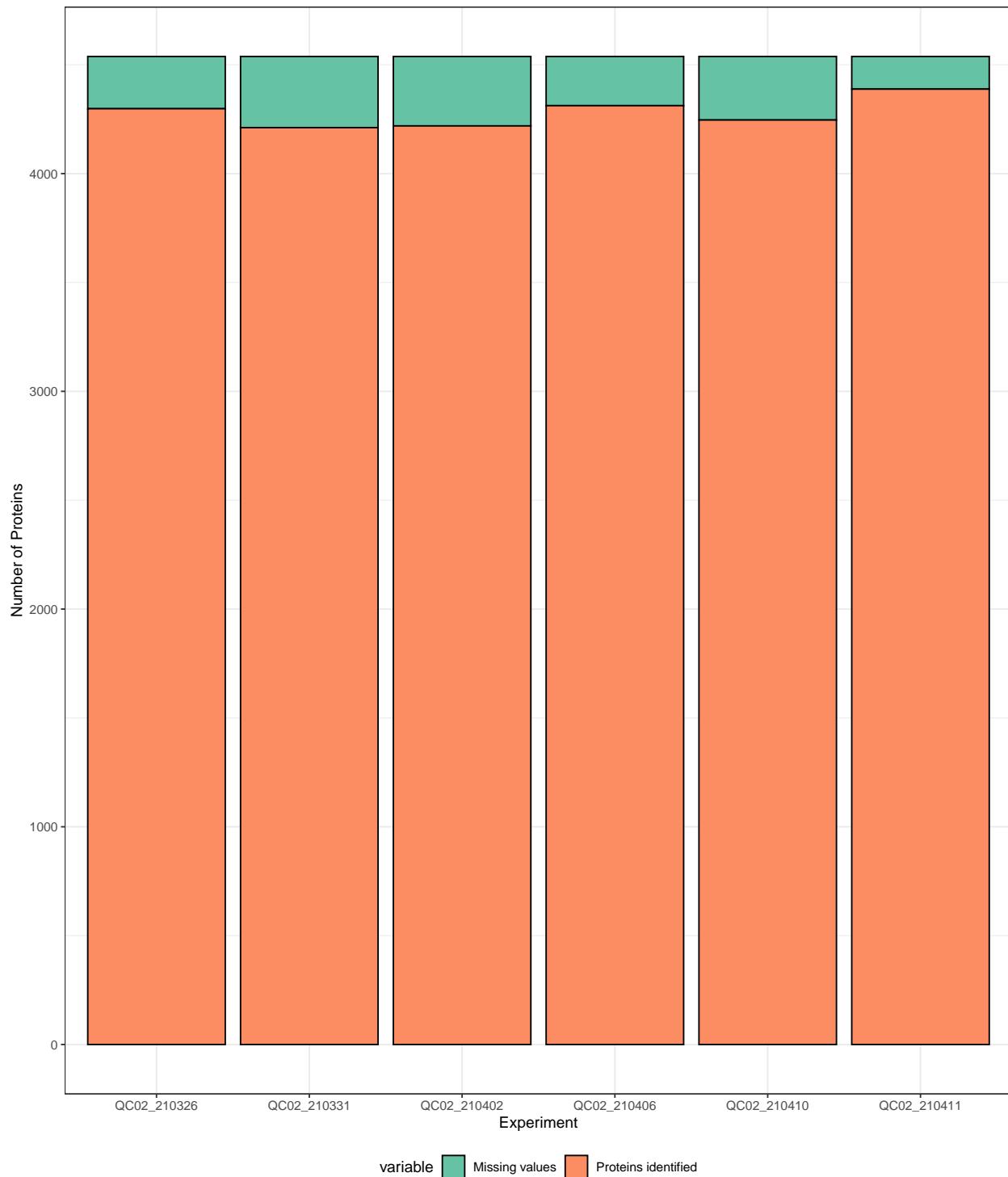


# MQmetrics Report

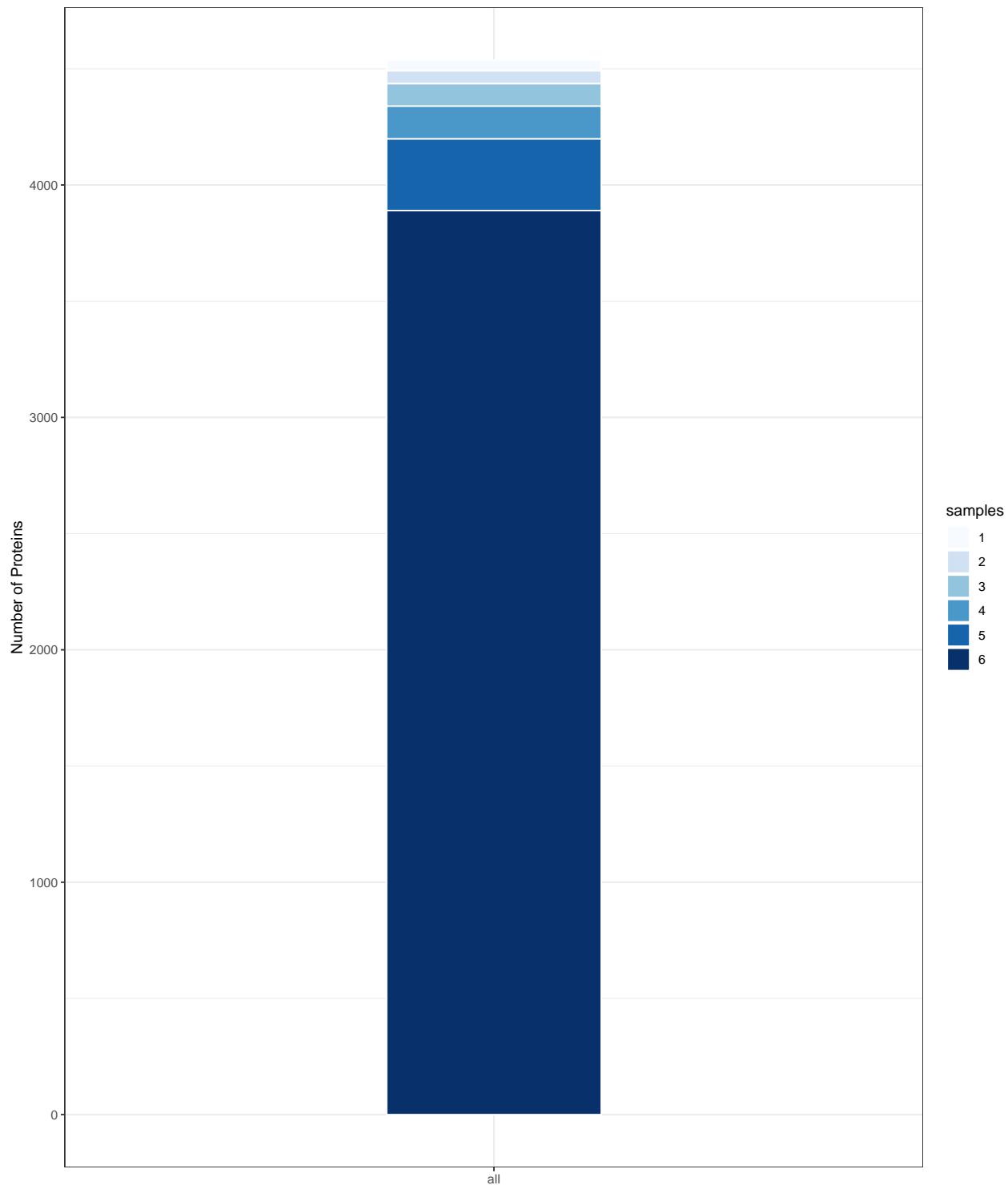
24 May, 2021

```
## [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: 0 days, 2 hours and 15 mins."
## [1] "The Experiment finished on: 16/04/2021 at: 20:22:40"
## [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)"
```

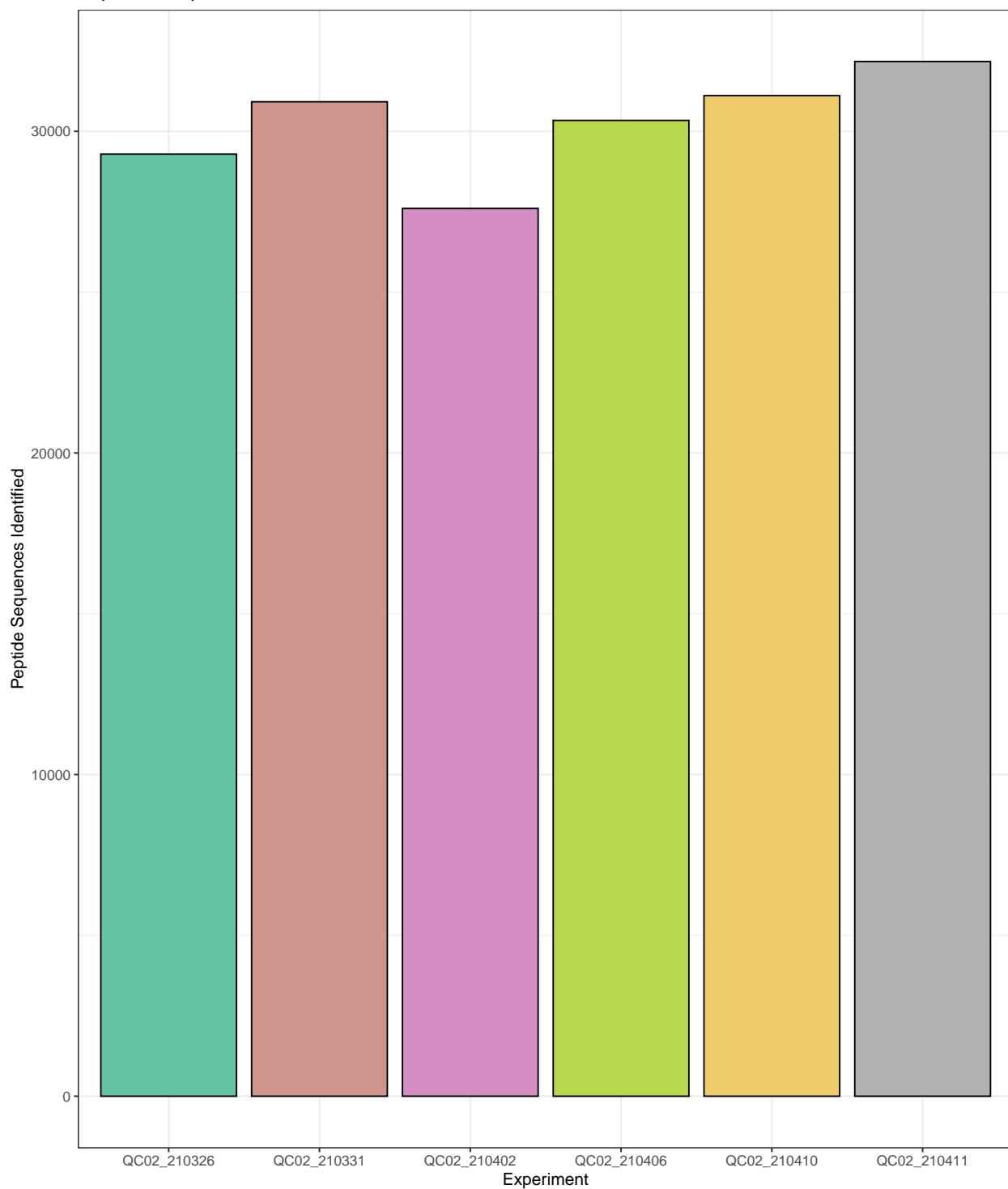
### Proteins Identified based on Intensity



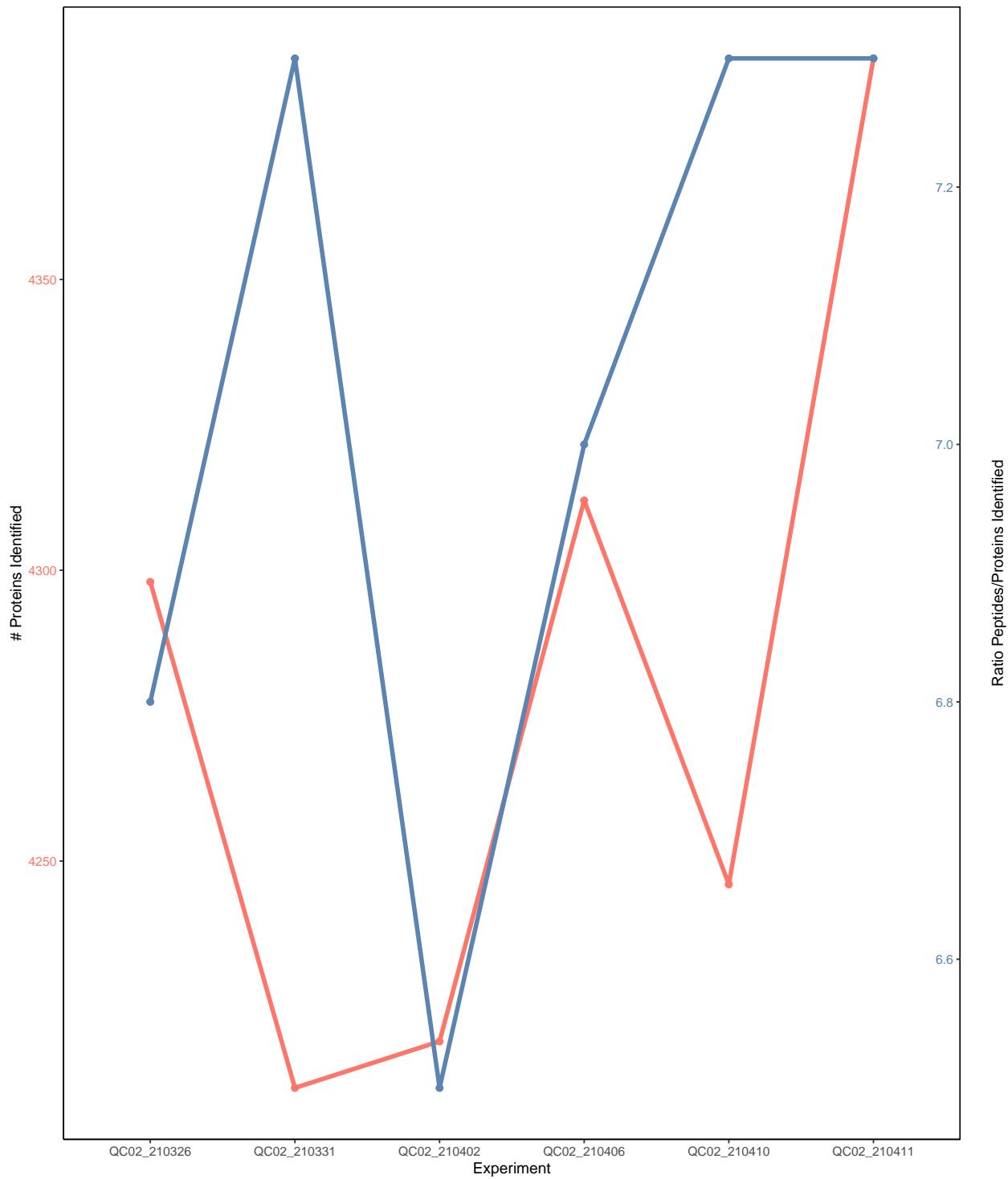
Protein Overlap Between samples

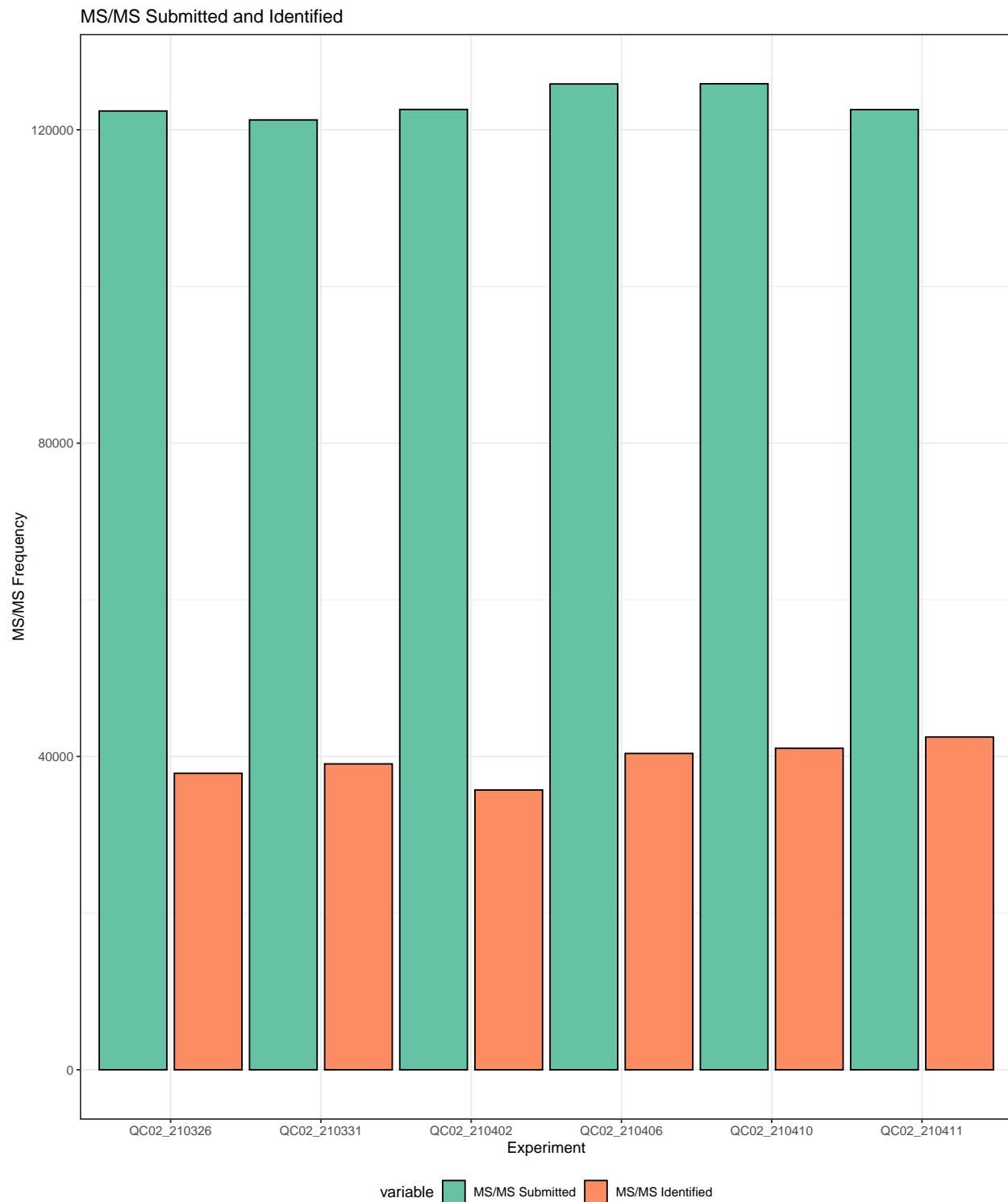


Peptides Sequences Identified

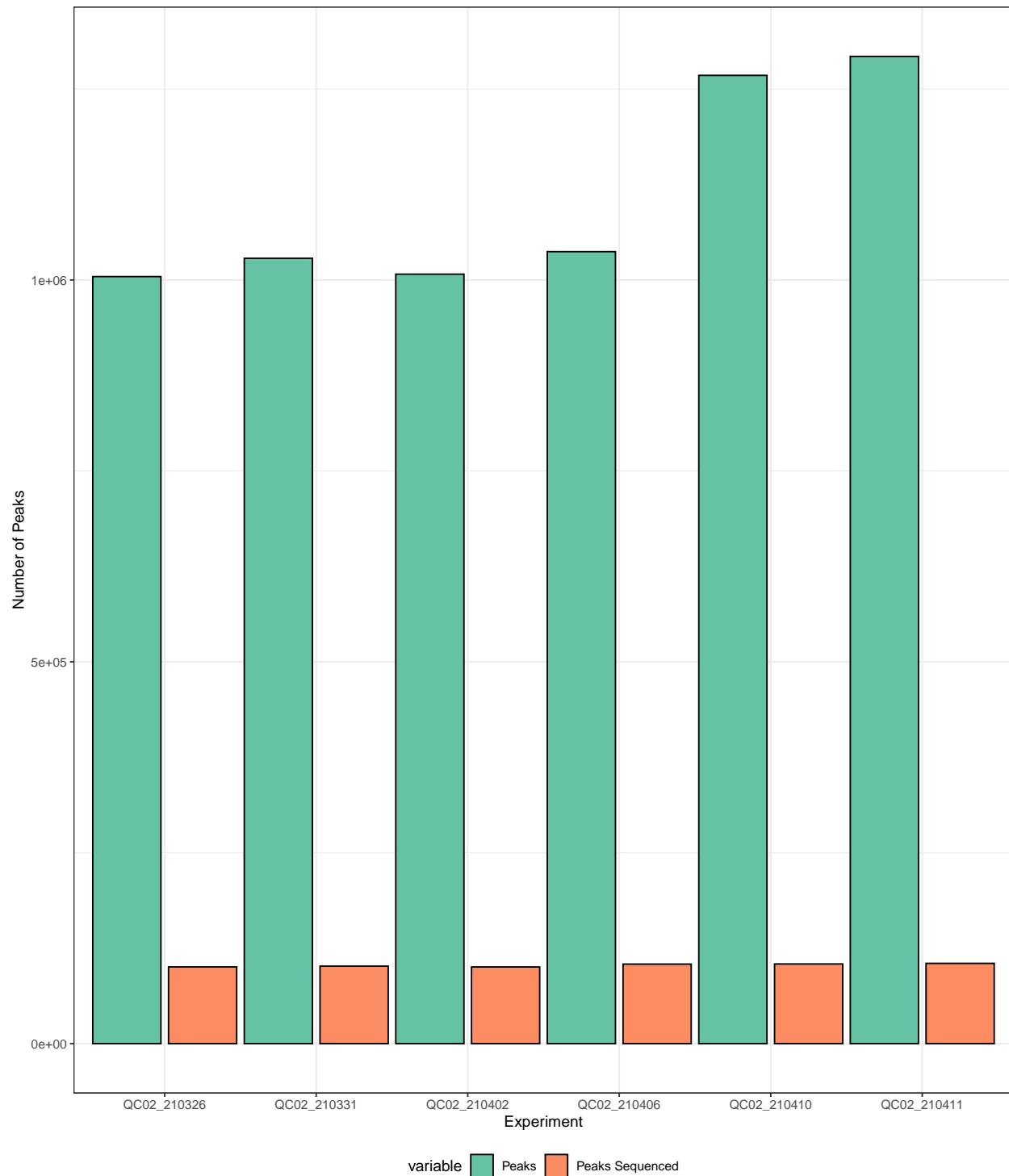


Proteins vs Peptide/Protein ratio based on Intensity

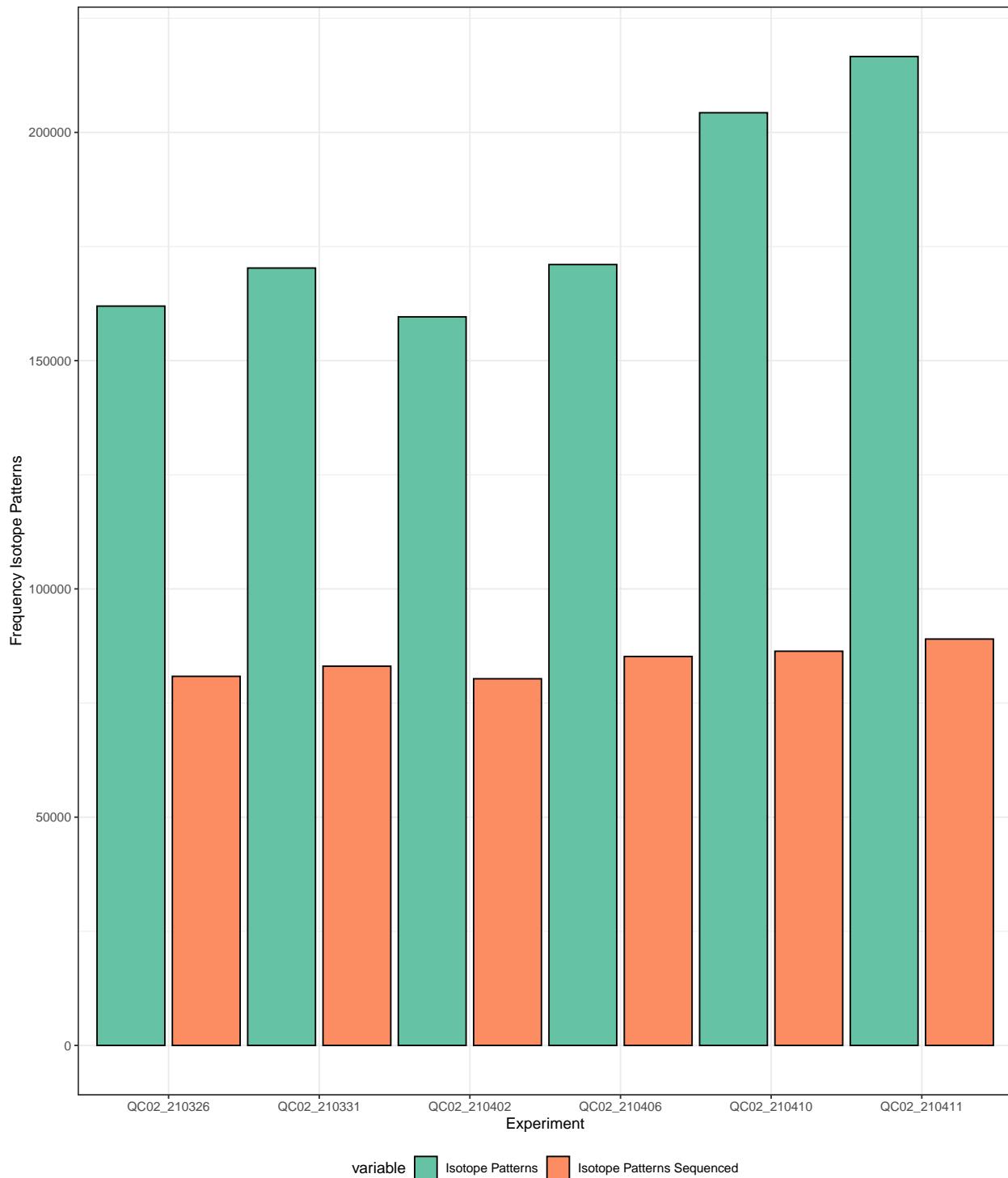




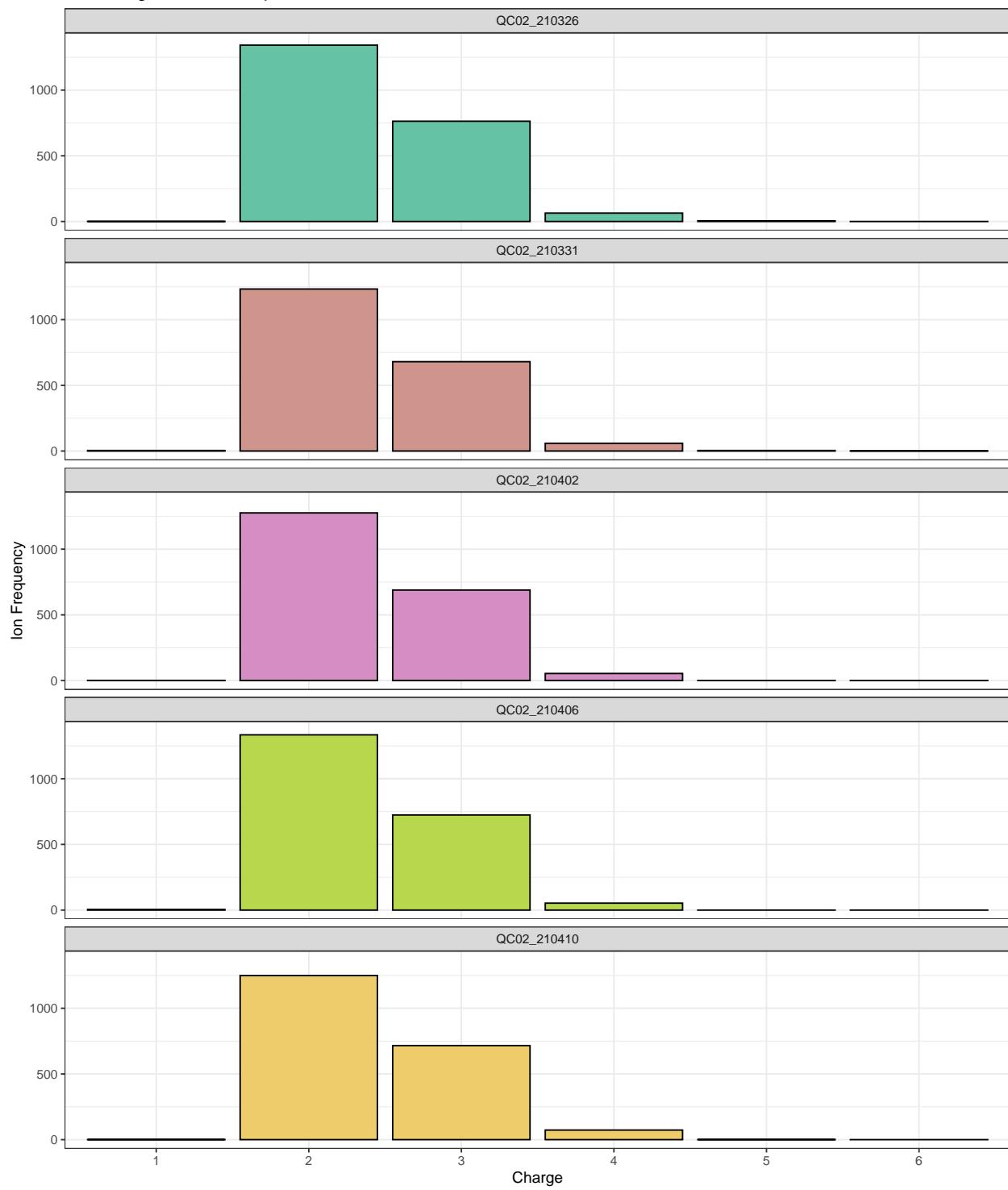
Peaks detected and sequenced in the full scans



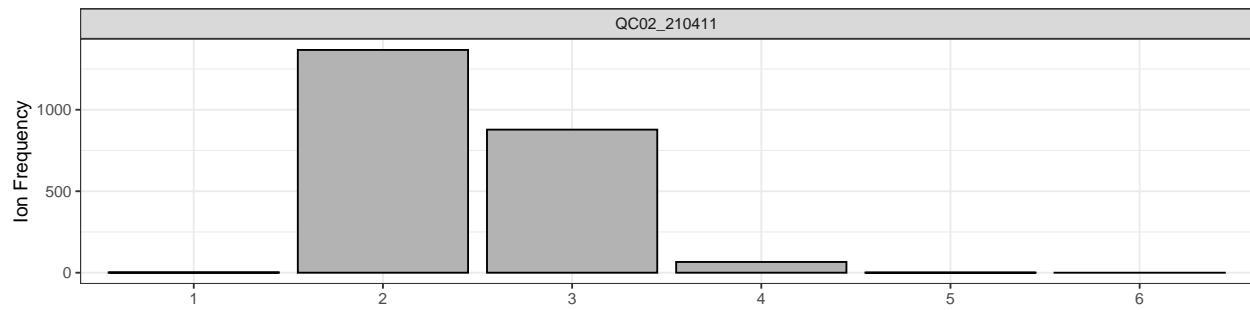
### Isotope Patterns detected and sequenced



The charge-state of the precursor ion.



The charge-state of the precursor ion.

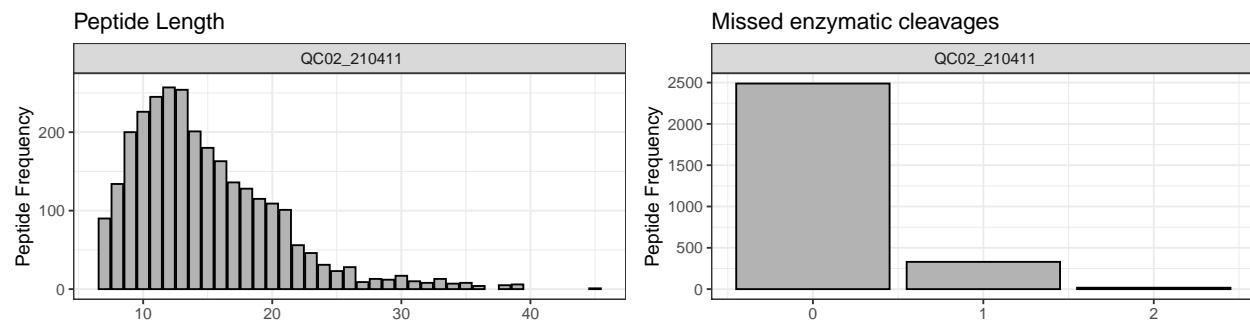


Charge

## Protease Specificity



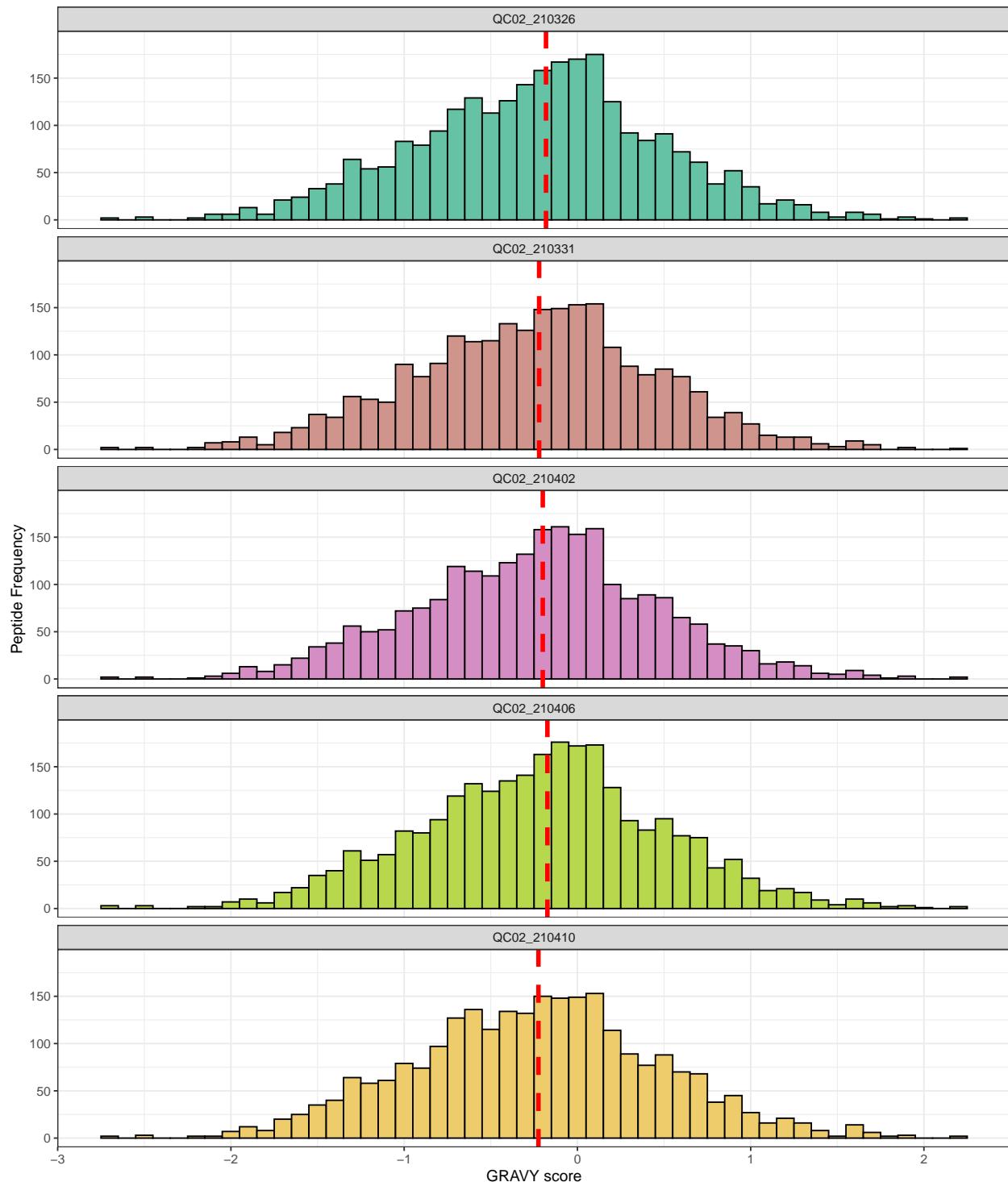
## Protease Specificity



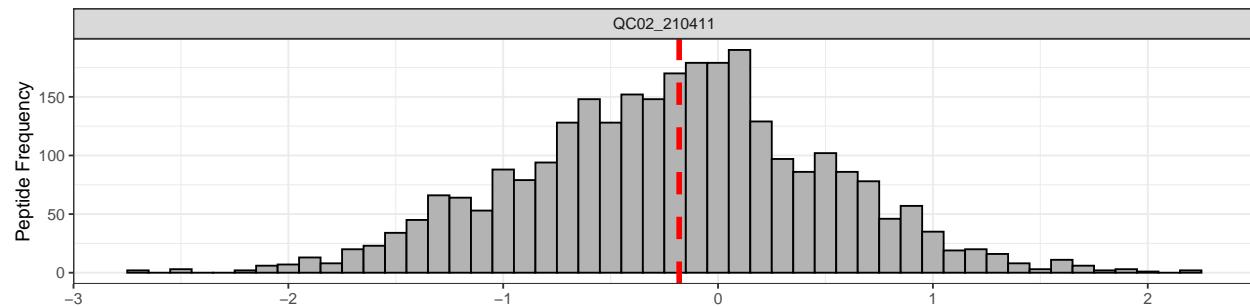
Peptide length

Missed Cleavages

### Peptide hydrophathy distribution

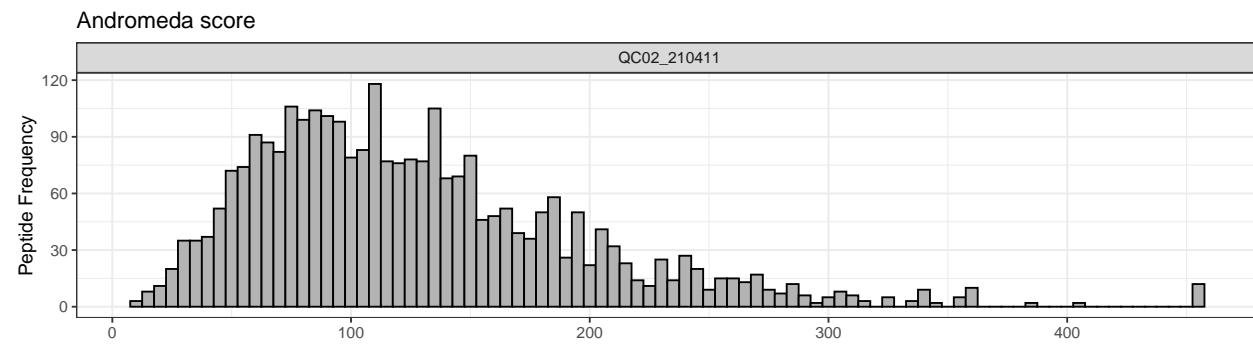


### Peptide hydrophathy distribution

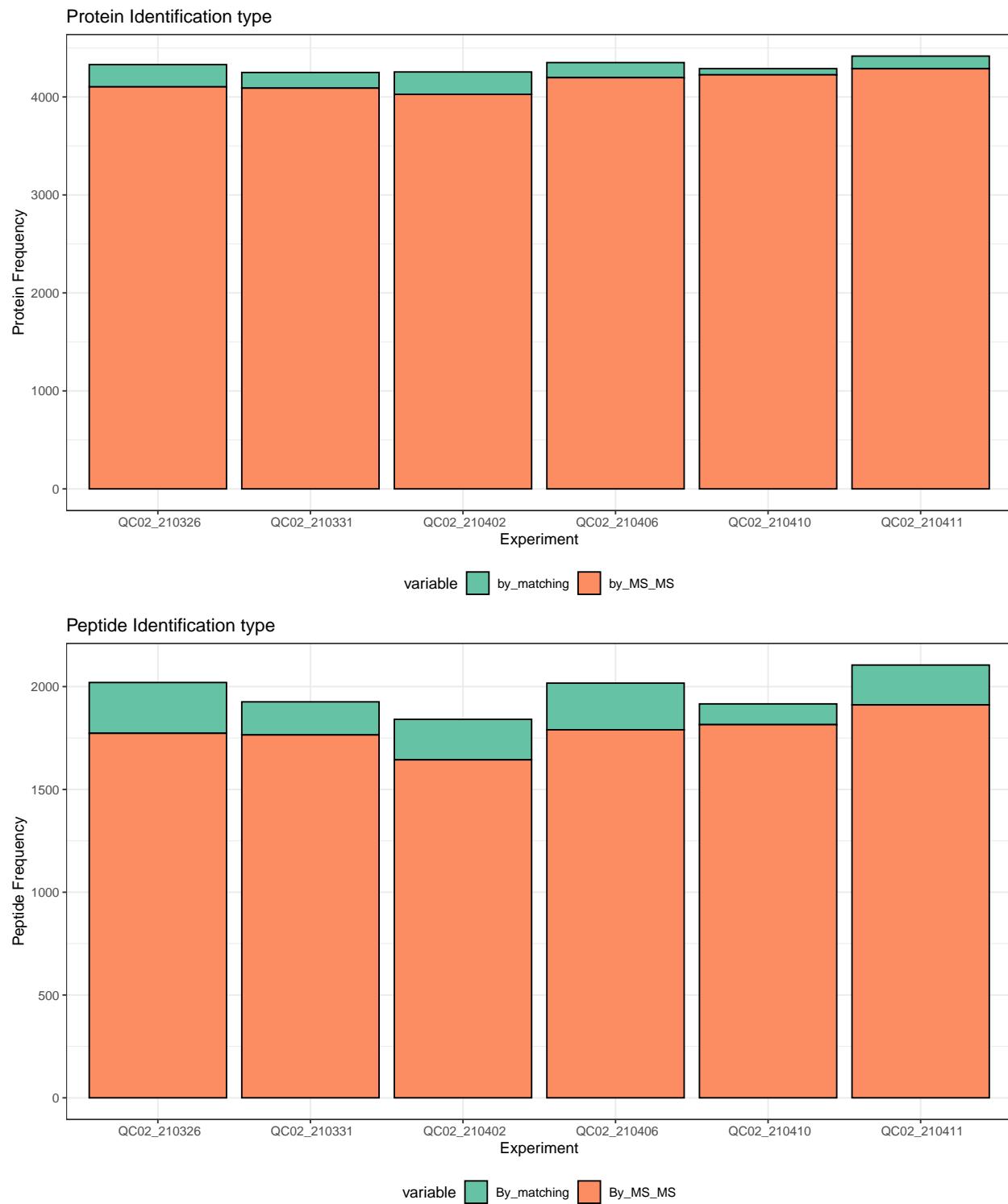


GRAVY score

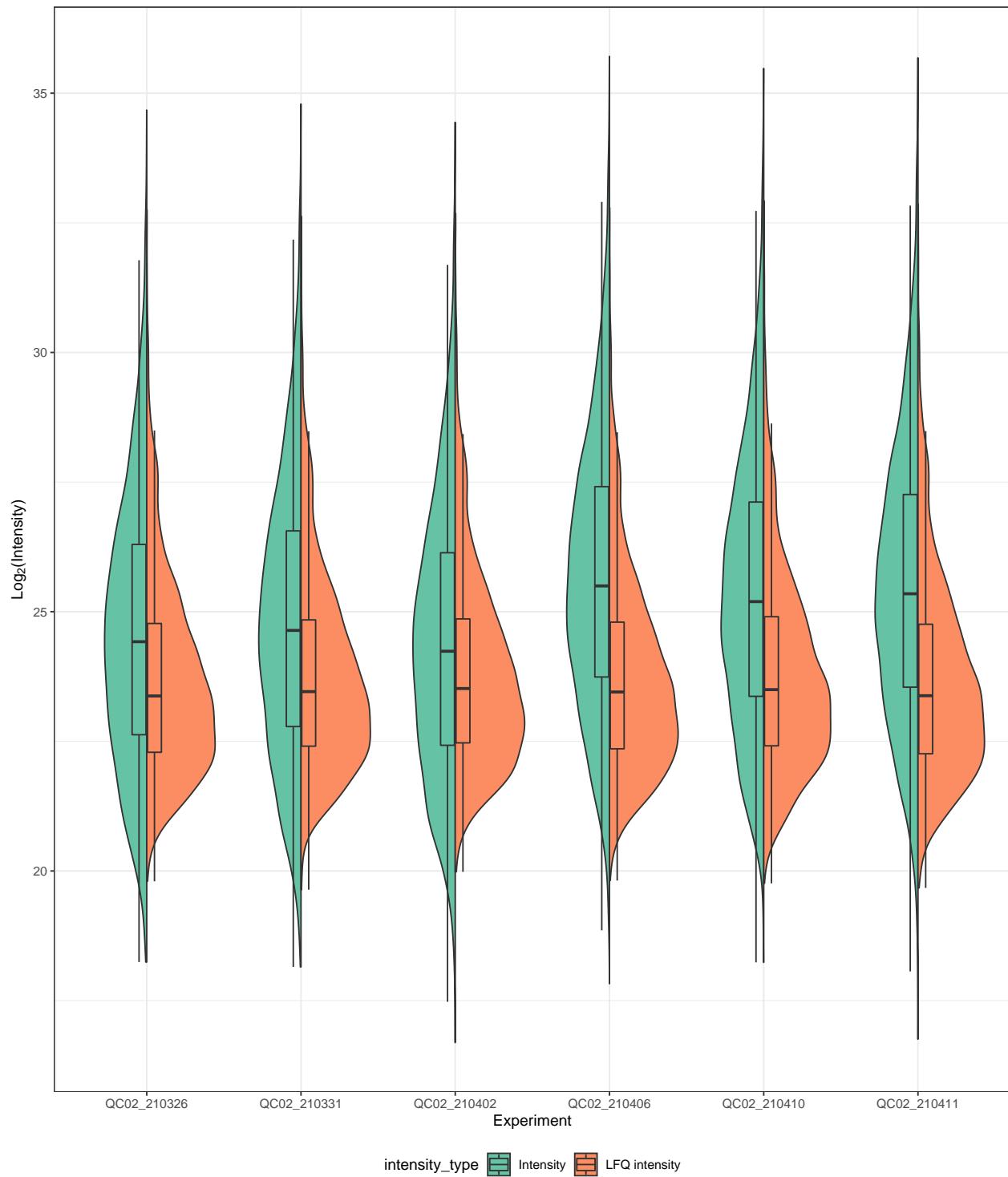


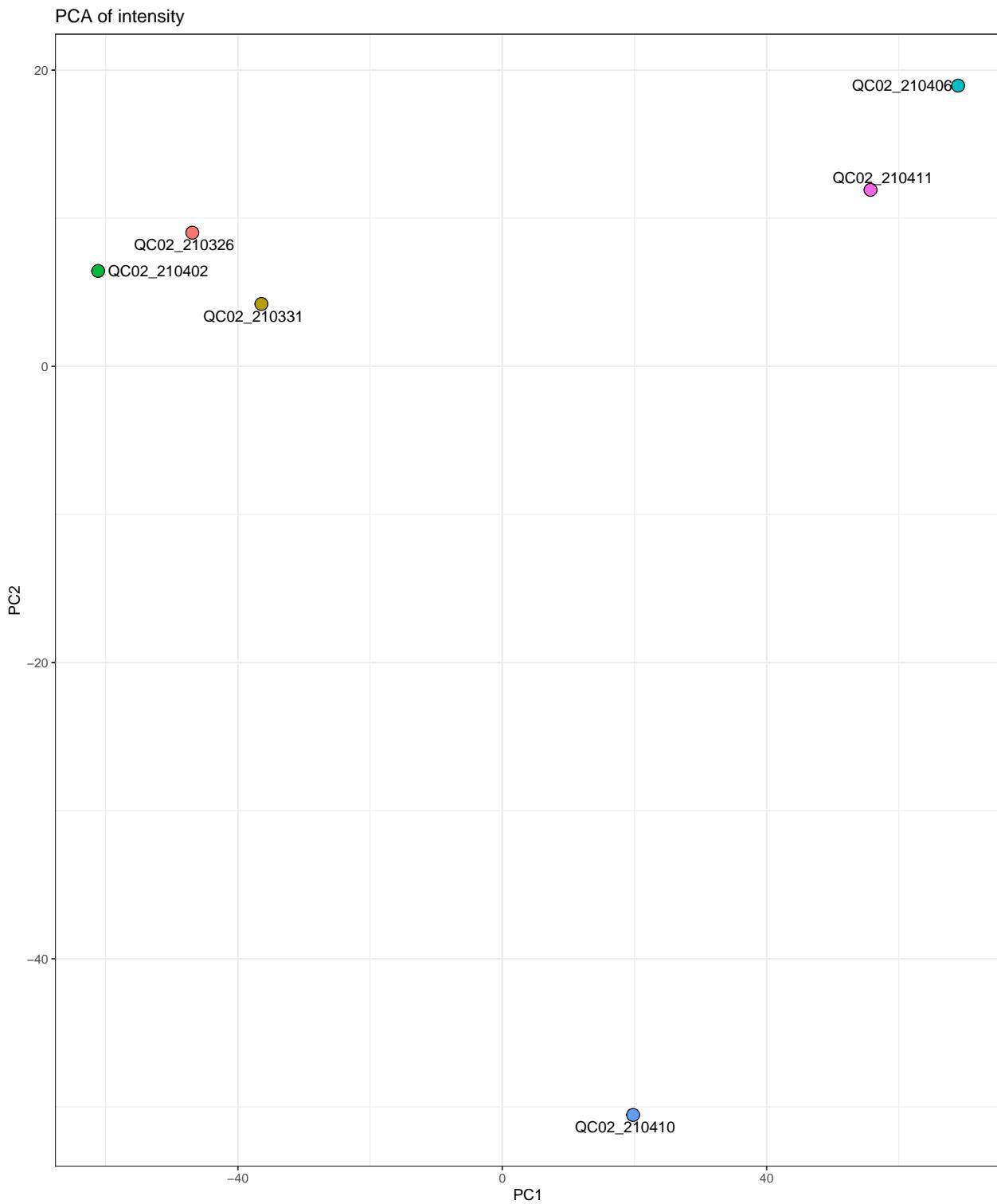


Score

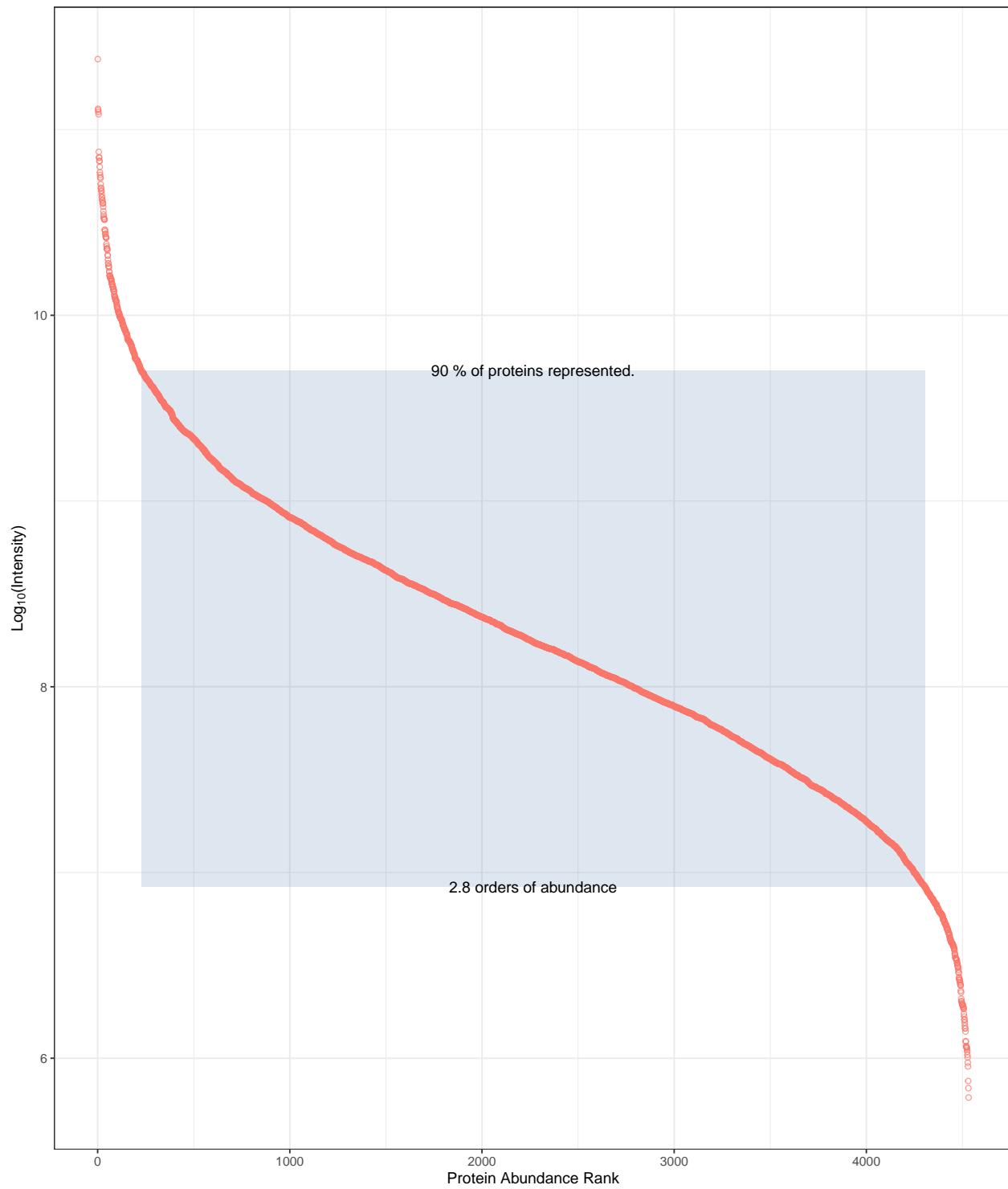


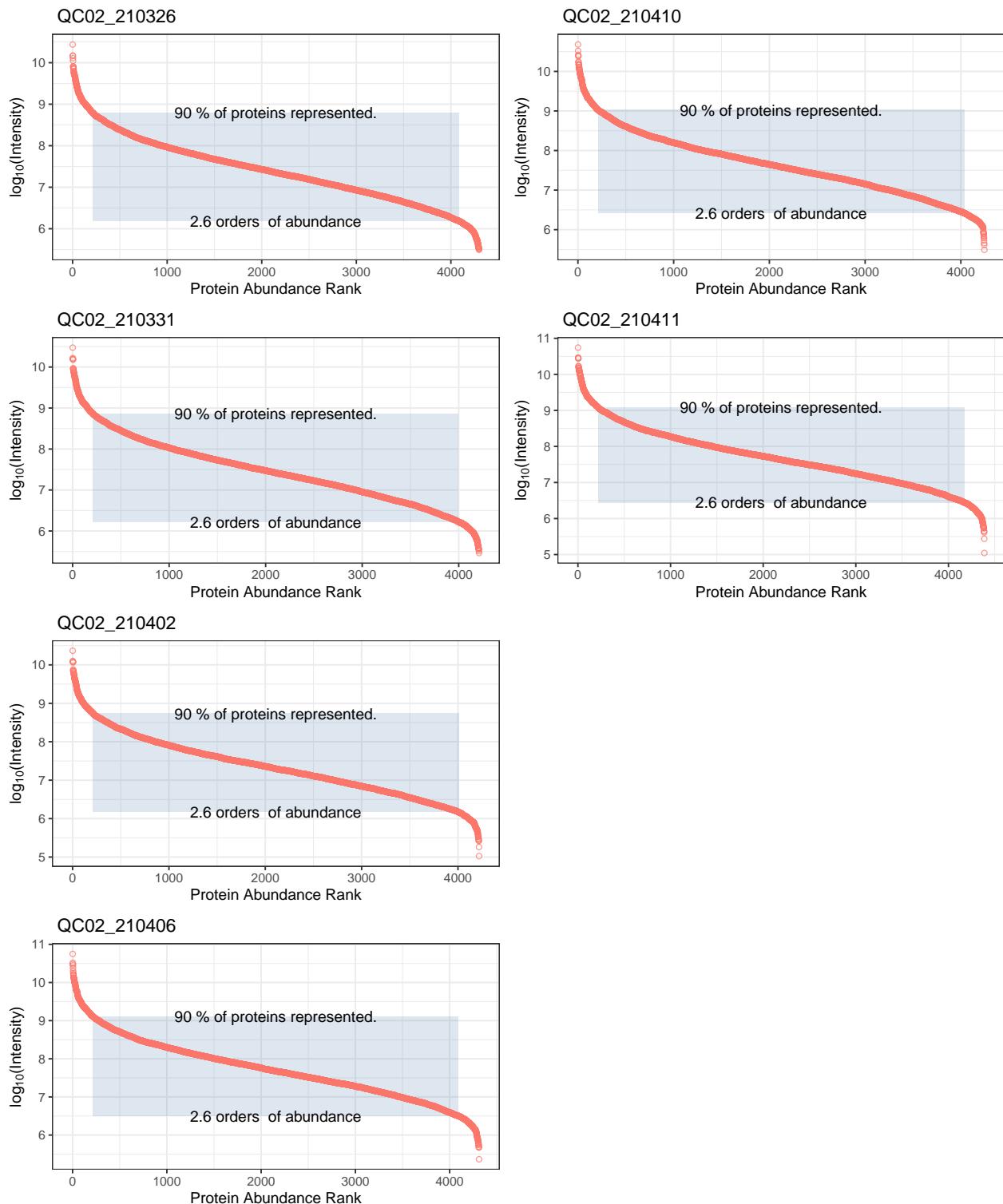
### Protein Intensity & LFQ intensity





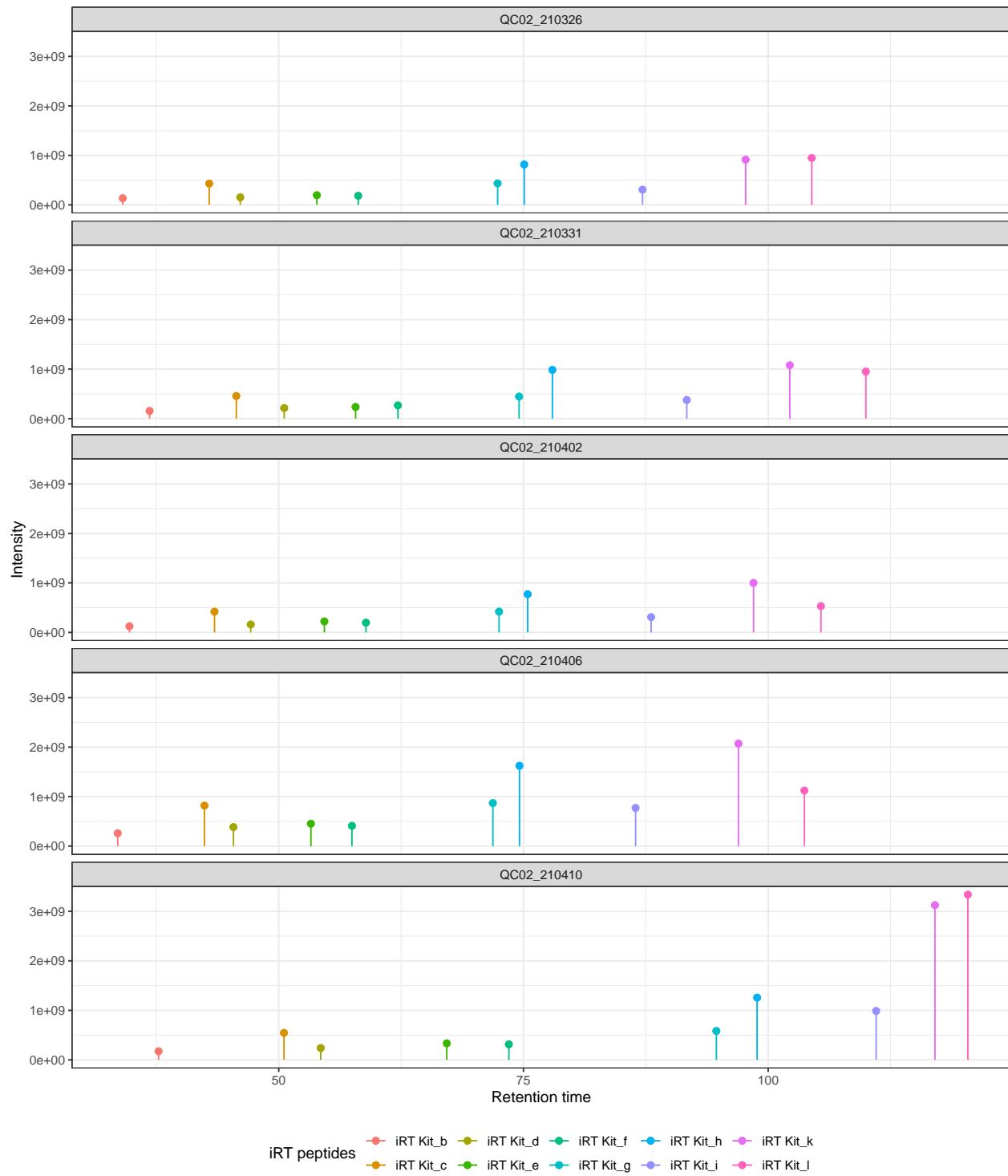
Dynamic range of protein abundance all samples



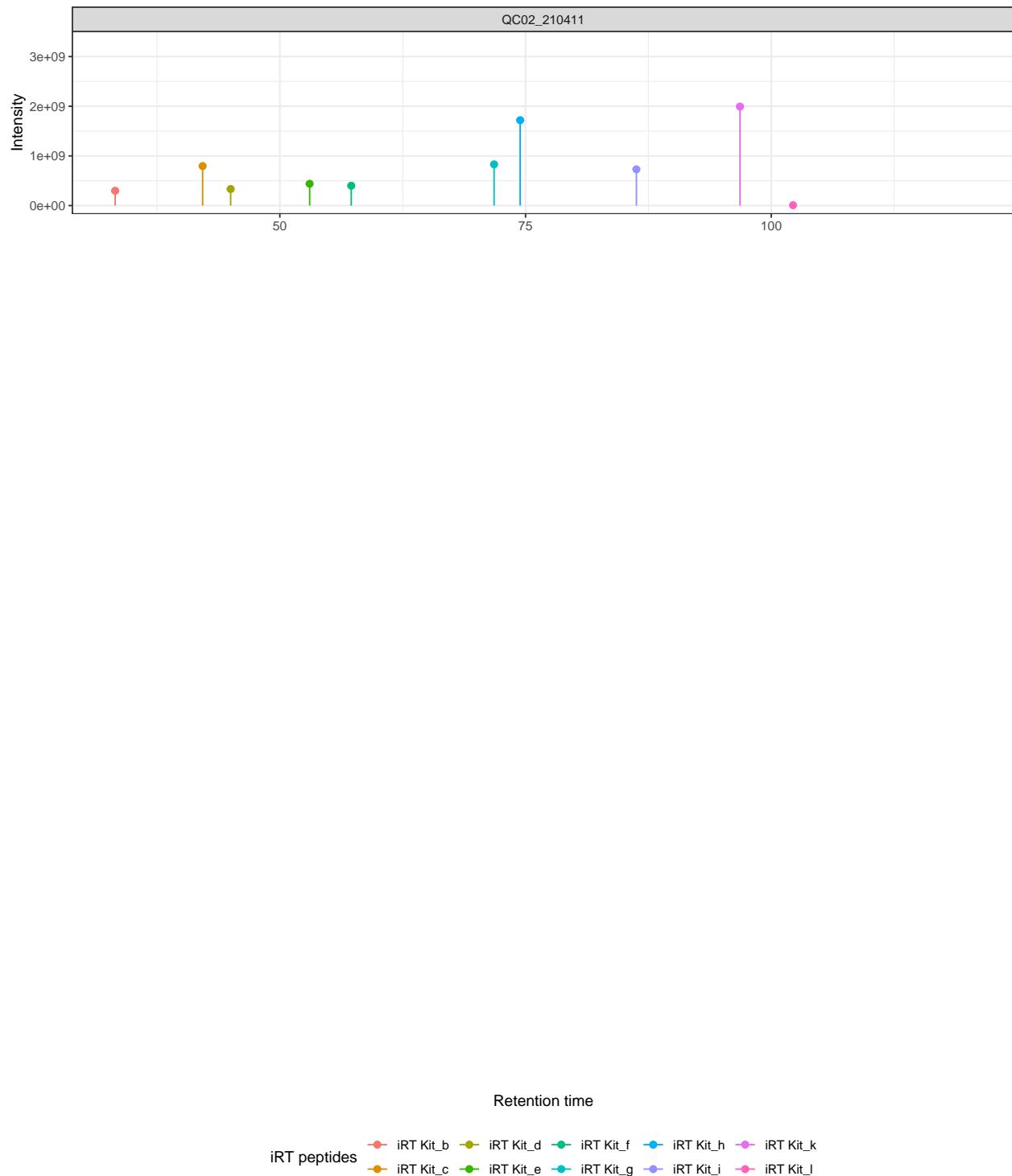


```
## [1] "No UniprotID provided."
```

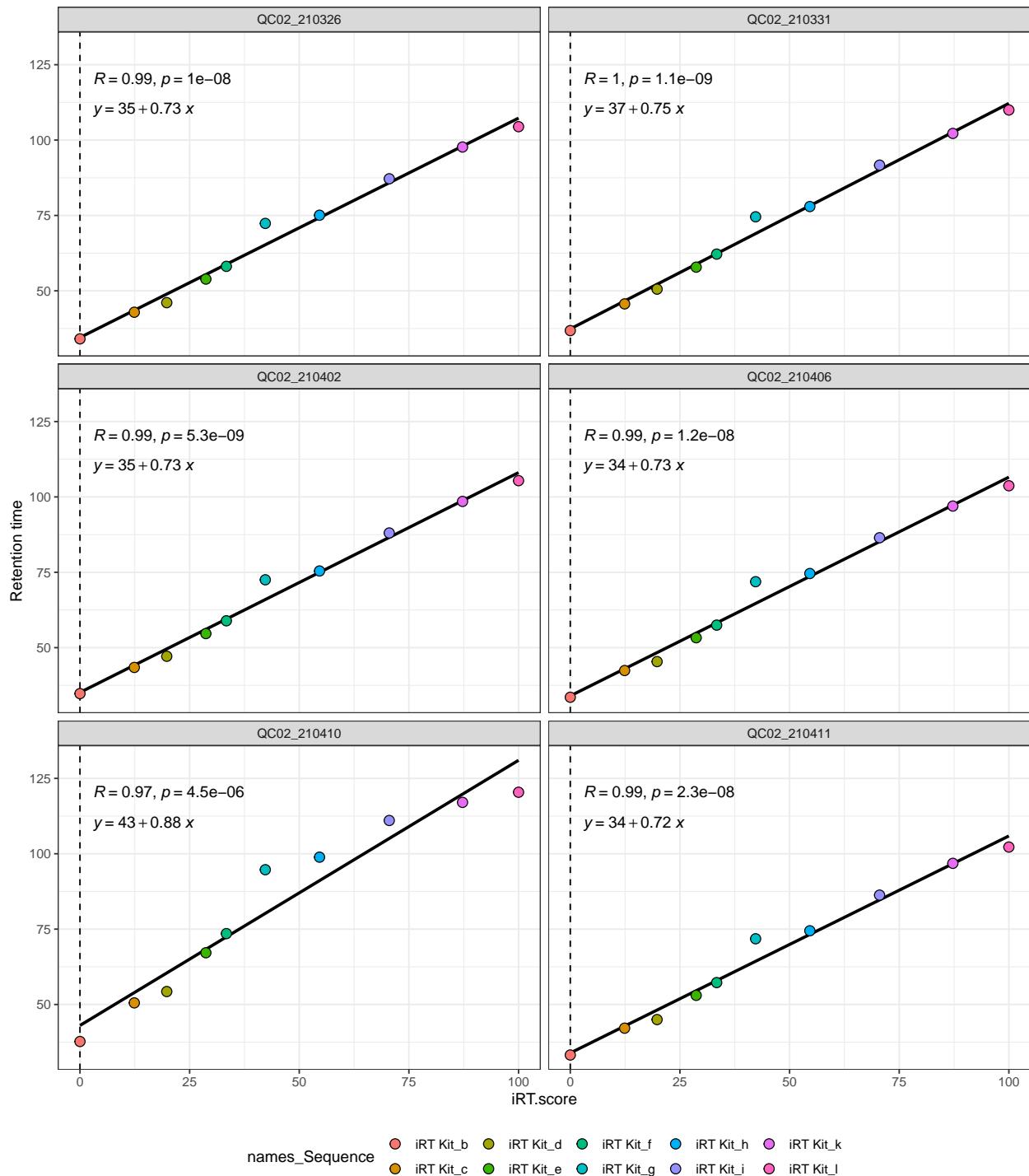
Biognosys iRT peptides in each sample.



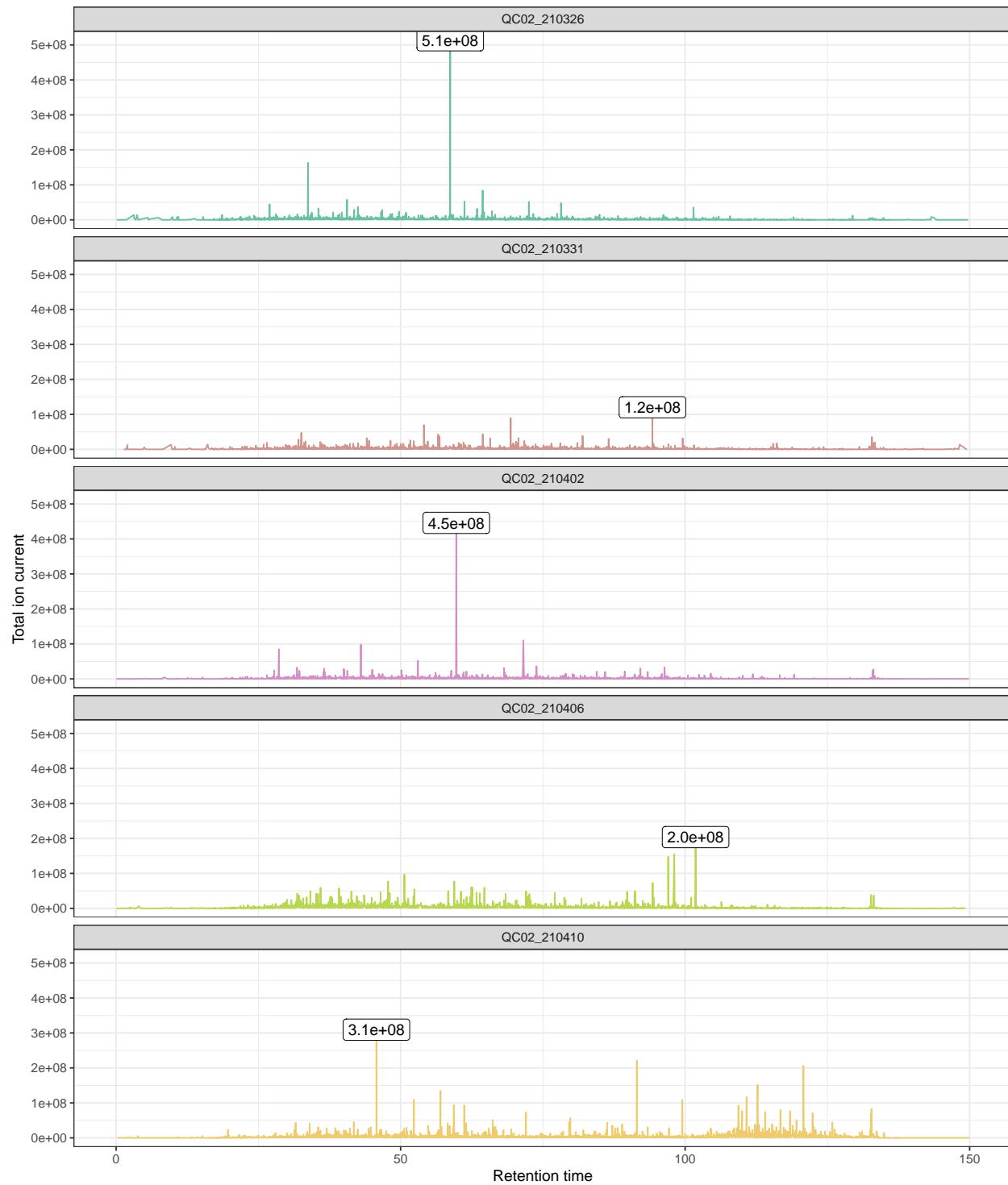
Biognosys iRT peptides in each sample.



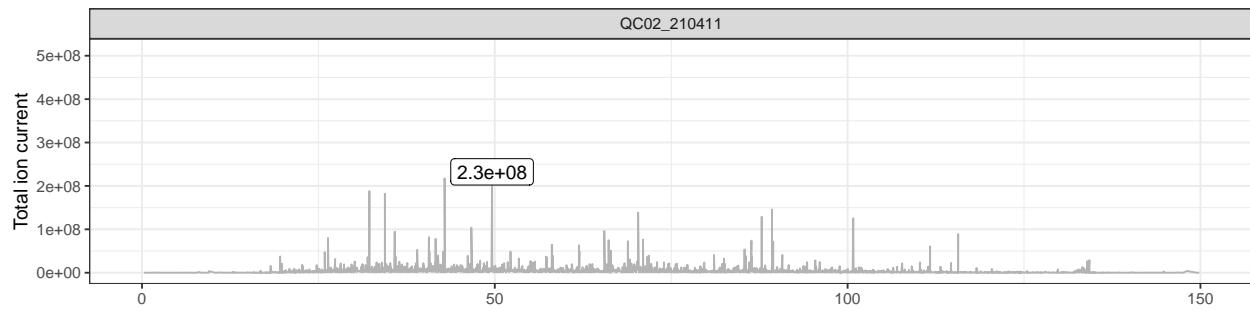
Retention time of  
the Biognosys iRT peptides.



### Total Ion Current

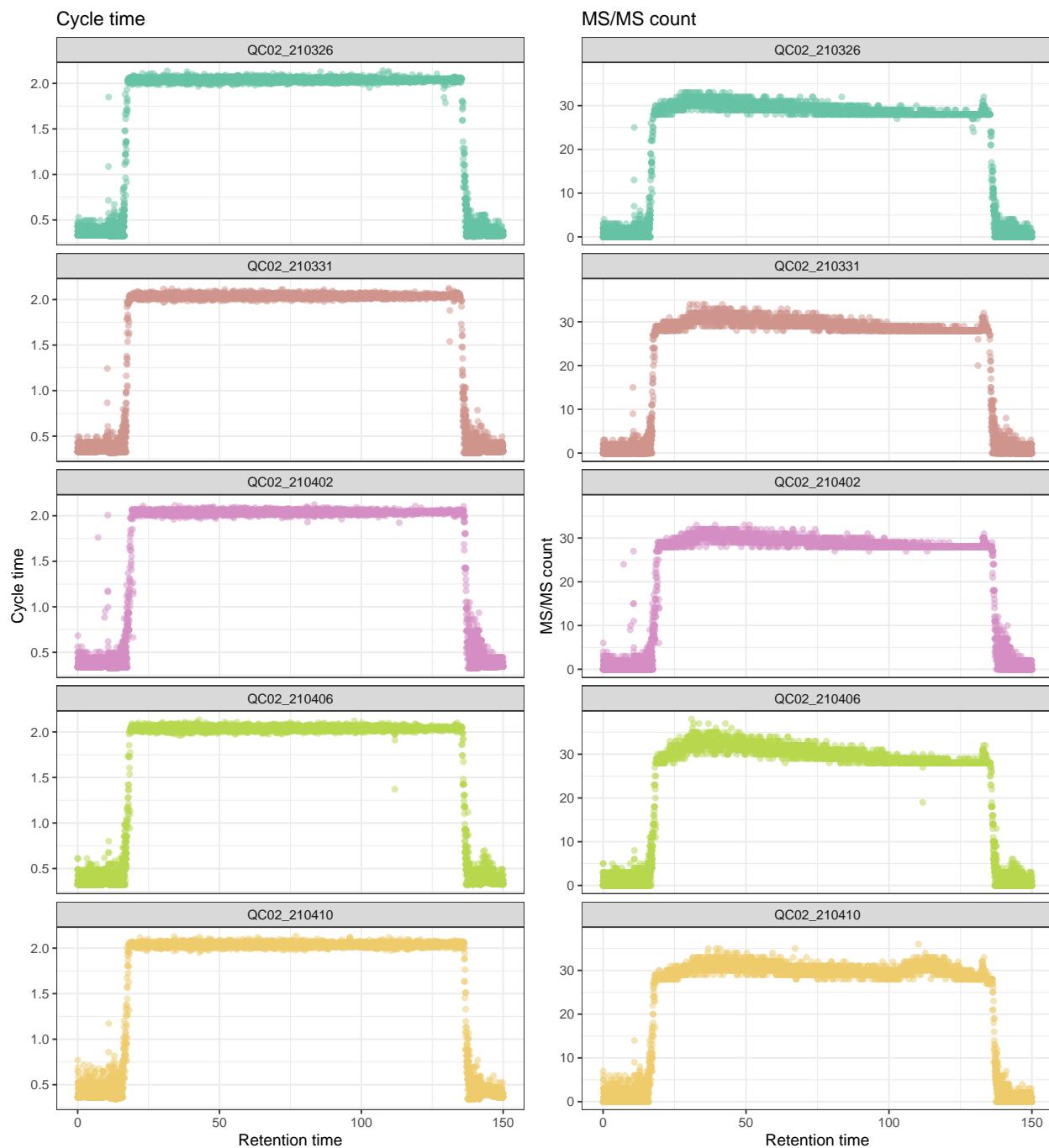


### Total Ion Current

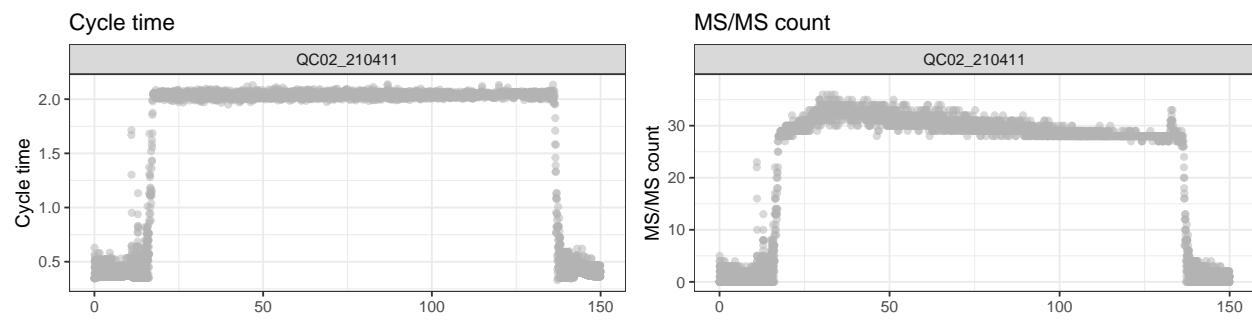


Retention time

### Acquisition Cycle



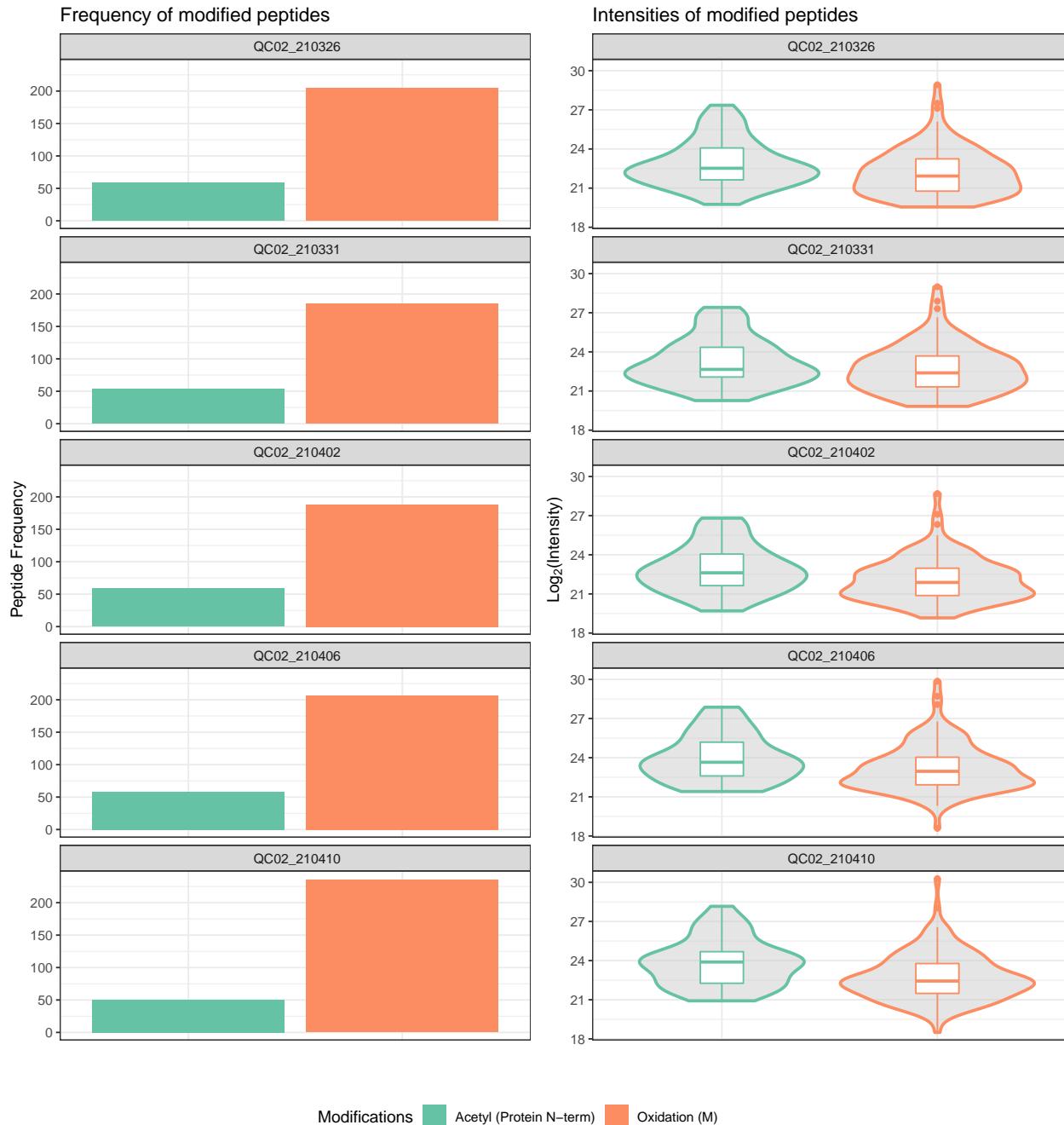
### Acquisition Cycle



Retention time

Retention time

## Post-Translational Modifications



## Post-Translational Modifications

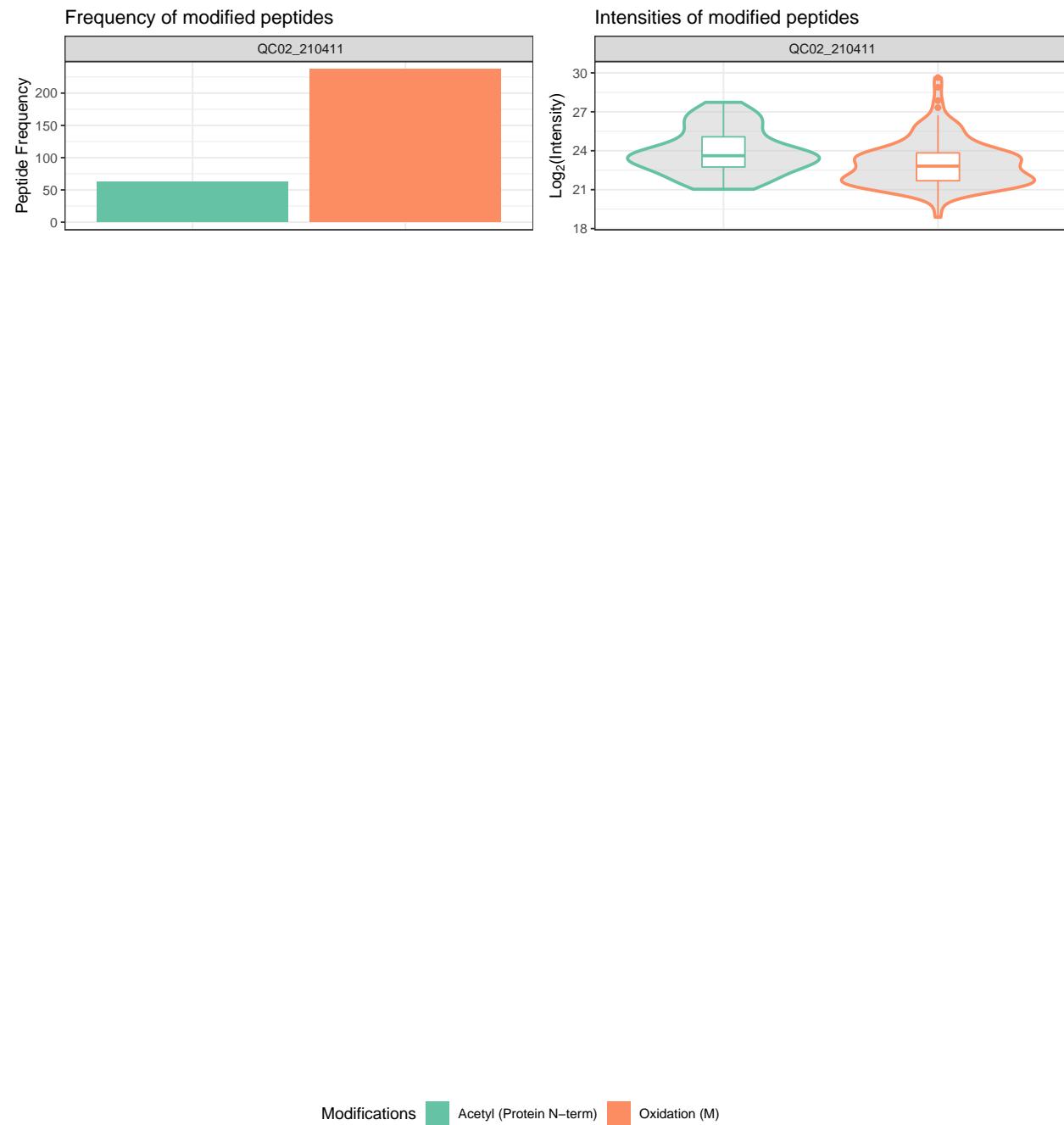


Table 1: Protein Information

	Proteins Identified	Missing values	Potential contaminants	Reversesite	Only identified by	Peptide Sequences Identified	Peptides/Proteins
Combined Samples	4751	NA	100	66	70	47126	9.9
QC02_210326456	295	91	43	33		29292	6.6
QC02_210331358	393	92	38	24		30920	7.1
QC02_210402380	371	94	42	36		27603	6.3
QC02_210406478	273	92	49	35		30341	6.8
QC02_210410404	347	94	47	30		31110	7.1
QC02_210414553	198	93	47	37		32170	7.1

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