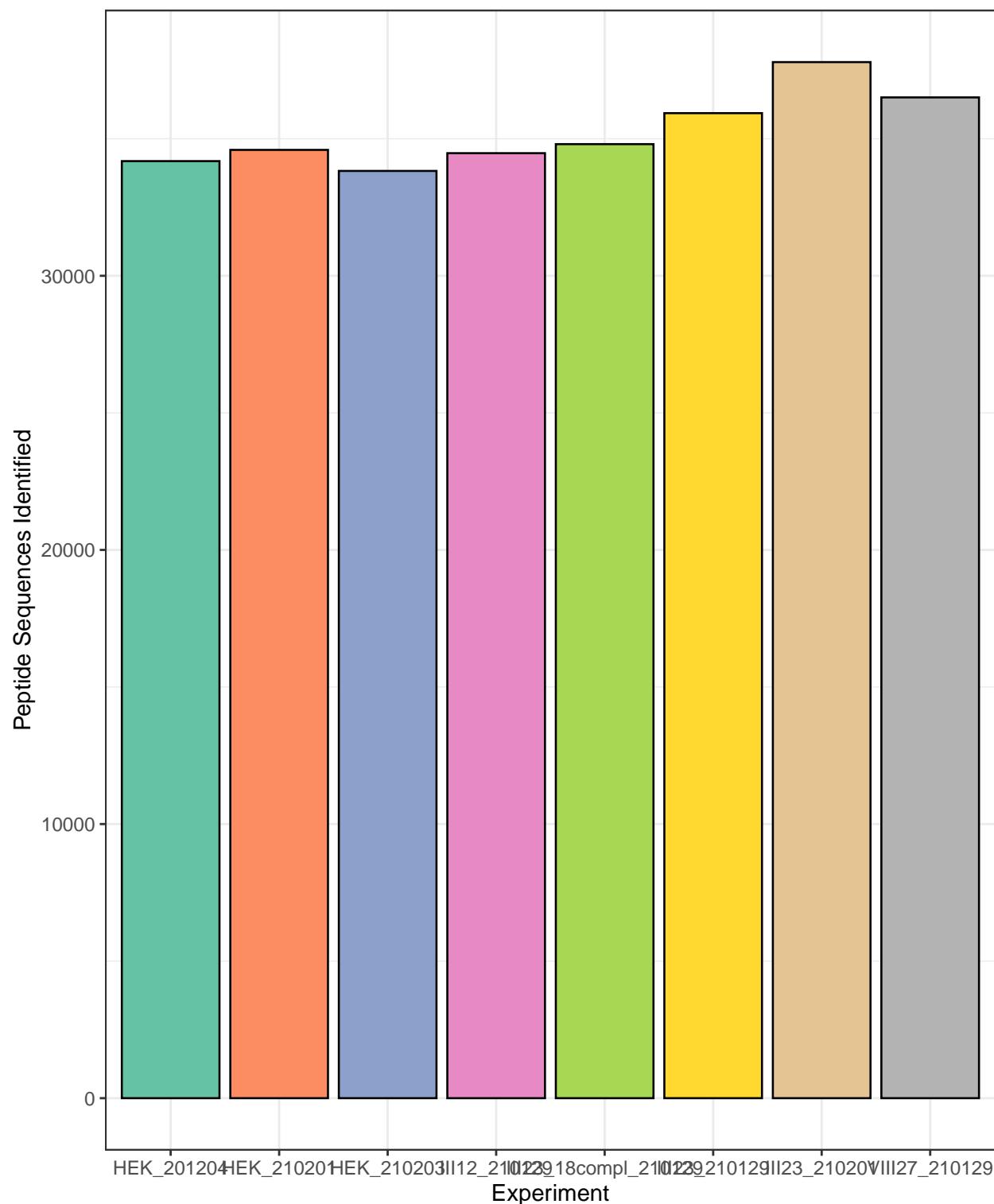


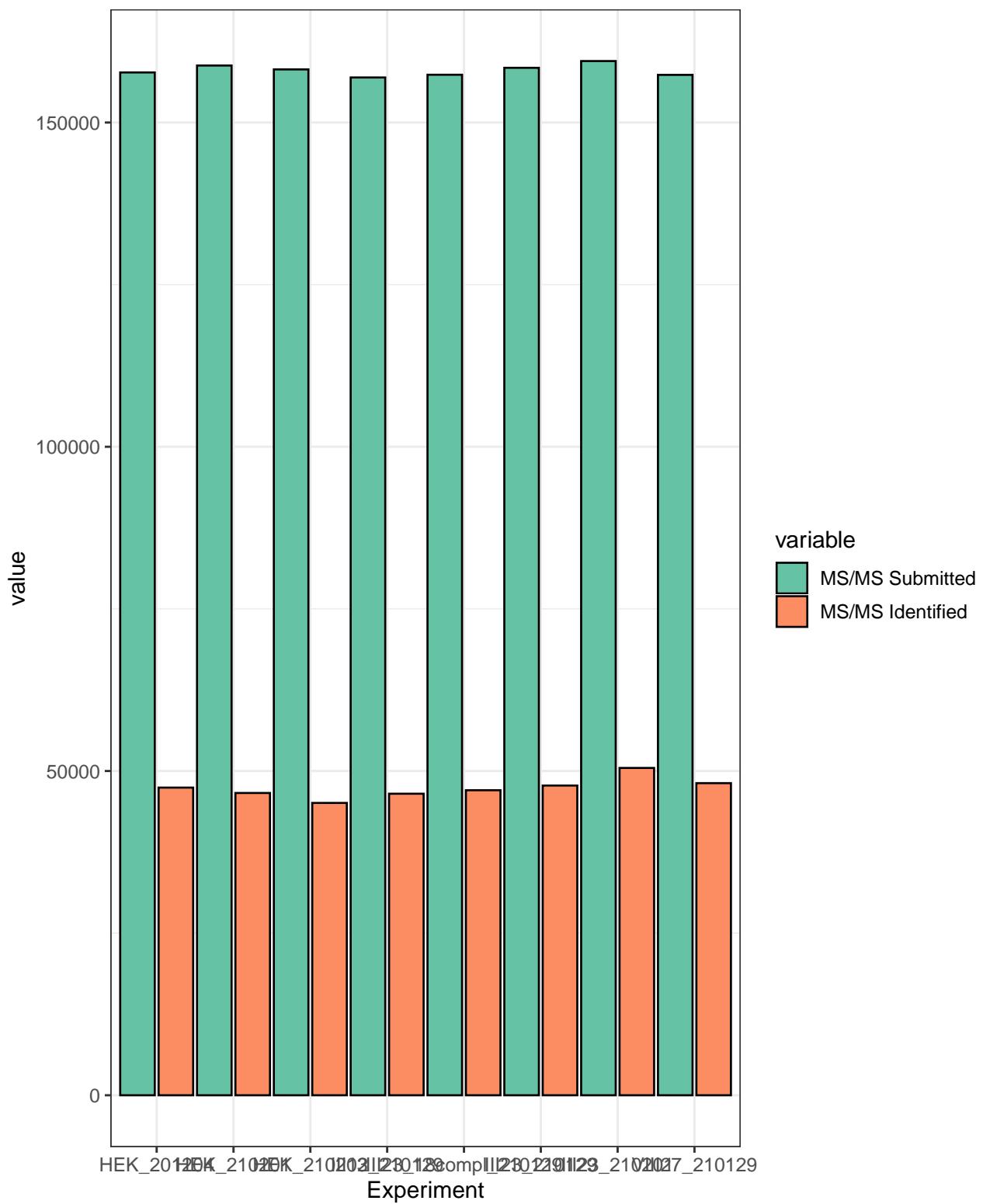
# Report

```
## [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 protein FDR was: 0.01"
## [1] "The match between runs was: True"
## [1] "The fasta file used was: C:\\MaxQuant_Databases\\UP000005640_9606.fasta"
```

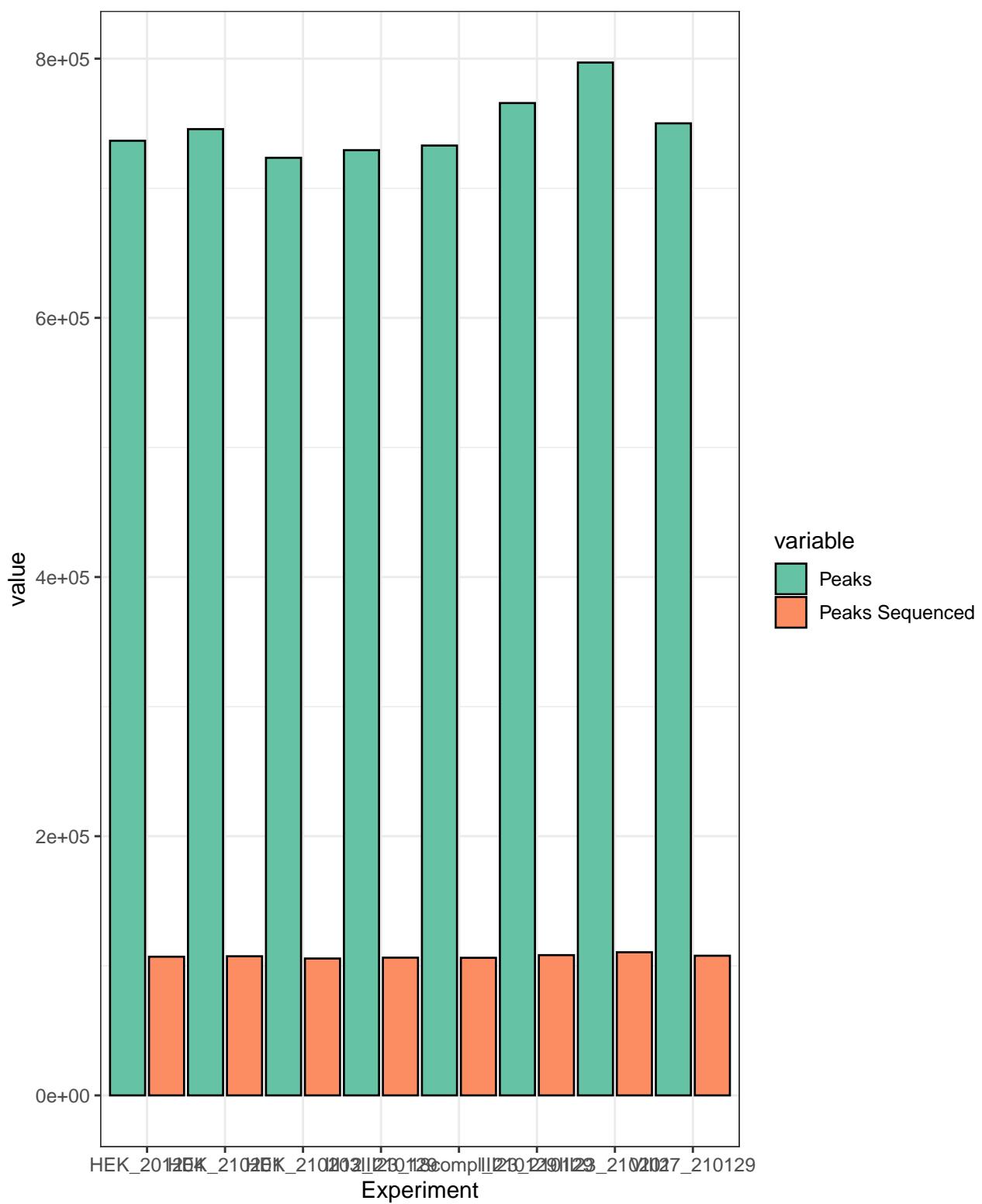
## Peptides Sequences Identified



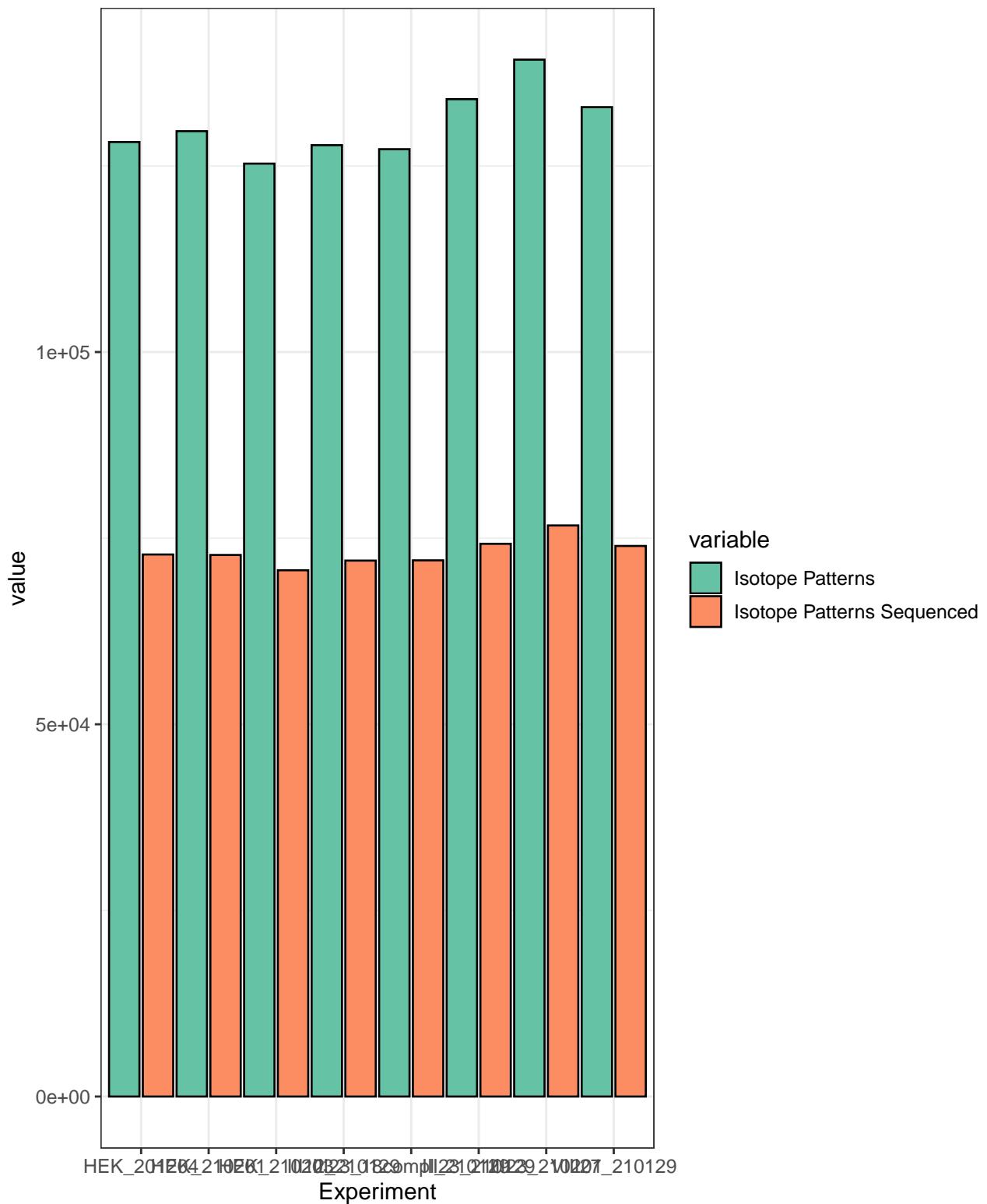
## MS/MS Submitted and Identified



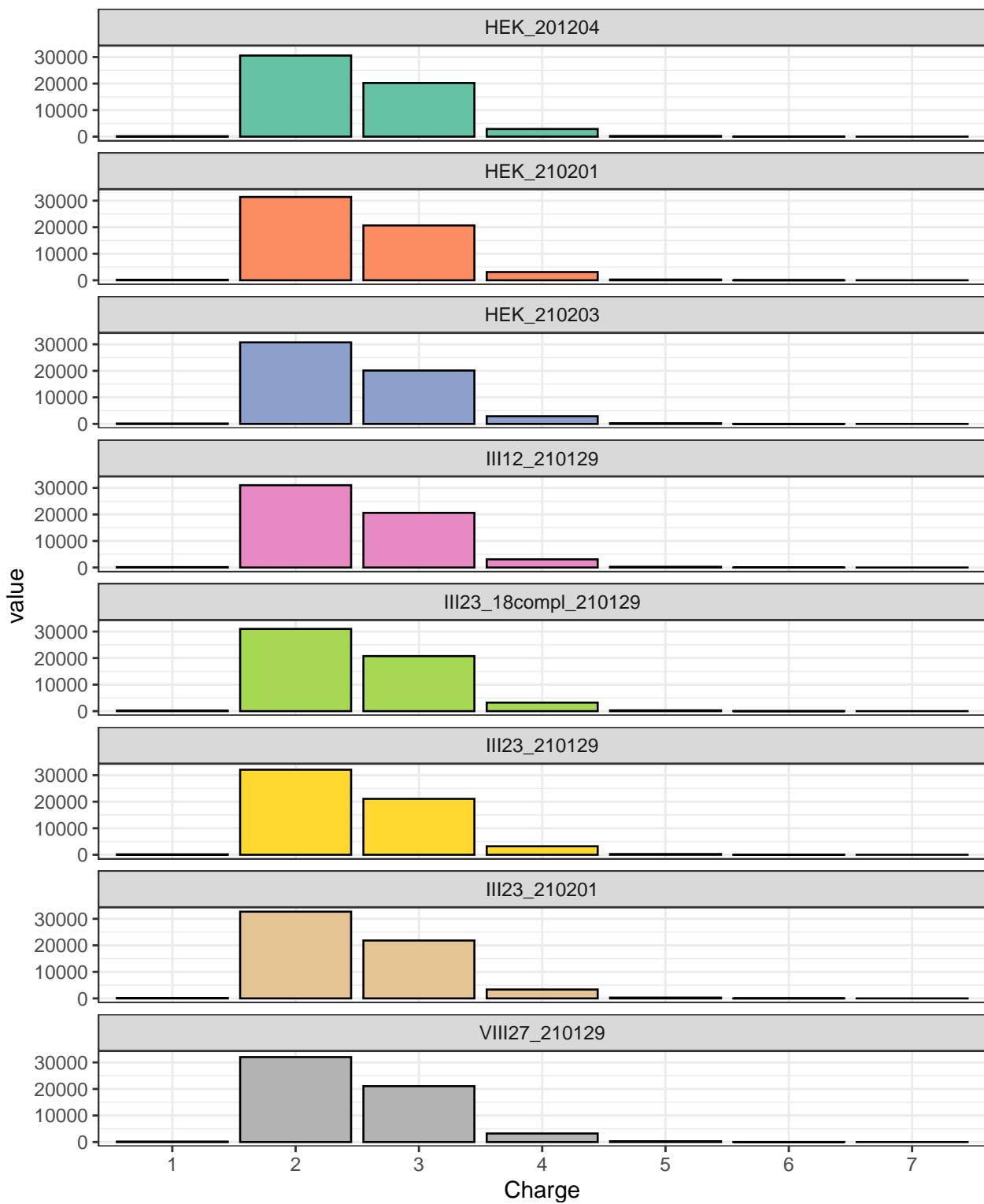
### Peaks detected and sequenced in the full scans



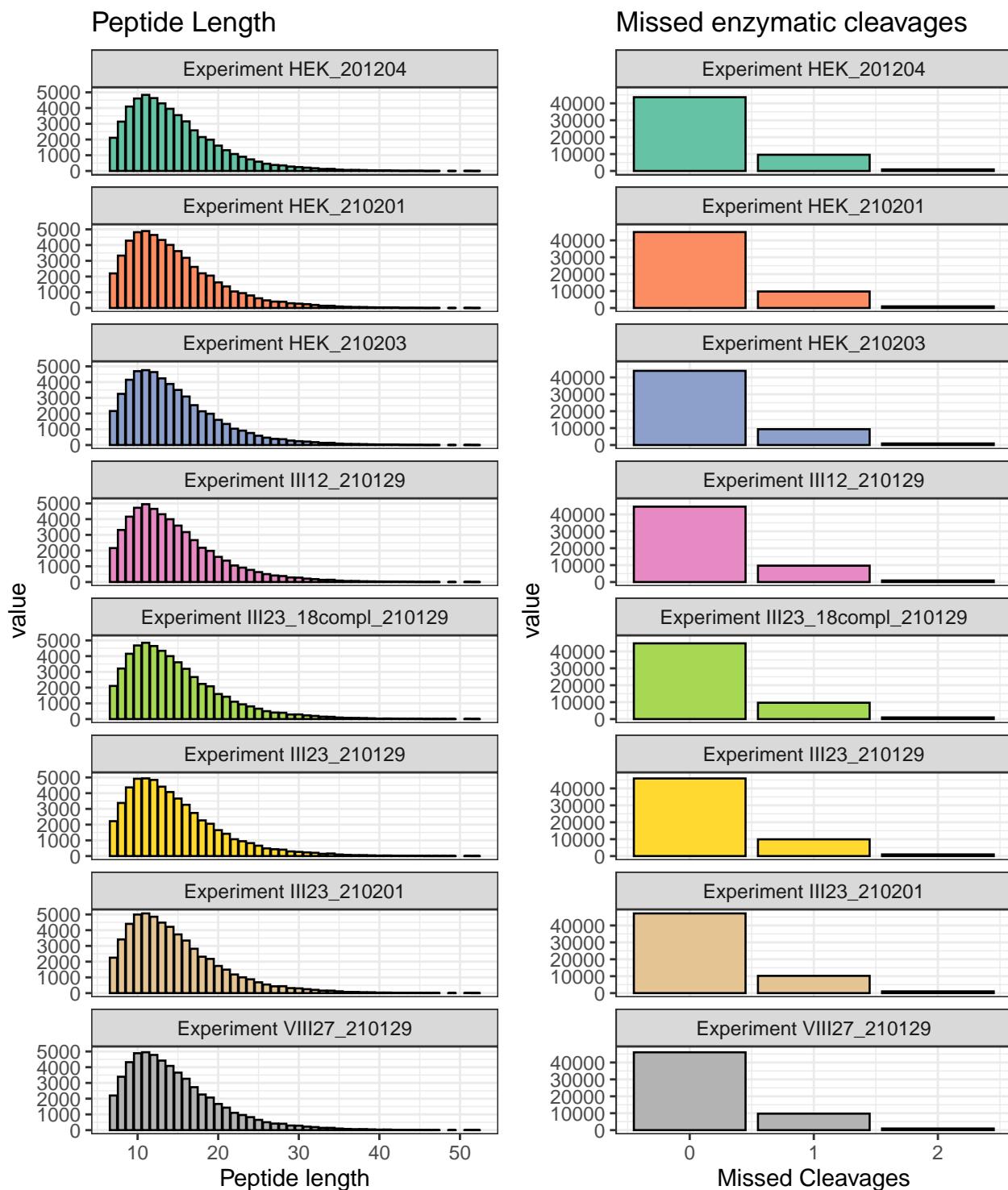
## Isotope Patterns detected and sequenced



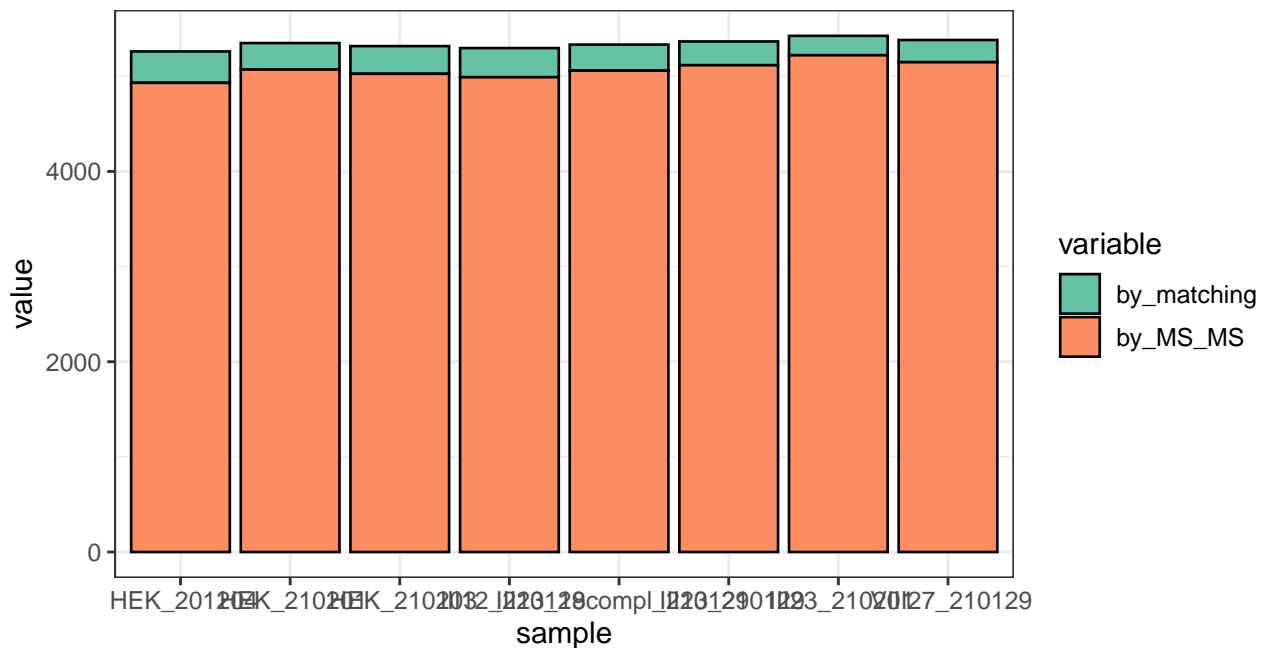
### The charge-state of the precursor ion.



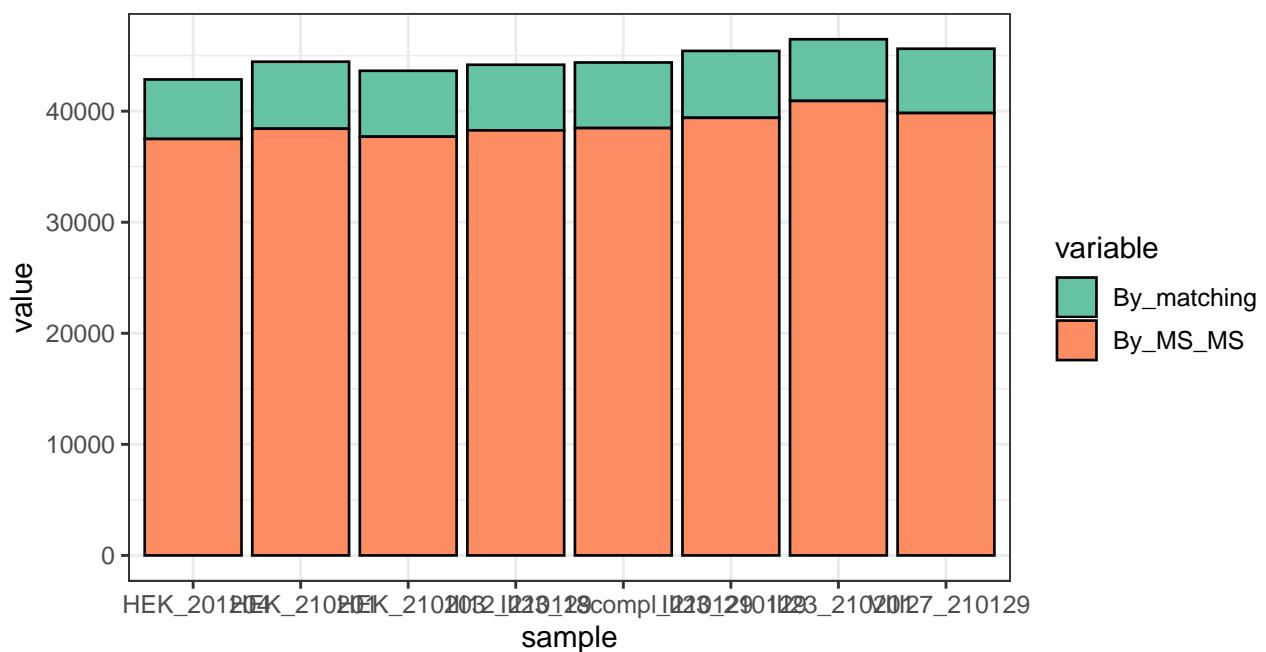
## Protease Specificity

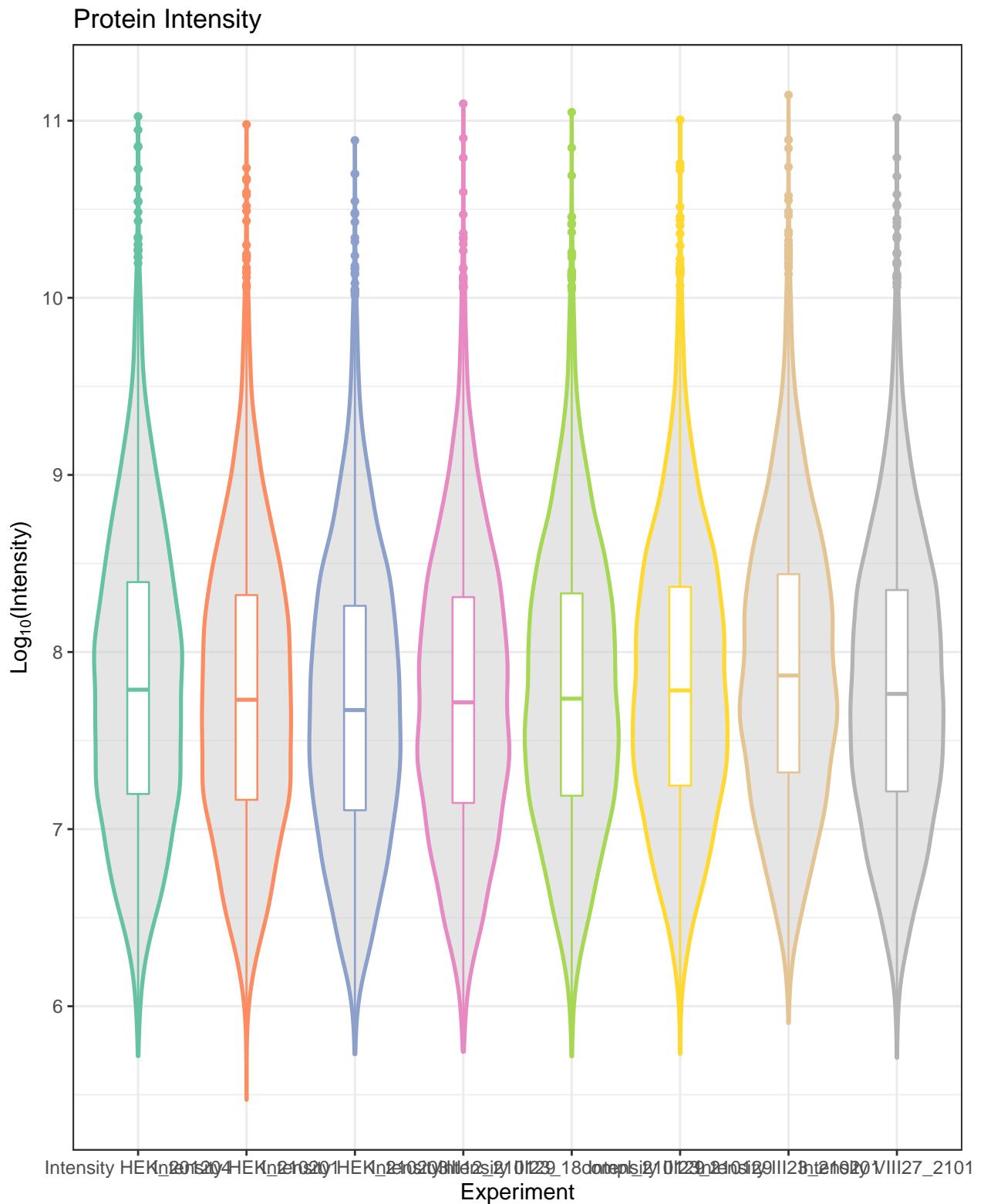


Protein Identification type

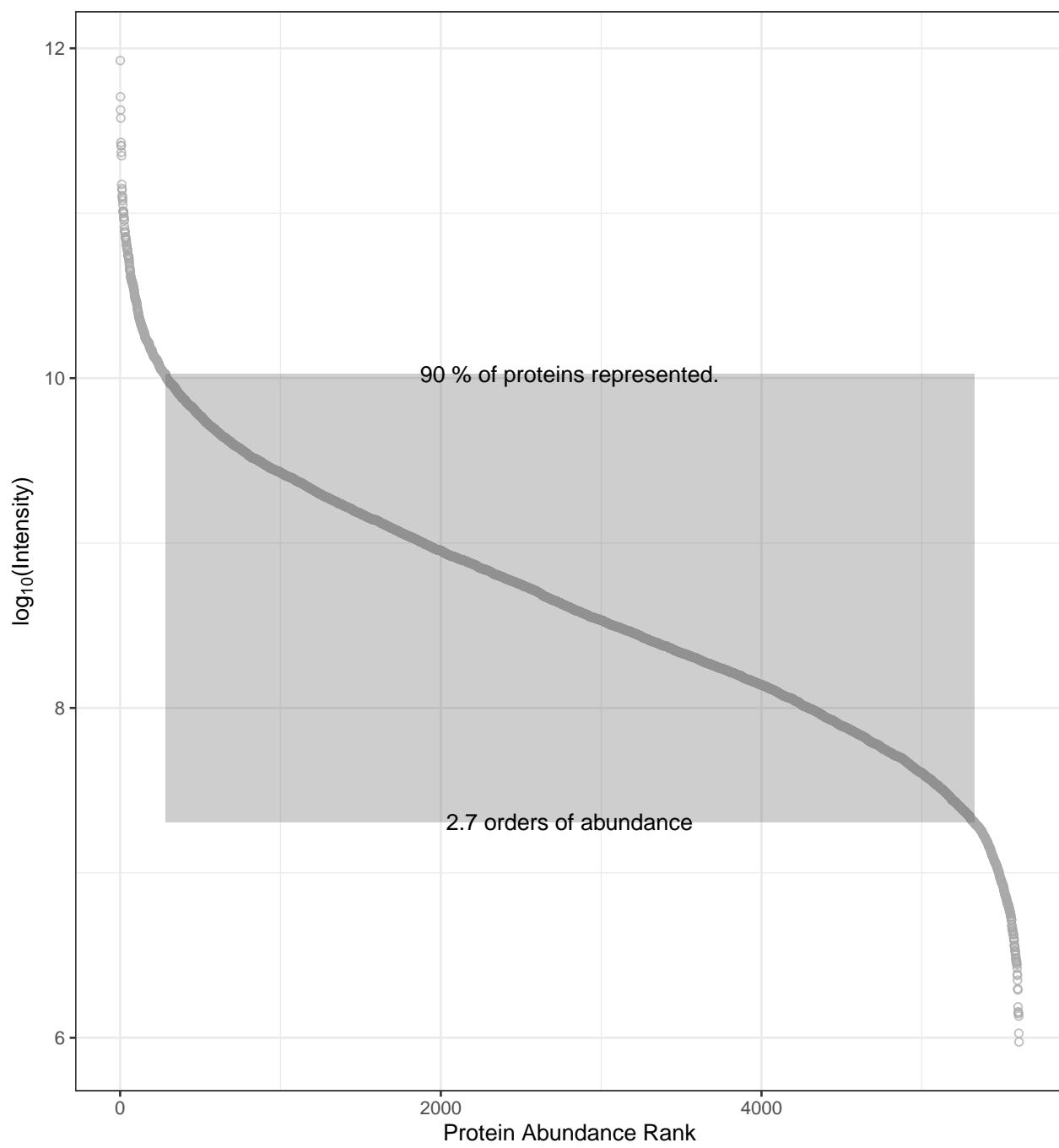


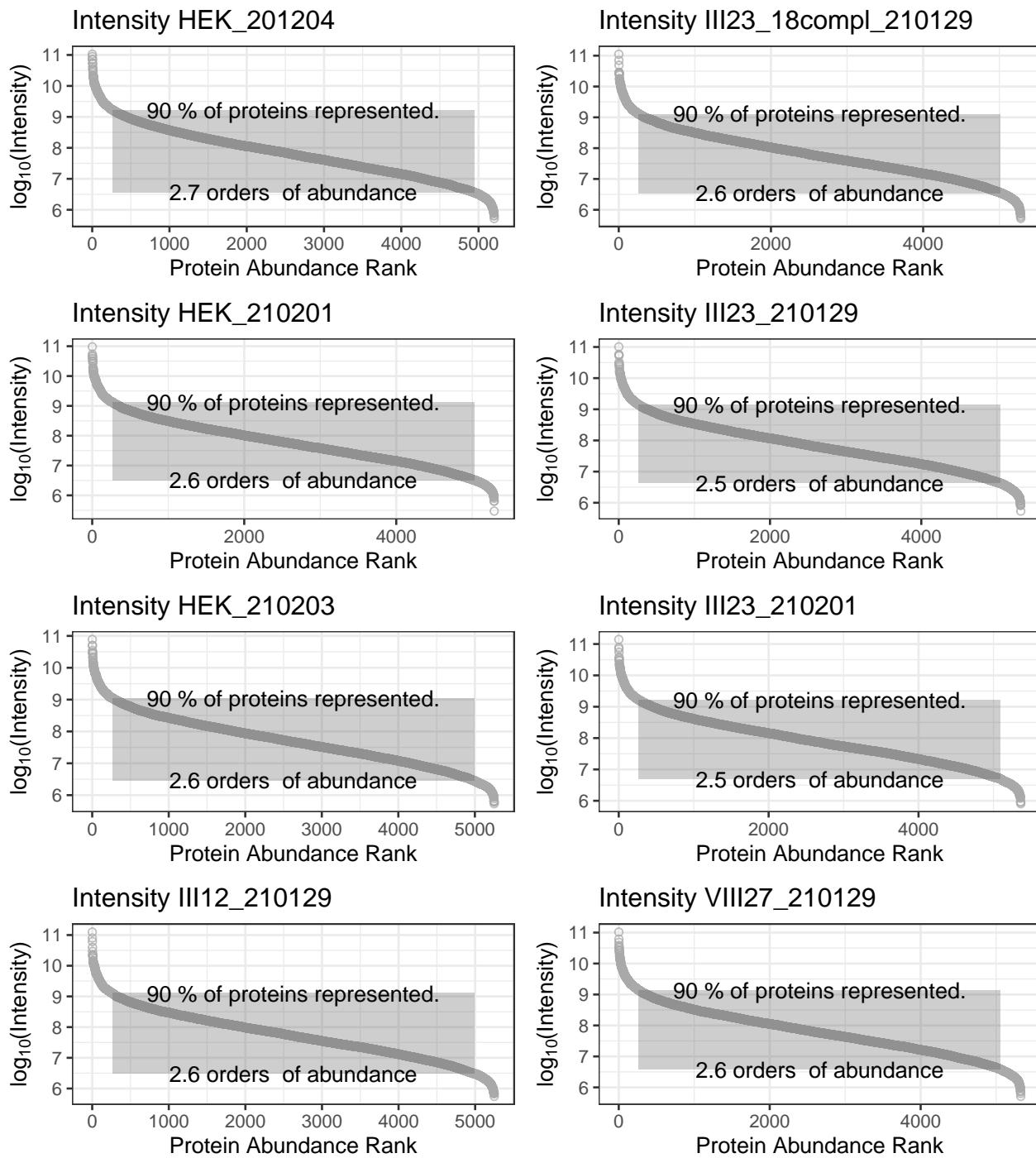
Peptide Identification type





### Dynamic range of protein abundance all samples



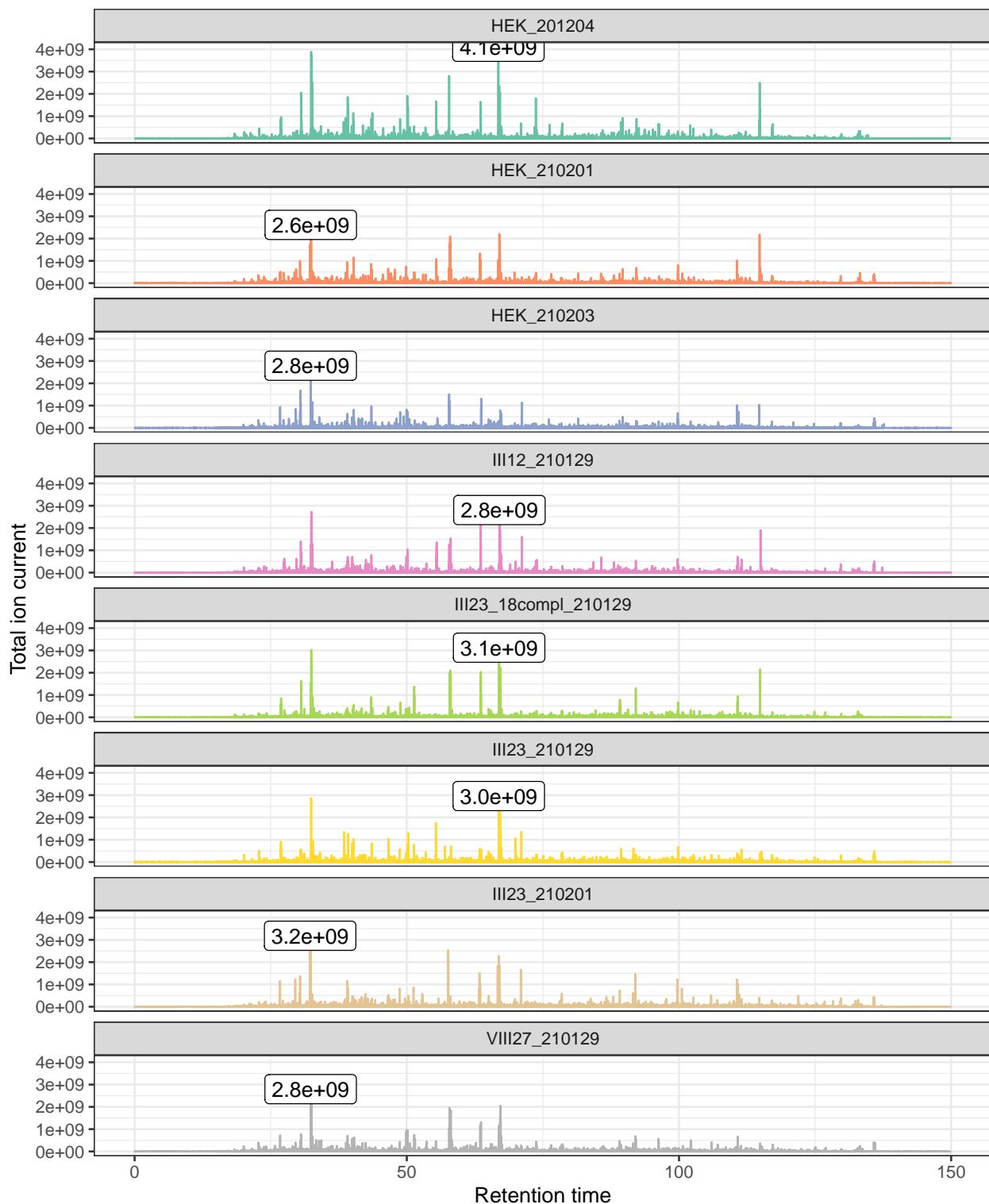


```
## [1] "No UniprotID provided."
```

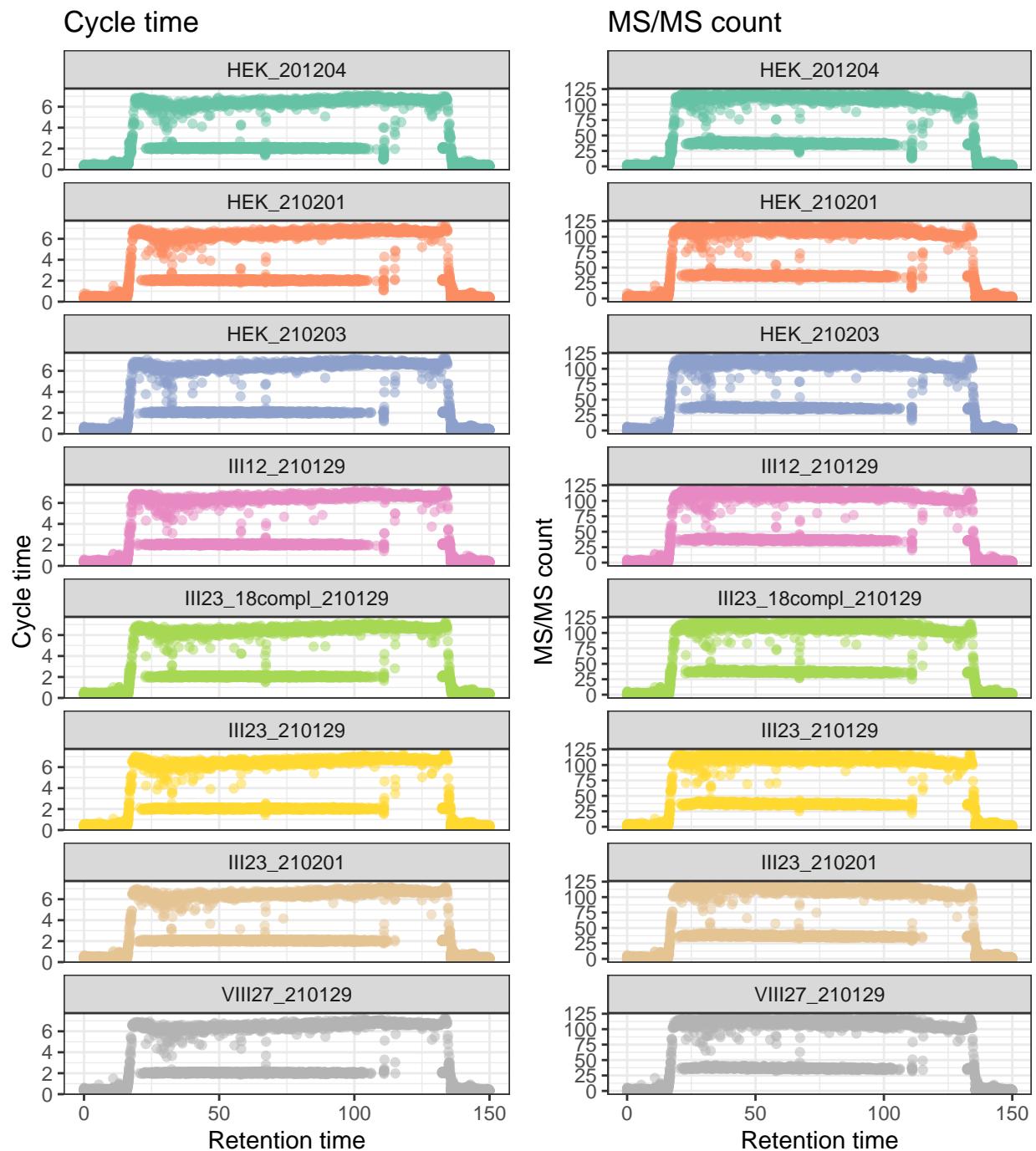
```
## [1] "No iRT peptides found in the MaxQuant output."
```

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

## Total Ion Current



## Acquisition Cycle



```
PlotPTM(modificationSpecificPeptides, freq_min = 3)
```

## Post-Translational Modifications

