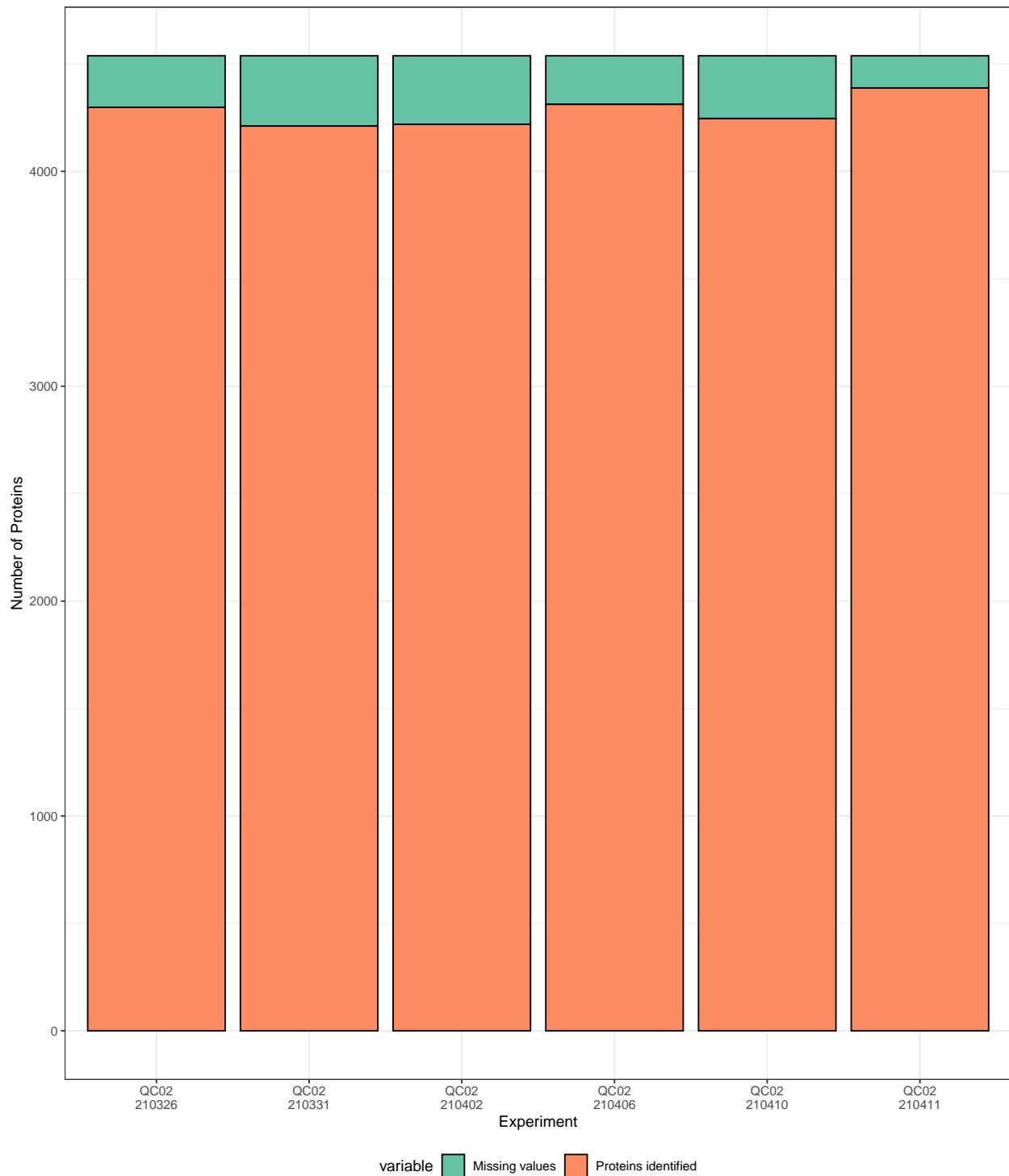


# MQmetrics Report

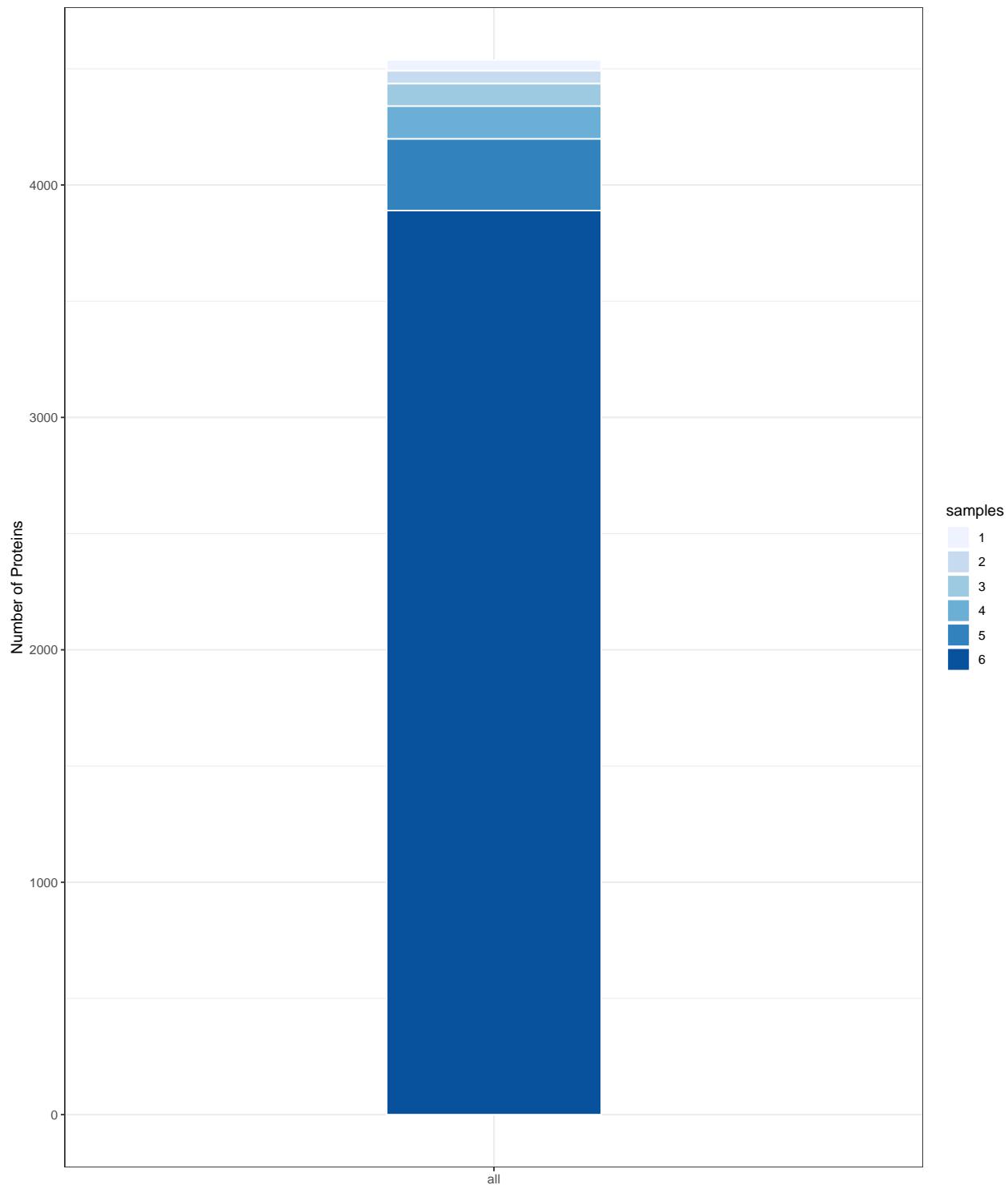
13 May, 2021

```
## [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: 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: "
## [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)"
```

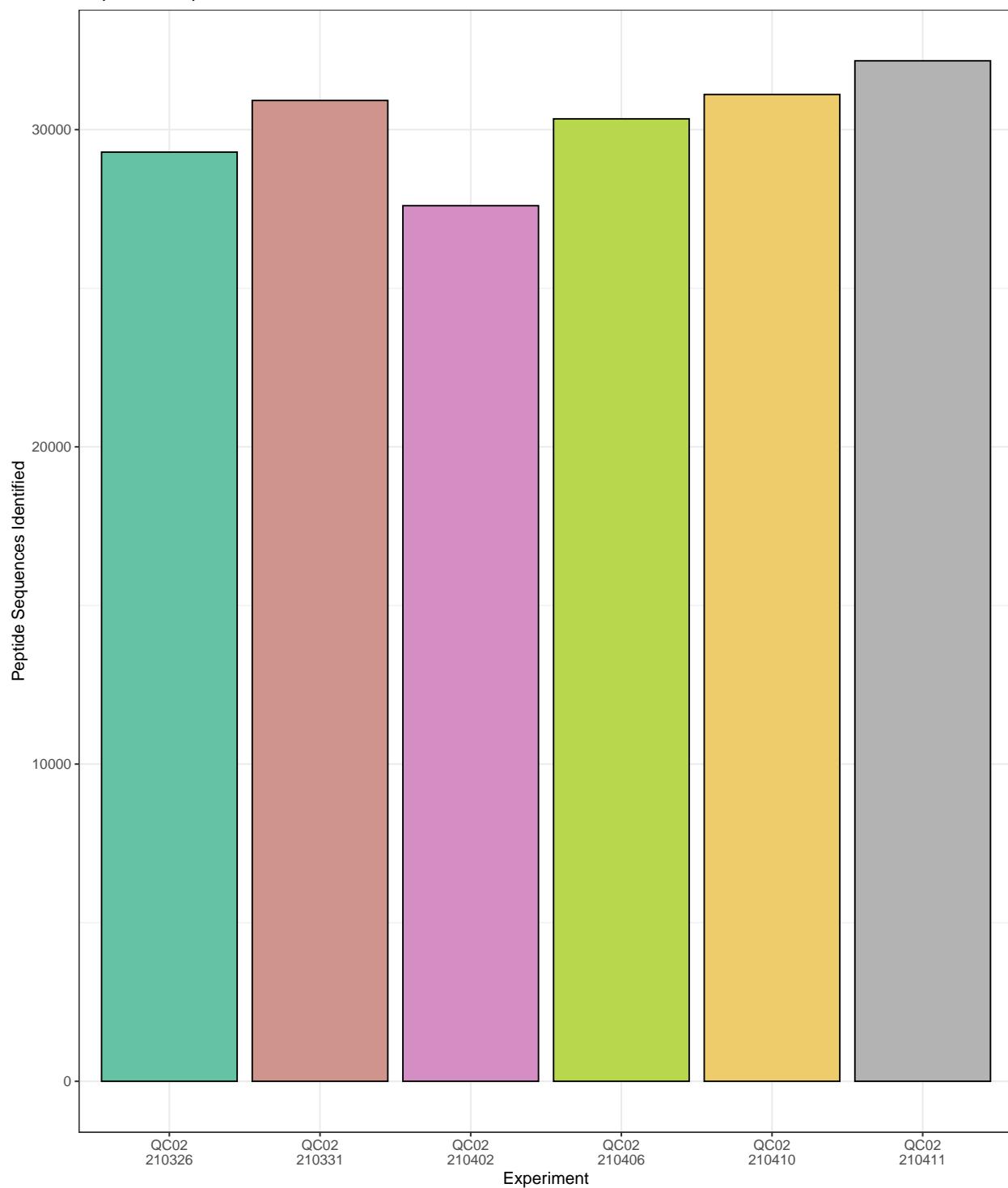
### Proteins Identified based on Intensity

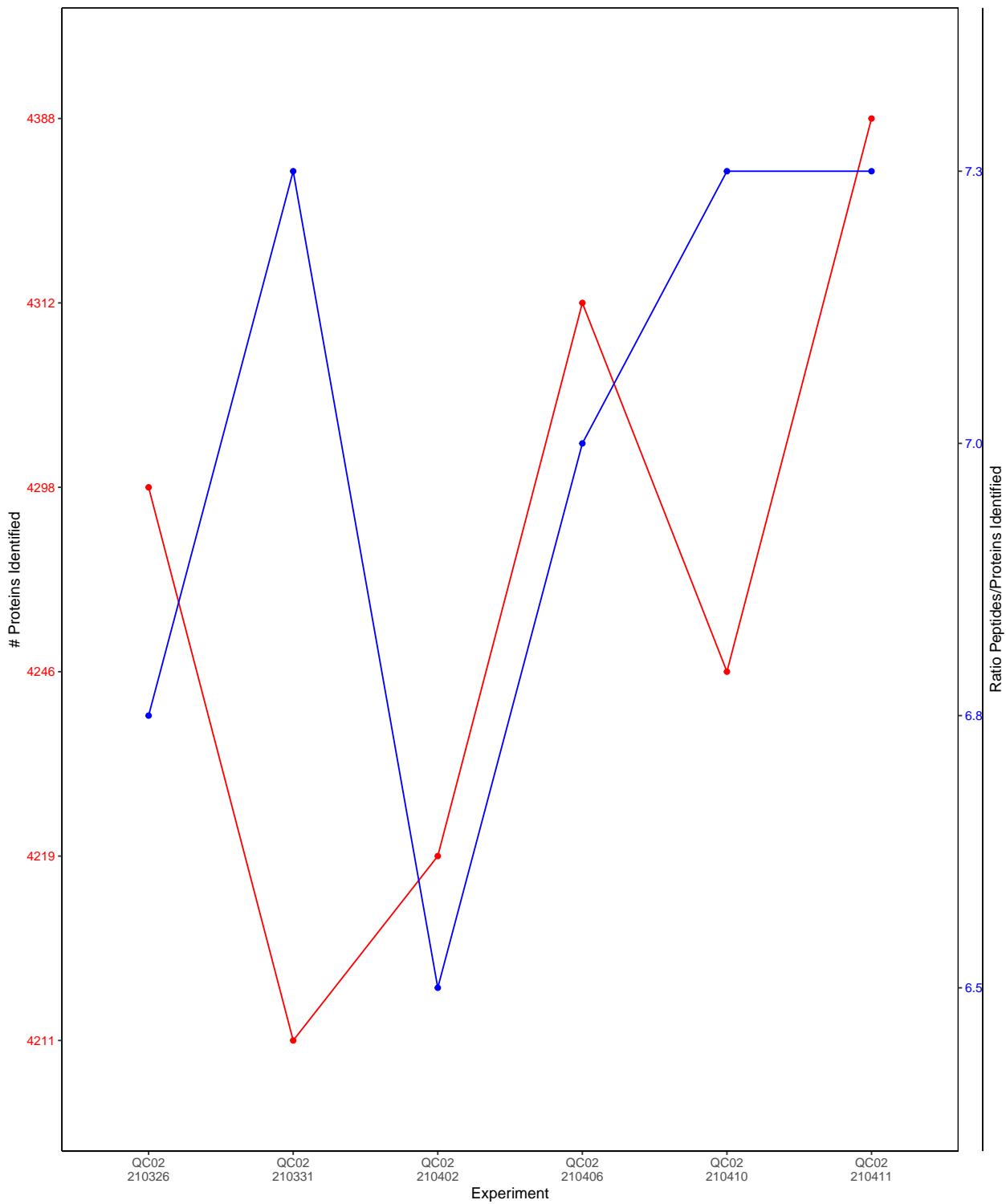


Protein Overlap Between samples

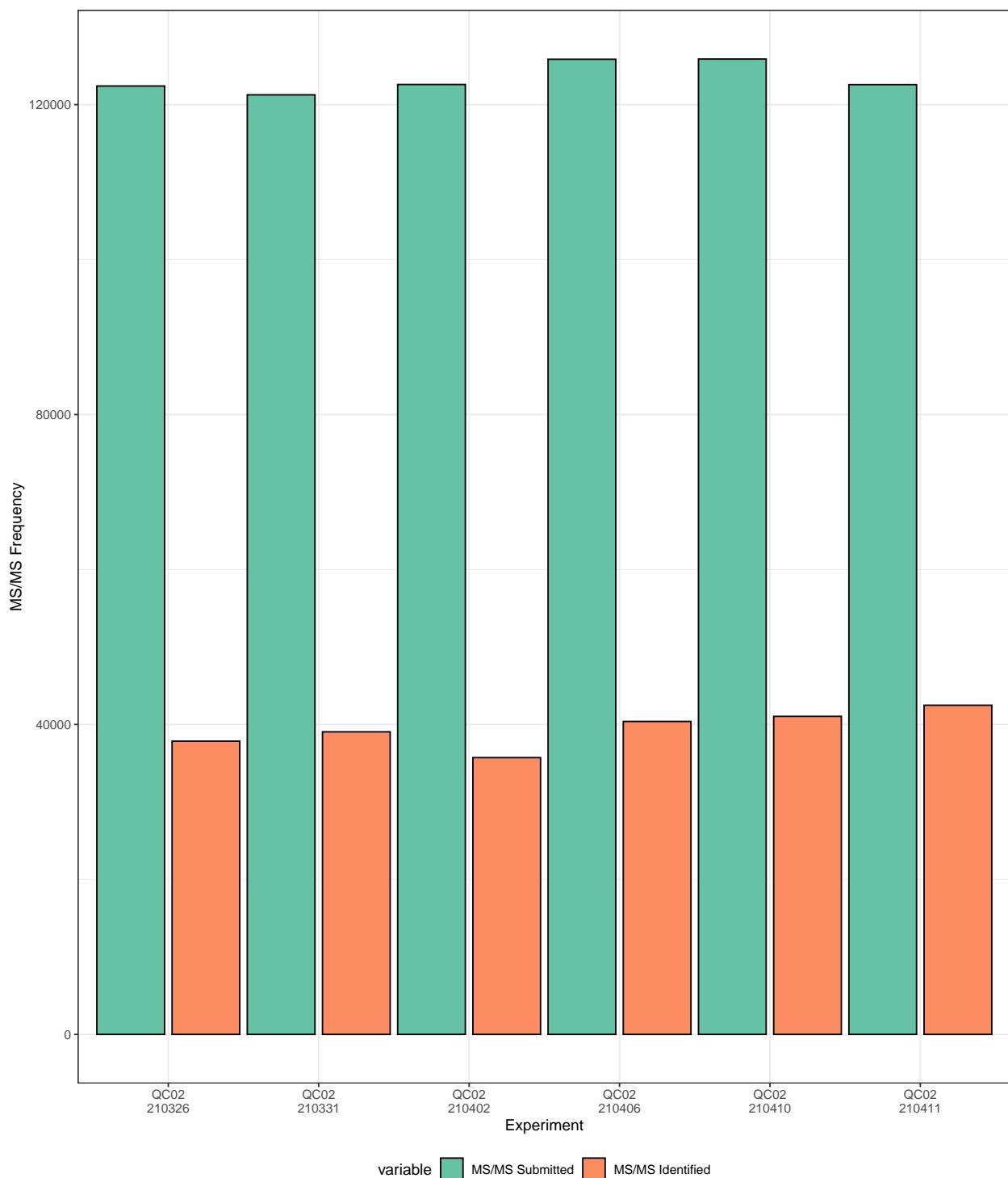


### Peptides Sequences Identified

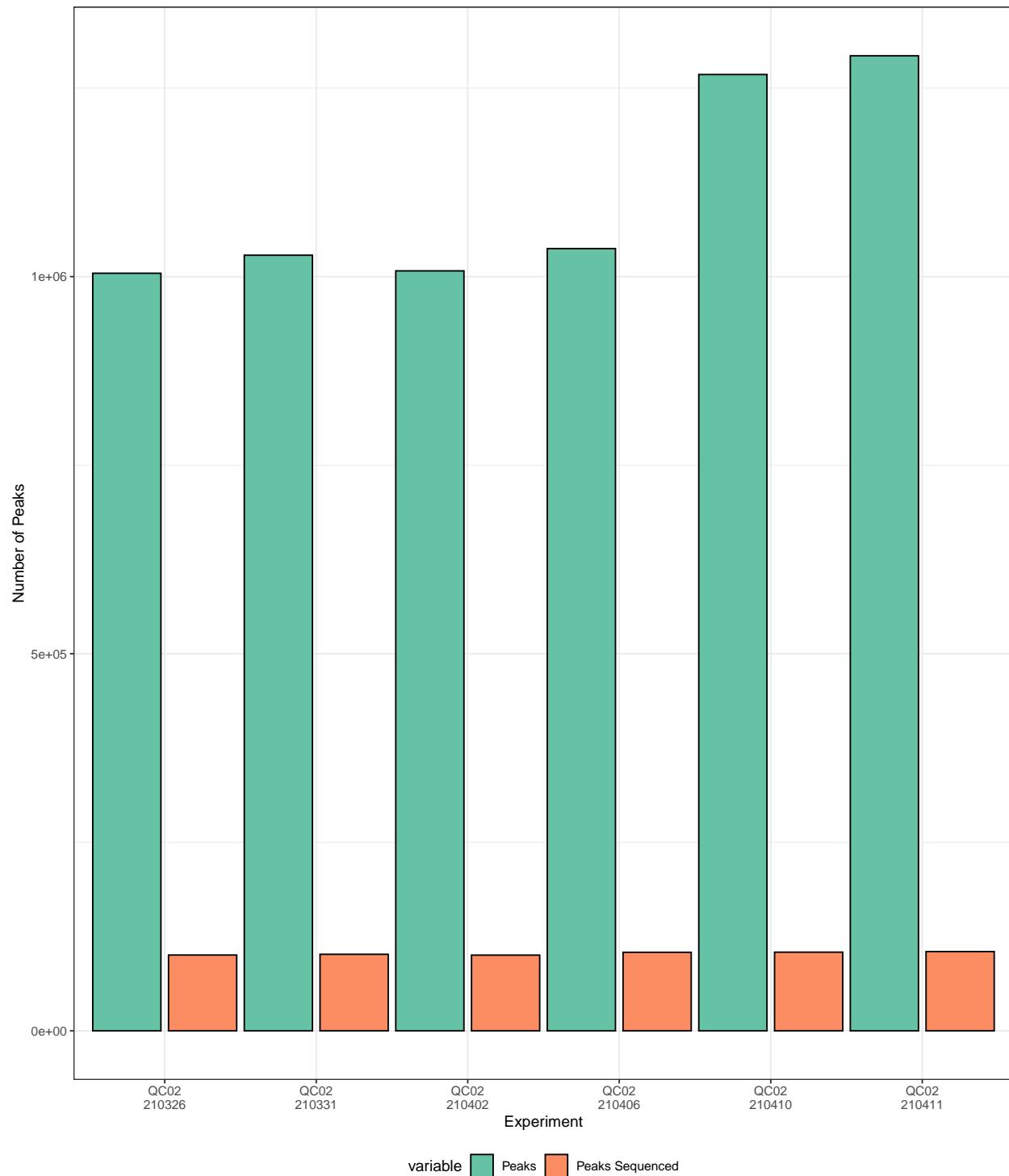




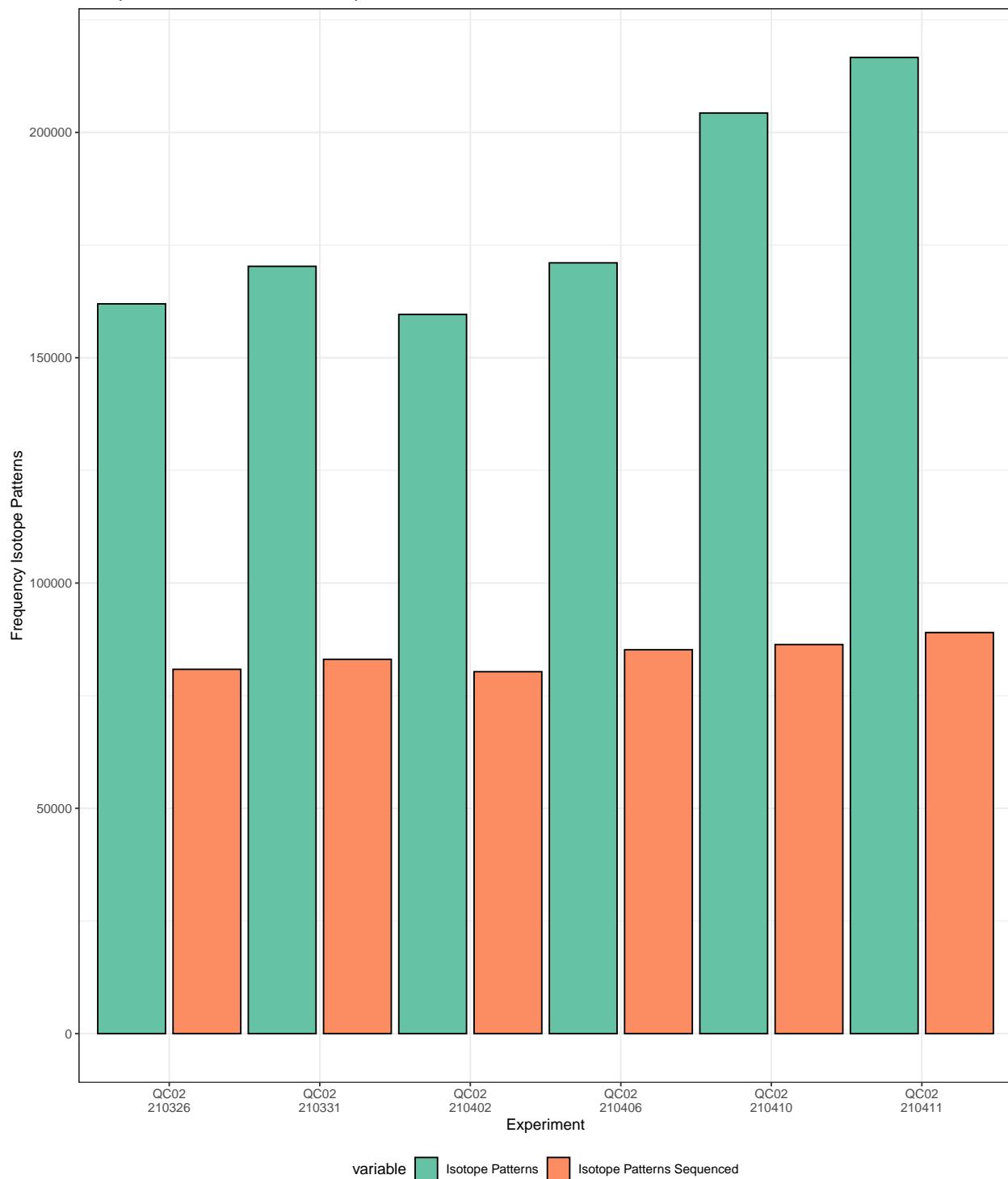
### MS/MS Submitted and Identified



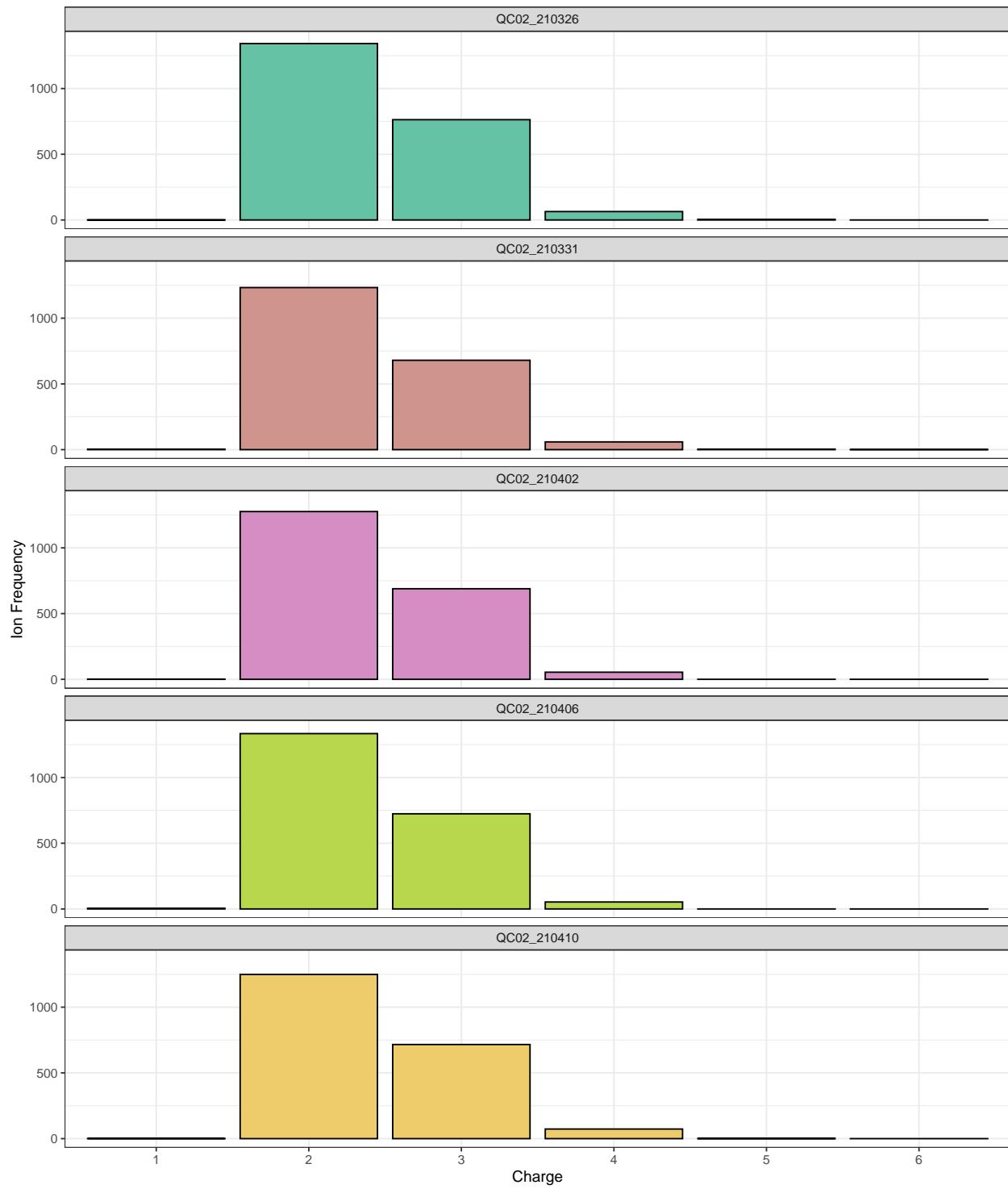
Peaks detected and sequenced in the full scans



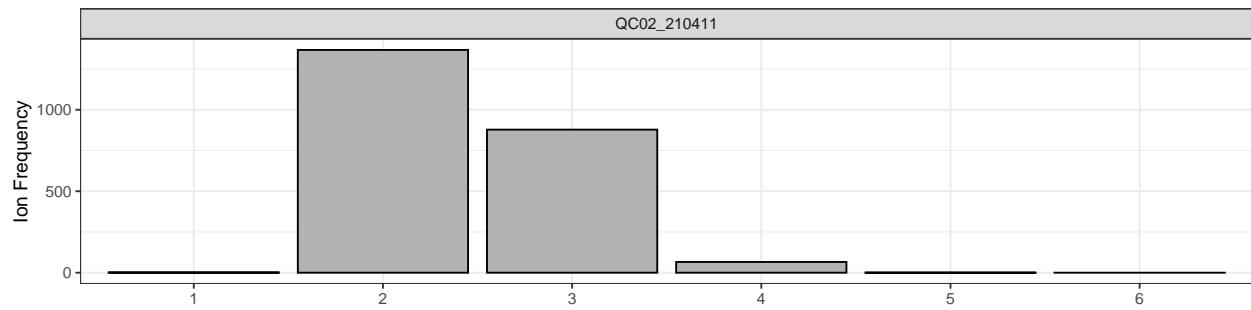
### Isotope Patterns detected and sequenced



The charge-state of the precursor ion.



The charge-state of the precursor ion.

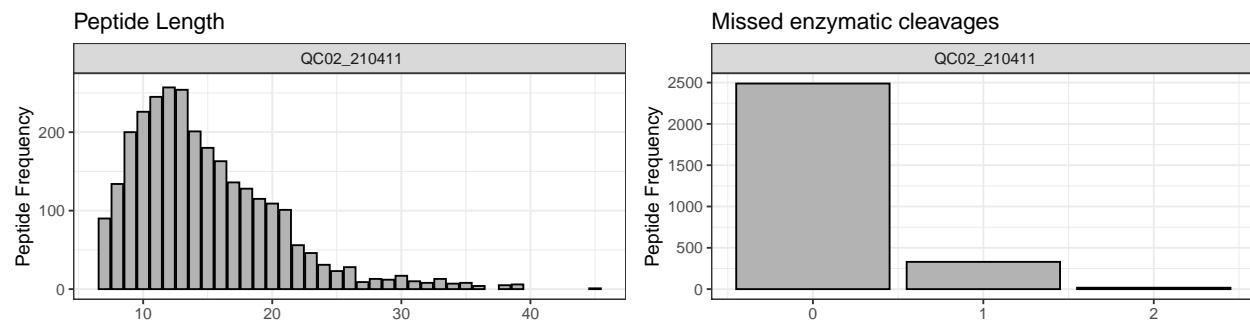


Charge

## Protease Specificity



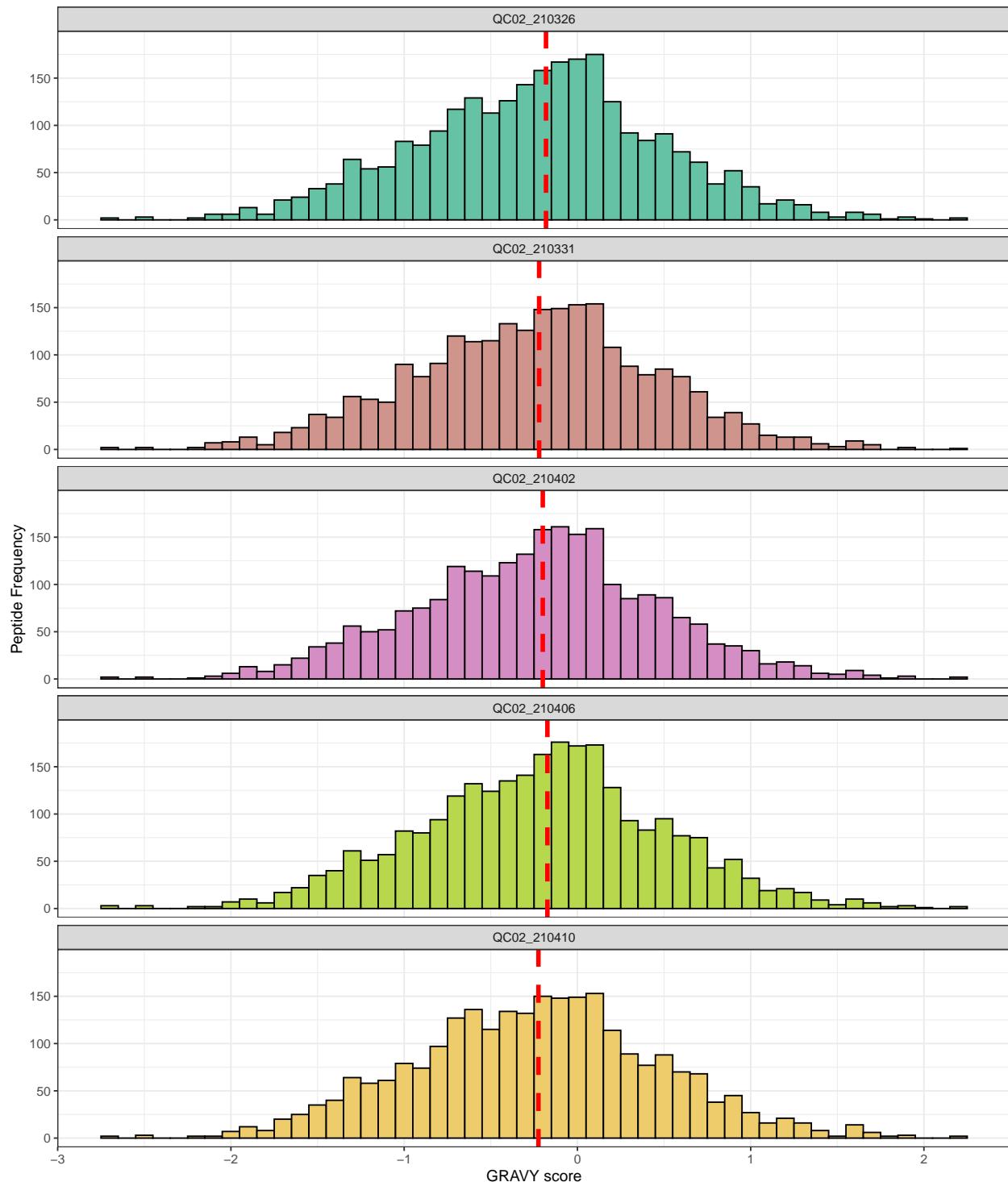
## Protease Specificity



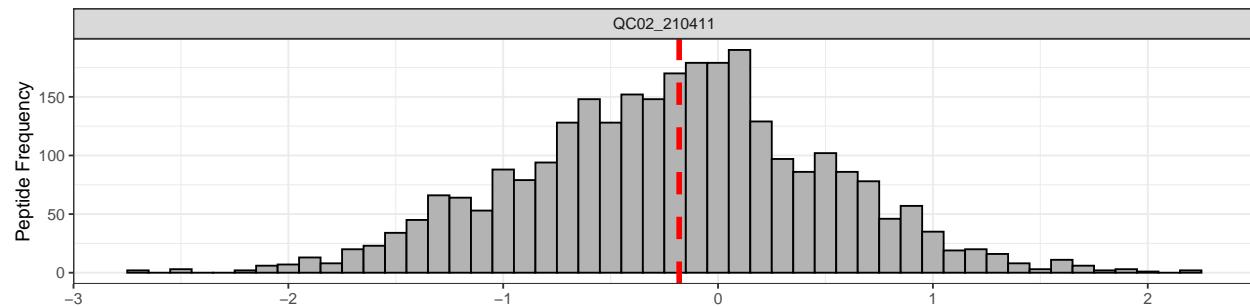
Peptide length

Missed Cleavages

### Peptide hydrophathy distribution

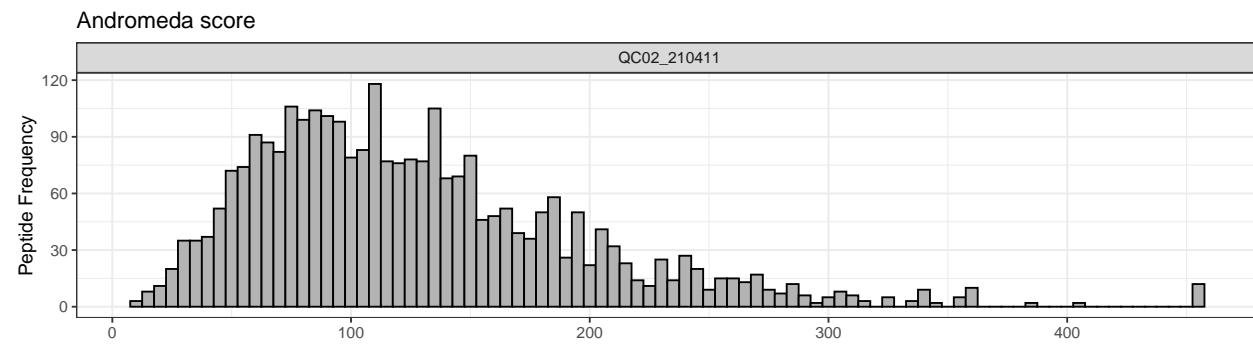


### Peptide hydrophathy distribution

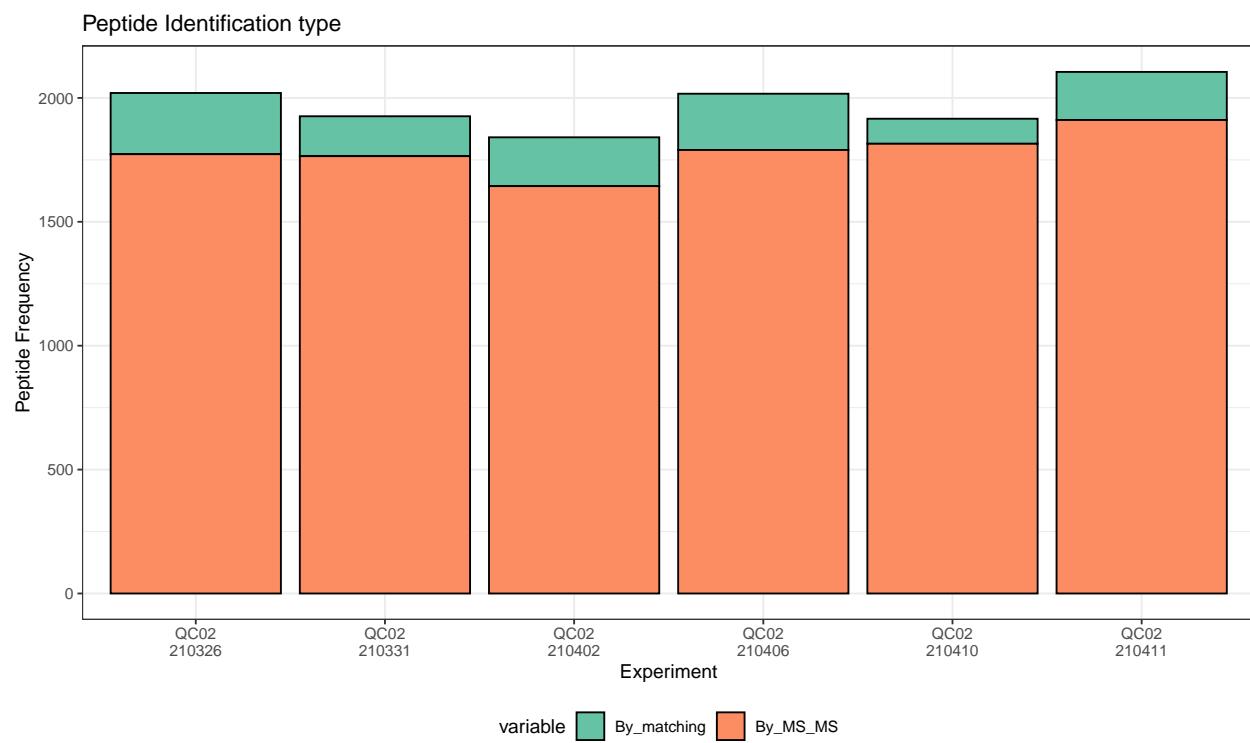
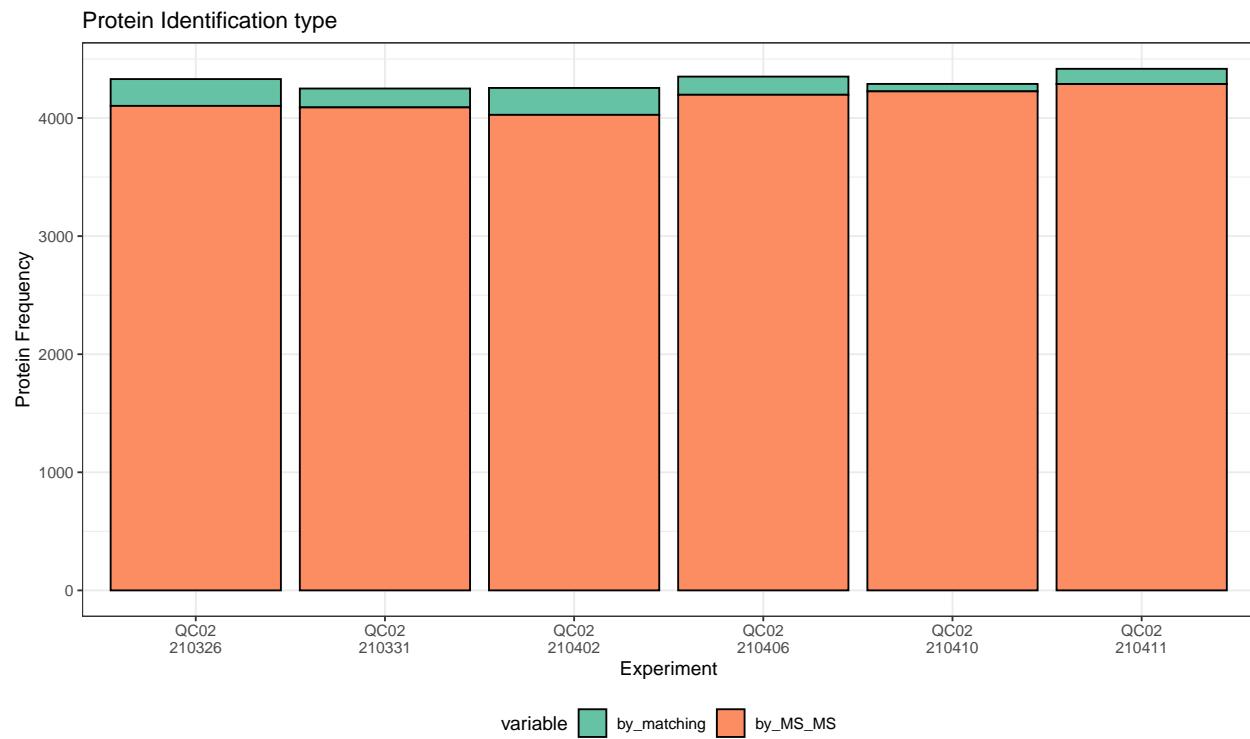


GRAVY score

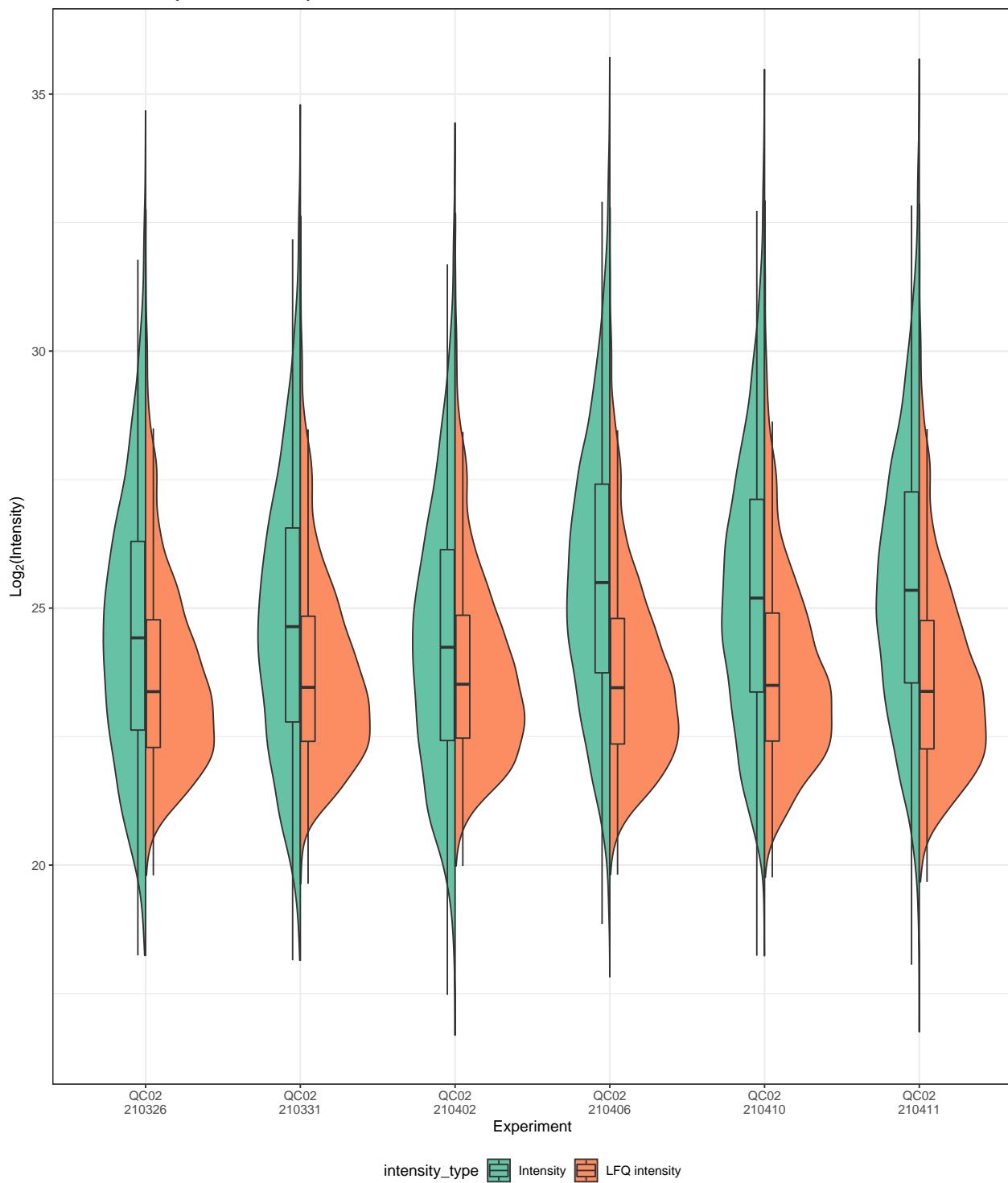


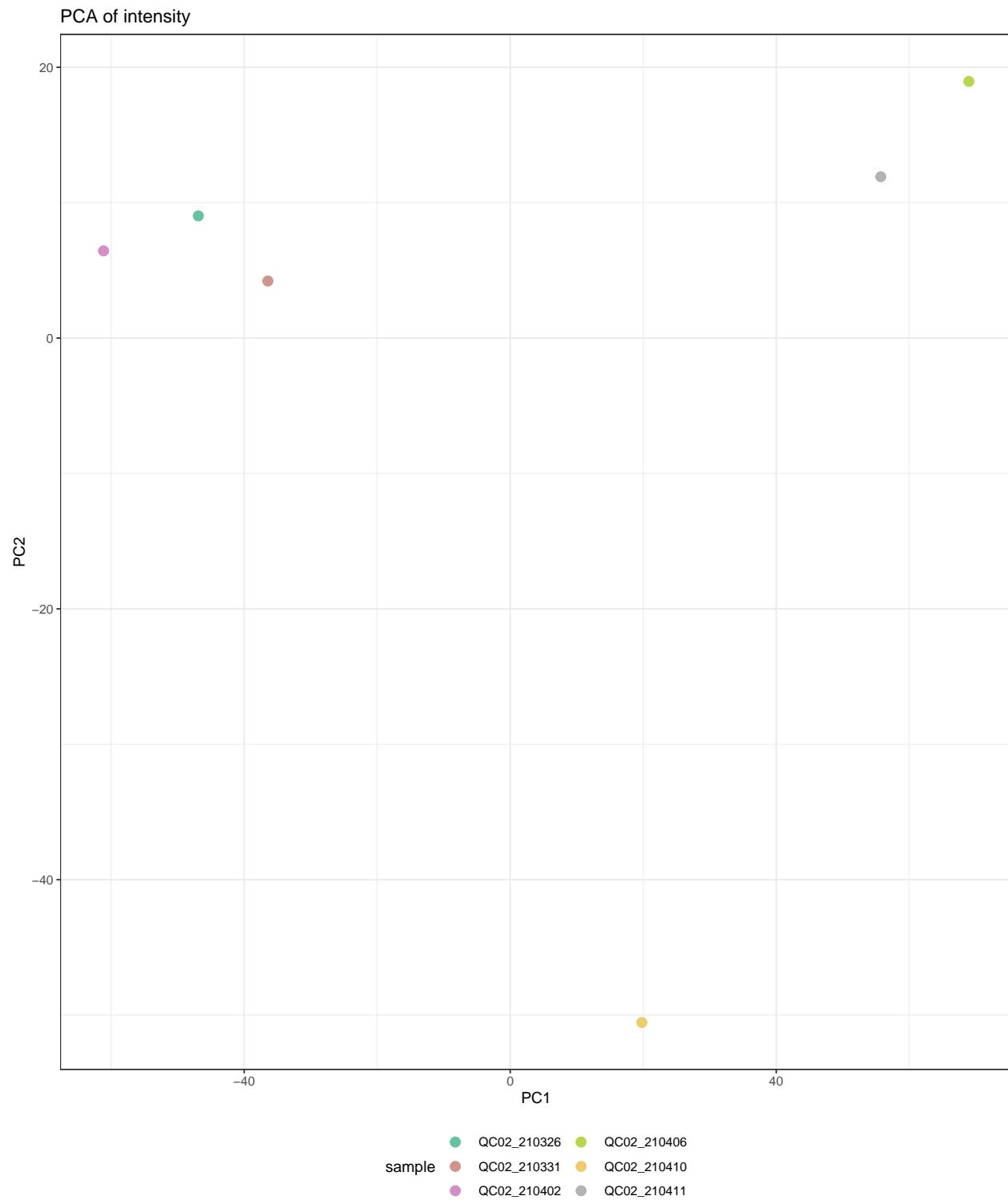


Score

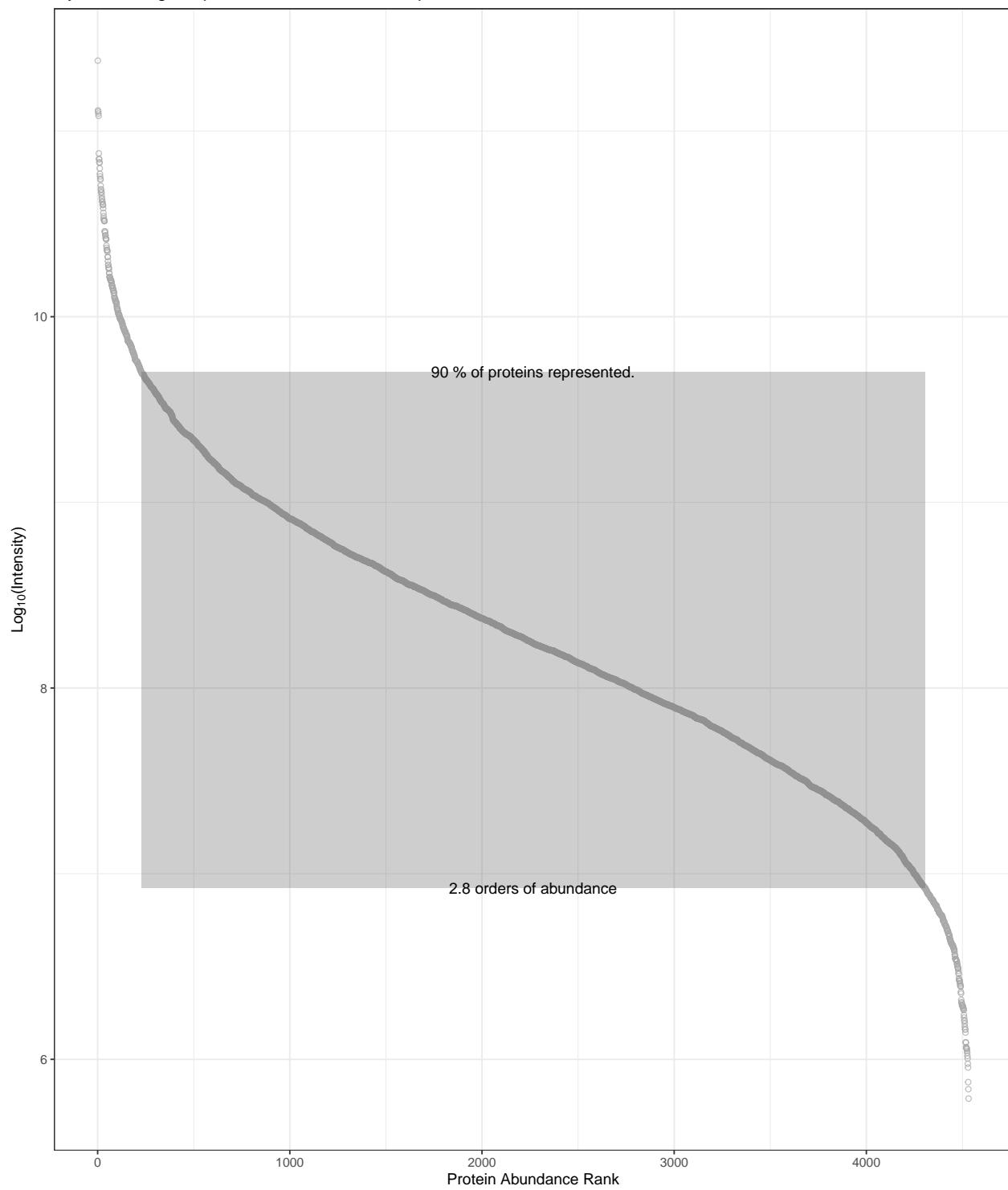


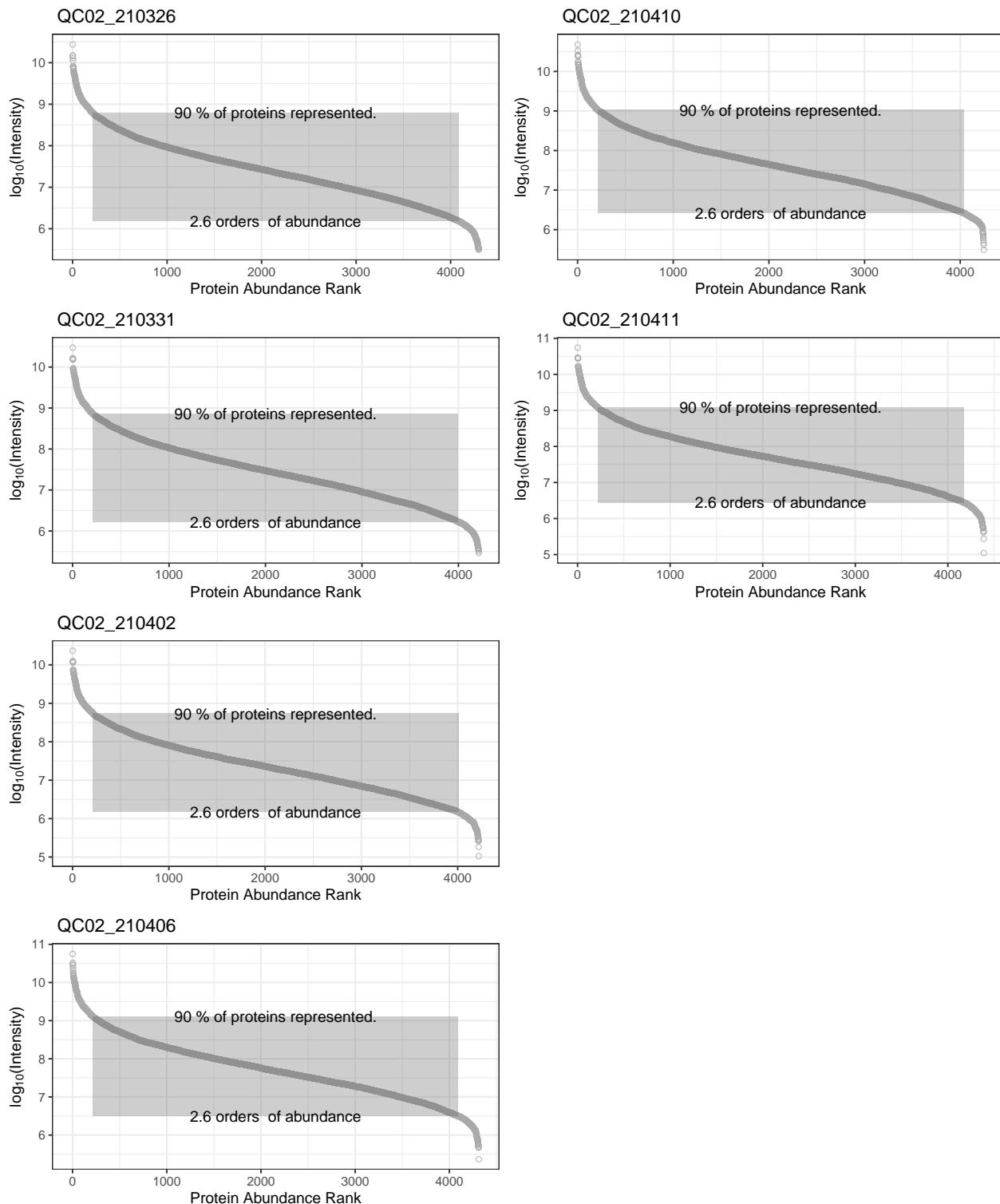
### Protein Intensity & LFQ intensity





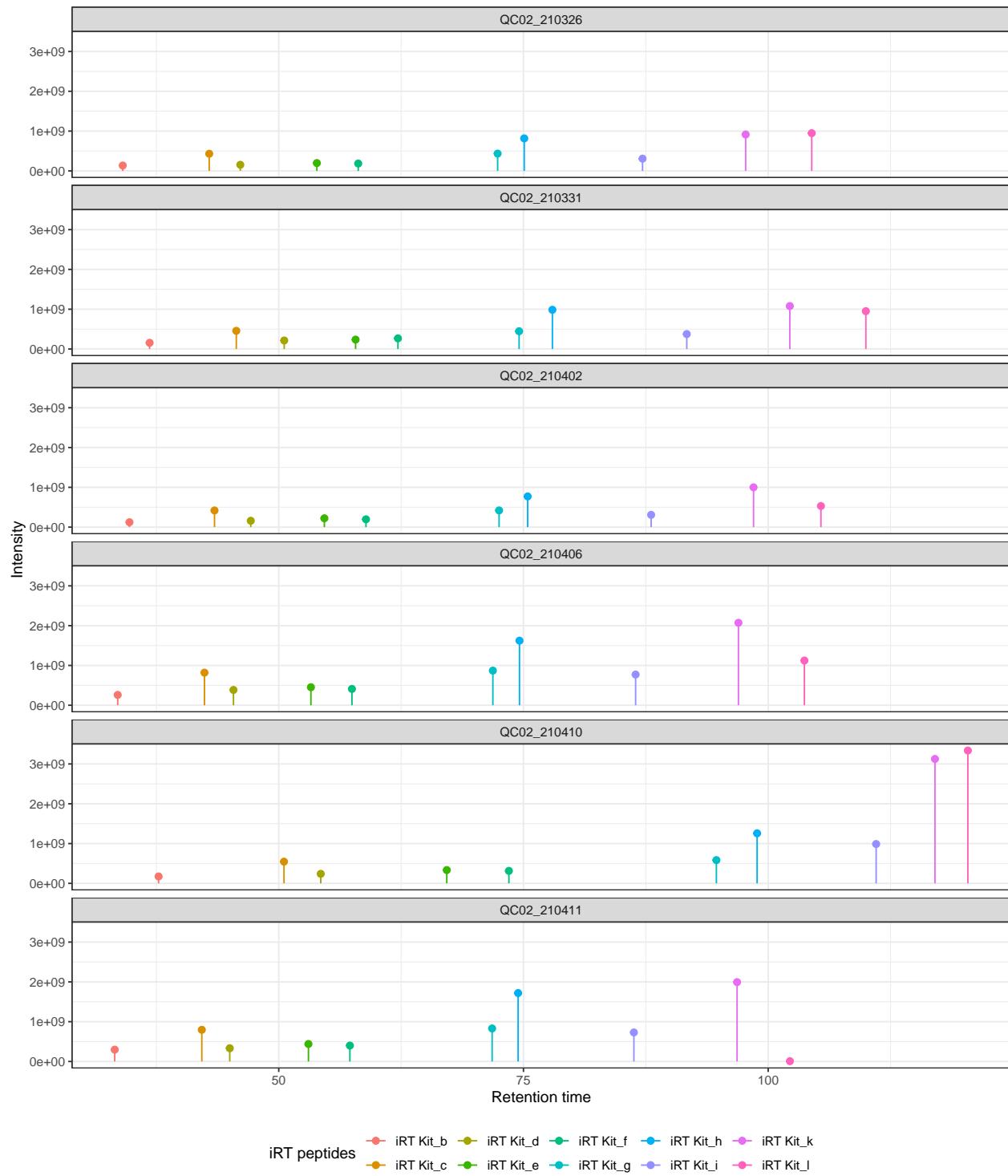
Dynamic range of protein abundance all samples



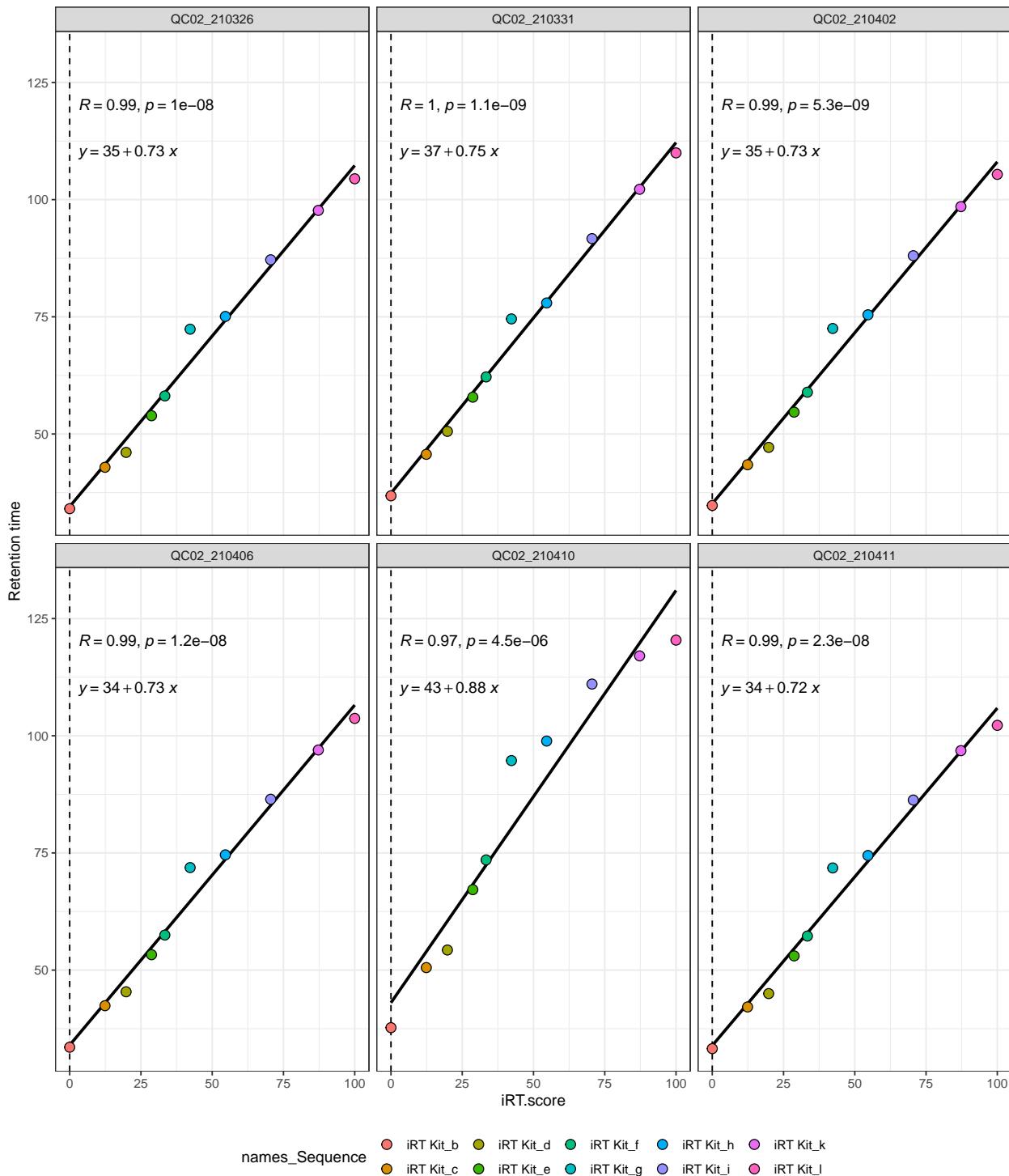


```
## [1] "No UniprotID provided."
```

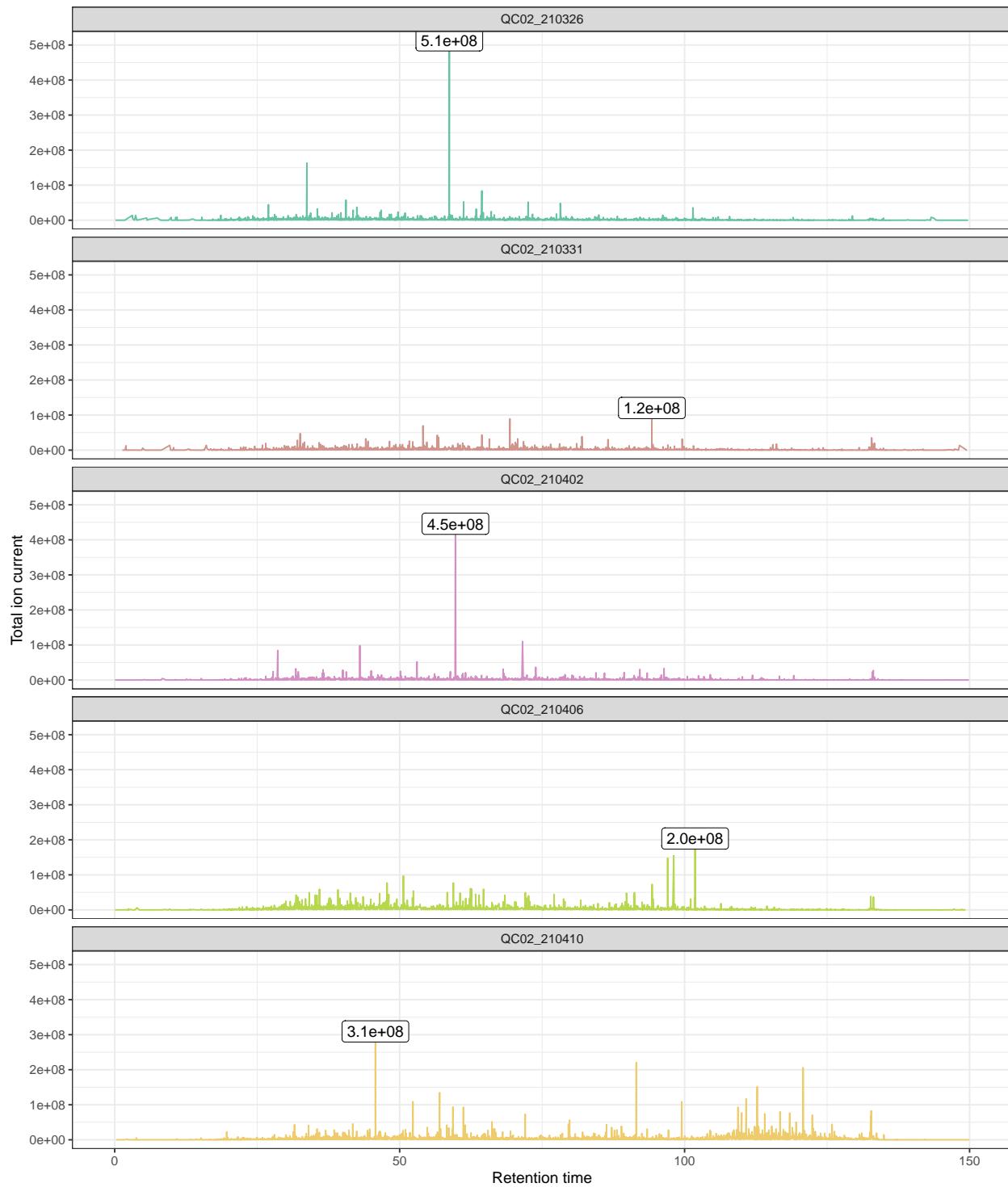
Biognosys iRT peptides in each sample.



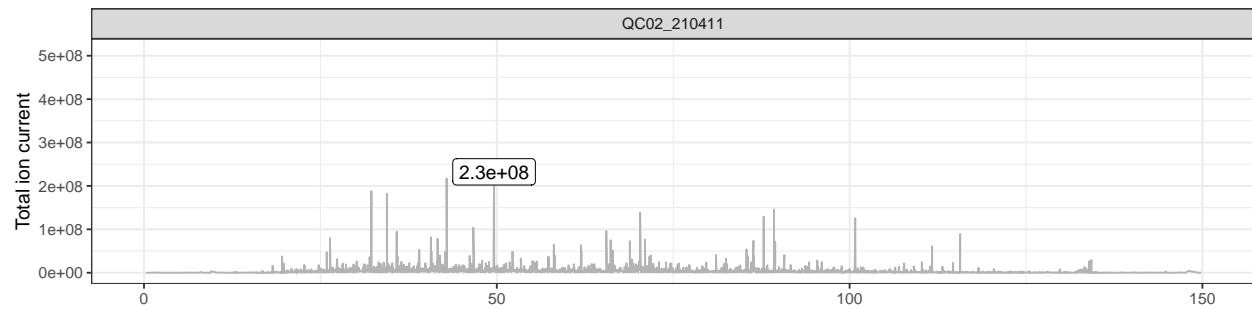
Retention time of the Biognosys iRT peptides.



### Total Ion Current

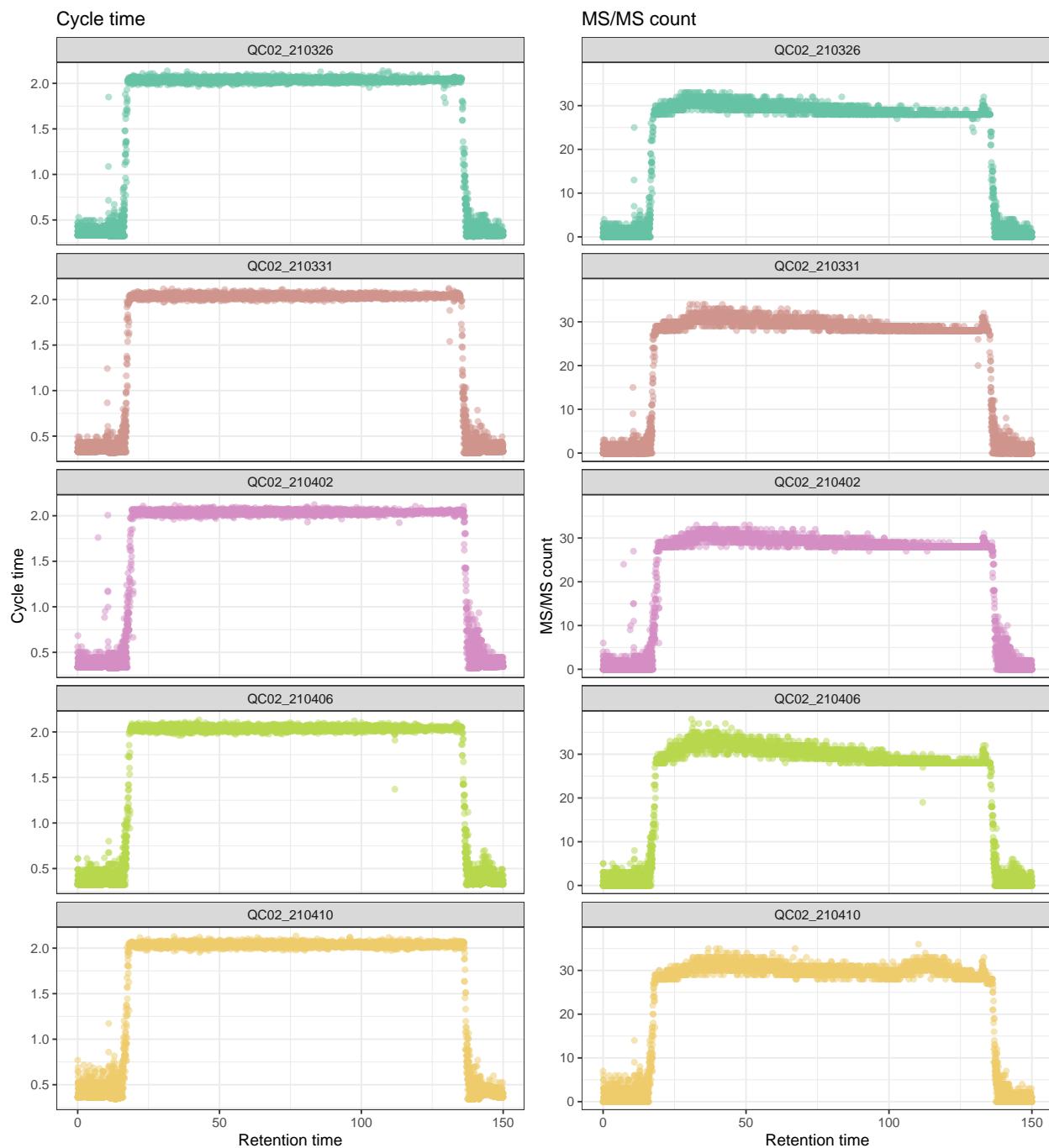


### Total Ion Current

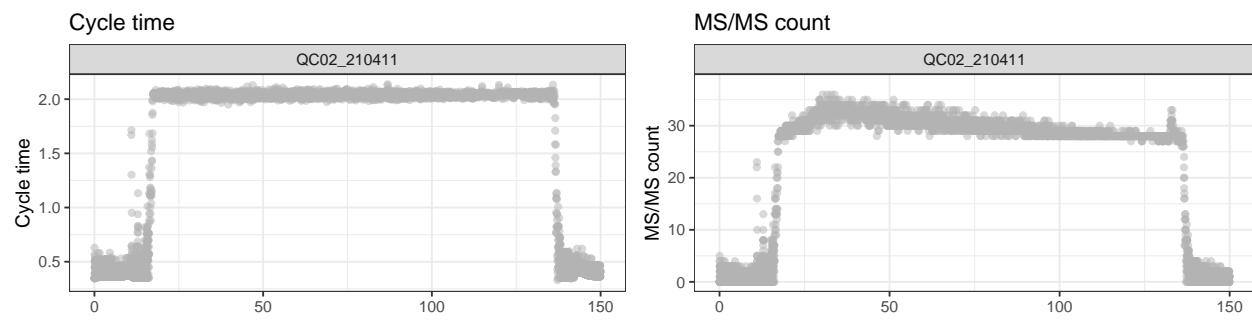


Retention time

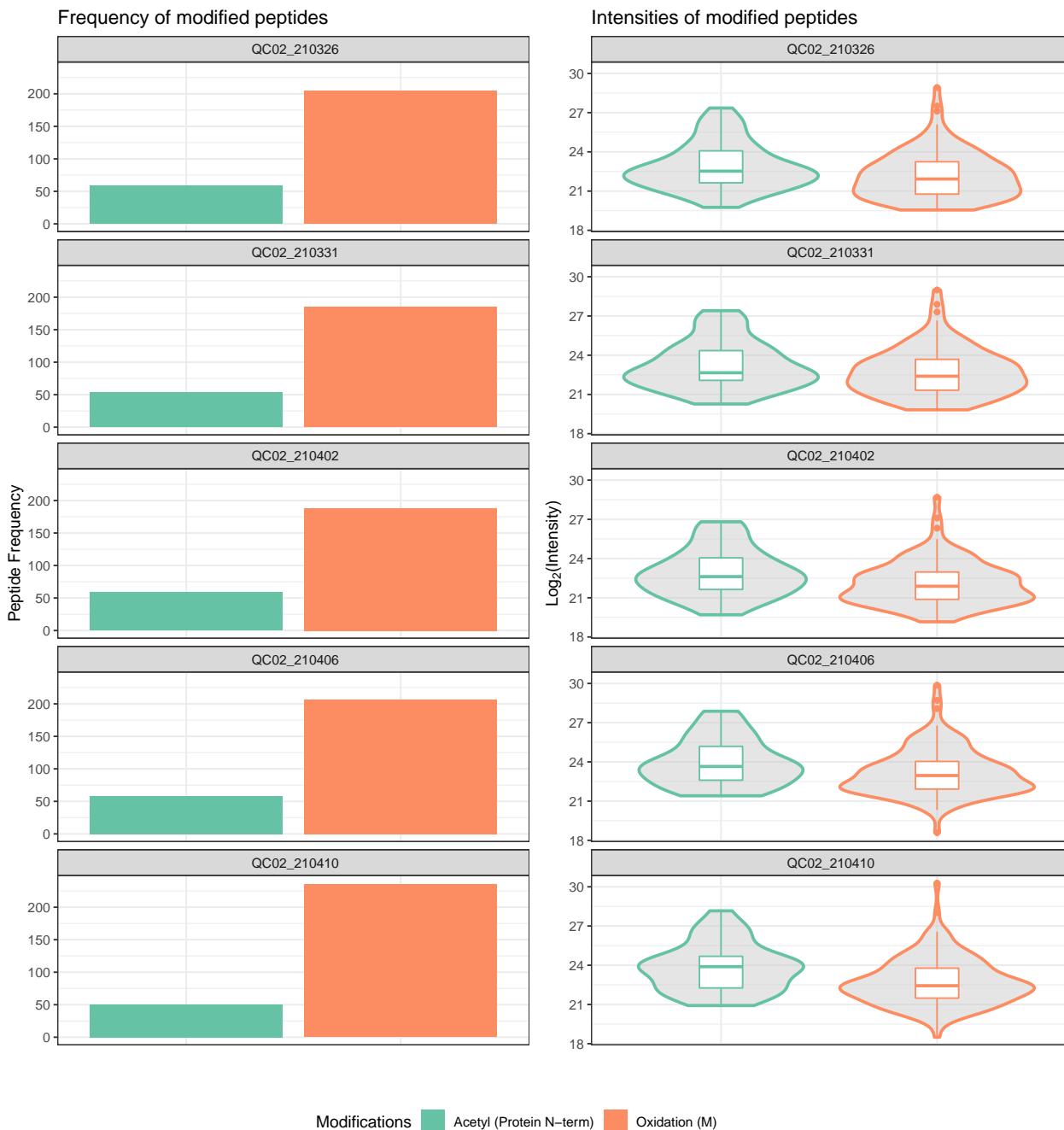
### Acquisition Cycle



### Acquisition Cycle



## Post-Translational Modifications



## Post-Translational Modifications

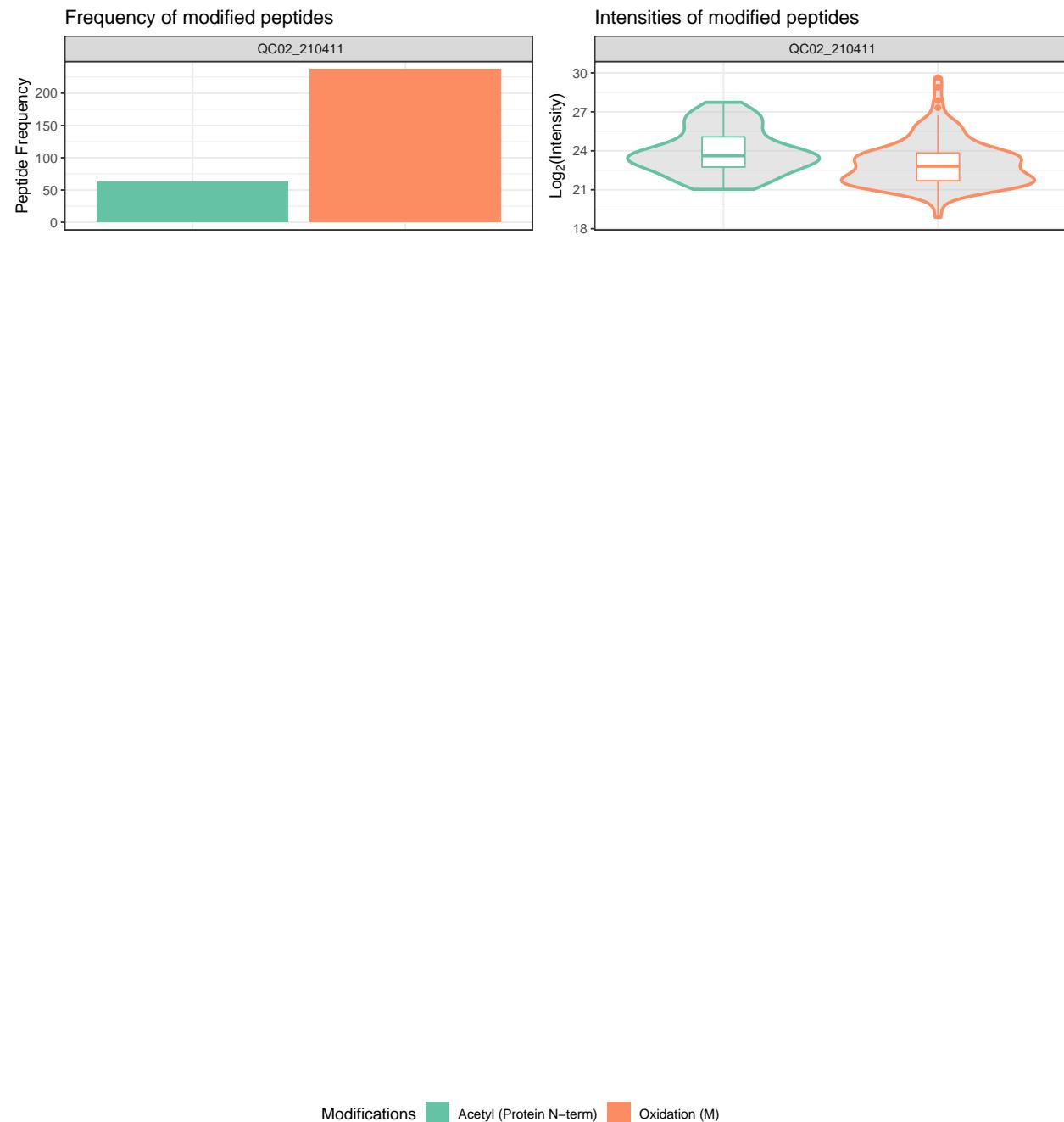


Table 1: Protein Information

	Proteins Identified	Missing values	Potential contaminants	Only identified by Reversesite		Peptide Sequences Identified	Peptides/Proteins
Combined Samples	4751	NA	100	66	70	47126	9.9
QC02 210326	4456	295	91	43	33	29292	6.6
QC02 210331	4358	393	92	38	24	30920	7.1
QC02 210402	4380	371	94	42	36	27603	6.3
QC02 210406	4478	273	92	49	35	30341	6.8
QC02 210410	4404	347	94	47	30	31110	7.1
QC02 210411	4553	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

Experiment	Mean	Max	Min	Median
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