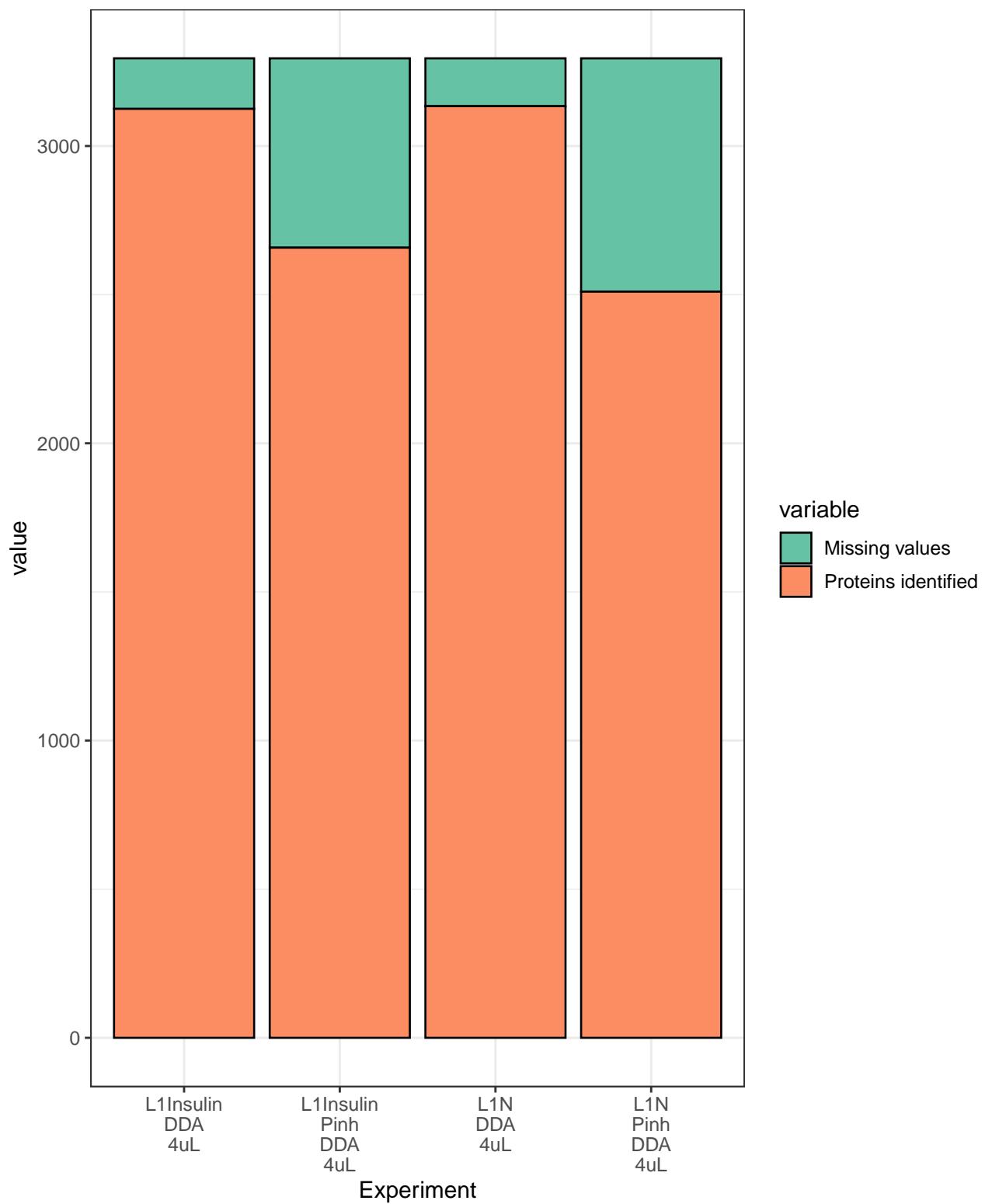


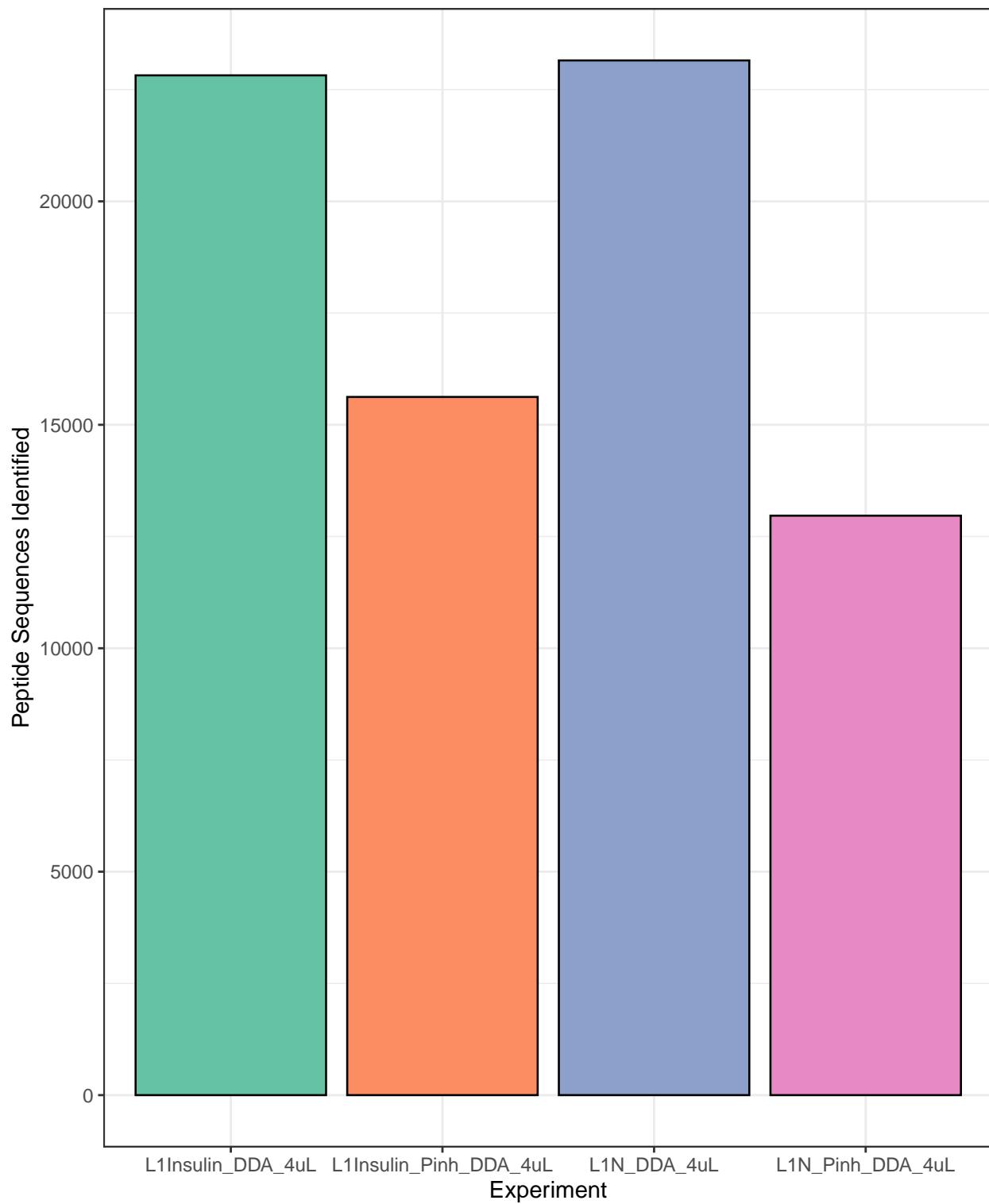
# Report

```
## [1] "The experiment started the day: 17/02/2021 at the time: 18:57:27."
## [1] "The whole experiment lasted: 05:48 (hours:minutes)."
## [1] "The MaxQuant version used was: 1.6.12.0"
## [1] "The user was: marek.vrbacky"
## [1] "The machine name was: FGU013PC029"
## [1] "The protein FDR was: 0.01"
## [1] "The match between runs was: True"
## [1] "The fasta file used was: C:\\MaxQuant_Databases\\UP000000589_10090.fasta"
```

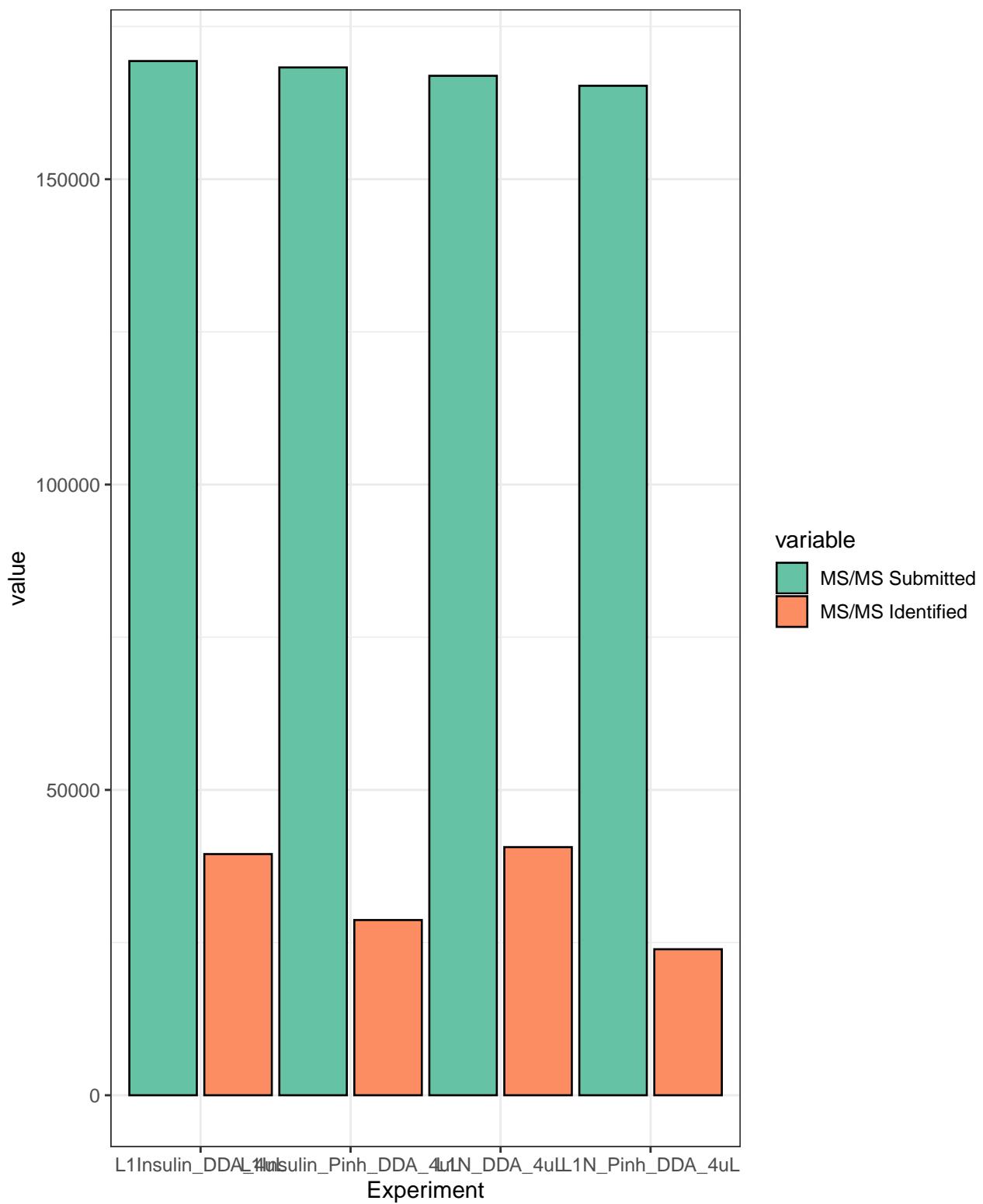
## Proteins Identified



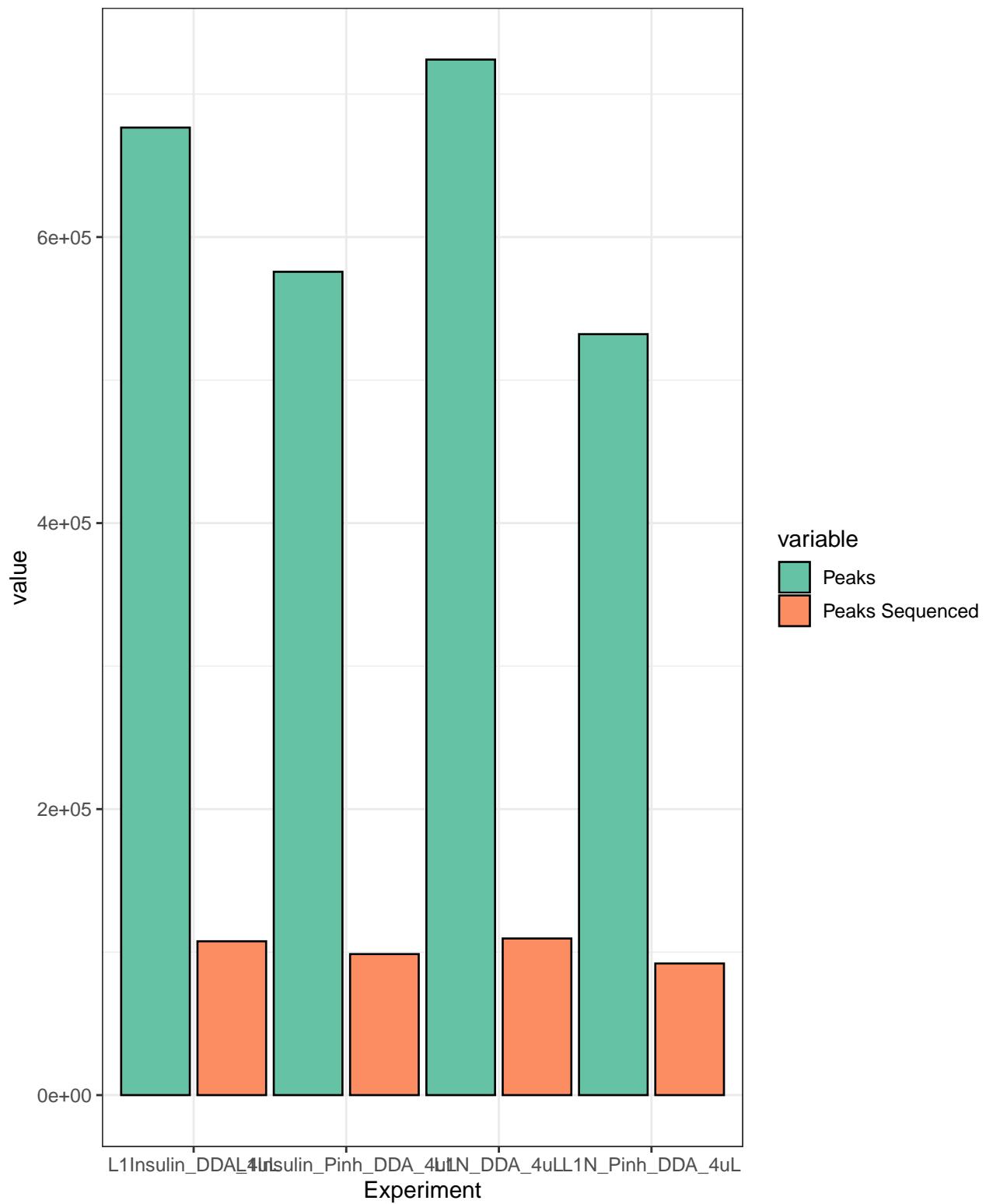
Peptides Sequences Identified



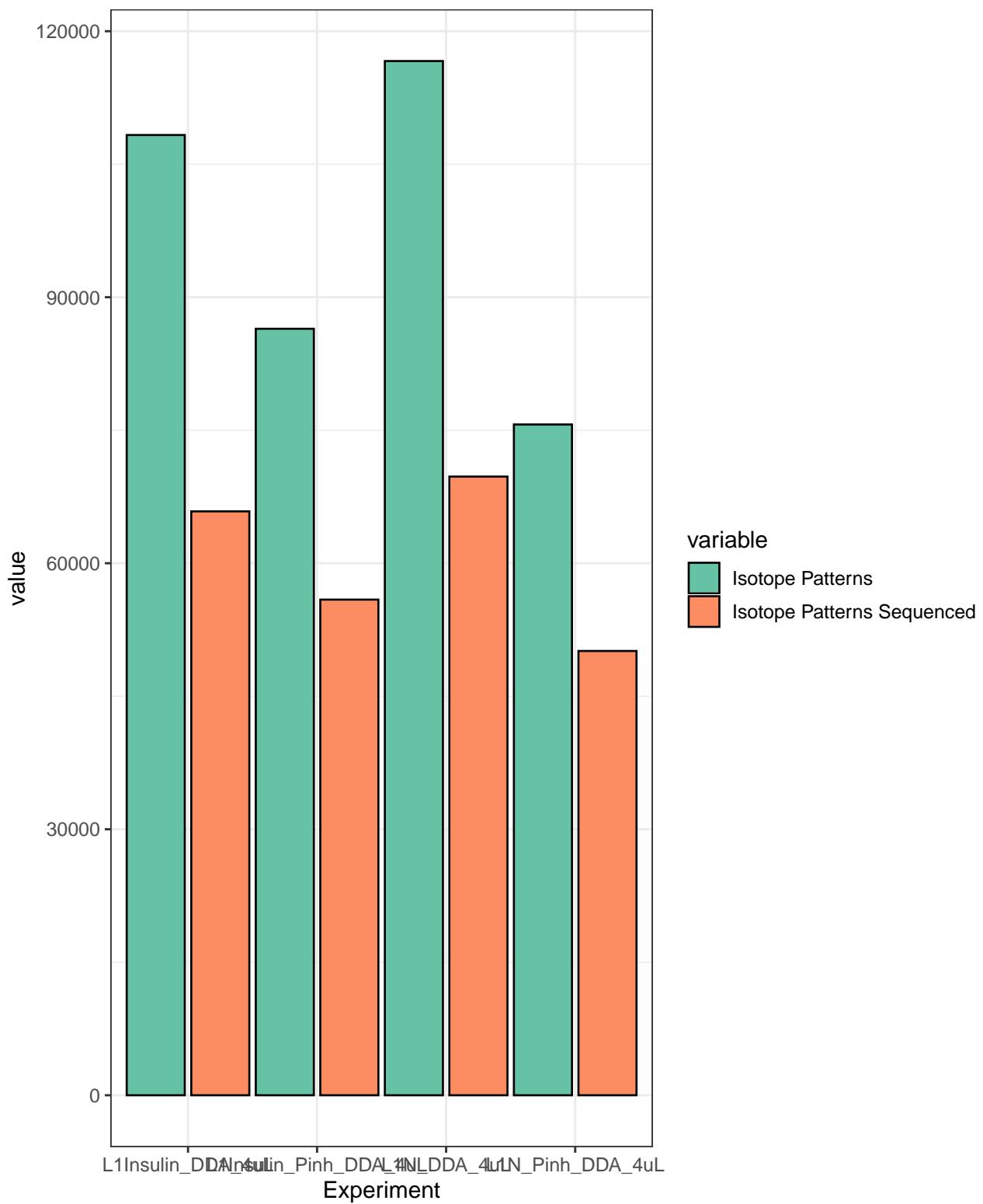
## MS/MS Submitted and Identified



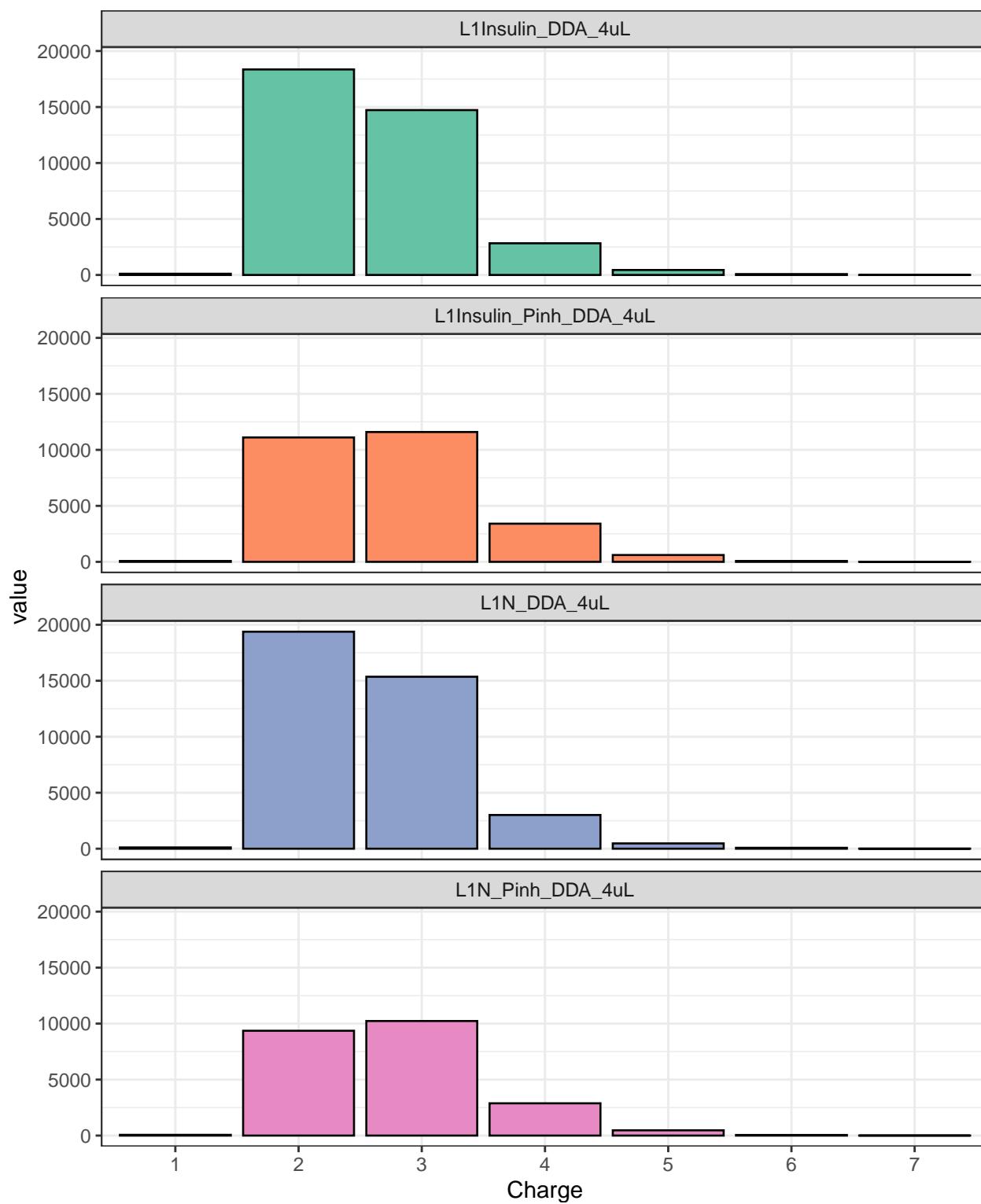
### Peaks detected and sequenced in the full scans



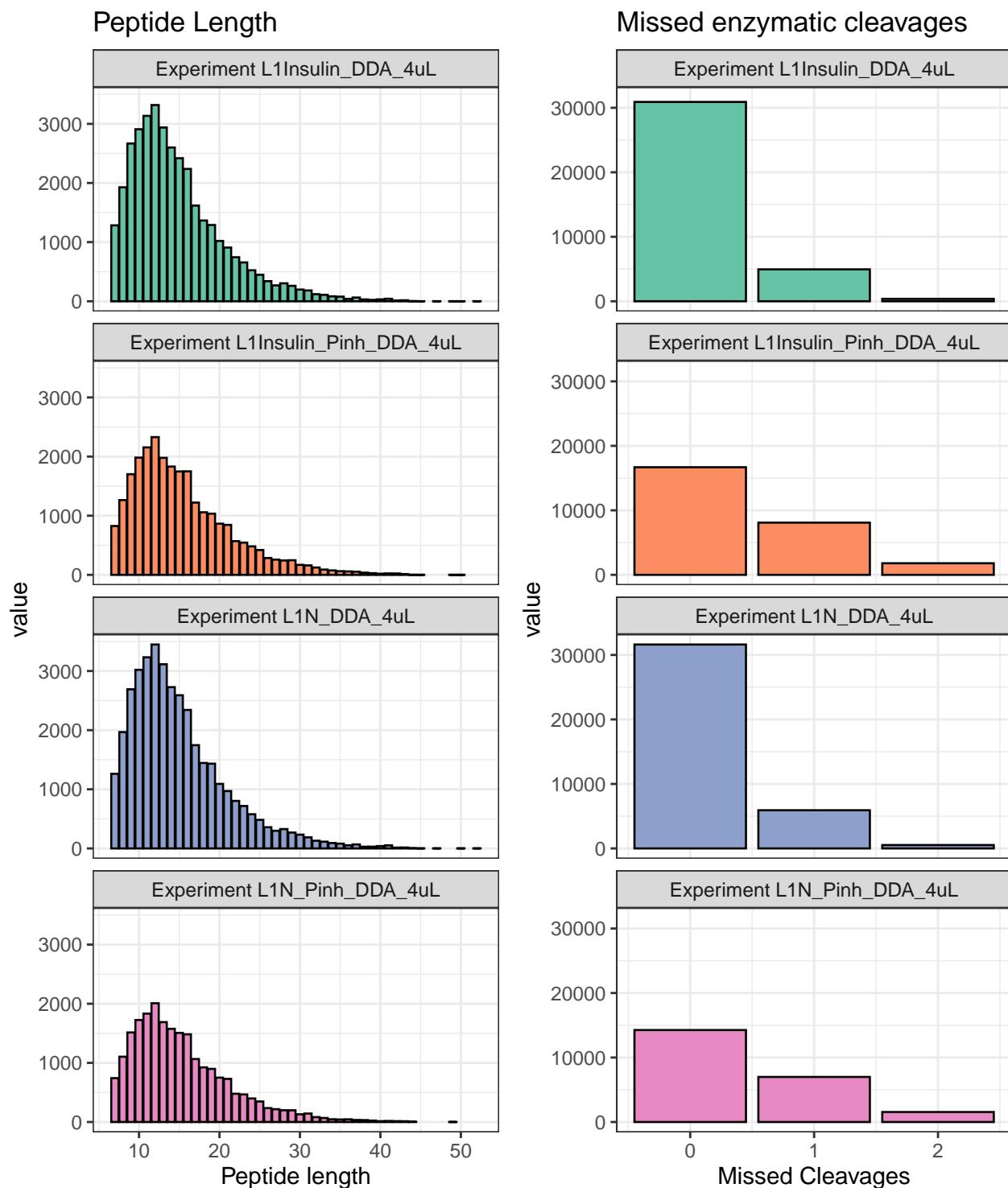
### Isotope Patterns detected and sequenced



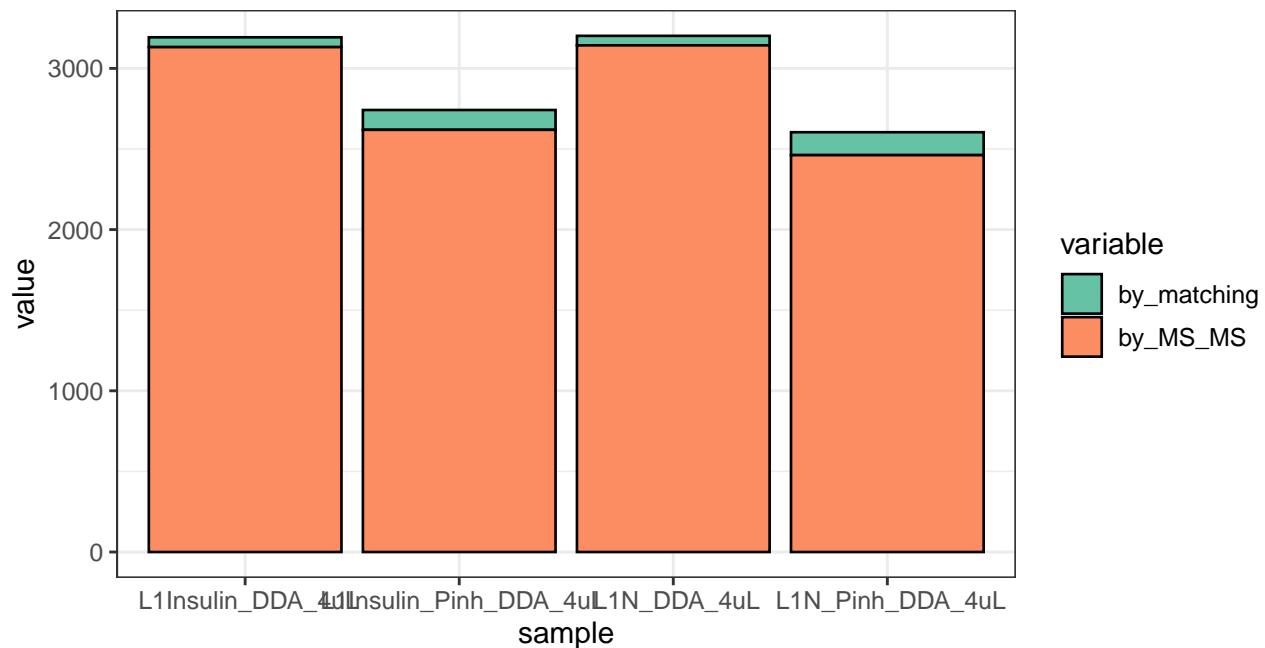
### The charge-state of the precursor ion.



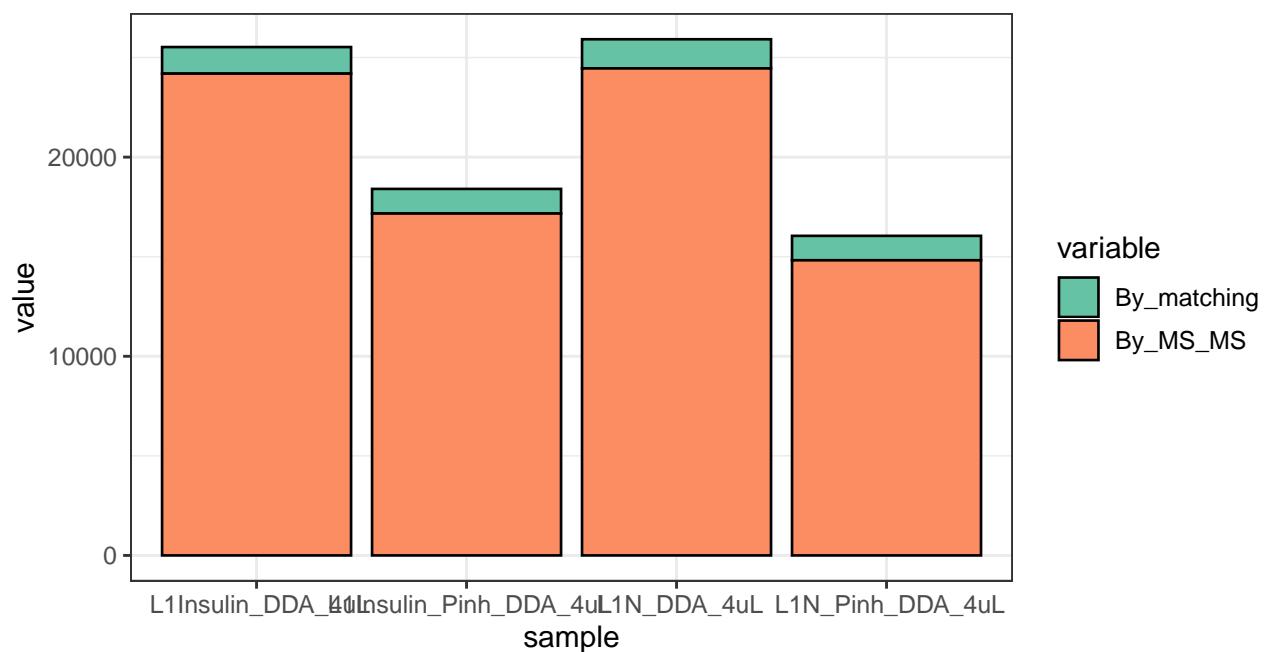
## Protease Specificity



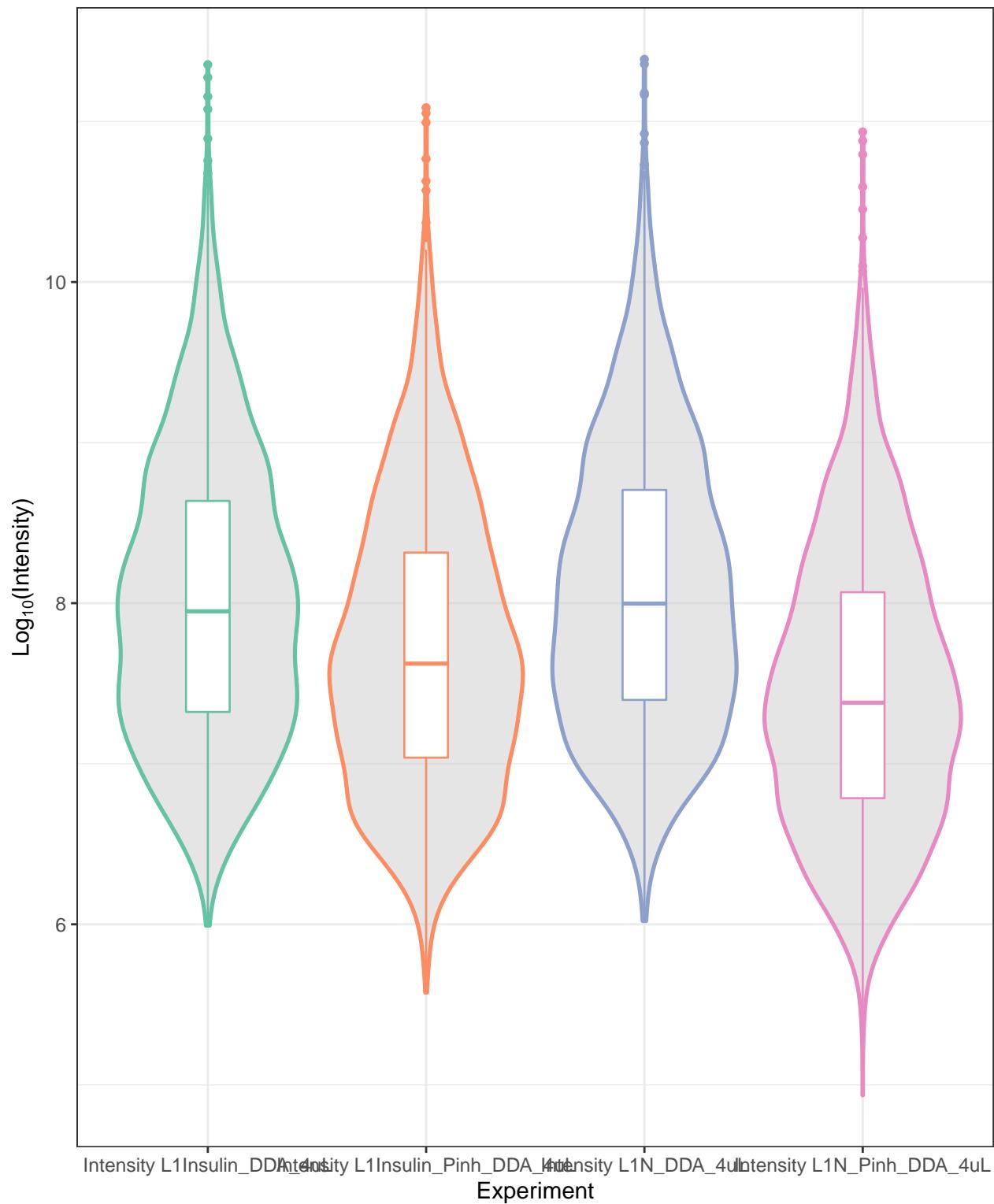
Protein Identification type



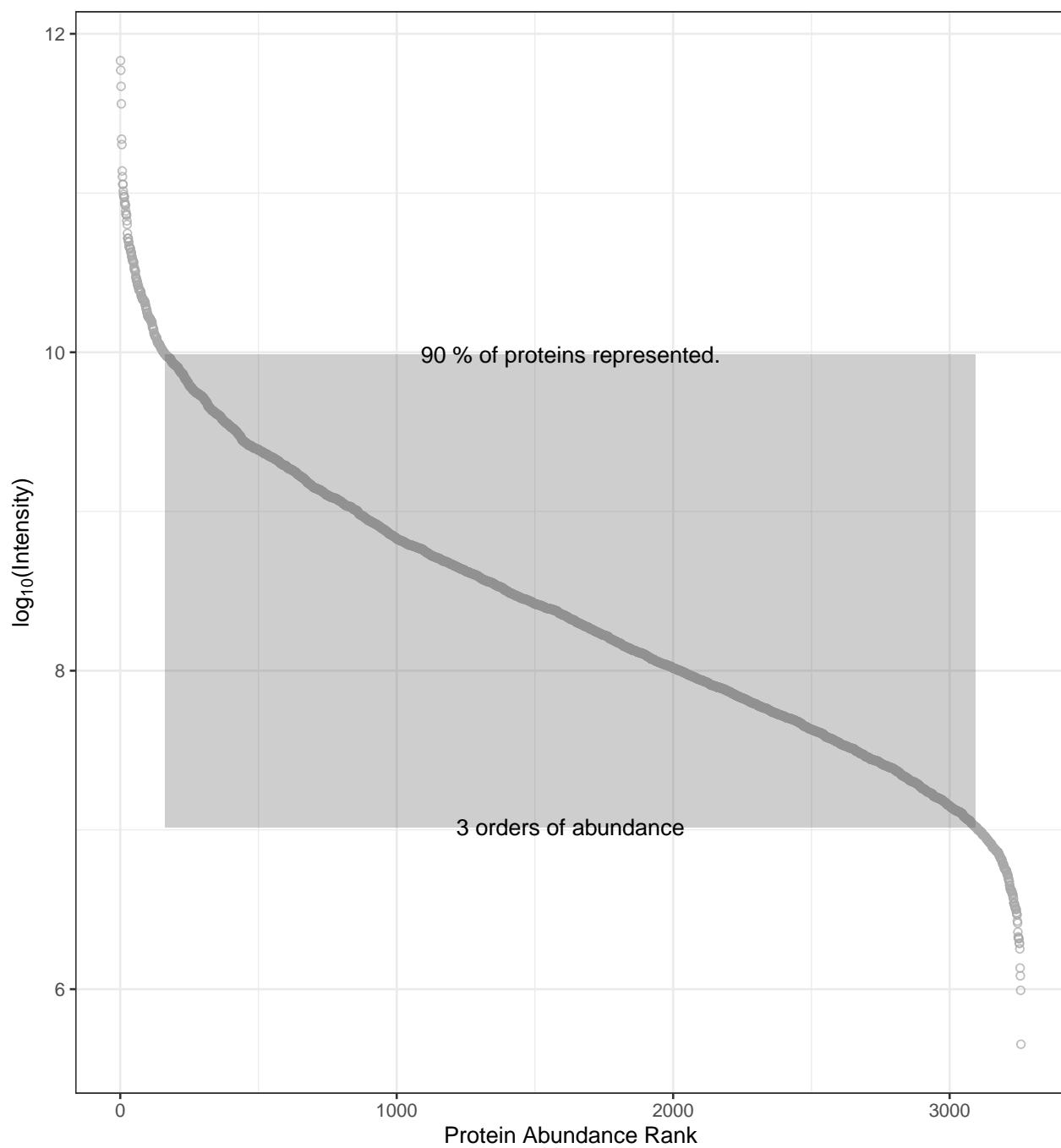
Peptide Identification type



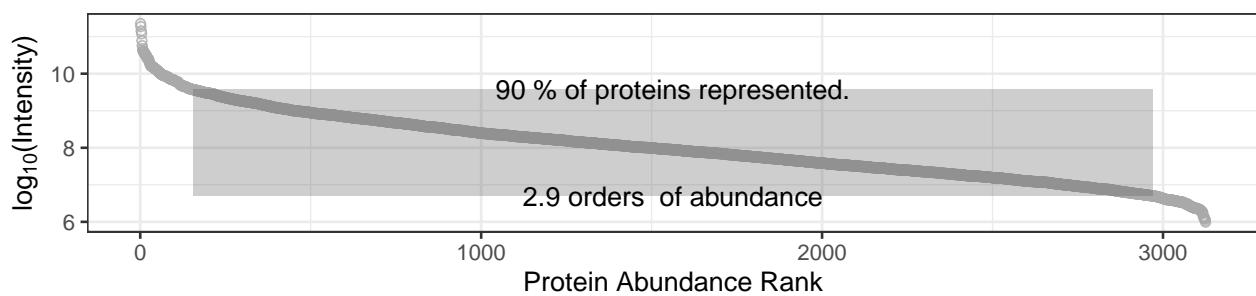
## Protein Intensity



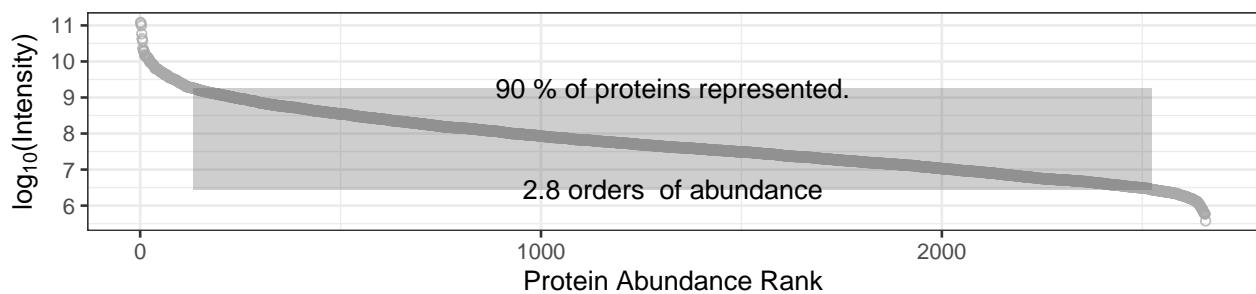
### Dynamic range of protein abundance all samples



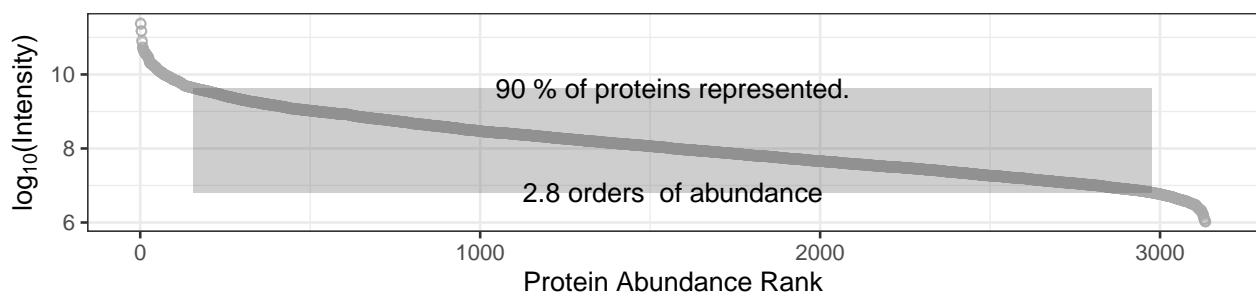
Intensity L1Insulin\_DDA\_4uL



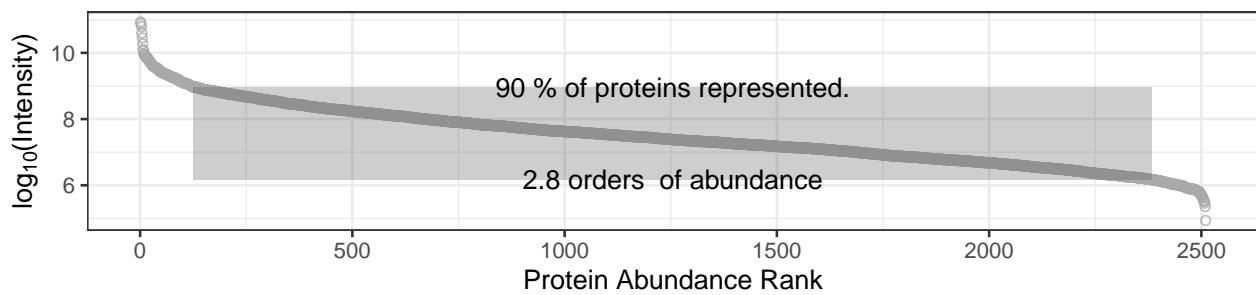
Intensity L1Insulin\_Pinh\_DDA\_4uL



Intensity L1N\_DDA\_4uL



Intensity L1N\_Pinh\_DDA\_4uL

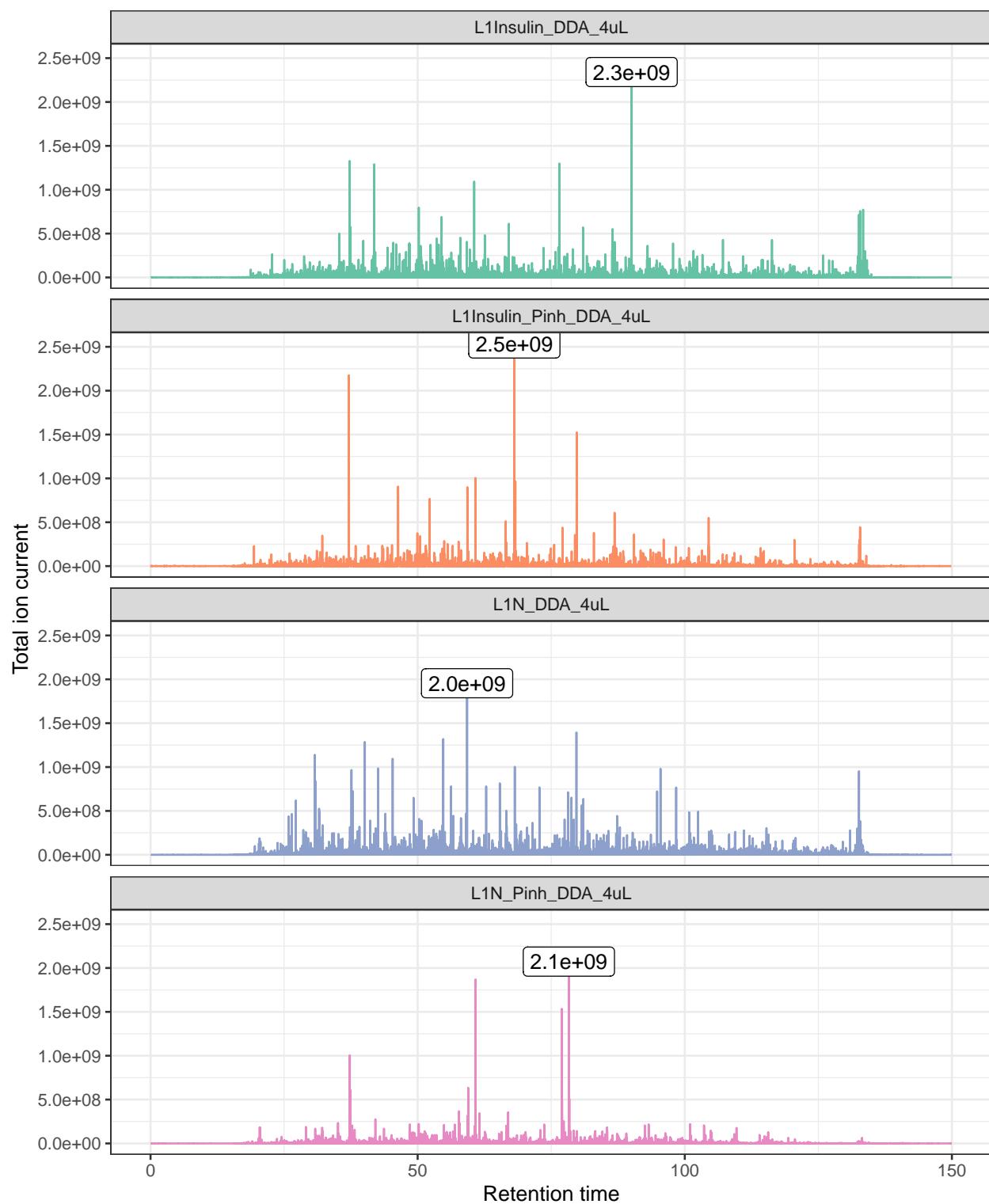


```
## [1] "No UniprotID provided."
```

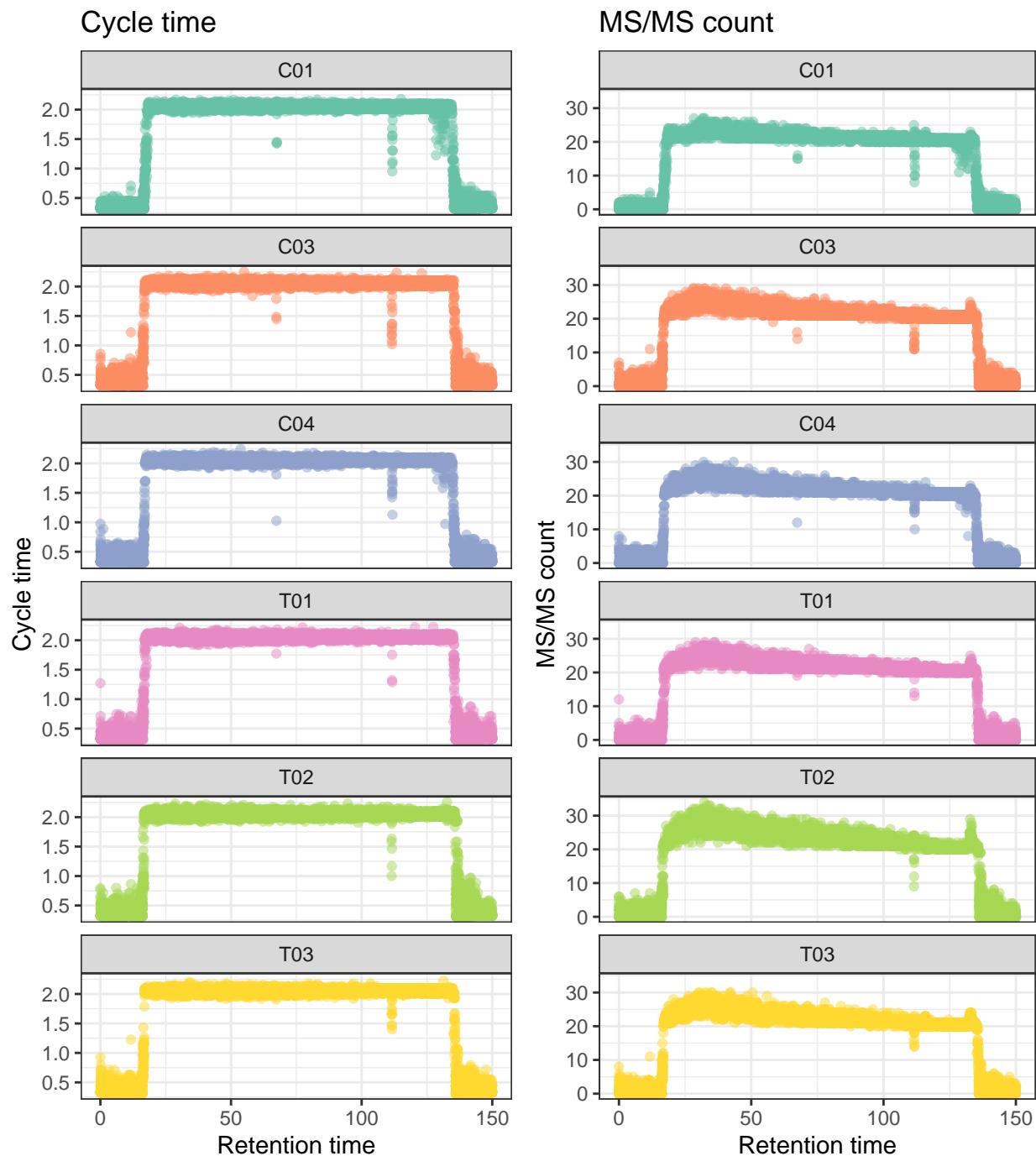
```
## [1] "No iRT peptides found in the MaxQuant output."
```

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

### Total Ion Current



## Acquisition Cycle



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

## Post–Translational Modifications

