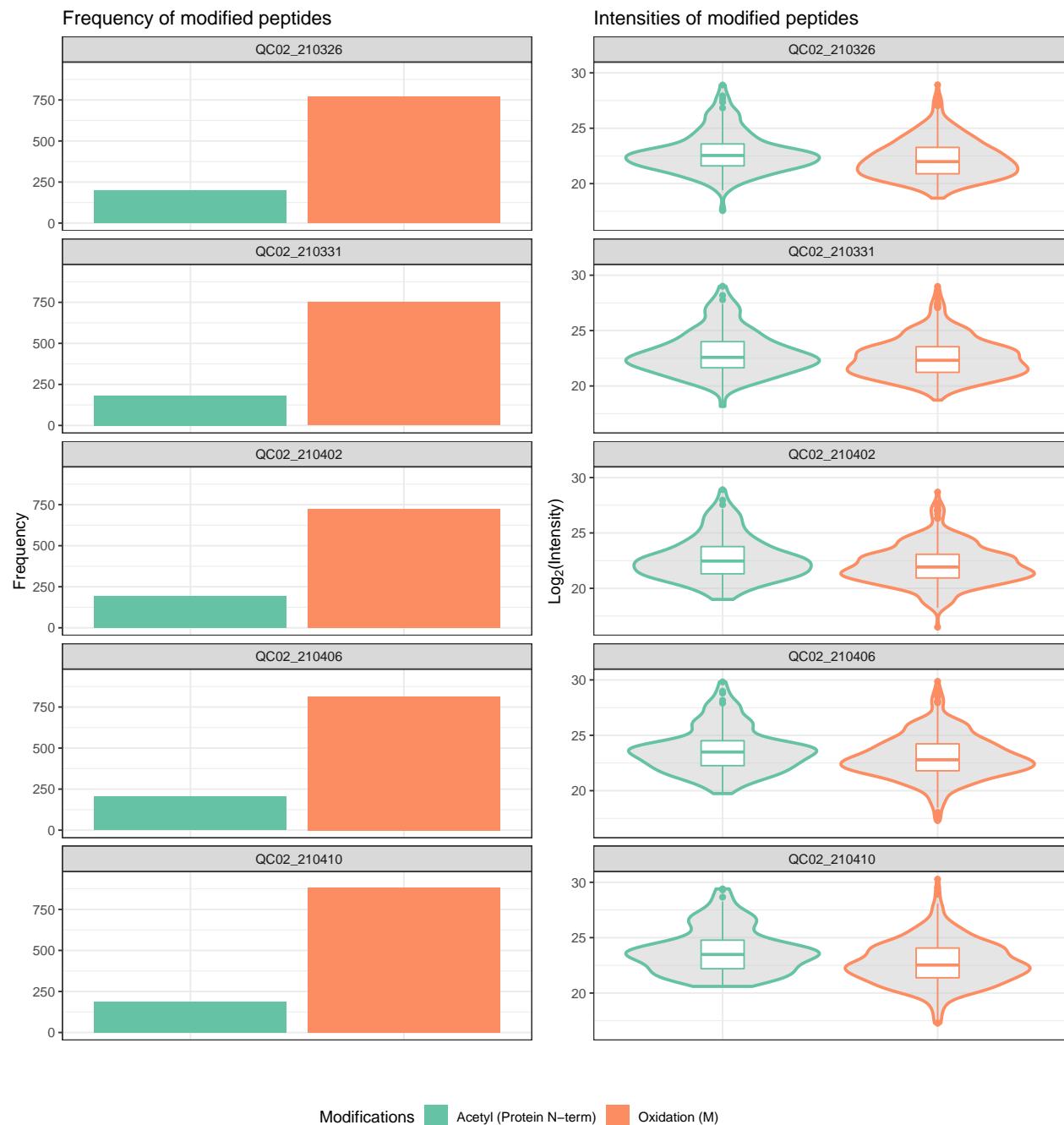
Acquisition Cycle



Retention time

Retention time

Post–Translational Modifications



Post–Translational Modifications

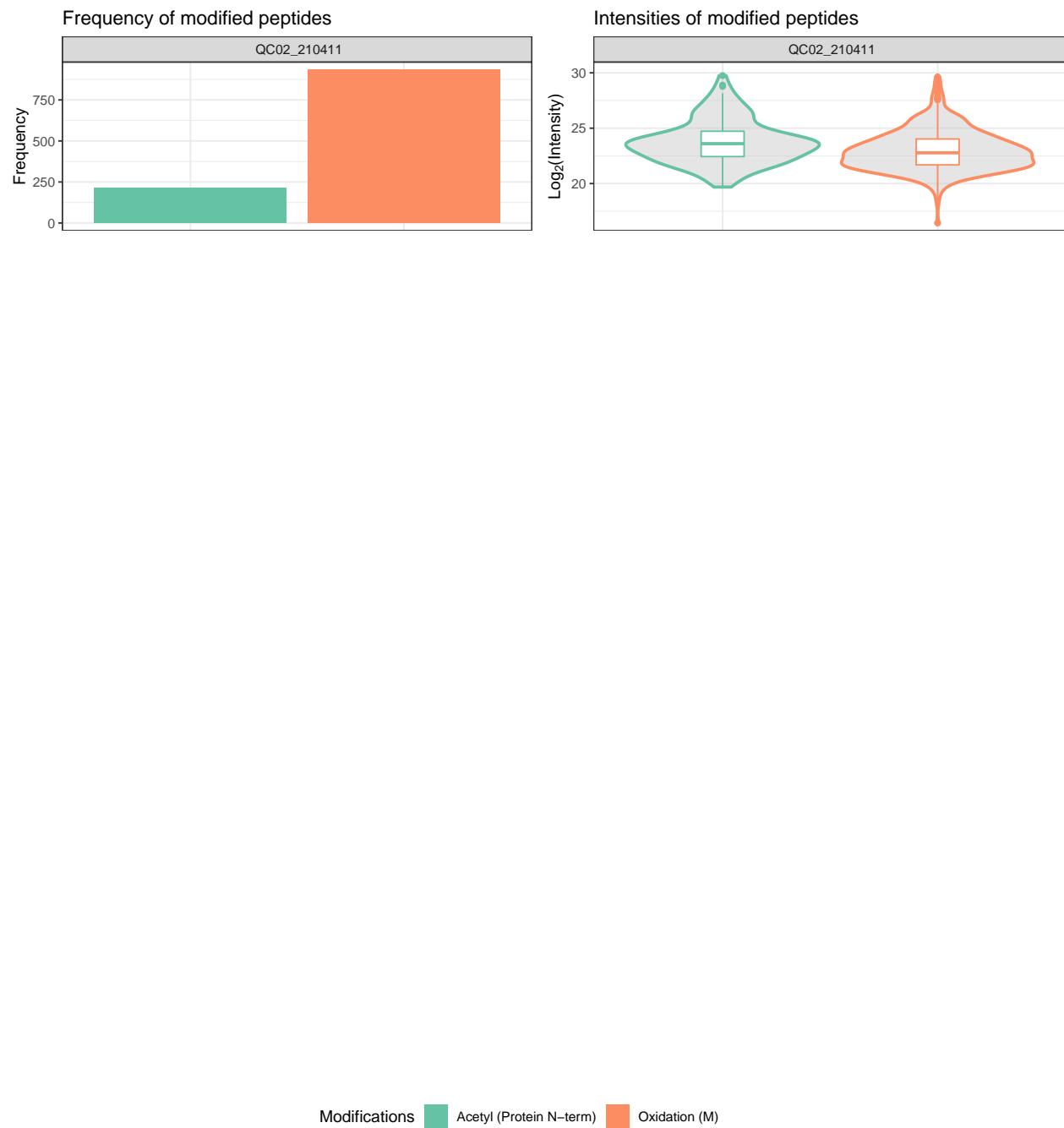


Table 1: Protein Information

Experiment	Proteins Identified	Missing values	Potential contaminants	Reverse	Only identified by site
Combined Samples	4751	NA	100	66	70
QC02_210326	4456	295	91	43	33
QC02_210331	4358	393	92	38	24
QC02_210402	4380	371	94	42	36
QC02_210406	4478	273	92	49	35
QC02_210410	4404	347	94	47	30
QC02_210411	4553	198	93	47	37

Table 2: Information of: Log2 Intensity

Experiment	mean	sd	median	min	max	n
QC02_210326	27.42	29.61	24.43	17.95	34.67	4456
QC02_210331	27.67	29.84	24.65	18.15	34.79	4358
QC02_210402	27.26	29.45	24.25	16.69	34.44	4380
QC02_210406	28.49	30.68	25.50	17.83	35.71	4478
QC02_210410	28.28	30.54	25.20	18.24	35.48	4404
QC02_210411	28.42	30.65	25.36	16.75	35.68	4553

Table 3: Charge Information

Experiment	1	2	3	4	5	6
QC02_210326	0.0	61.7	35.1	2.9	0.2	0.0
QC02_210331	0.2	62.2	34.3	3.0	0.2	0.1
QC02_210402	0.0	63.2	34.1	2.7	0.0	0.0
QC02_210406	0.2	63.0	34.2	2.5	0.0	0.0
QC02_210410	0.0	61.2	35.1	3.6	0.0	0.0
QC02_210411	0.1	59.1	37.9	2.9	0.0	0.0

Table 4: Peptide hydrophobicity (GRAVY)

Experiment	Mean	Max	Min	Median
QC02_210326	-0.22	2.24	-2.69	-0.18
QC02_210331	-0.25	2.24	-2.69	-0.22
QC02_210402	-0.23	2.24	-2.69	-0.2
QC02_210406	-0.2	2.24	-2.69	-0.17
QC02_210410	-0.24	2.24	-2.69	-0.23
QC02_210411	-0.21	2.24	-2.69	-0.18

Table 5: Missed Enzymatic Cleavages

Experiment	0	1	2
QC02_210326	2300	304	14
QC02_210331	2153	282	10
QC02_210402	2151	265	8
QC02_210406	2355	309	15
QC02_210410	2203	324	12
QC02_210411	2489	330	17

Table 6: Protein Identification Overlap Between Samples

samples	Freq
1	47
2	55
3	97
4	141
5	308
6	3890