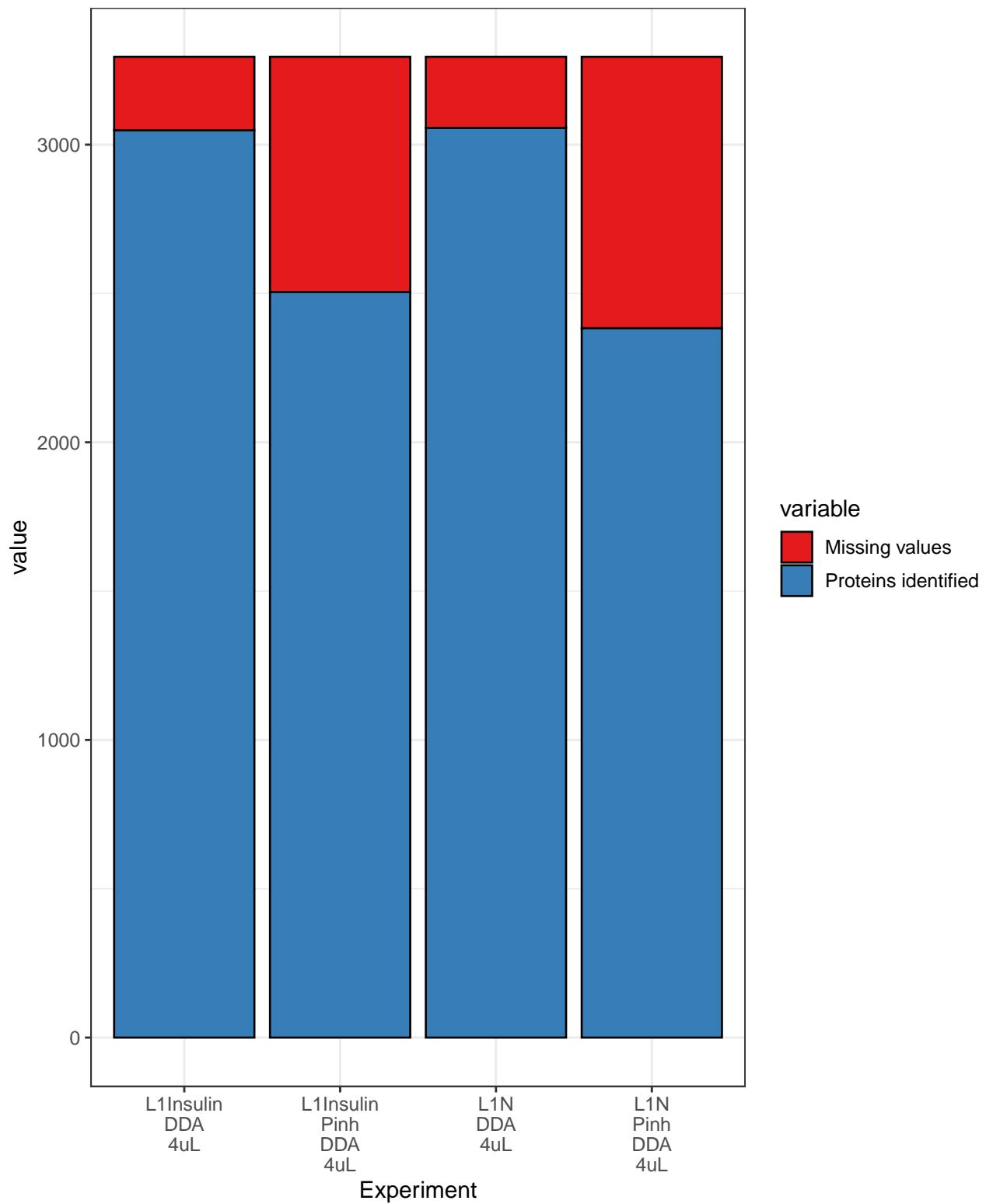


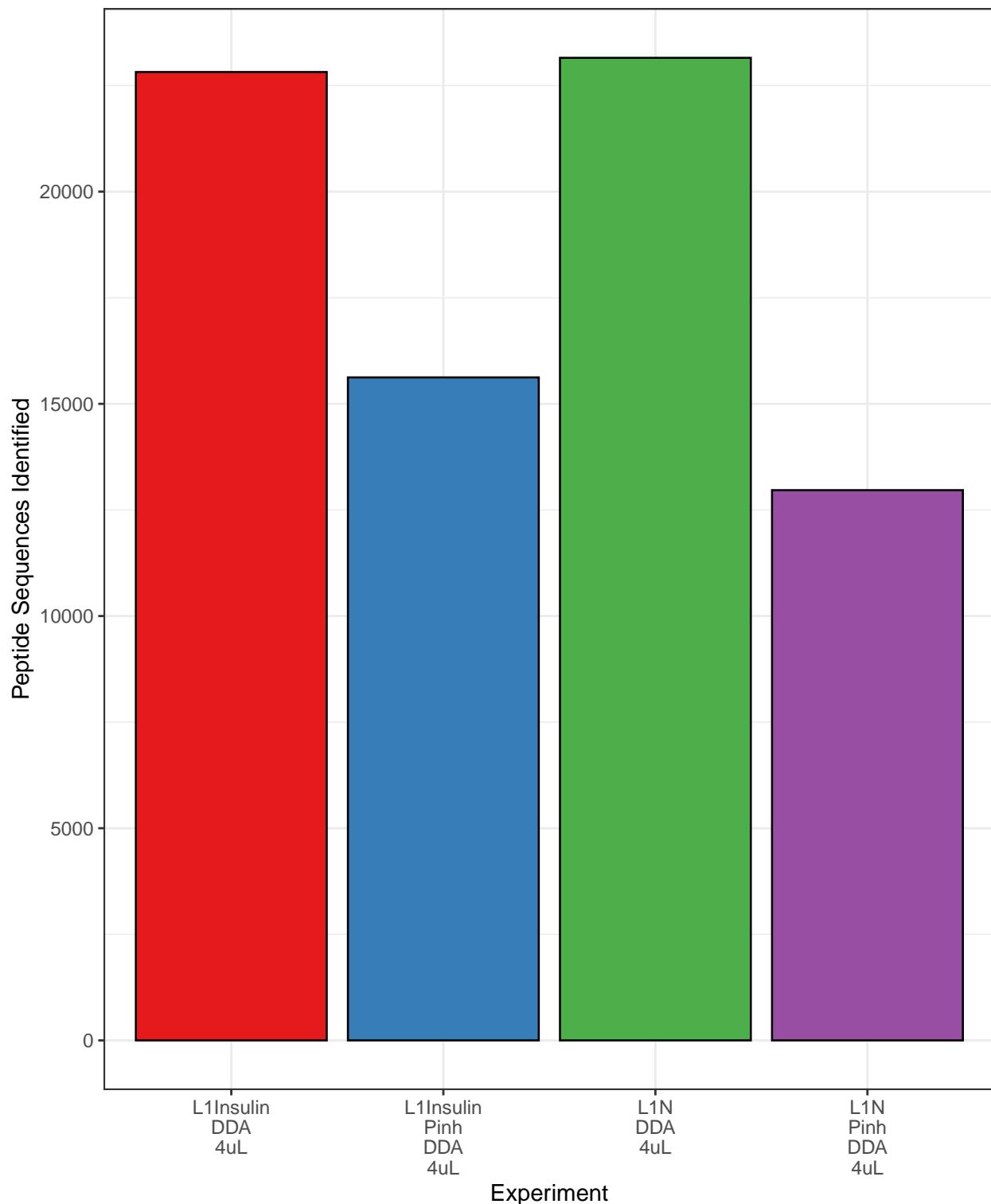
Report

```
## [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"
```

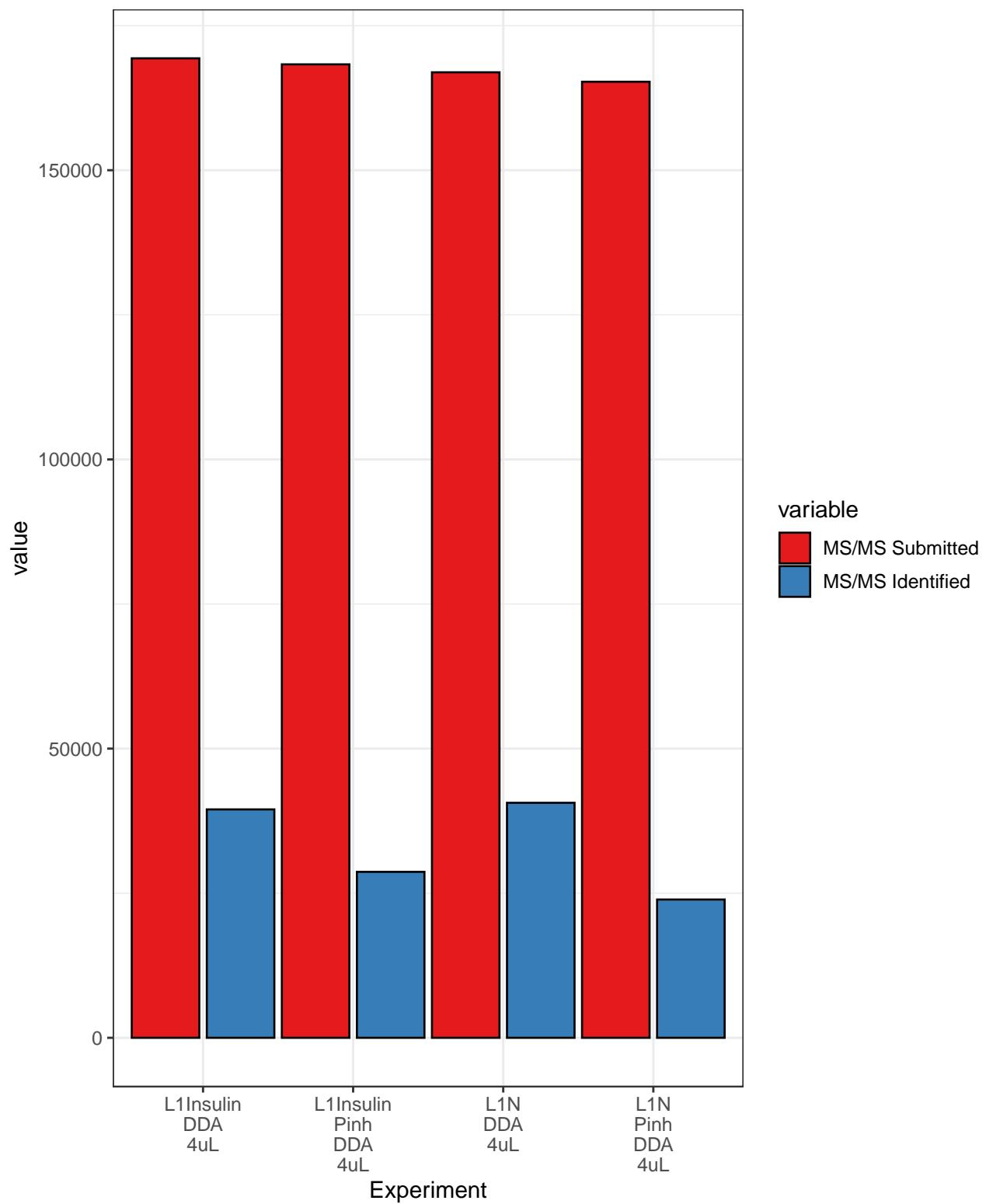
Proteins Identified based on LFQ intensity



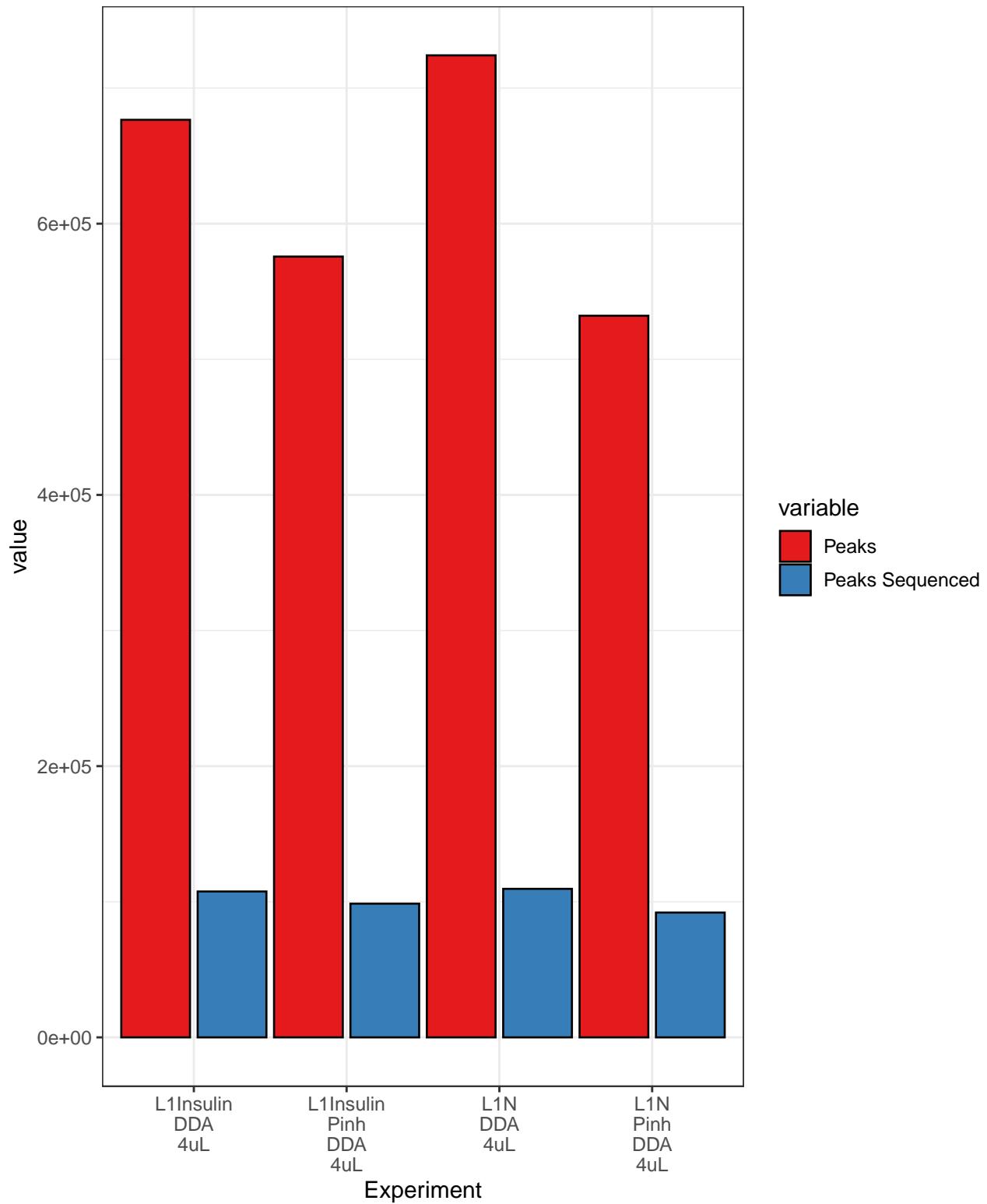
Peptides Sequences Identified



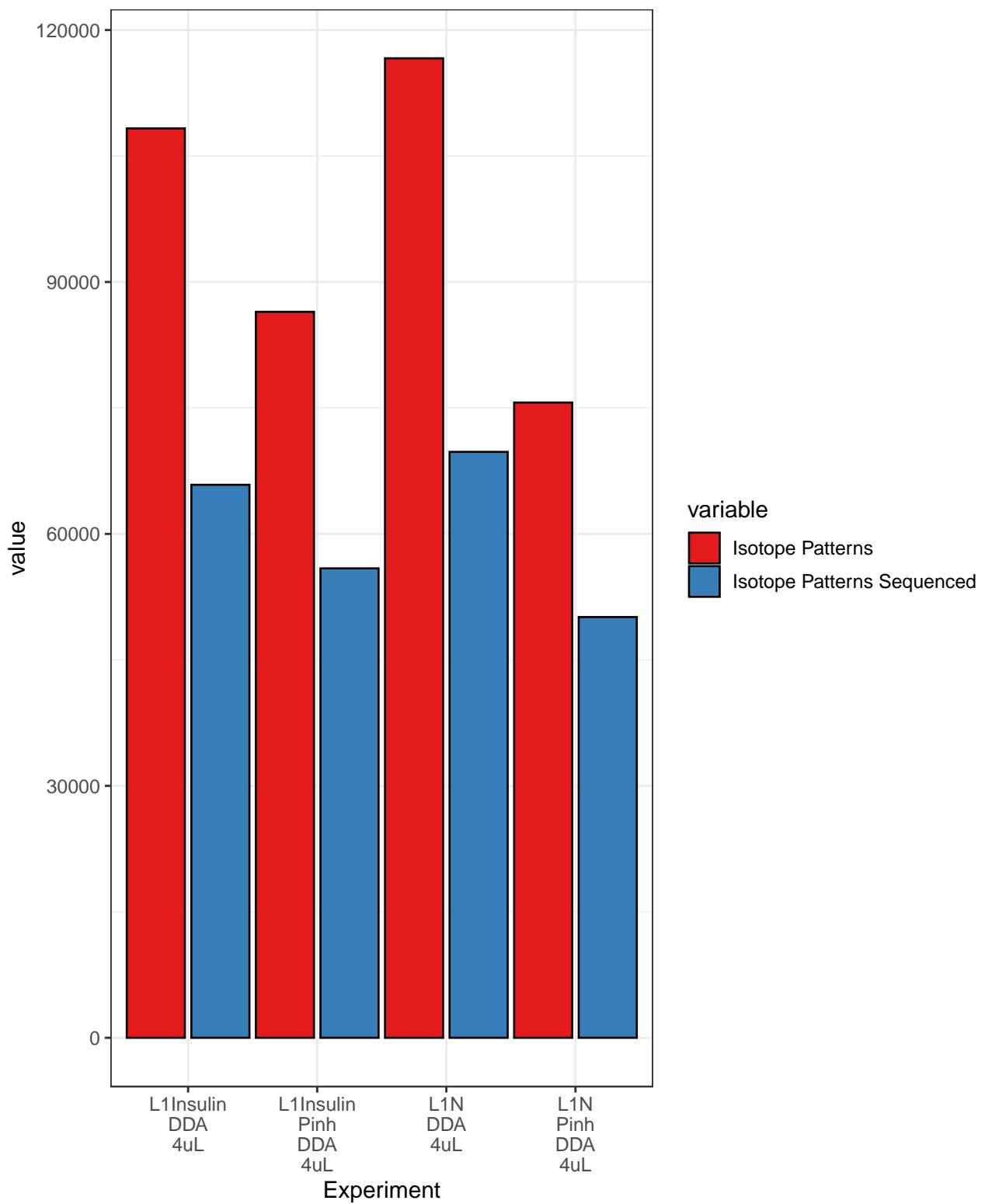
MS/MS Submitted and Identified



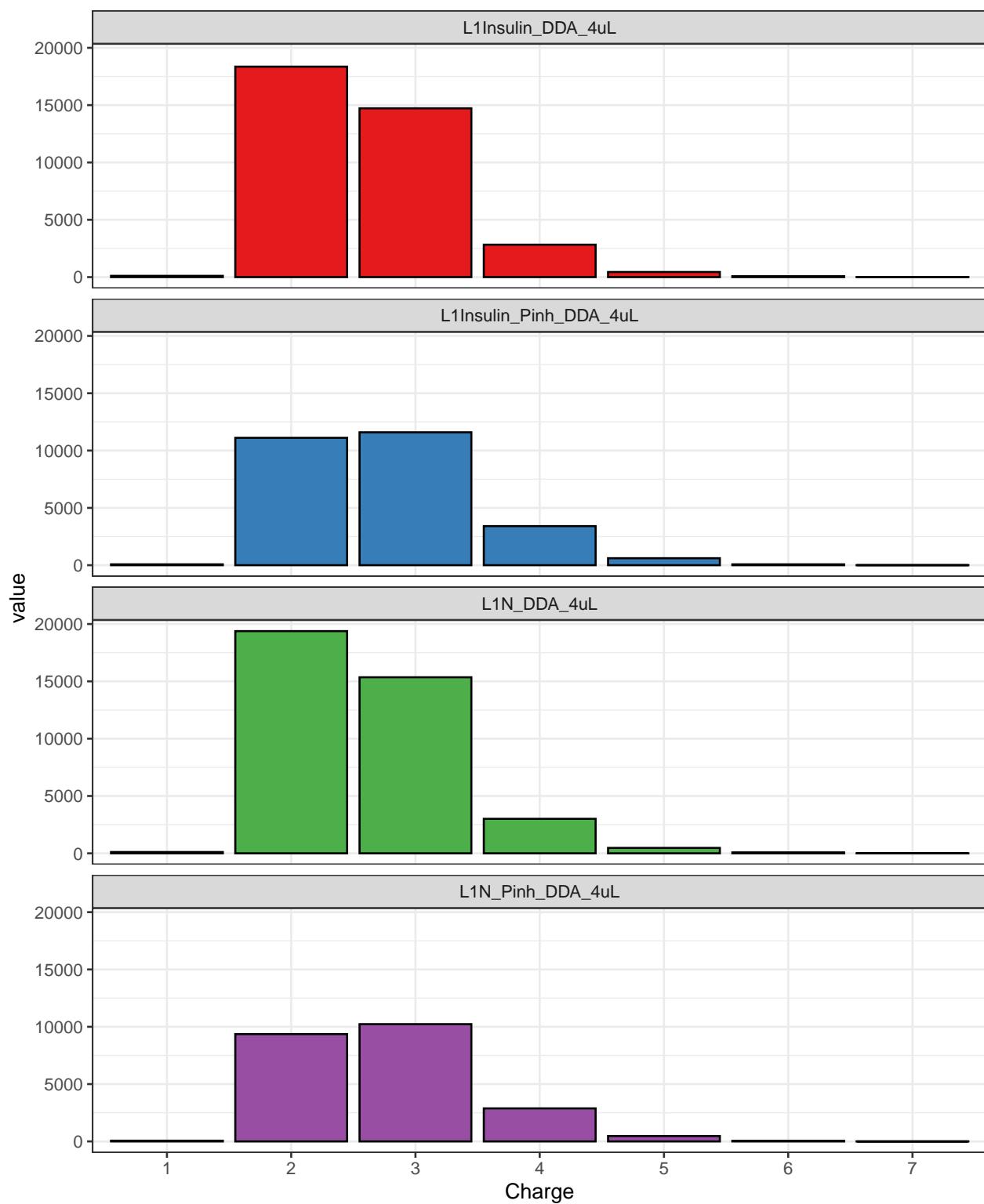
Peaks detected and sequenced in the full scans



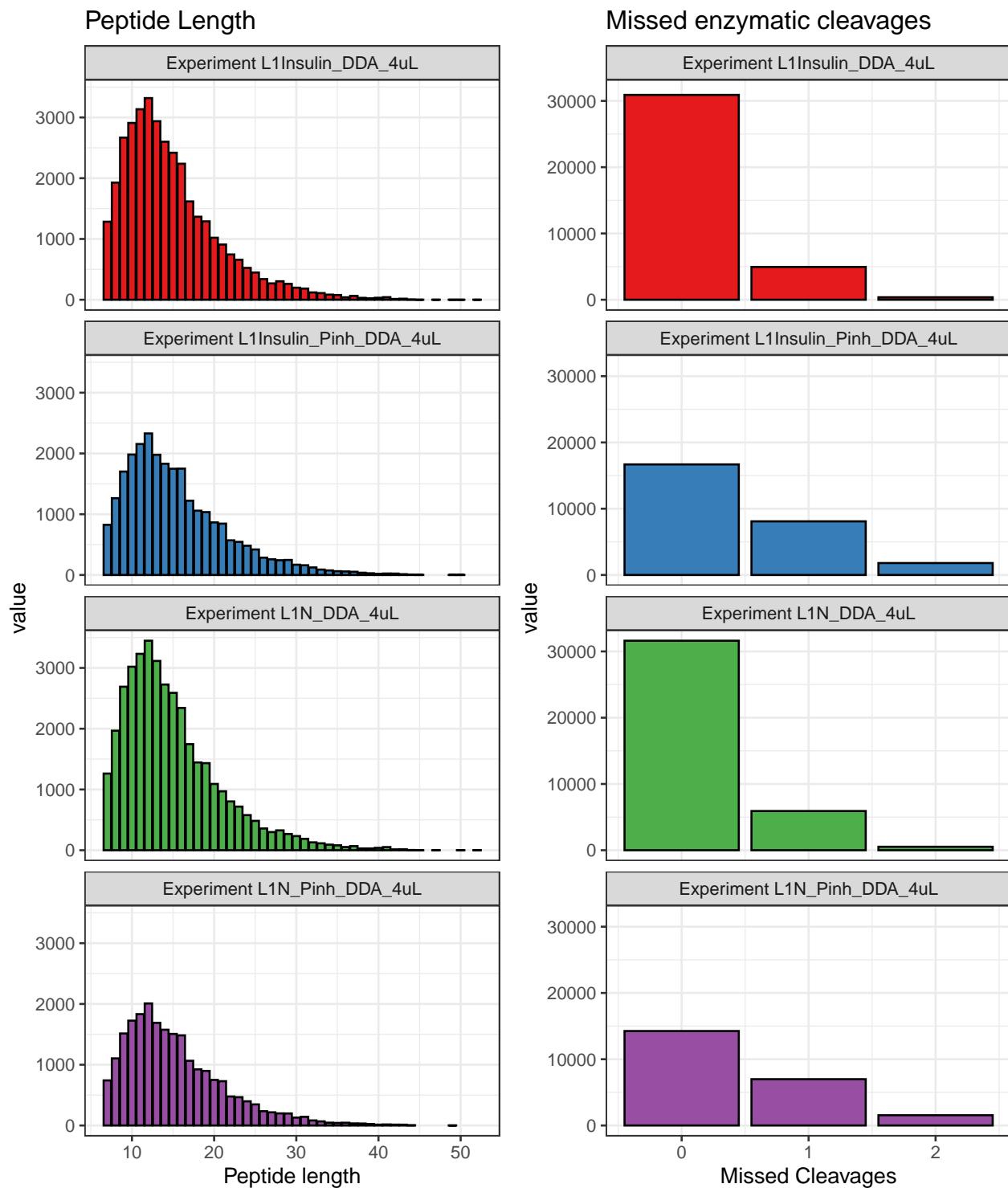
Isotope Patterns detected and sequenced



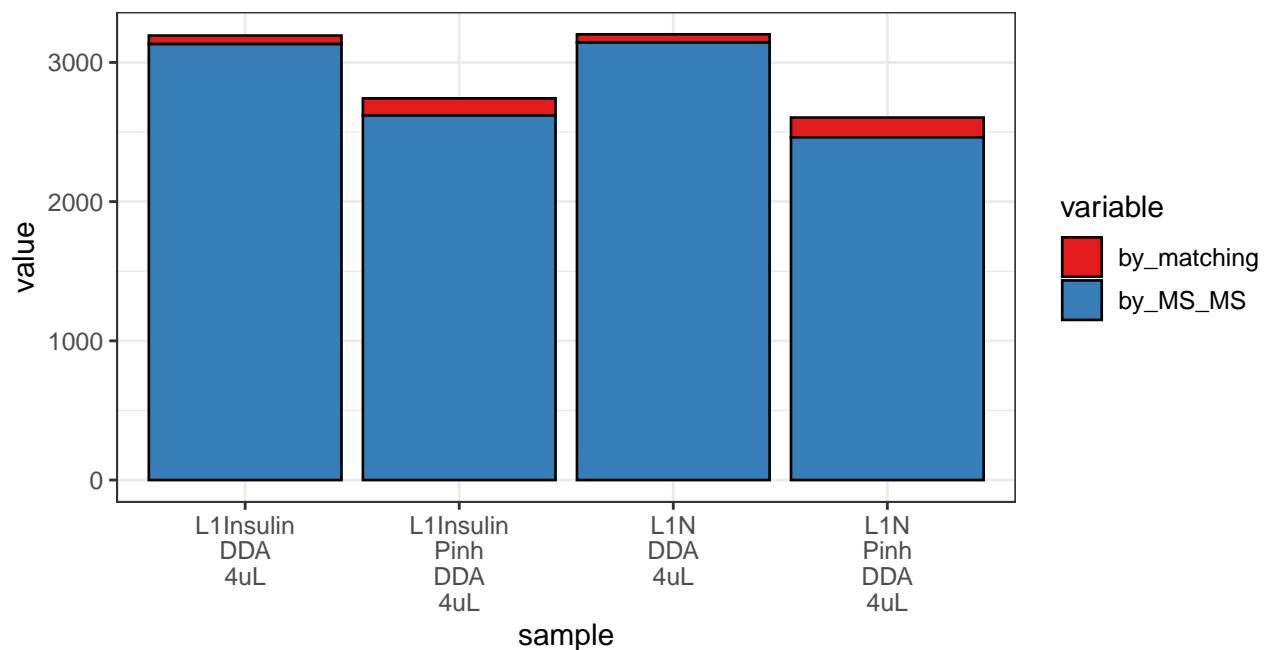
The charge-state of the precursor ion.



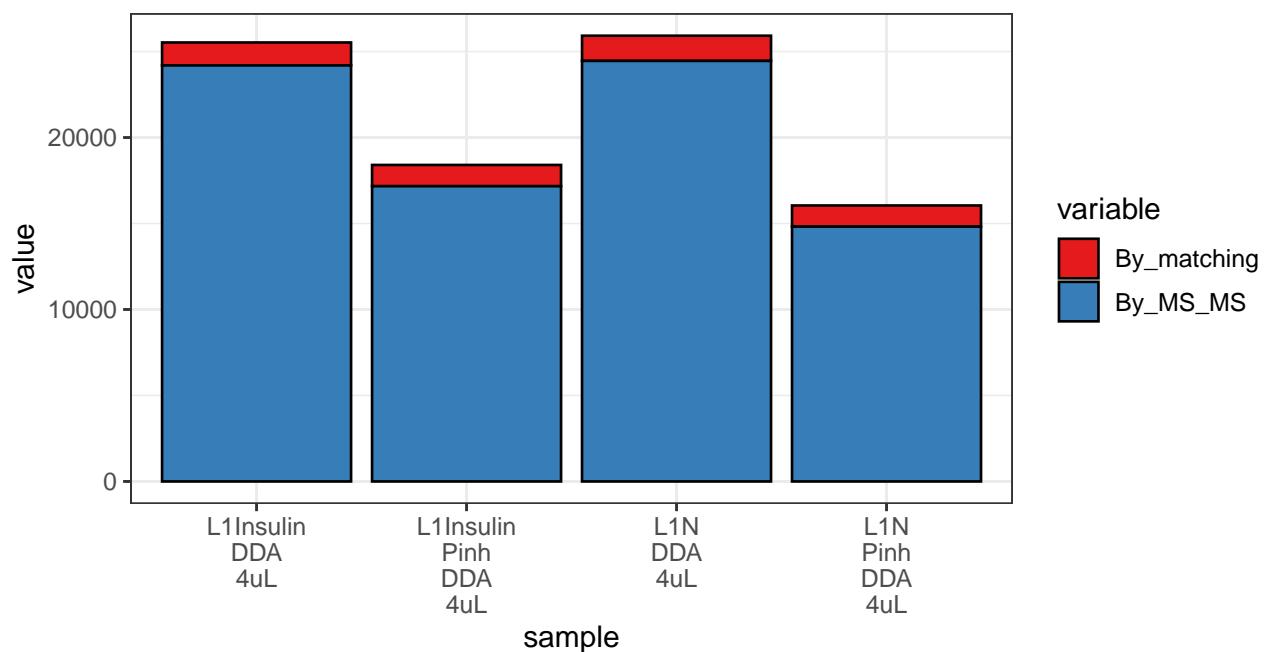
Protease Specificity



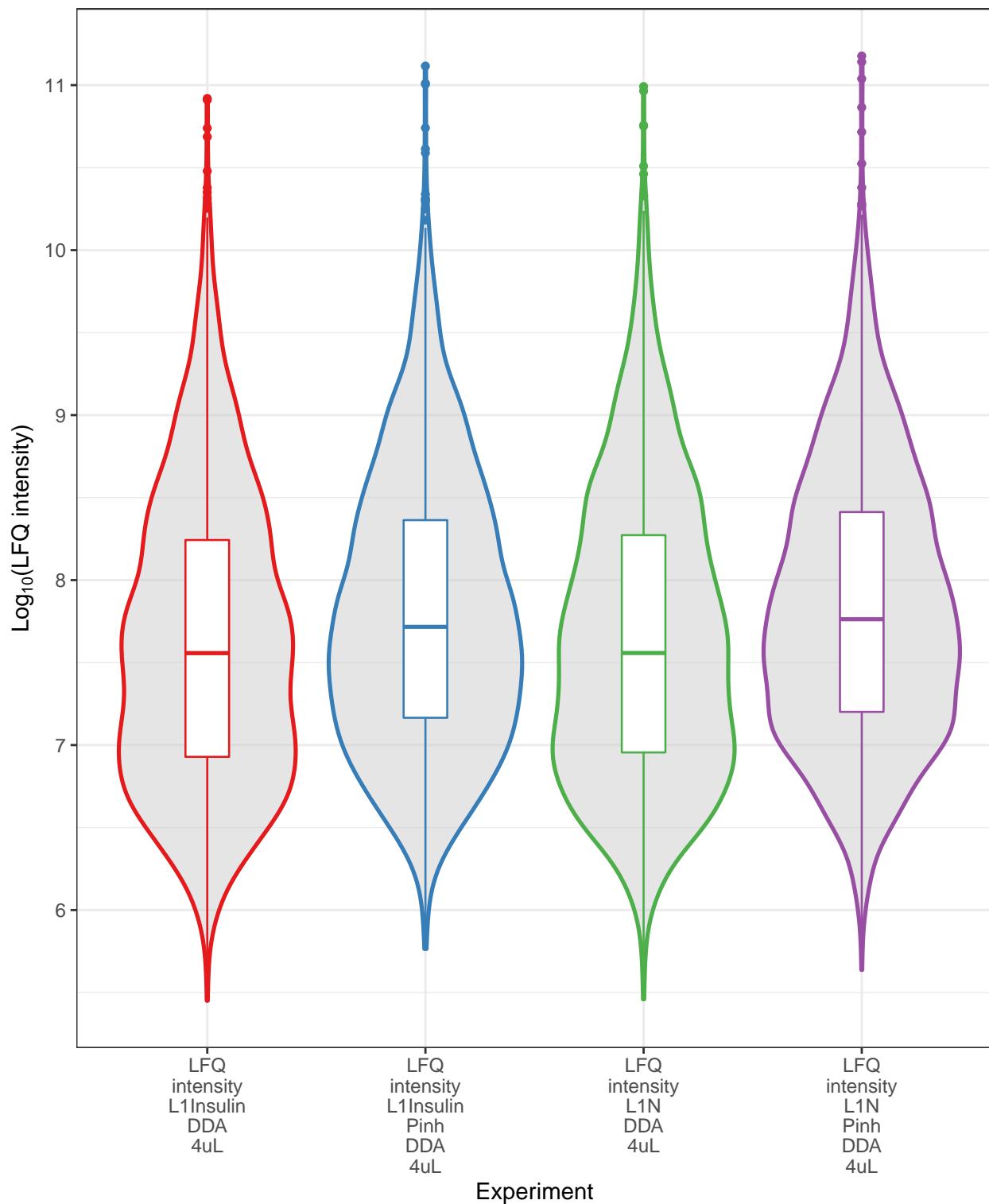
Protein Identification type



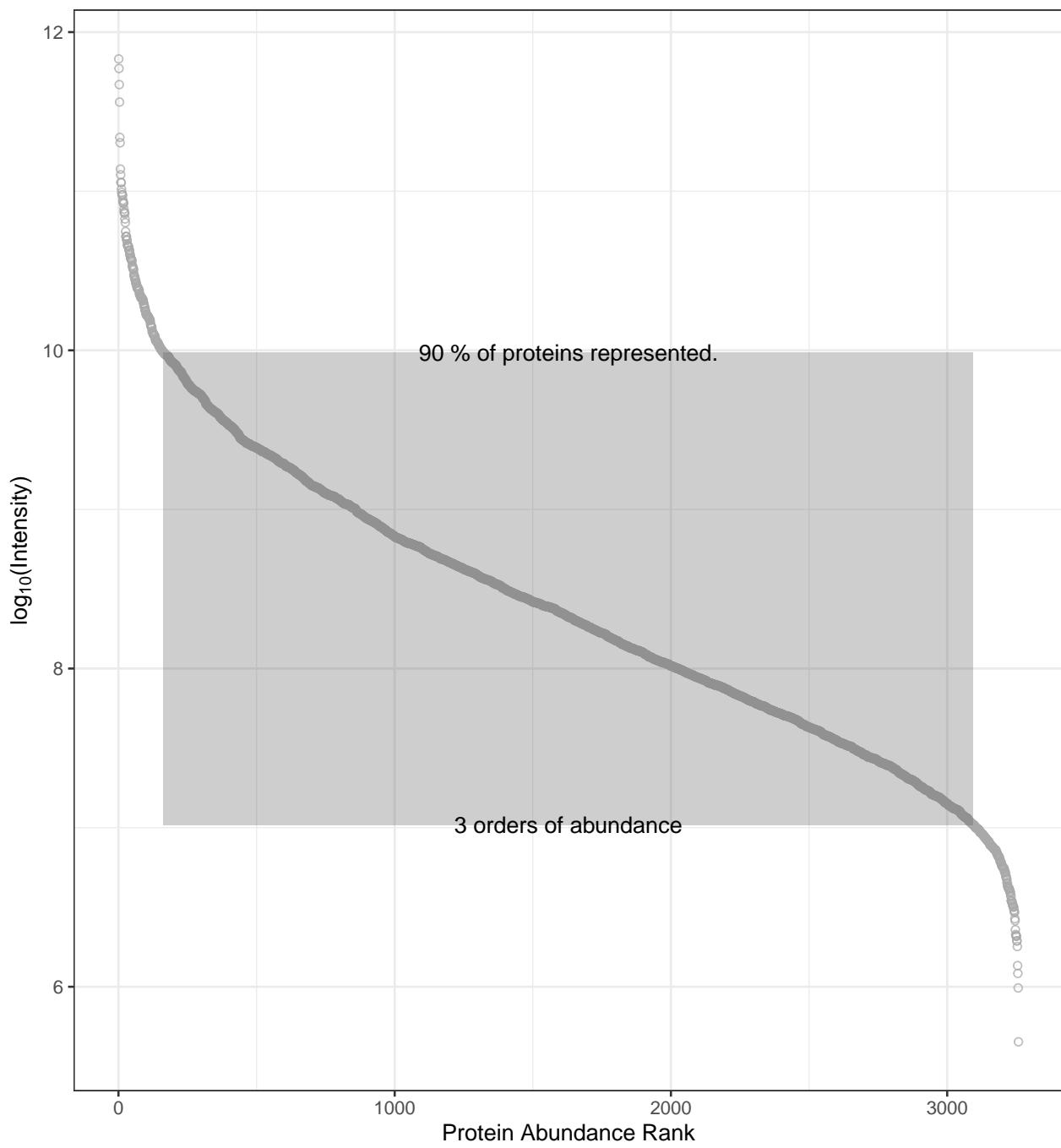
Peptide Identification type



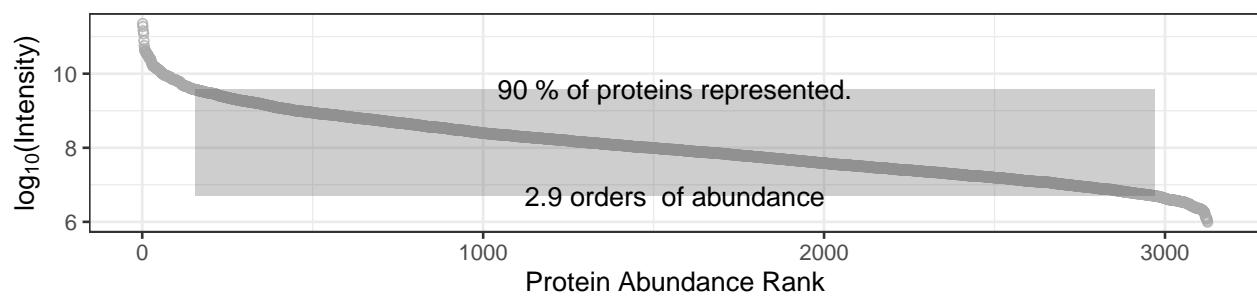
Protein Intensity



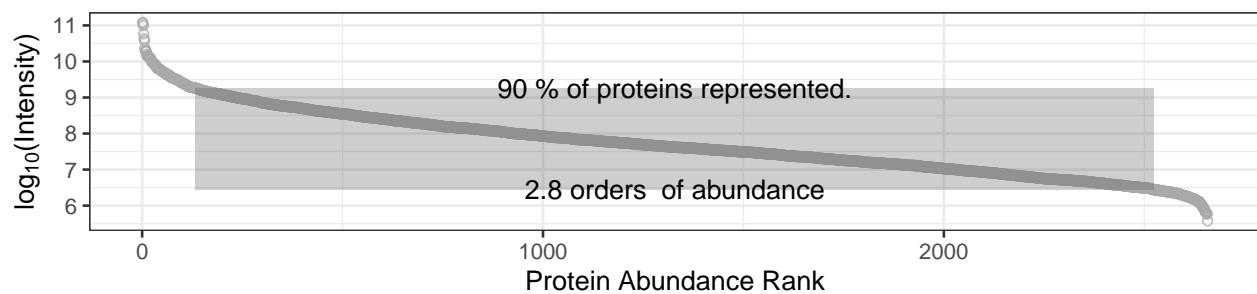
Dynamic range of protein abundance all samples



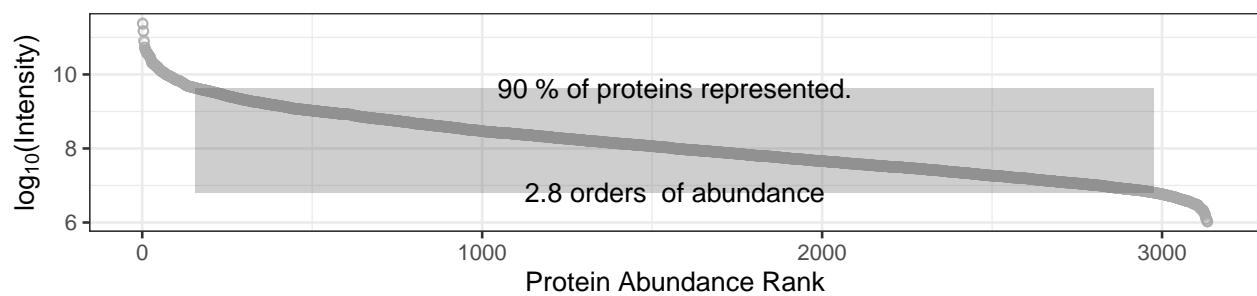
Intensity L1Insulin_DDA_4uL



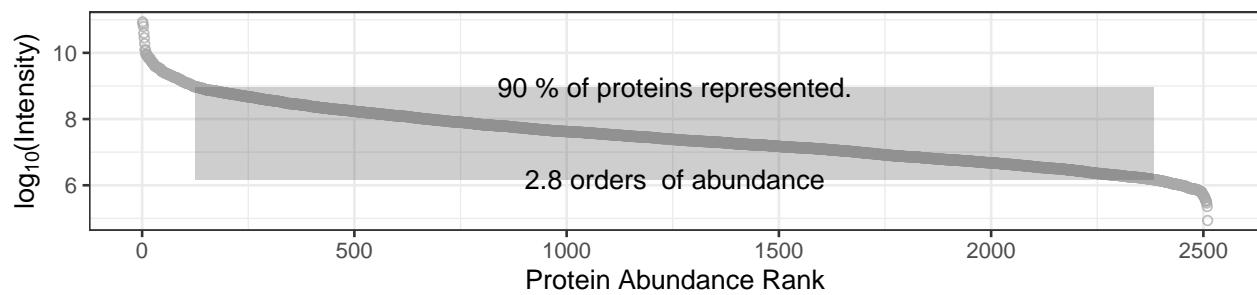
Intensity L1Insulin_Pinh_DDA_4uL



Intensity L1N_DDA_4uL



Intensity L1N_Pinh_DDA_4uL

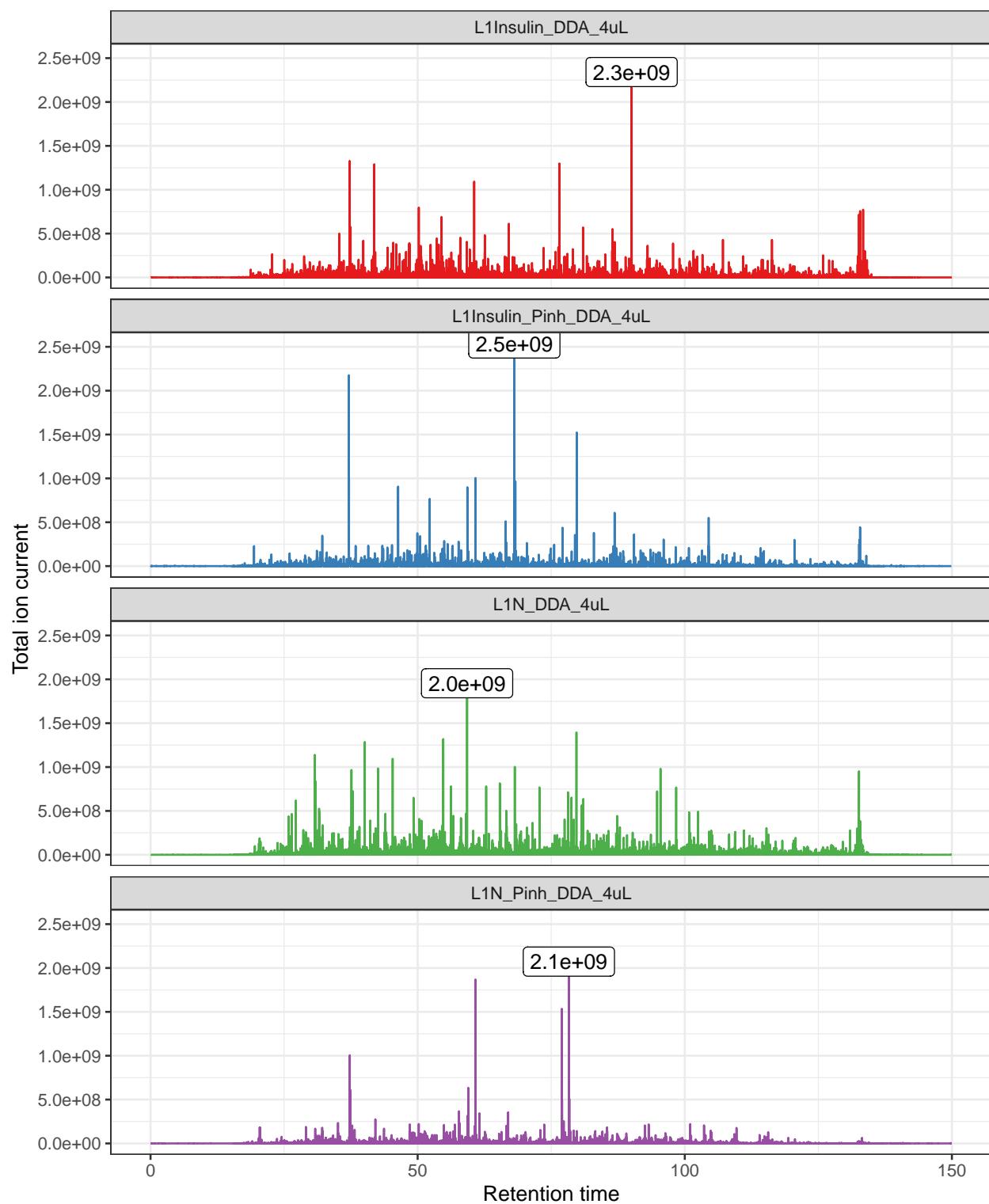


```
## [1] "No UniprotID provided."
```

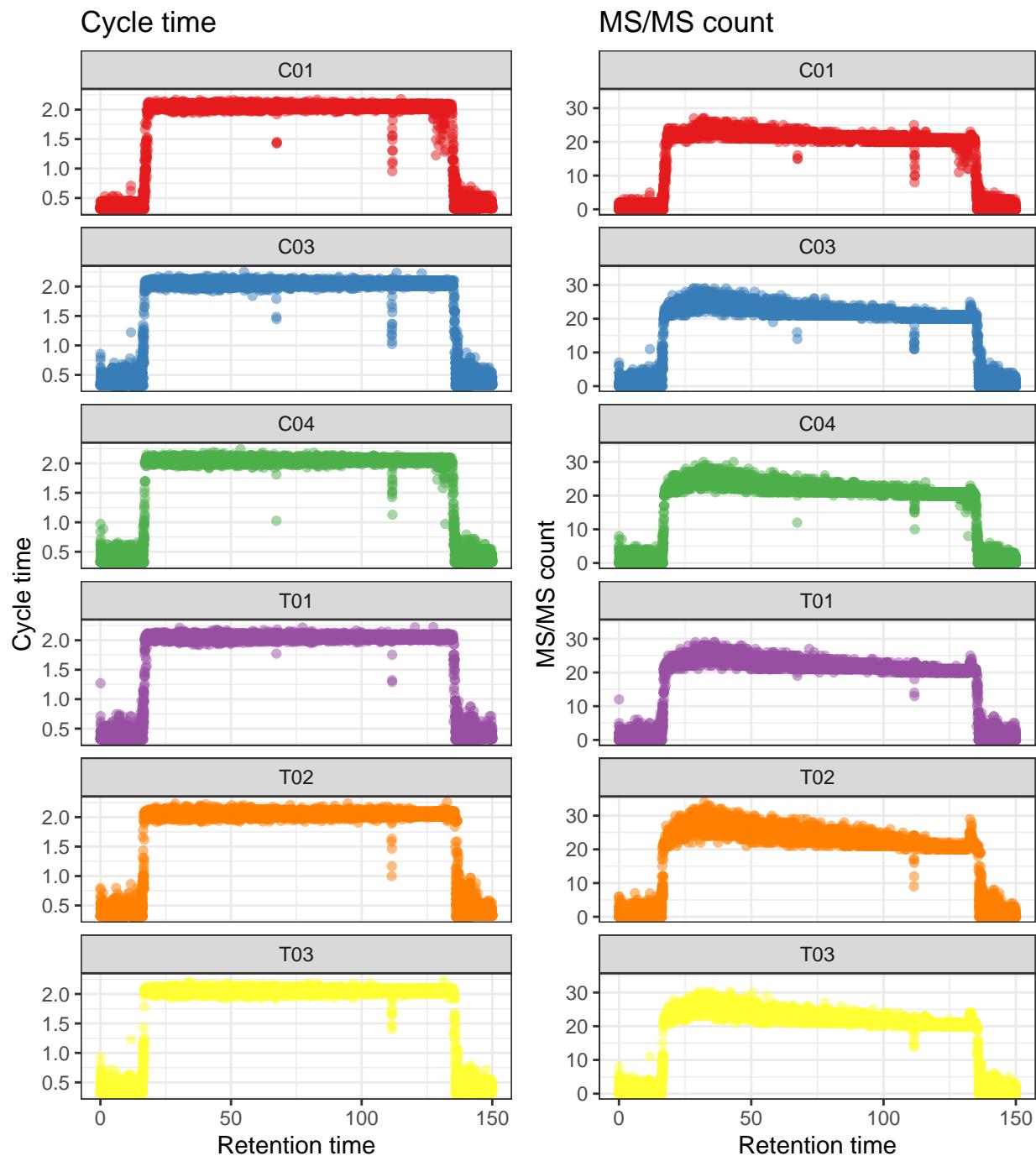
```
## [1] "No iRT peptides found in the MaxQuant output."
```

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

Total Ion Current



Acquisition Cycle



```
PlotPTM(modificationSpecificPeptides,
        freq_min = 3,
        palette = params$palette)
```

Post-Translational Modifications

