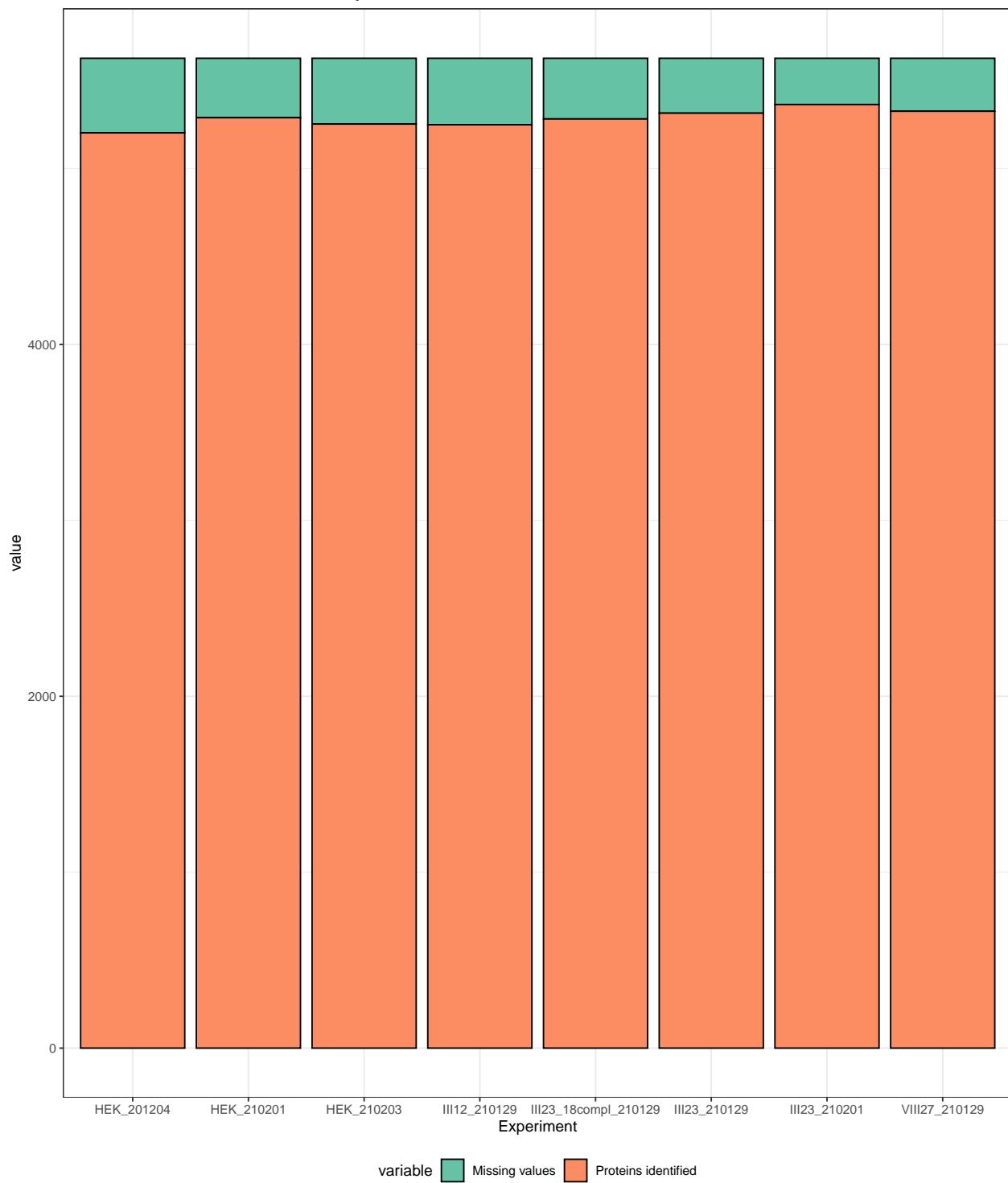


# MQmetrics Report

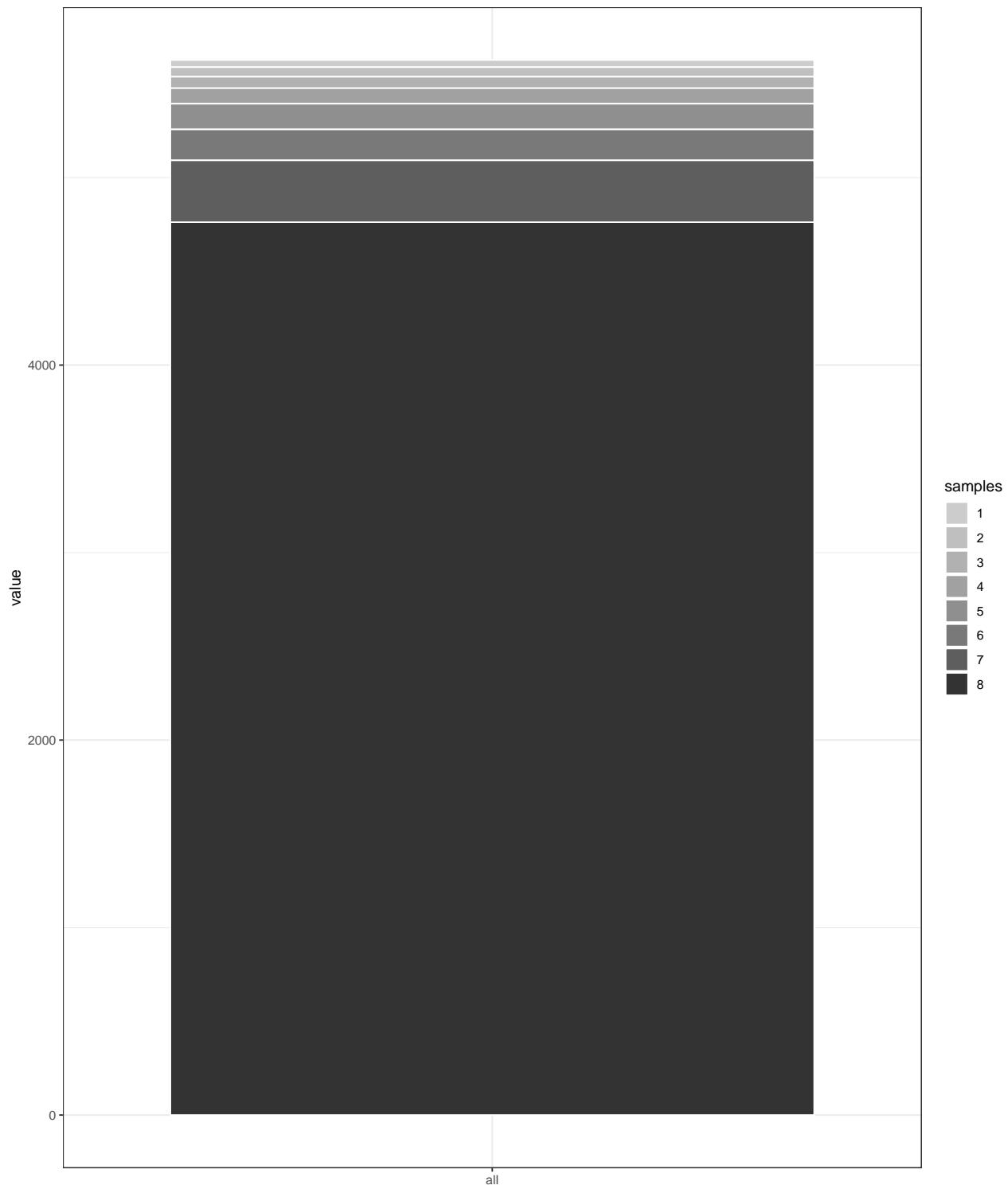
19 April, 2021

```
## [1] "The MaxQuant output directory is: /home/alvaro/Documents/MaxQuant/example5/combined/"
## [1] "The experiment started the day: 07/03/2021 at the time: 13:06:24."
## [1] "The whole experiment lasted: 02:07 (hours:minutes)."
## [1] "The MaxQuant version used was: 1.6.12.0"
## [1] "The user was: marek.vrbacky"
## [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\\UP000005640_9606.fasta"
## [1] "The iBAQ presence is: True"
## [1] "The PTM selected is/are: Oxidation (M);Acetyl (Protein N-term)"
```

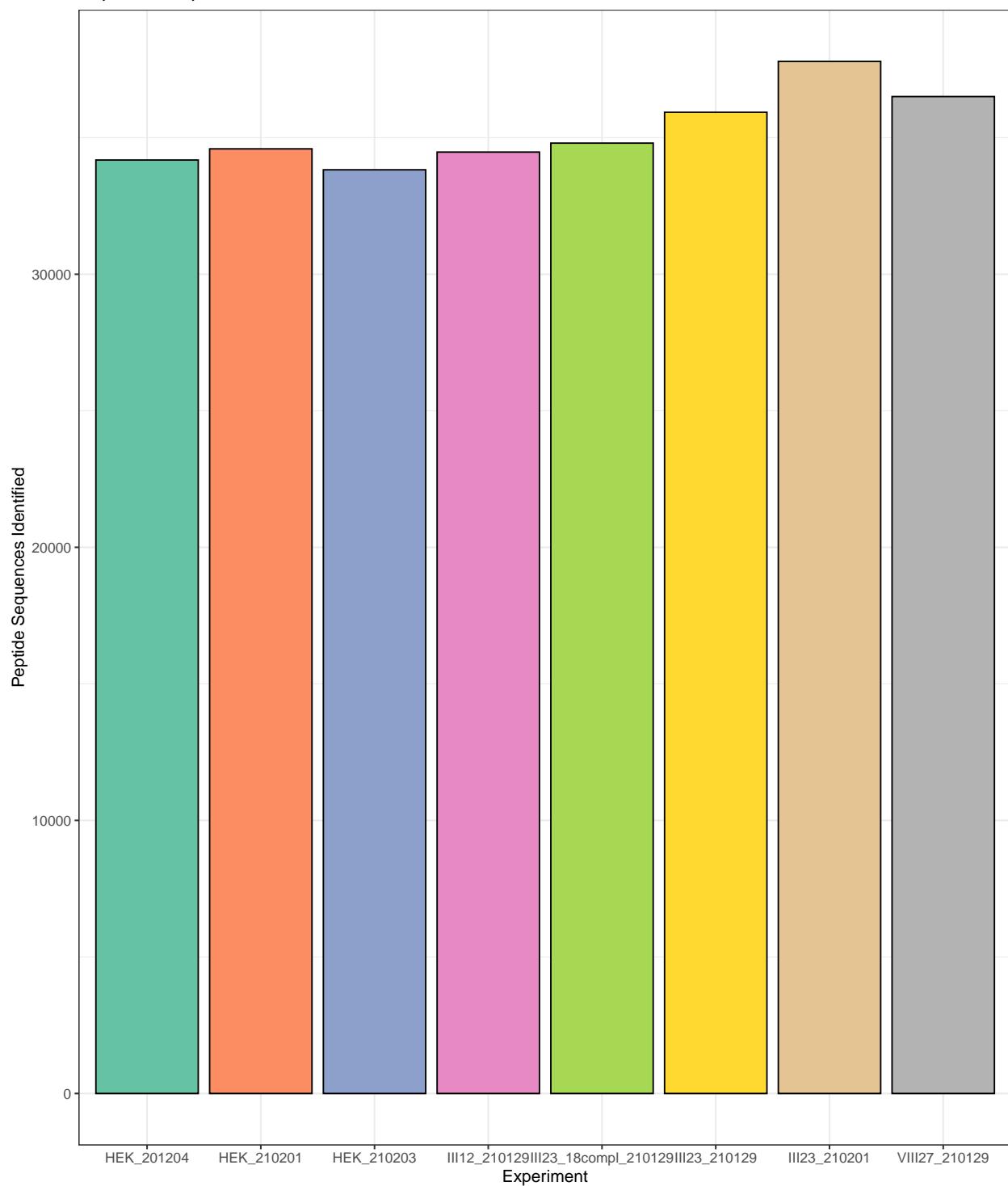
Proteins Identified based on Intensity



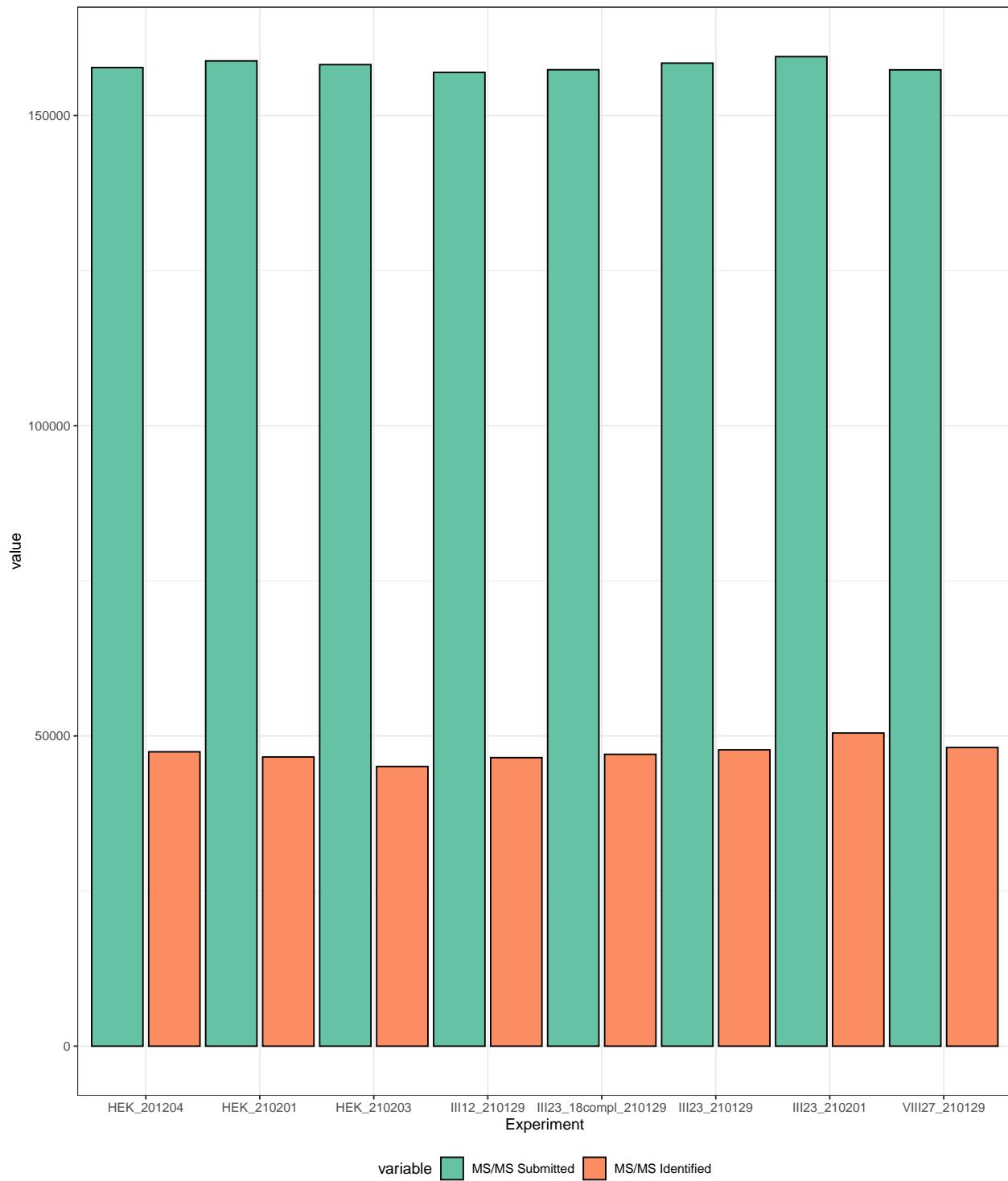
Protein Coverage of all samples



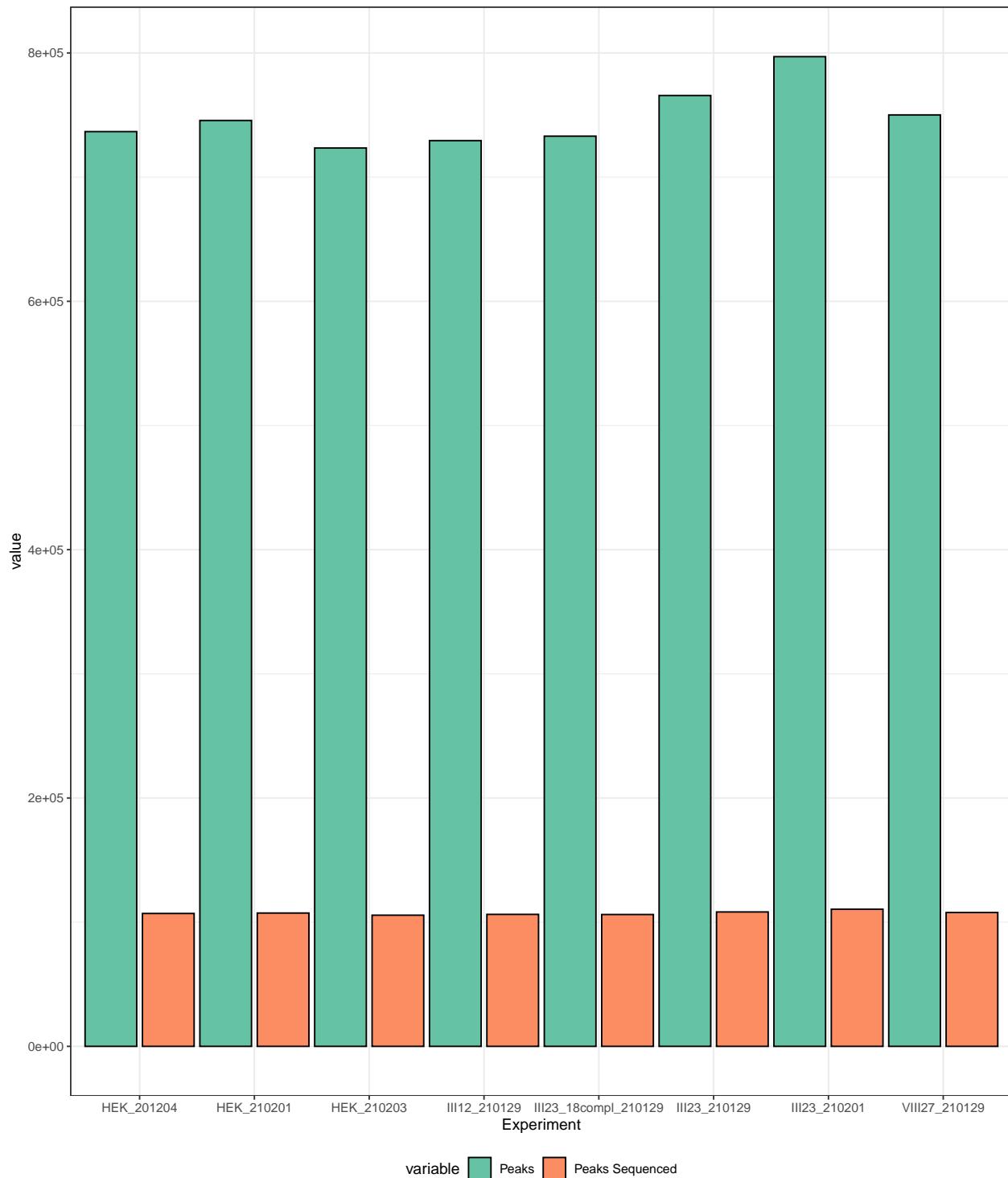
### Peptides Sequences Identified



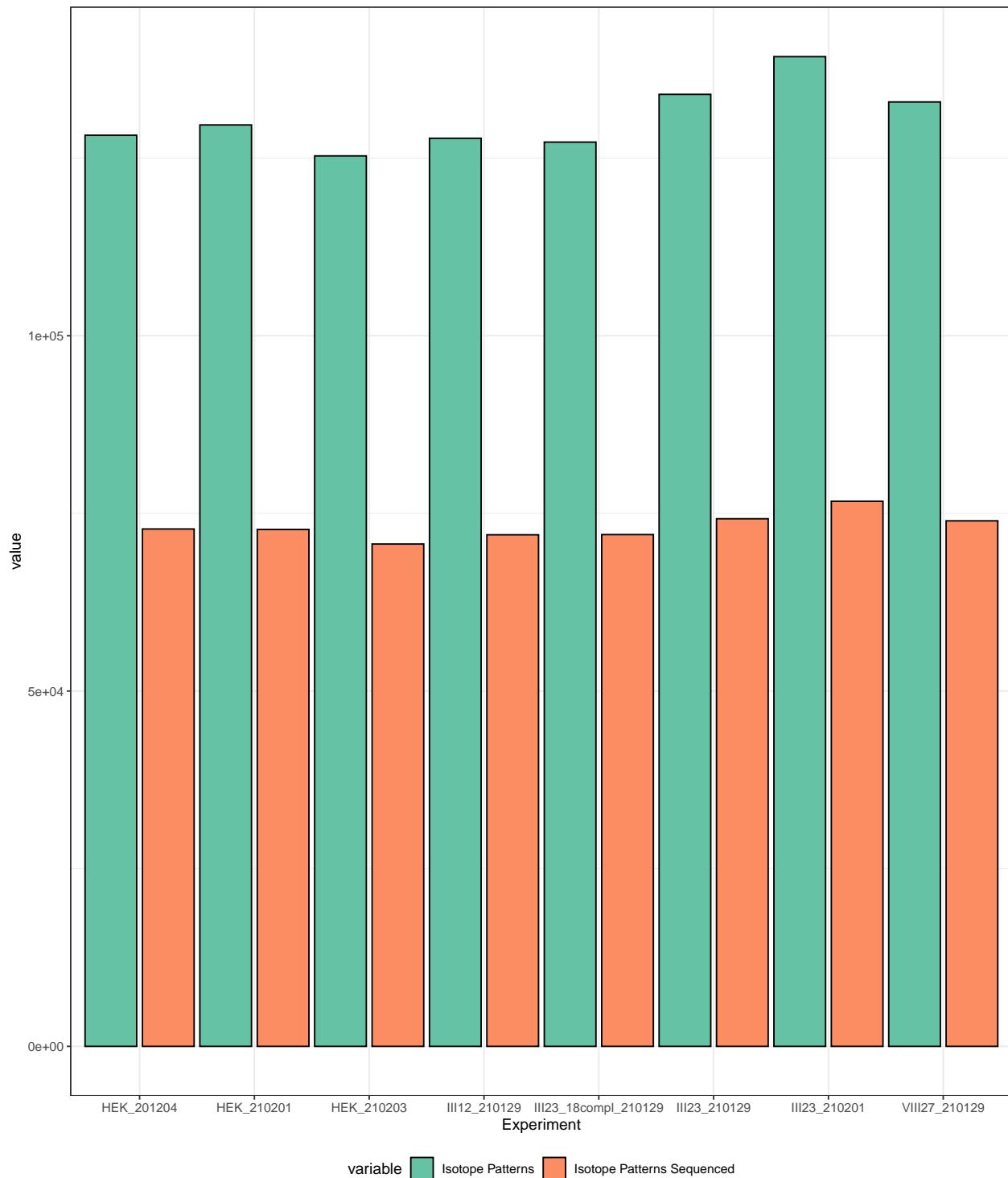
### MS/MS Submitted and Identified



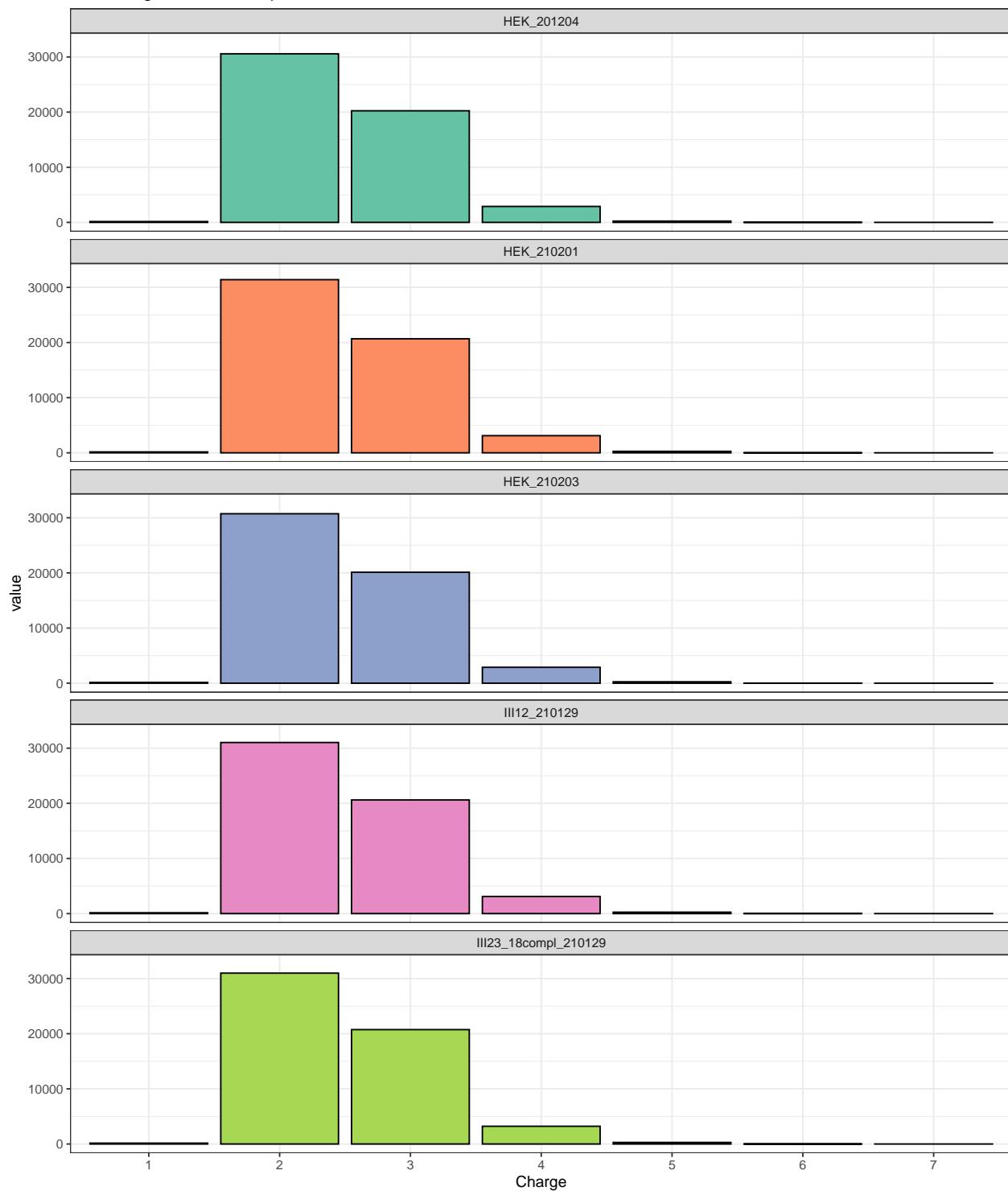
Peaks detected and sequenced in the full scans



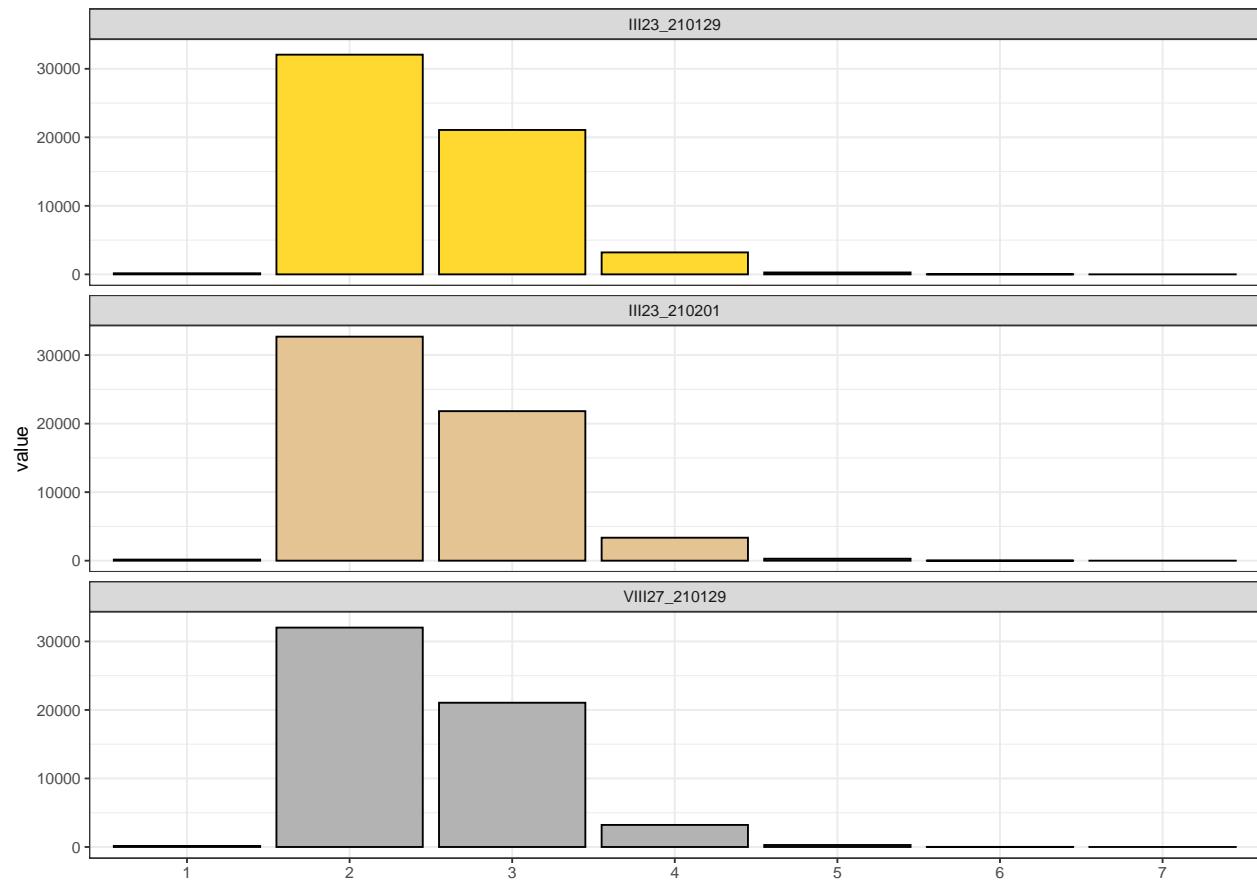
### Isotope Patterns detected and sequenced



The charge-state of the precursor ion.

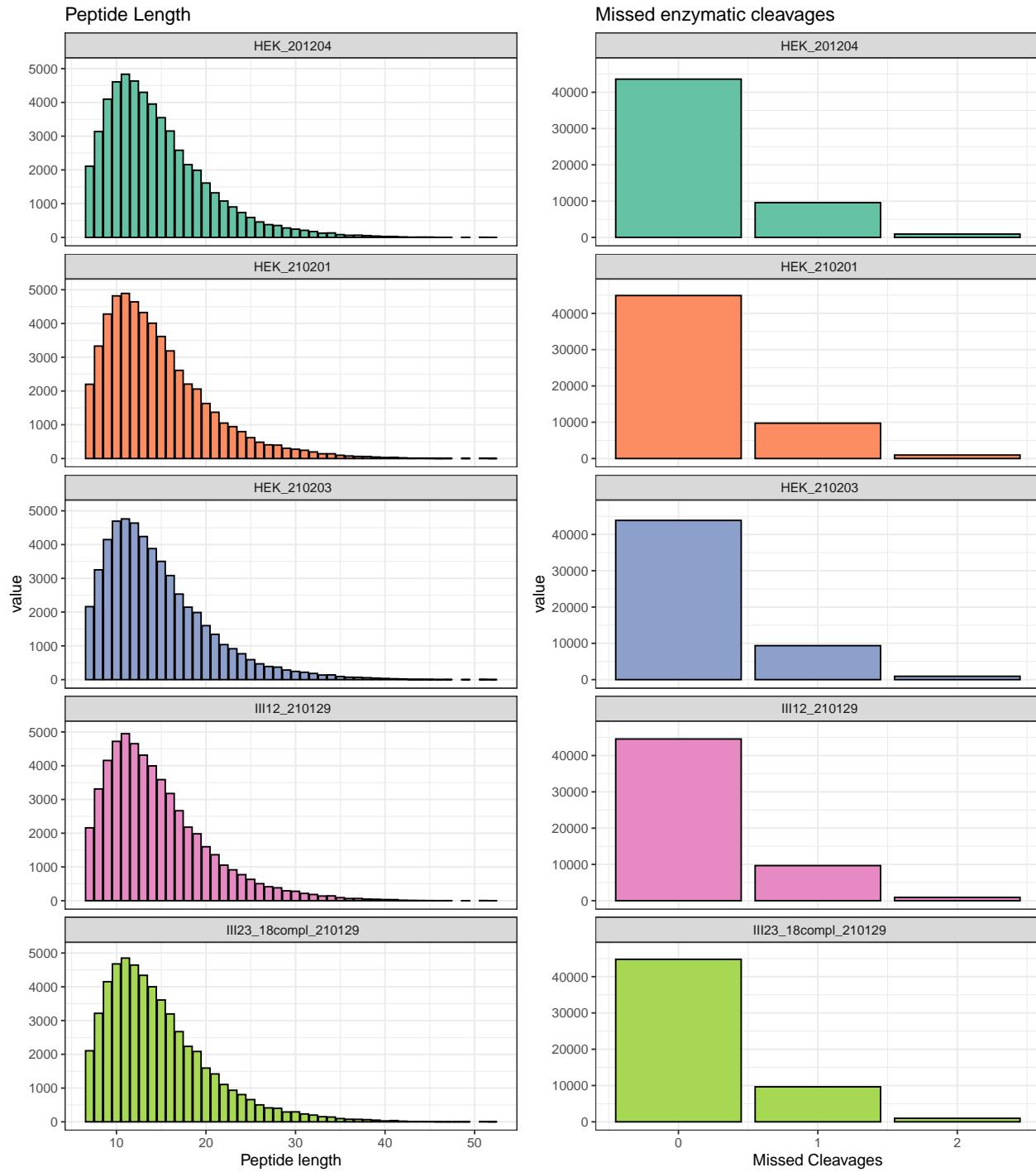


The charge-state of the precursor ion.

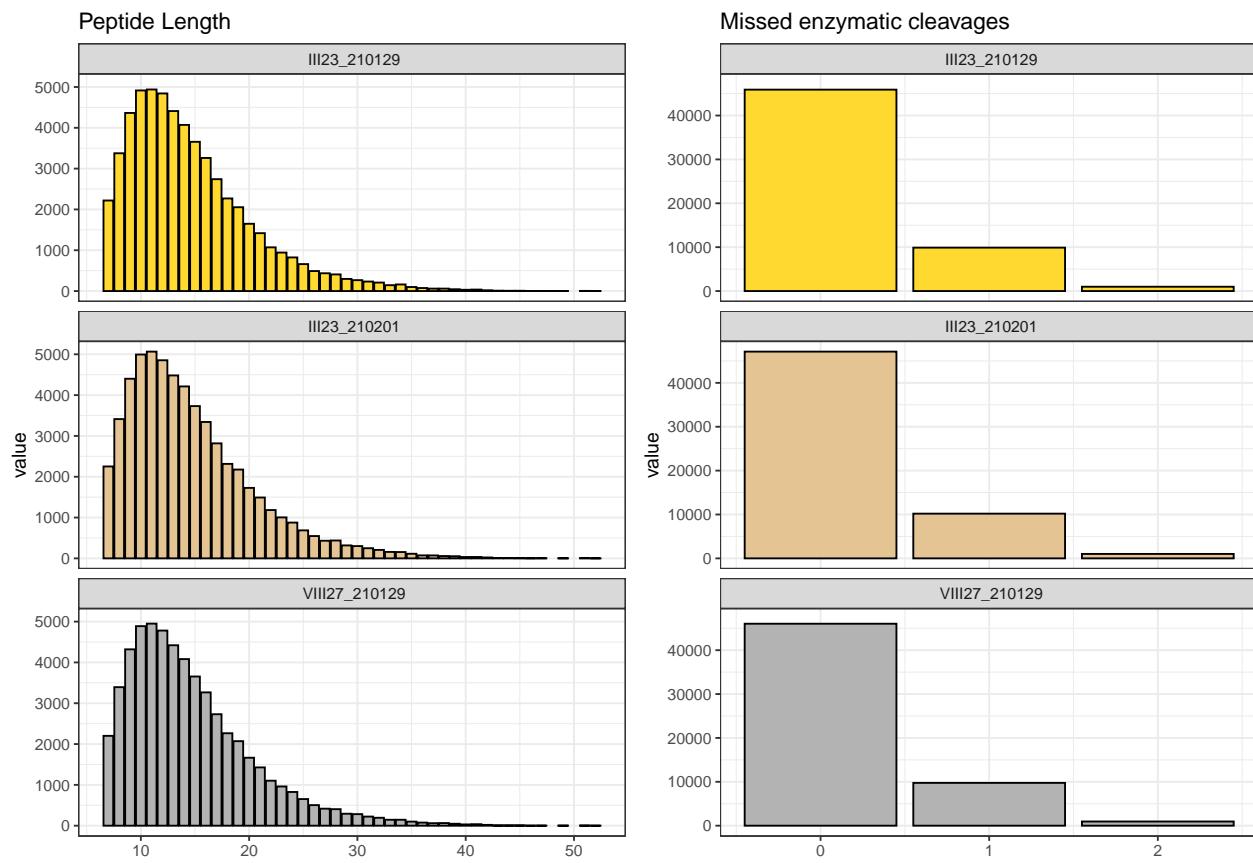


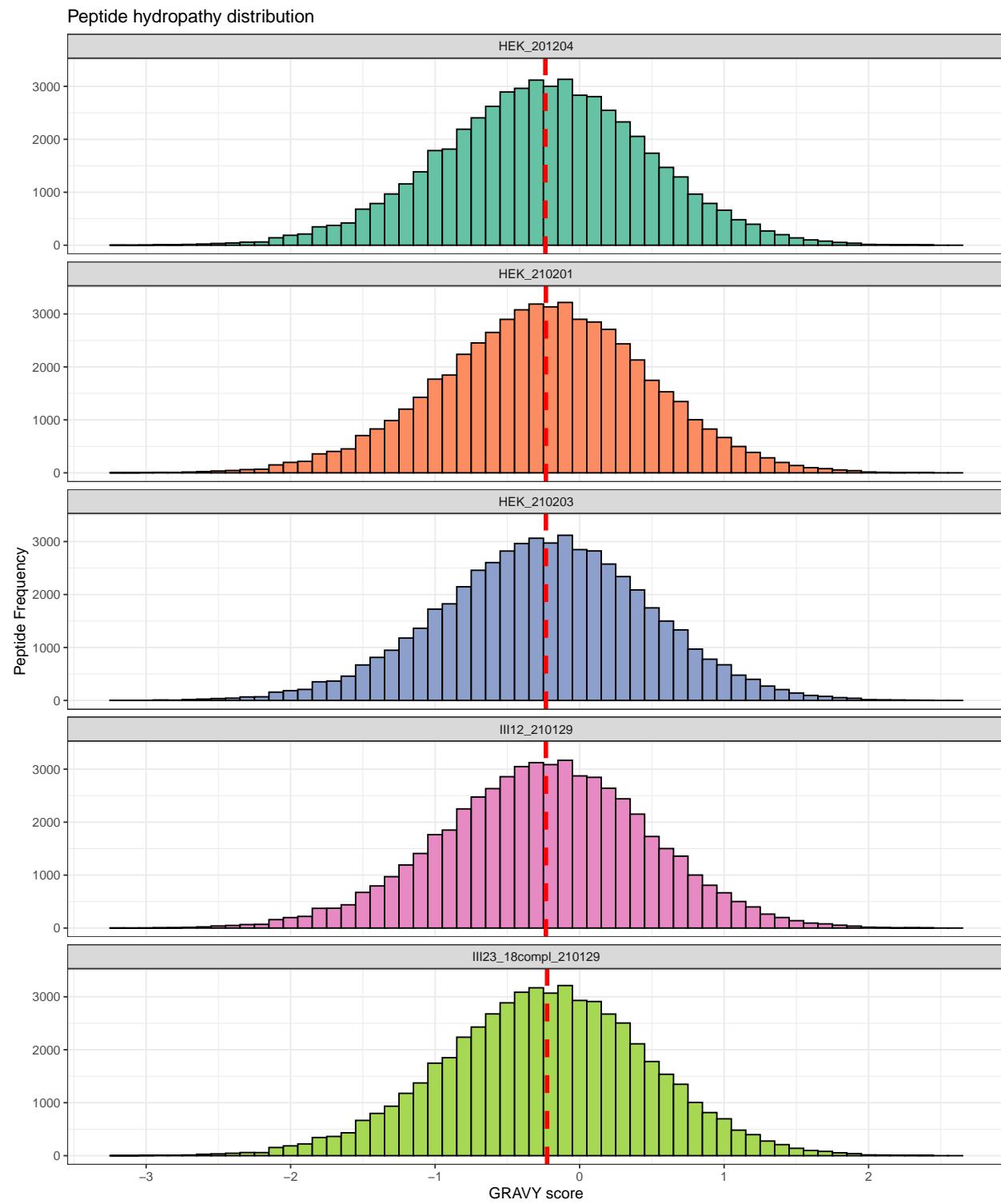
Charge

## Protease Specificity

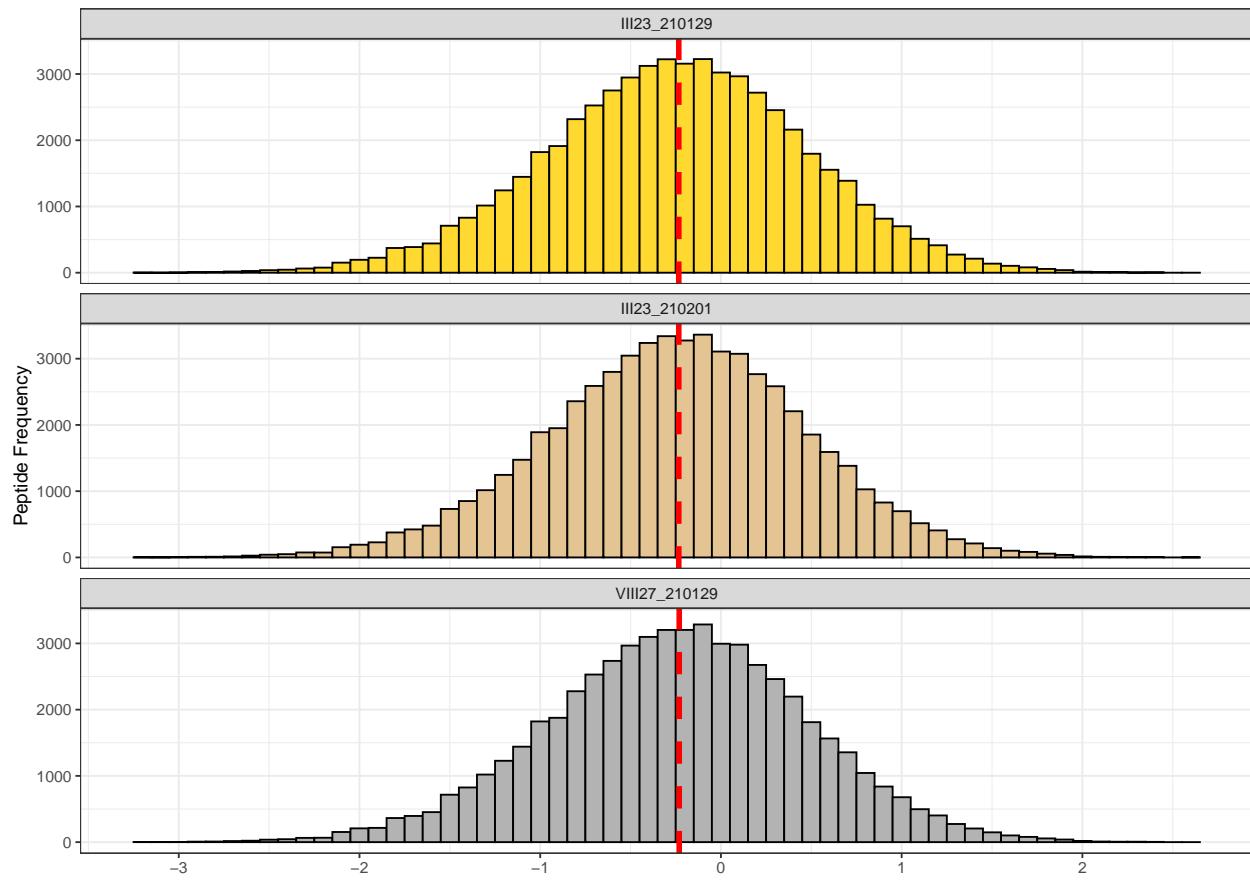


## Protease Specificity

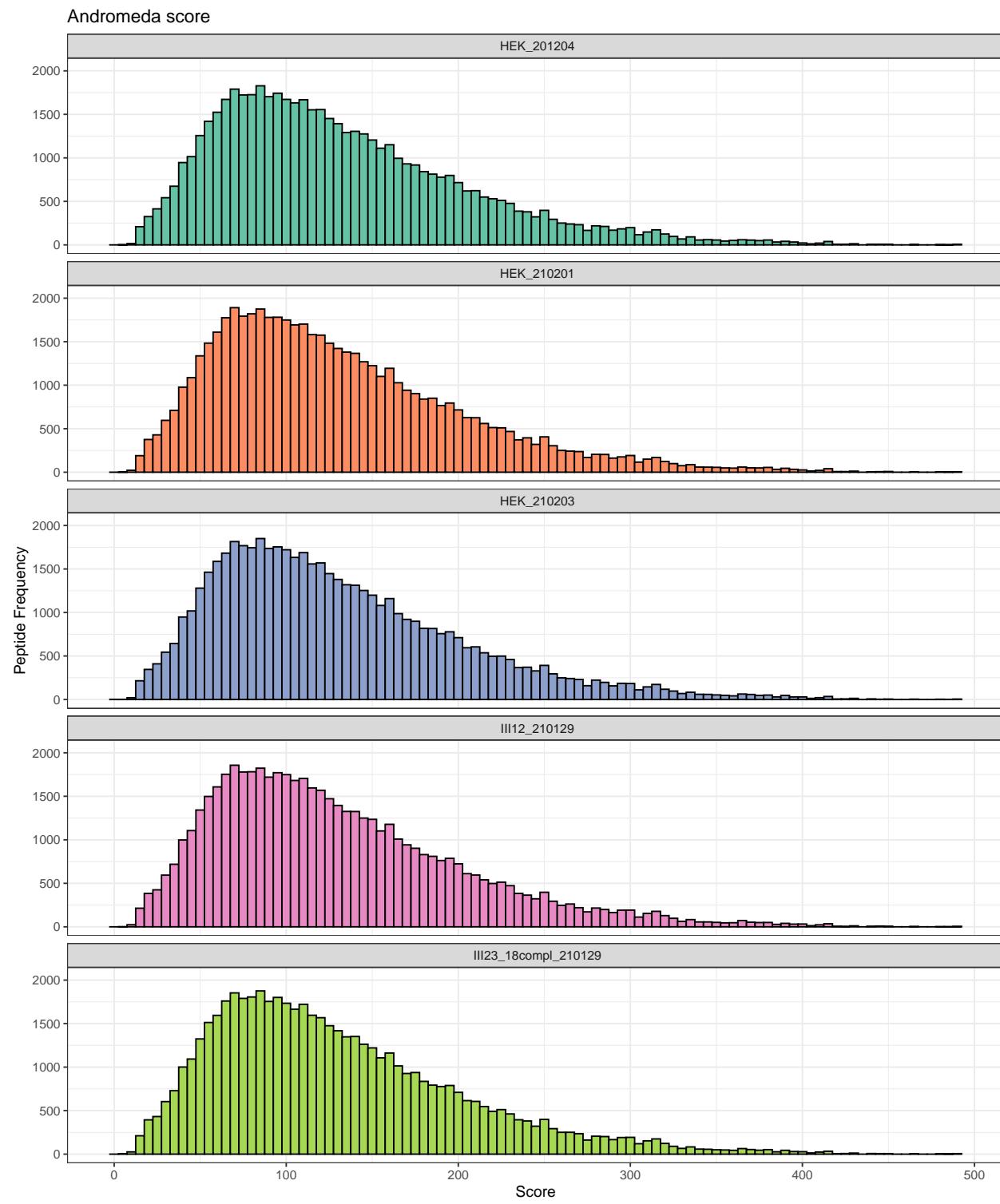


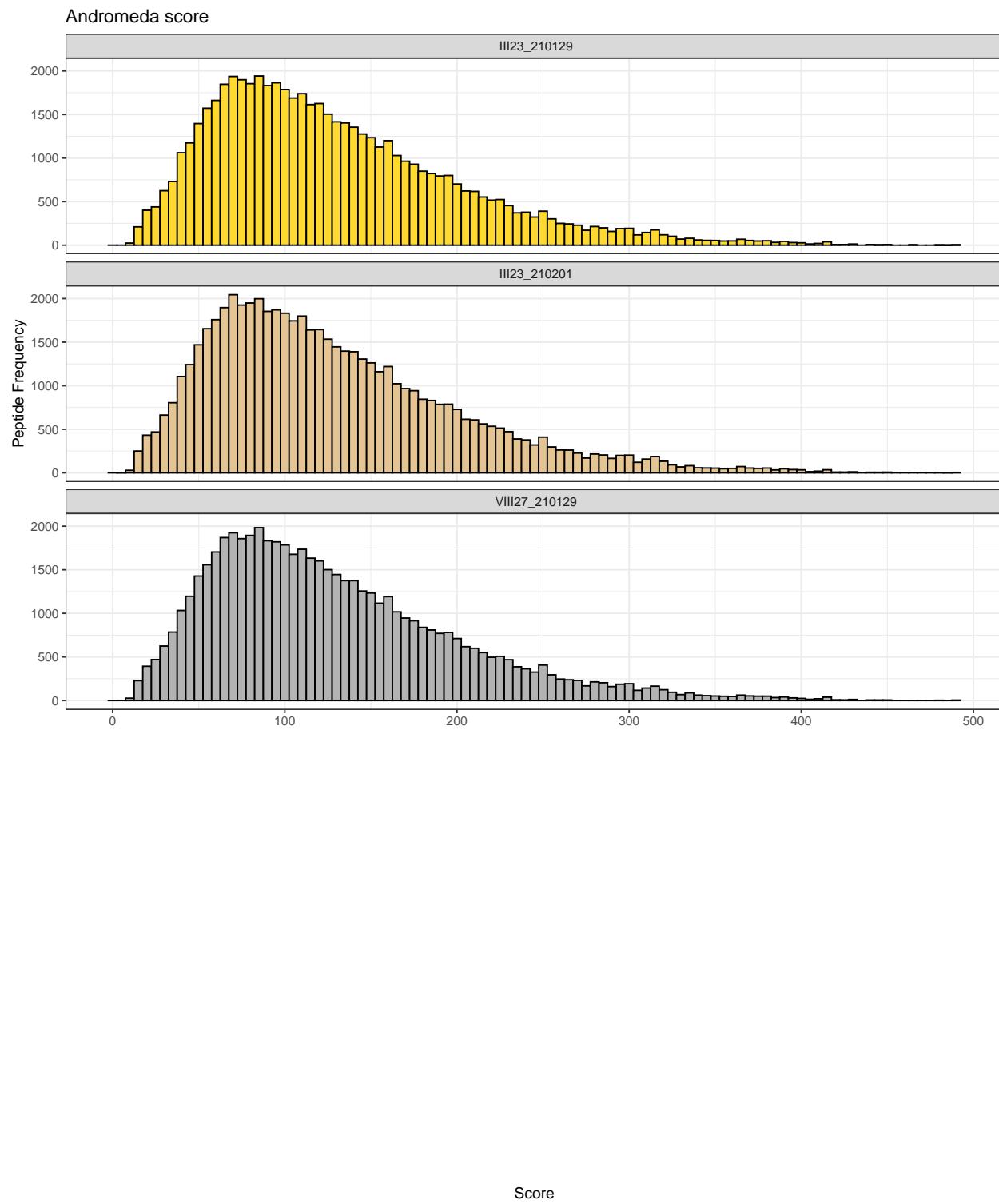


### Peptide hydrophathy distribution

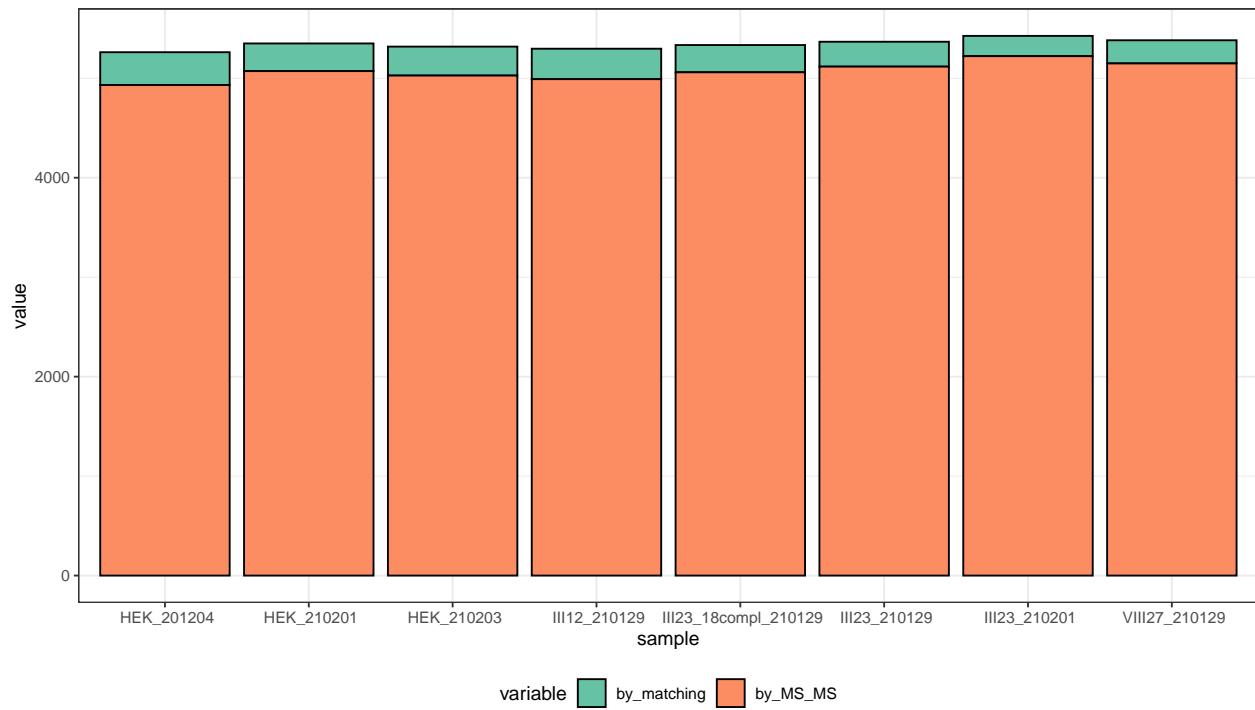


GRAY score

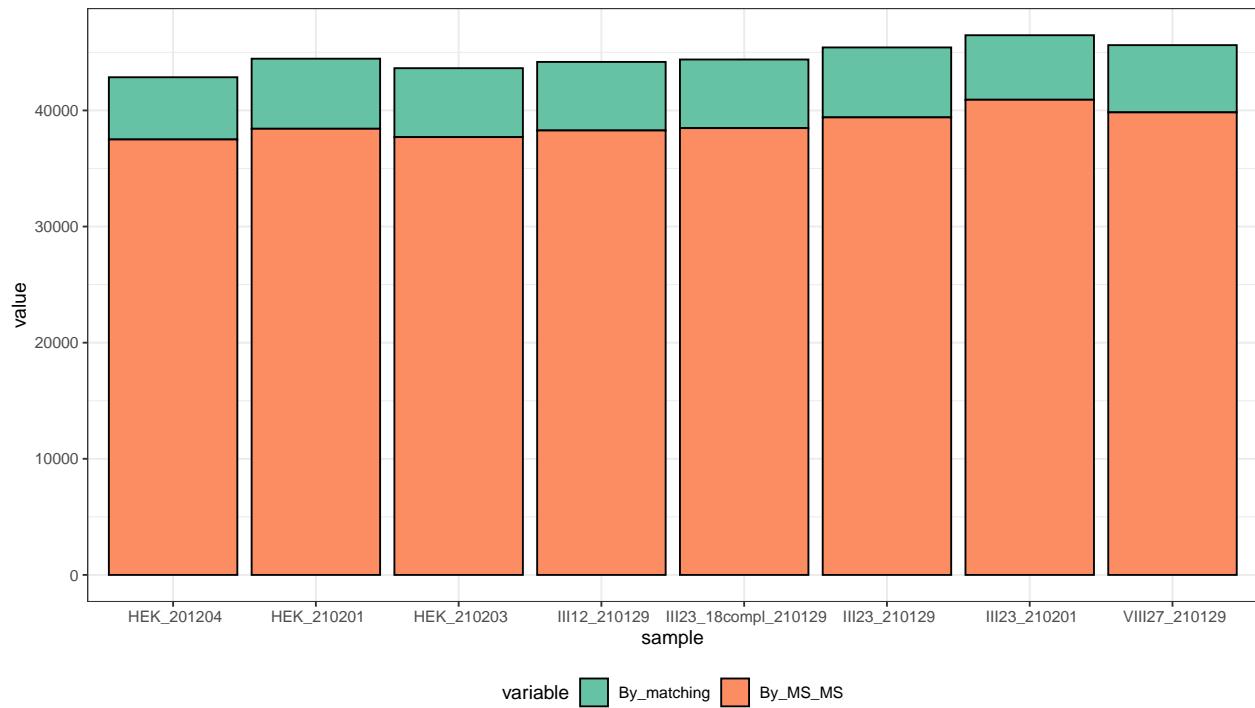




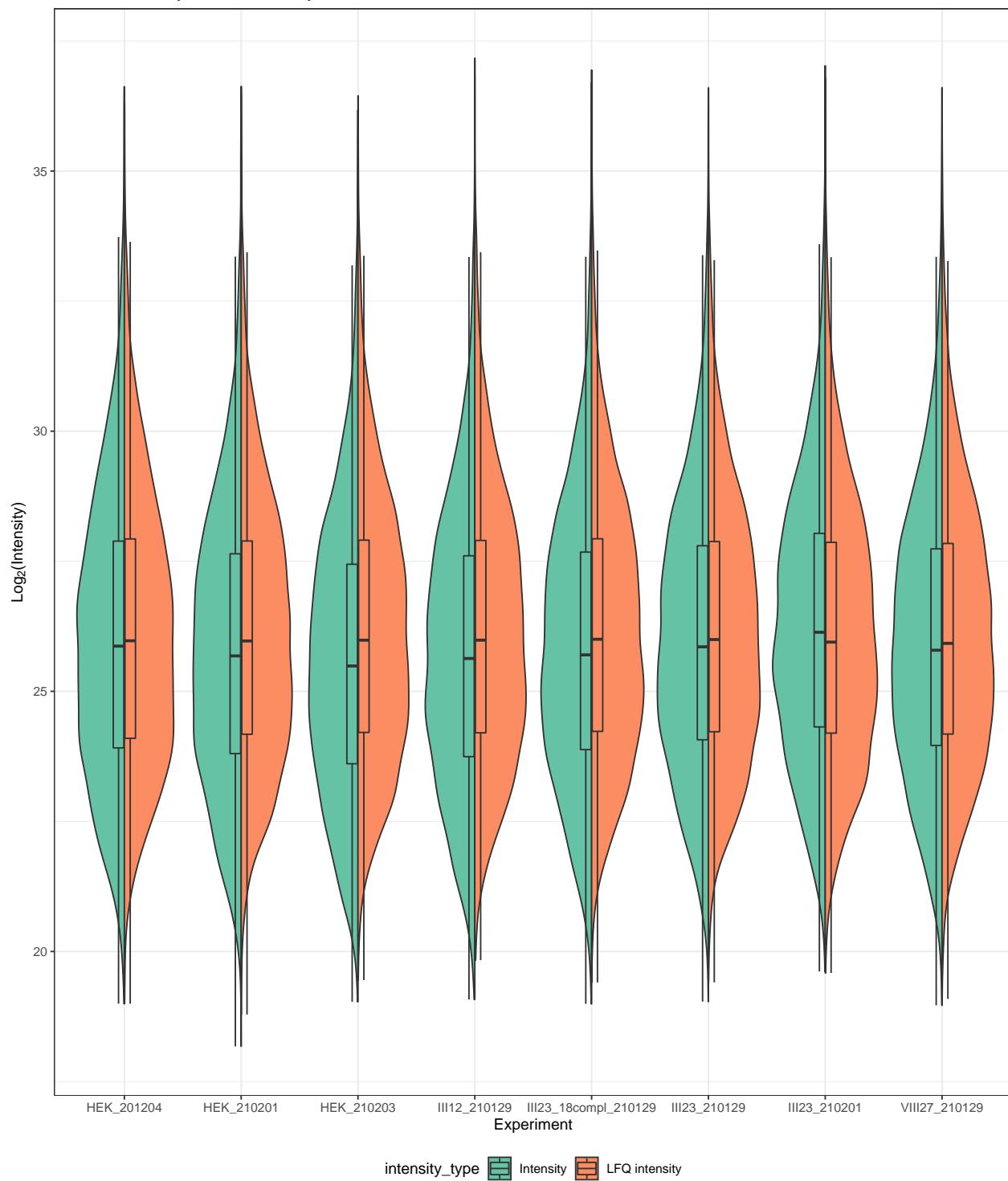
Protein Identification type

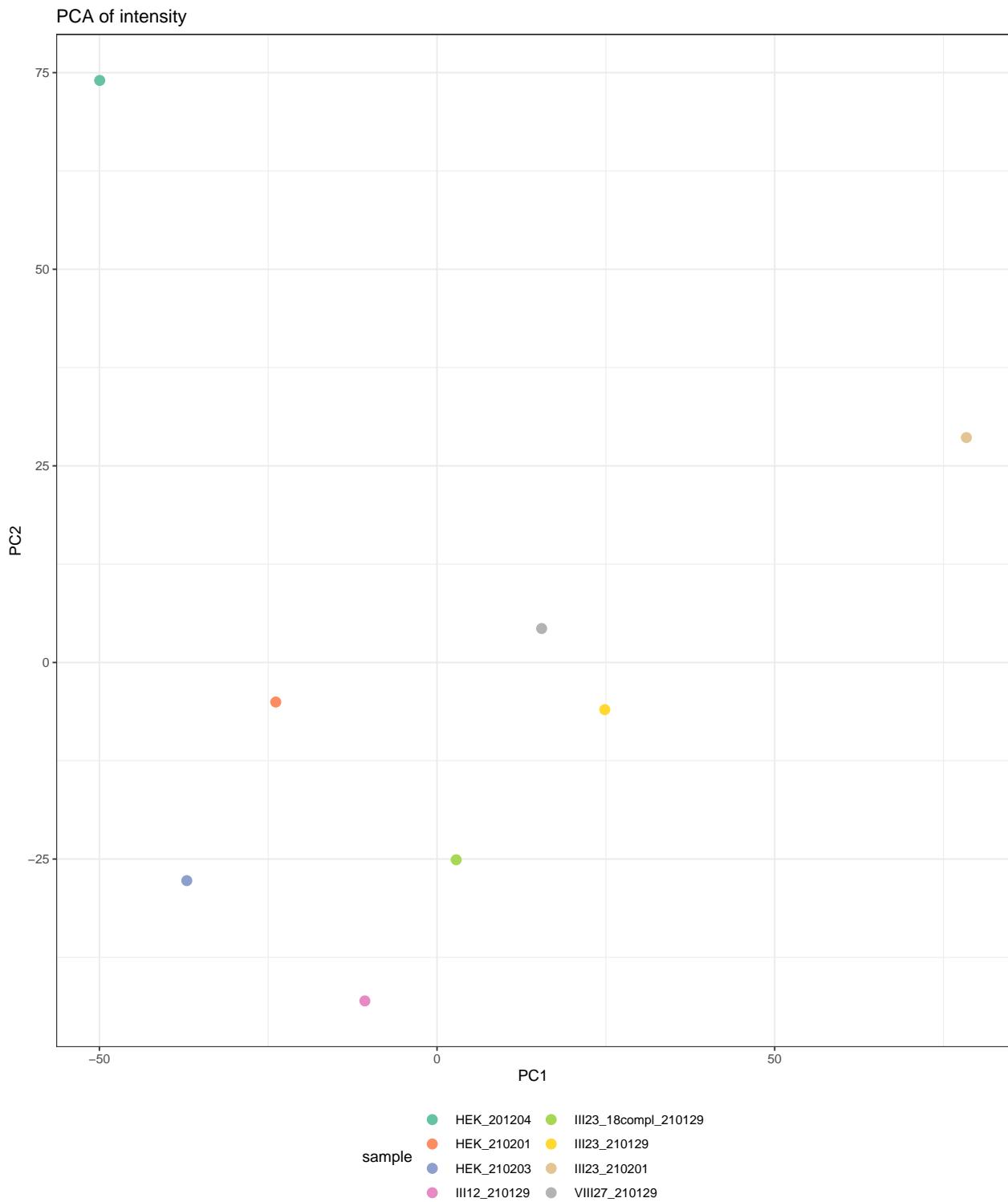


Peptide Identification type

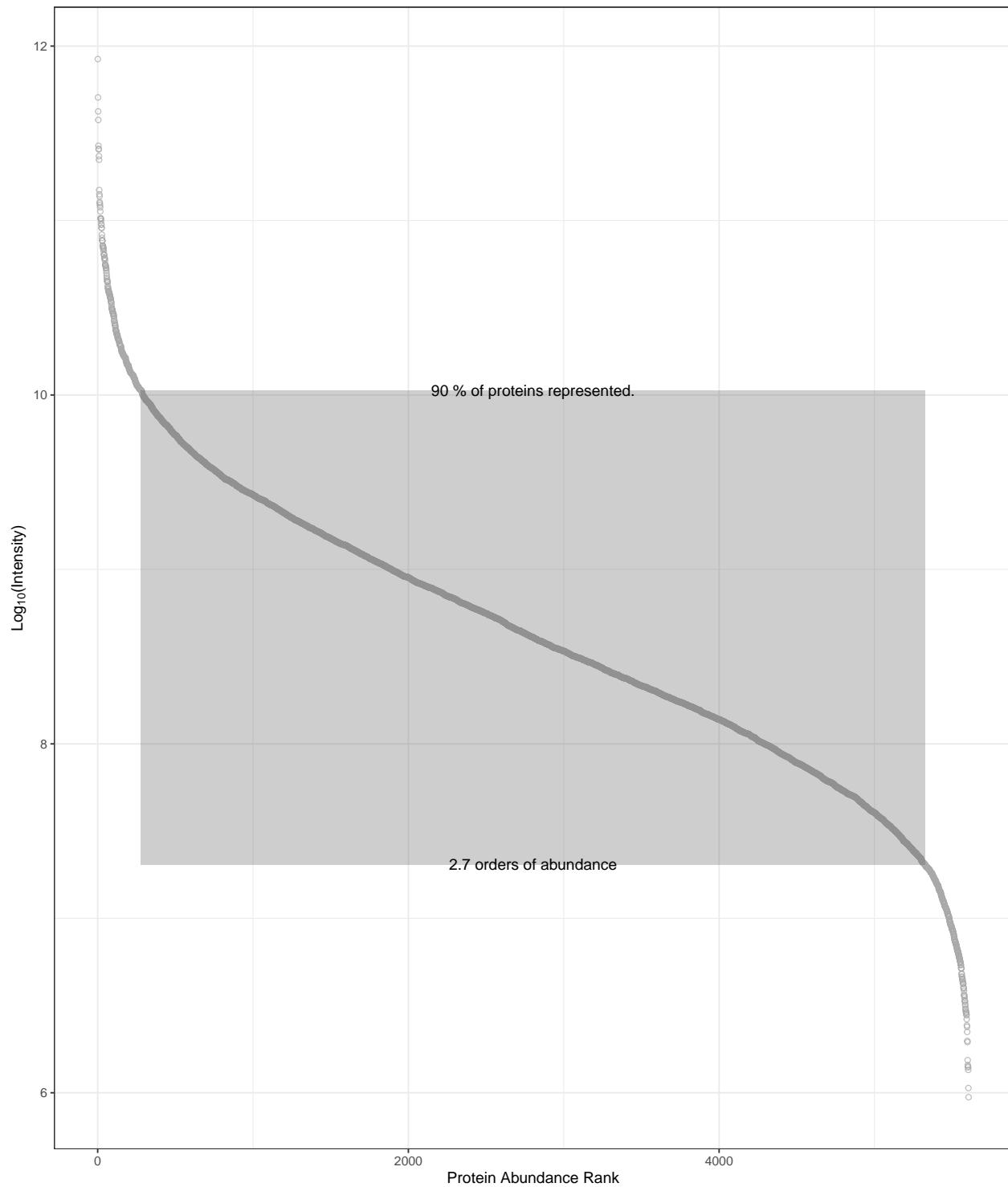


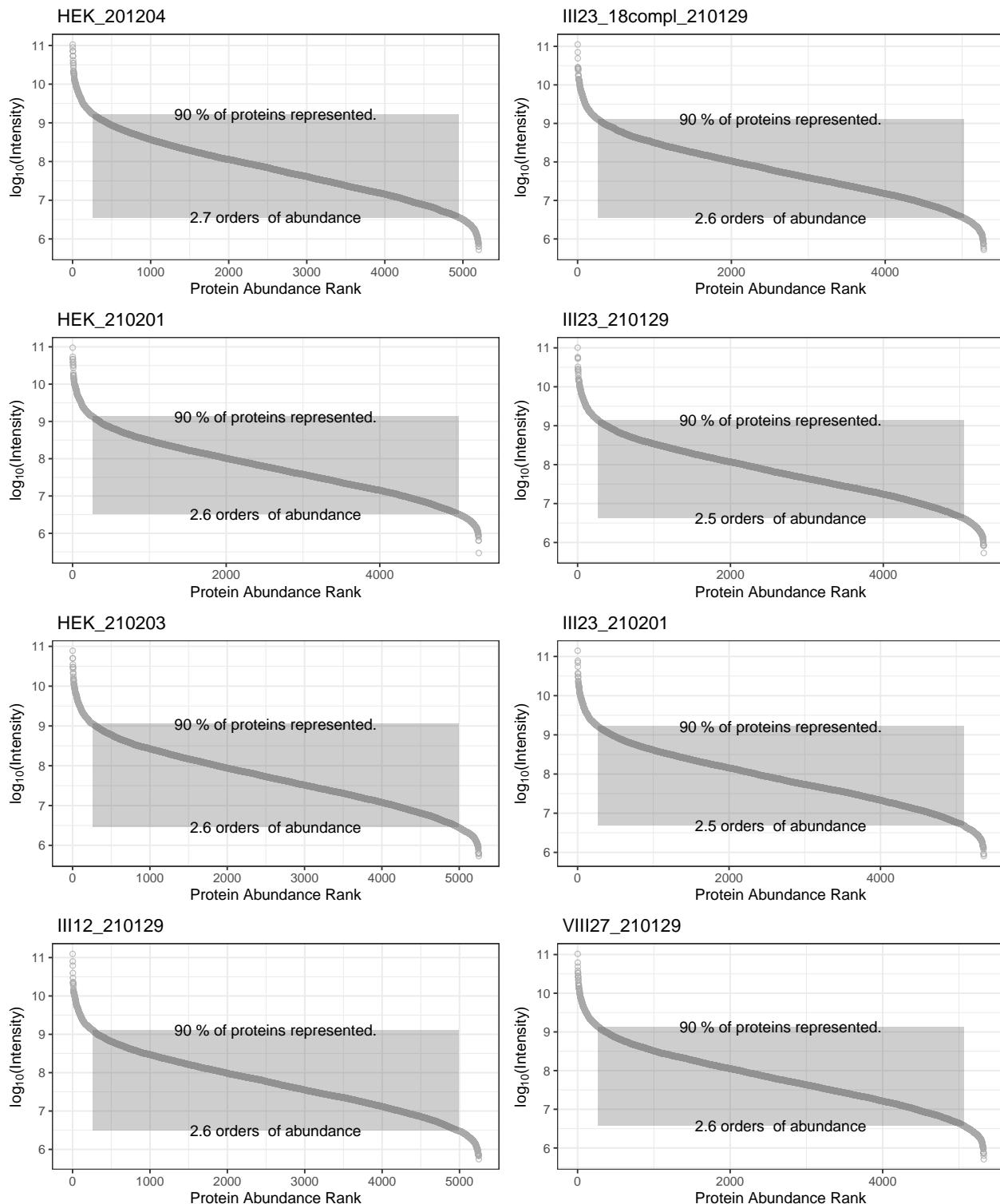
### Protein Intensity & LFQ intensity





Dynamic range of protein abundance all samples



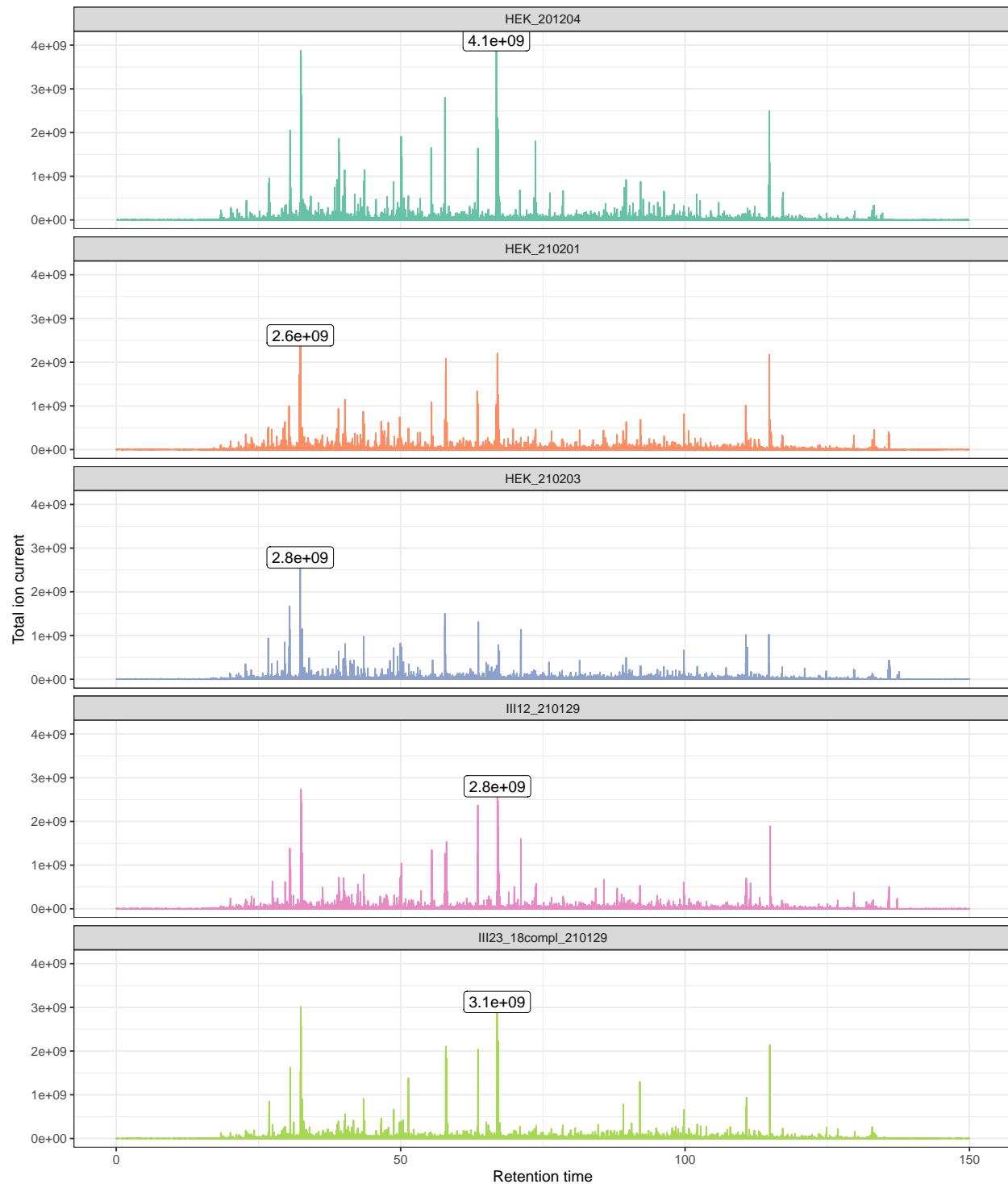


```
## [1] "No UniprotID provided."
```

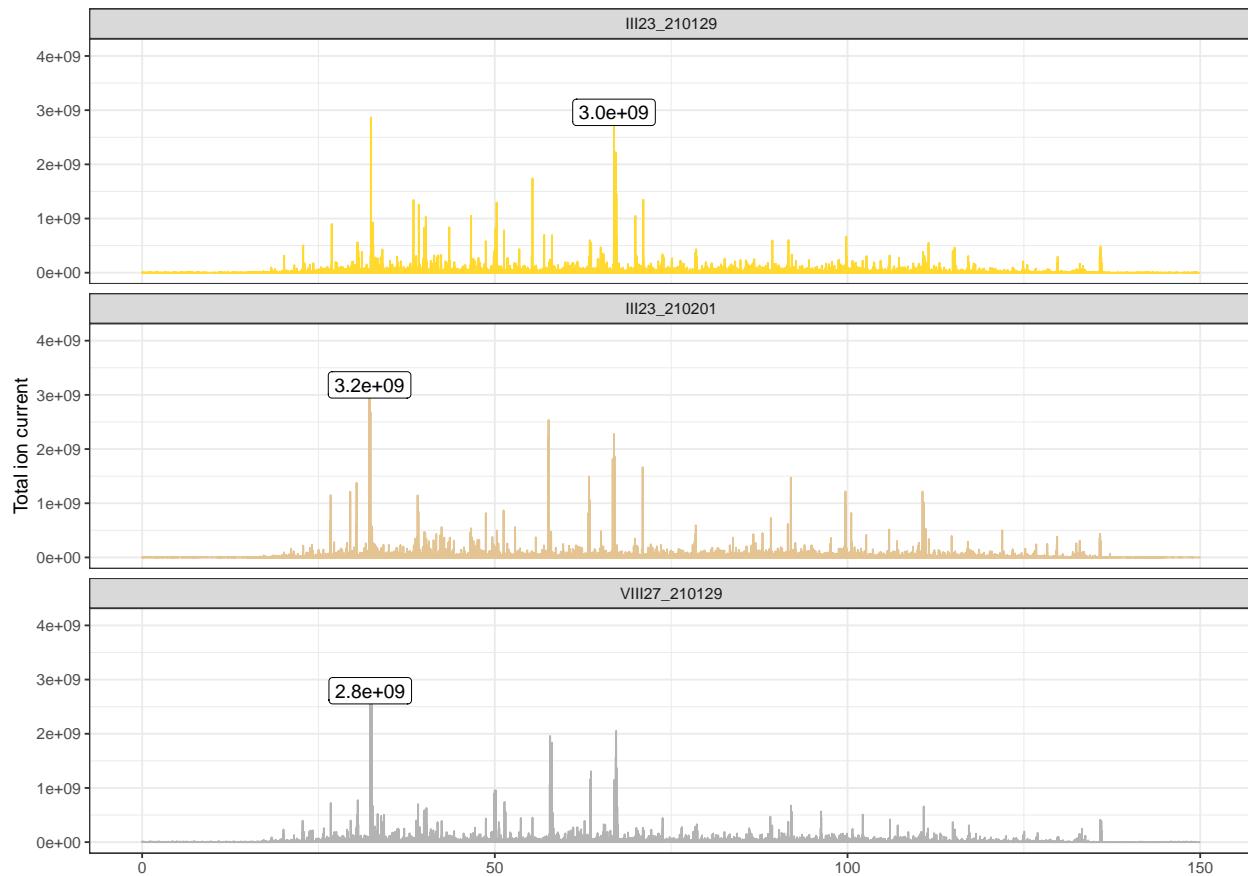
```
## [1] "No iRT peptides found in the MaxQuant output."
```

```
## [1] "No iRT peptides found in the MaxQuant output."
```

### Total Ion Current

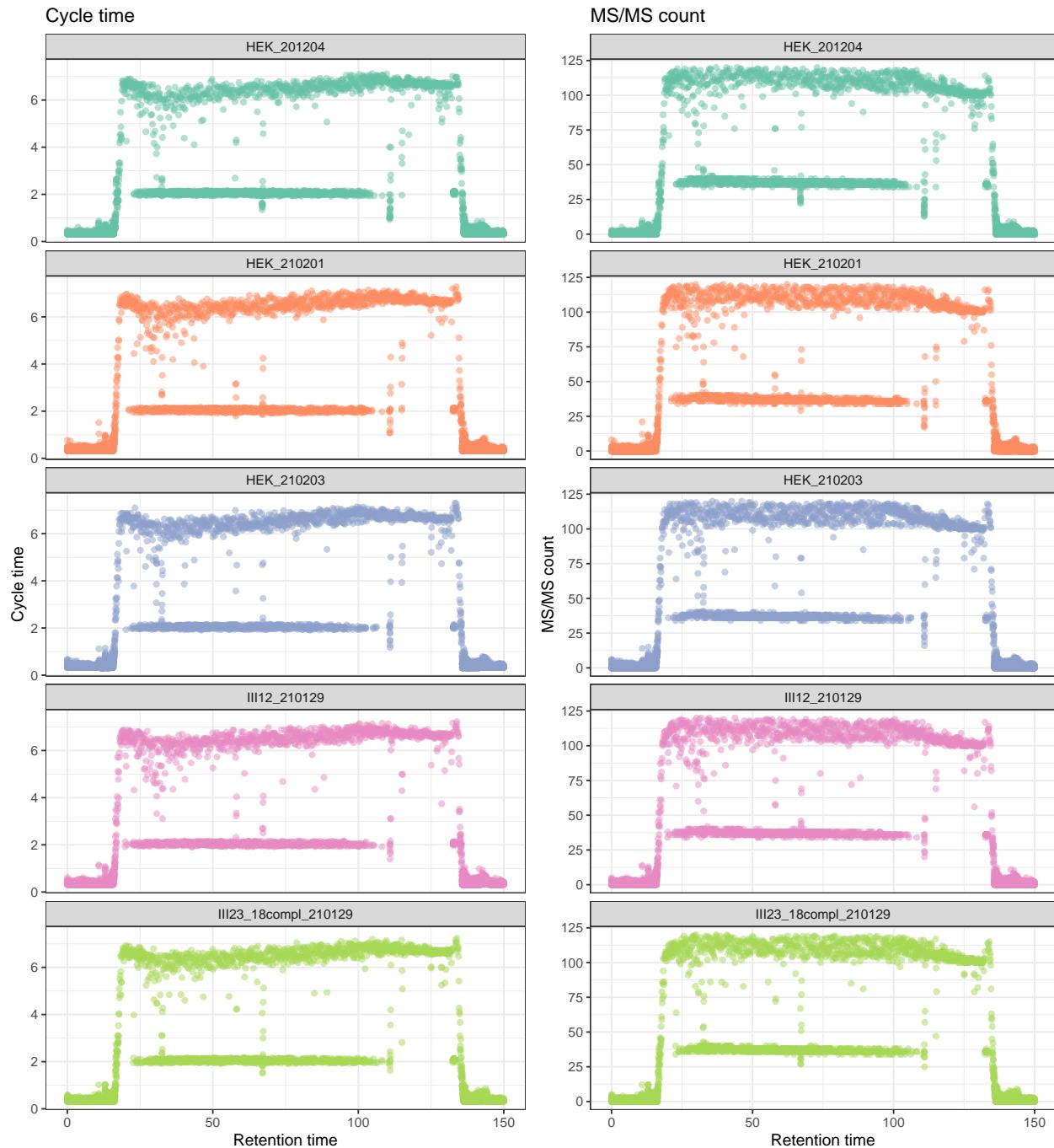


### Total Ion Current

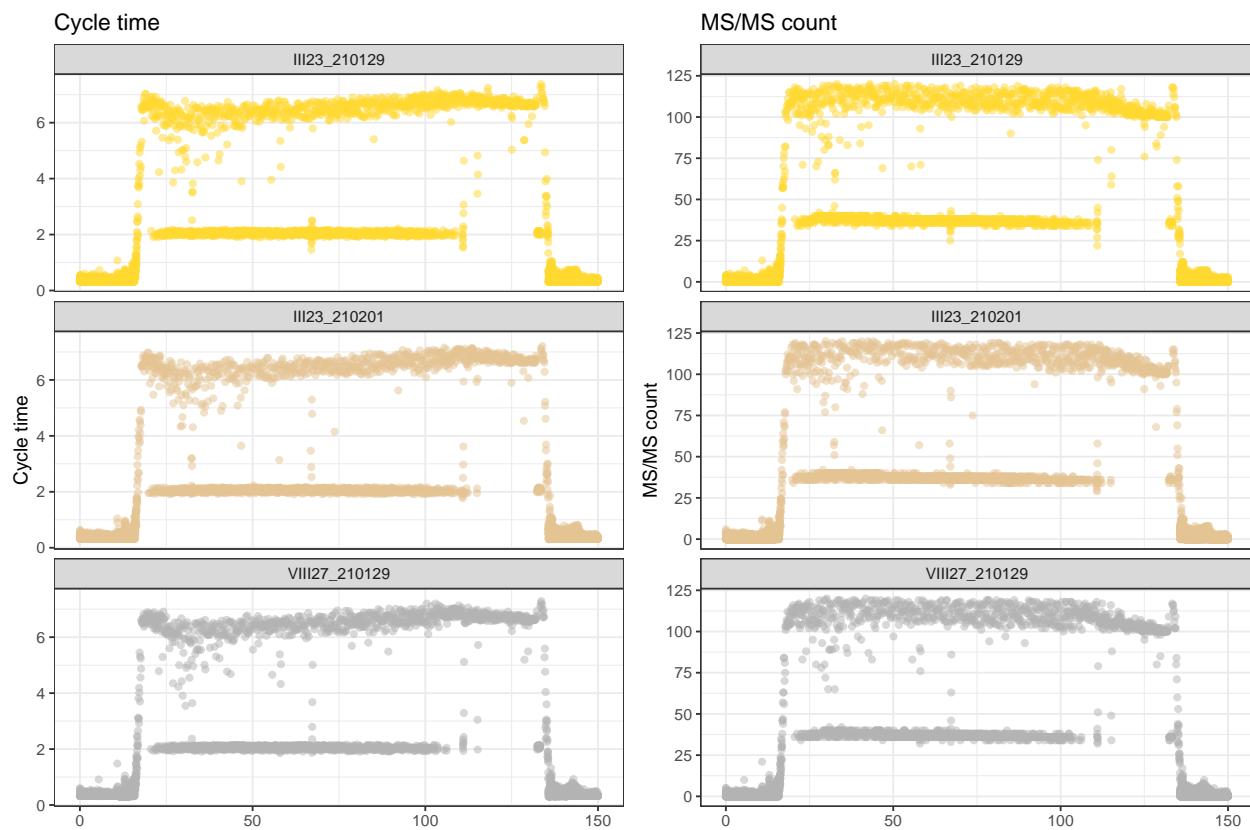


Retention time

### Acquisition Cycle



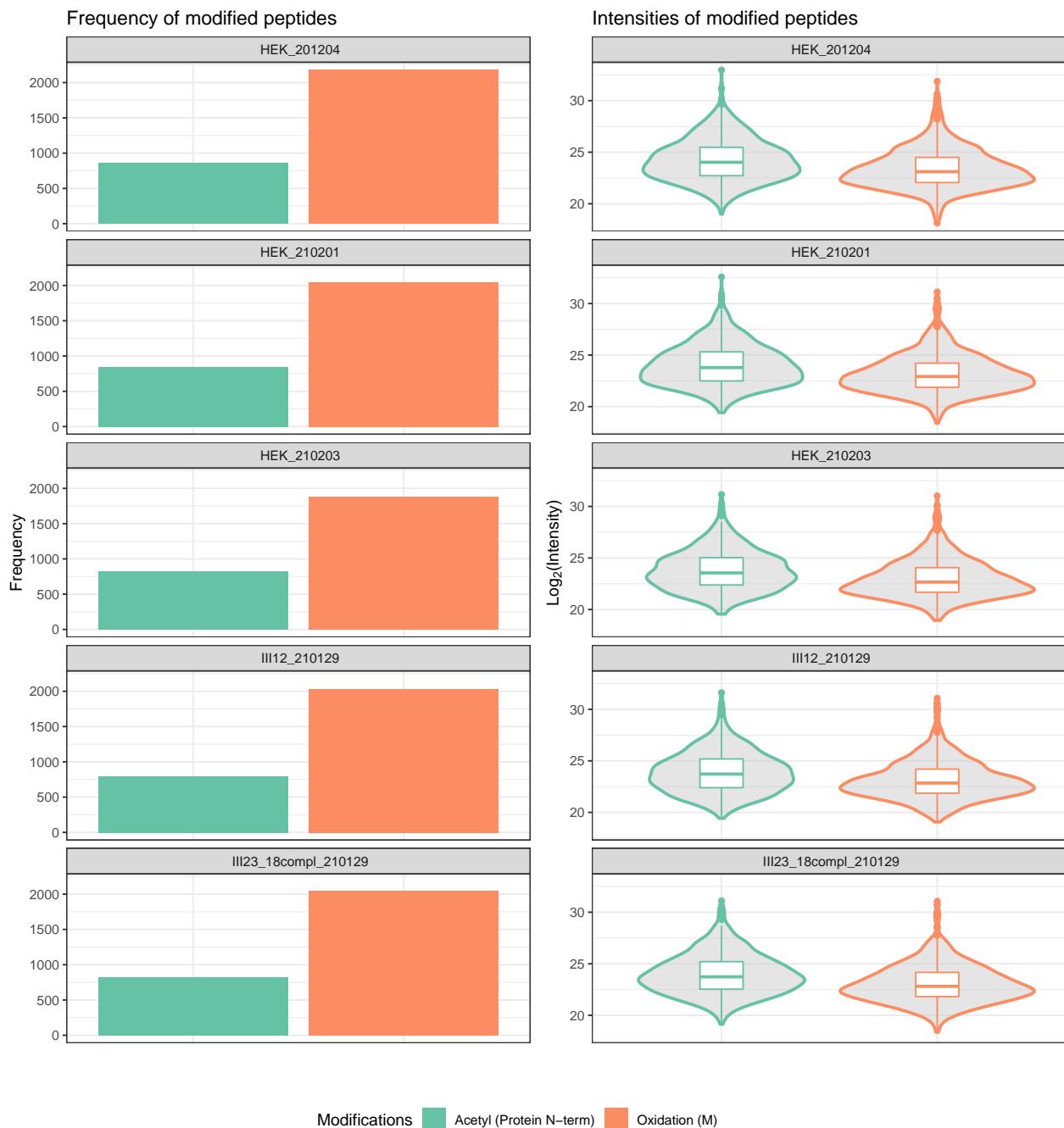
### Acquisition Cycle



Retention time

Retention time

## Post–Translational Modifications



## Post–Translational Modifications

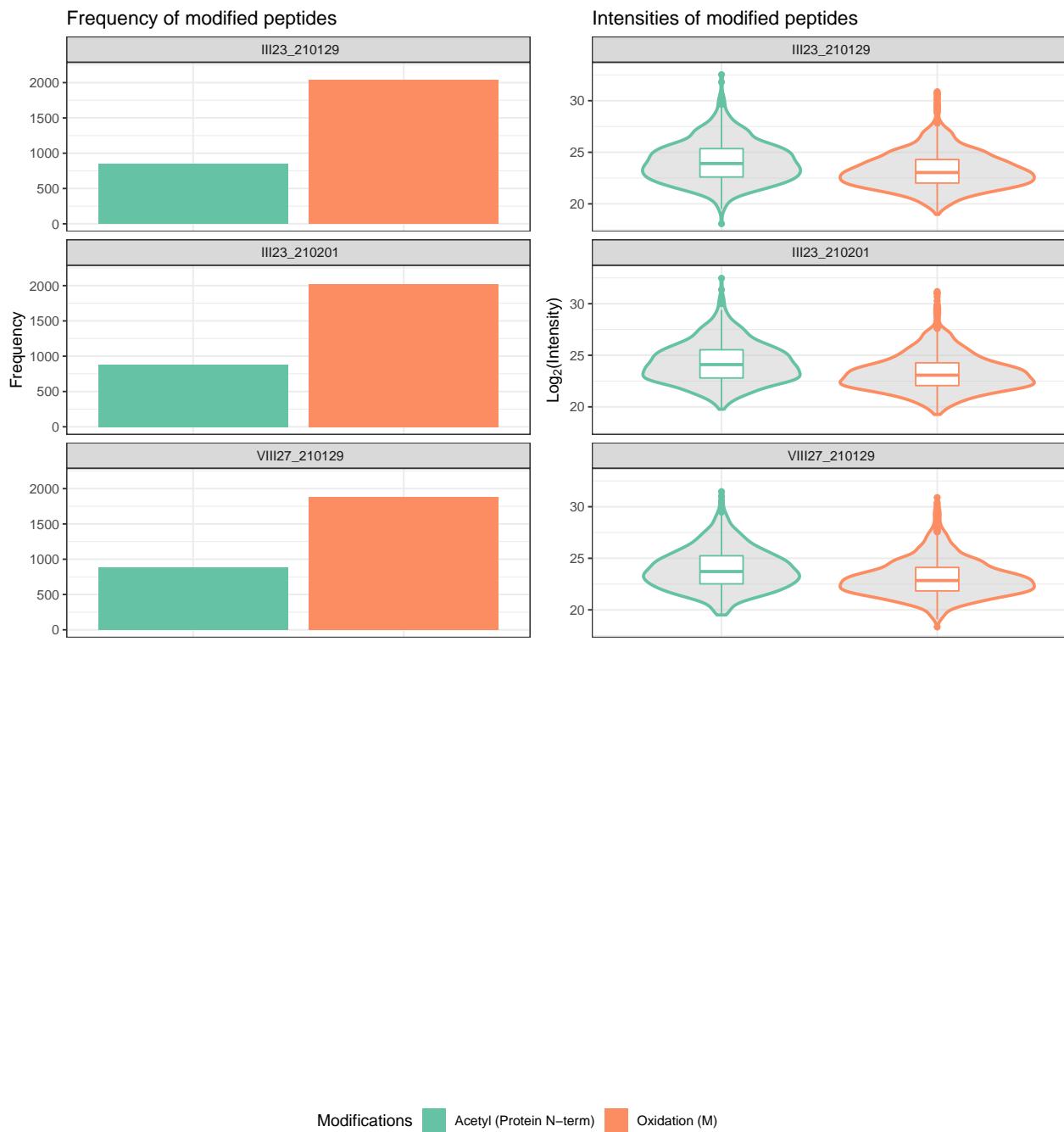


Table 1: Protein Information

Experiment	Proteins Identified	Missing values	Potential contaminants	Reverse	Only identified by site
HEK_201204	5275	447	58	0	15
HEK_210201	5360	362	55	0	17
HEK_210203	5329	393	63	0	15
III12_210129	5323	399	59	0	17
III23_18compl_210129	5351	371	54	0	17
III23_210129	5388	334	60	0	15
III23_210201	5444	278	63	0	18
VIII27_210129	5406	316	66	0	17

Table 2: Information of: Log2 Intensity

Experiment	mean	sd	median	min	max	n
HEK_201204	28.97	31.53	25.86	19.00	36.62	5275
HEK_210201	28.60	31.11	25.67	18.18	36.47	5360
HEK_210203	28.39	30.88	25.48	19.03	36.17	5329
III12_210129	28.56	31.29	25.62	19.08	36.86	5323
III23_18compl_210129	28.59	31.17	25.69	18.99	36.70	5351
III23_210129	28.67	31.15	25.85	19.04	36.56	5388
III23_210201	28.93	31.49	26.12	19.62	37.02	5444
VIII27_210129	28.65	31.15	25.78	18.96	36.59	5406

Table 3: Charge Information

Experiment	1	2	3	4	5	6	7
HEK_201204	0.3	56.5	37.4	5.4	0.4	0.0	0.0
HEK_210201	0.3	56.5	37.2	5.6	0.5	0.0	0.0
HEK_210203	0.3	56.8	37.2	5.3	0.5	0.0	0.0
III12_210129	0.3	56.3	37.4	5.6	0.5	0.0	0.0
III23_18compl_210129	0.3	55.9	37.4	5.8	0.5	0.0	0.0
III23_210129	0.3	56.5	37.1	5.6	0.5	0.0	0.0
III23_210201	0.3	56.0	37.4	5.7	0.5	0.0	0.0
VIII27_210129	0.3	56.4	37.1	5.7	0.5	0.0	0.0

Table 4: Peptide hydrophobicity (GRAVY)

Experiment	Mean	Max	Min	Median
HEK_201204	-0.24	2.44	-3.19	-0.24
HEK_210201	-0.24	2.44	-3.19	-0.23
HEK_210203	-0.24	2.44	-3.19	-0.23
III12_210129	-0.24	2.44	-3.19	-0.23
III23_18compl_210129	-0.24	2.44	-3.19	-0.22
III23_210129	-0.24	2.44	-3.19	-0.23
III23_210201	-0.25	2.57	-3.19	-0.23
VIII27_210129	-0.24	2.43	-3.19	-0.23

Table 5: Missed Enzymatic Cleavages

Experiment	0	1	2
HEK_201204	43615	9572	922
HEK_210201	44910	9746	963
HEK_210203	43871	9356	920
III12_210129	44563	9676	915
III23_18compl_210129	44776	9650	975
III23_210129	45902	9893	987
III23_210201	47122	10191	1014
VIII27_210129	46029	9755	953