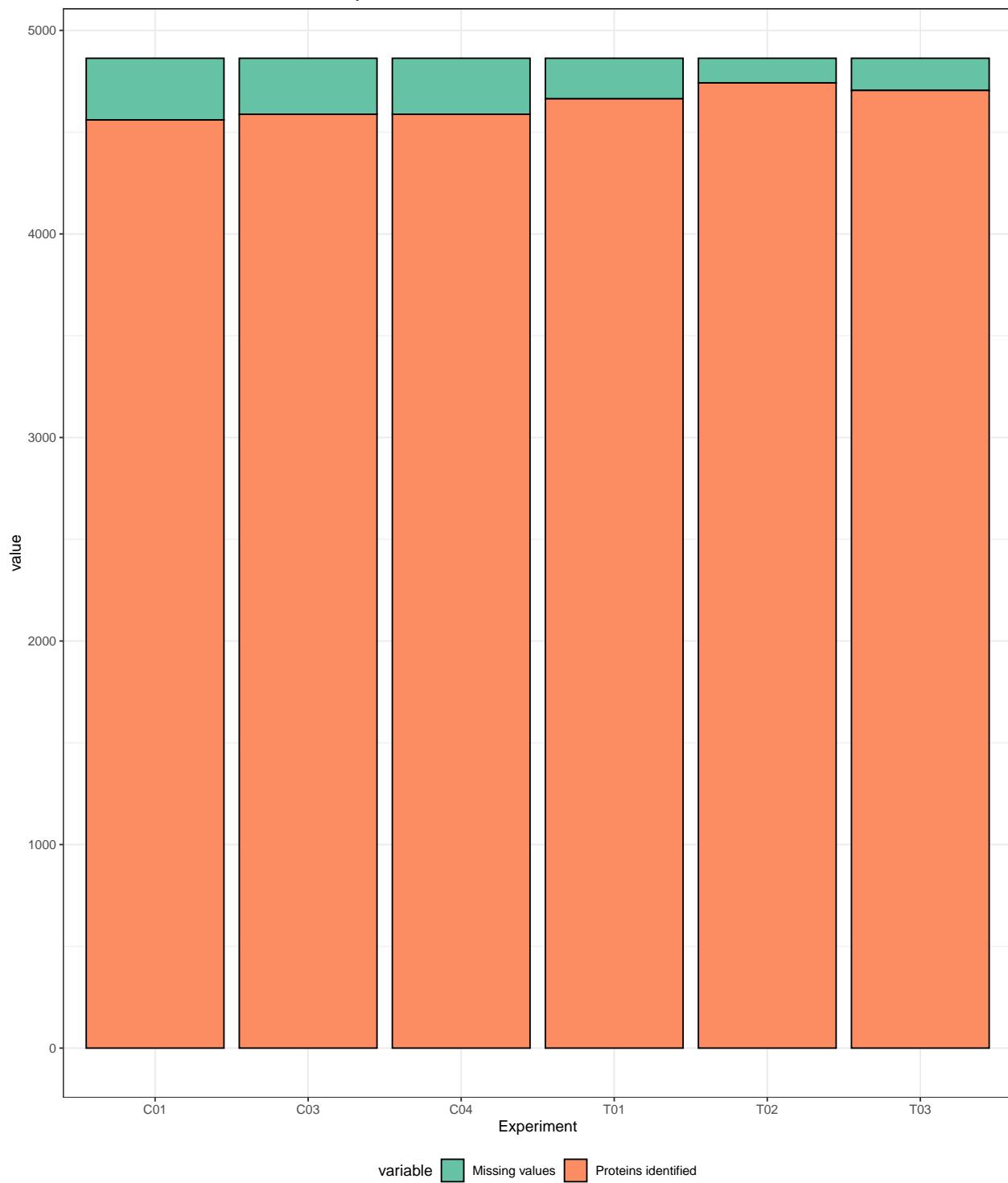


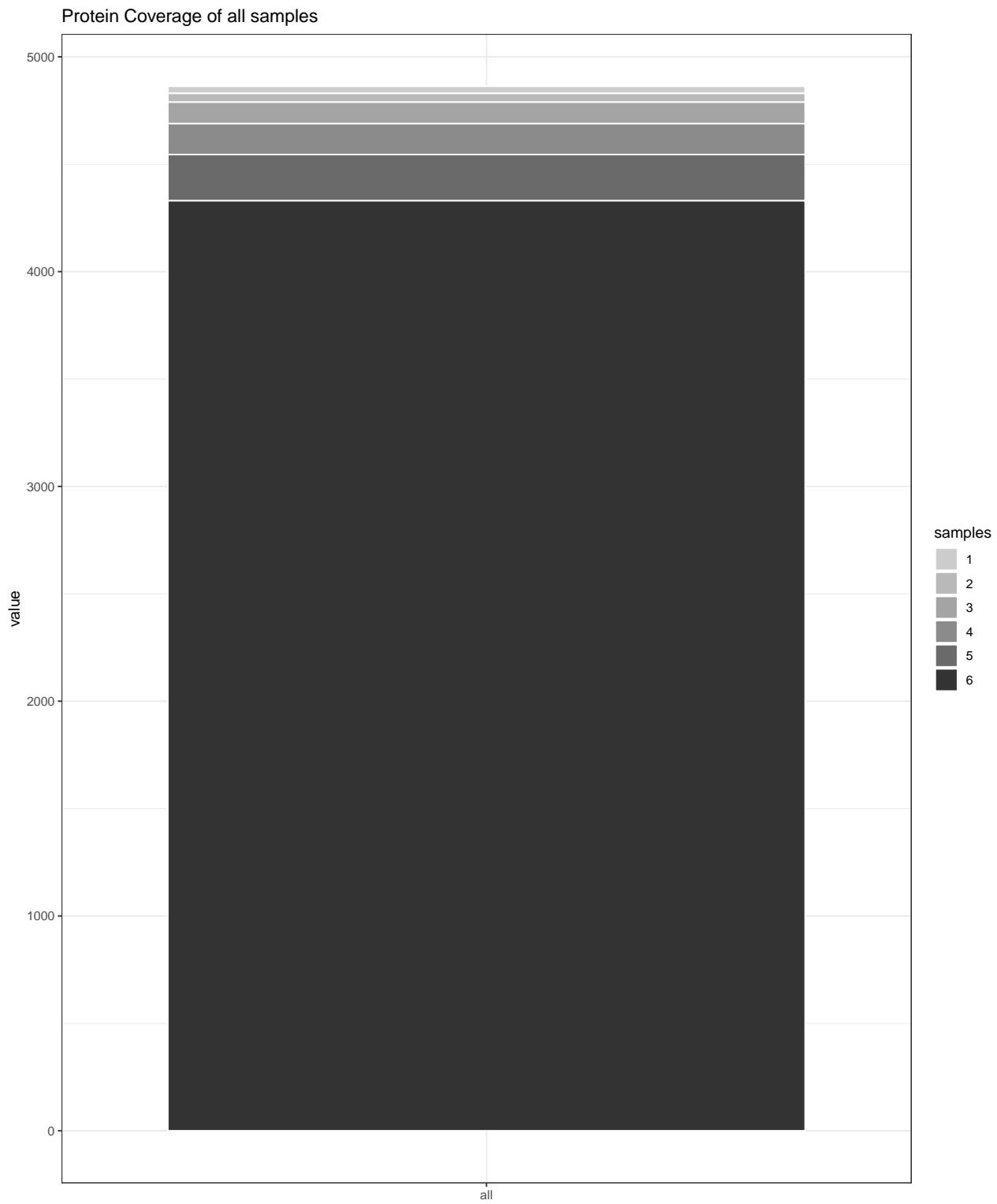
MQmetrics Report

13 April, 2021

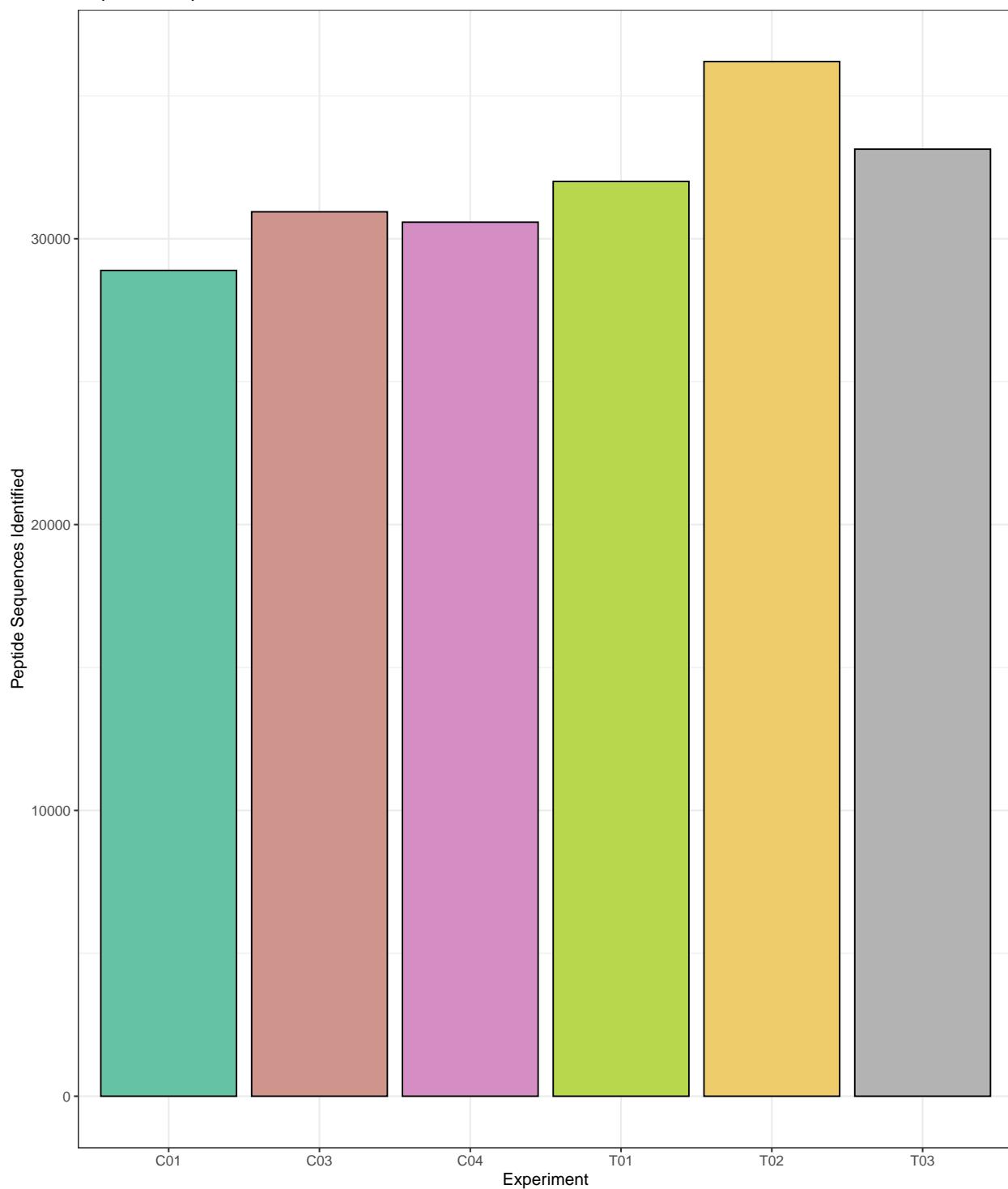
```
## [1] "The experiment started the day: 17/12/2020 at the time: 01:18:03."
## [1] "The whole experiment lasted: 01:19 (hours:minutes)."
## [1] "The MaxQuant version used was: 1.6.12.0"
## [1] "The user was: marek.vrbacky"
## [1] "The machine name was: FGU045PC004"
## [1] "The protein FDR was: 0.01"
## [1] "The match between runs was: True"
## [1] "The fasta file used was: C:\\MaxQuant_Databases\\\\UP000005640_9606.fasta"
```

Proteins Identified based on Intensity

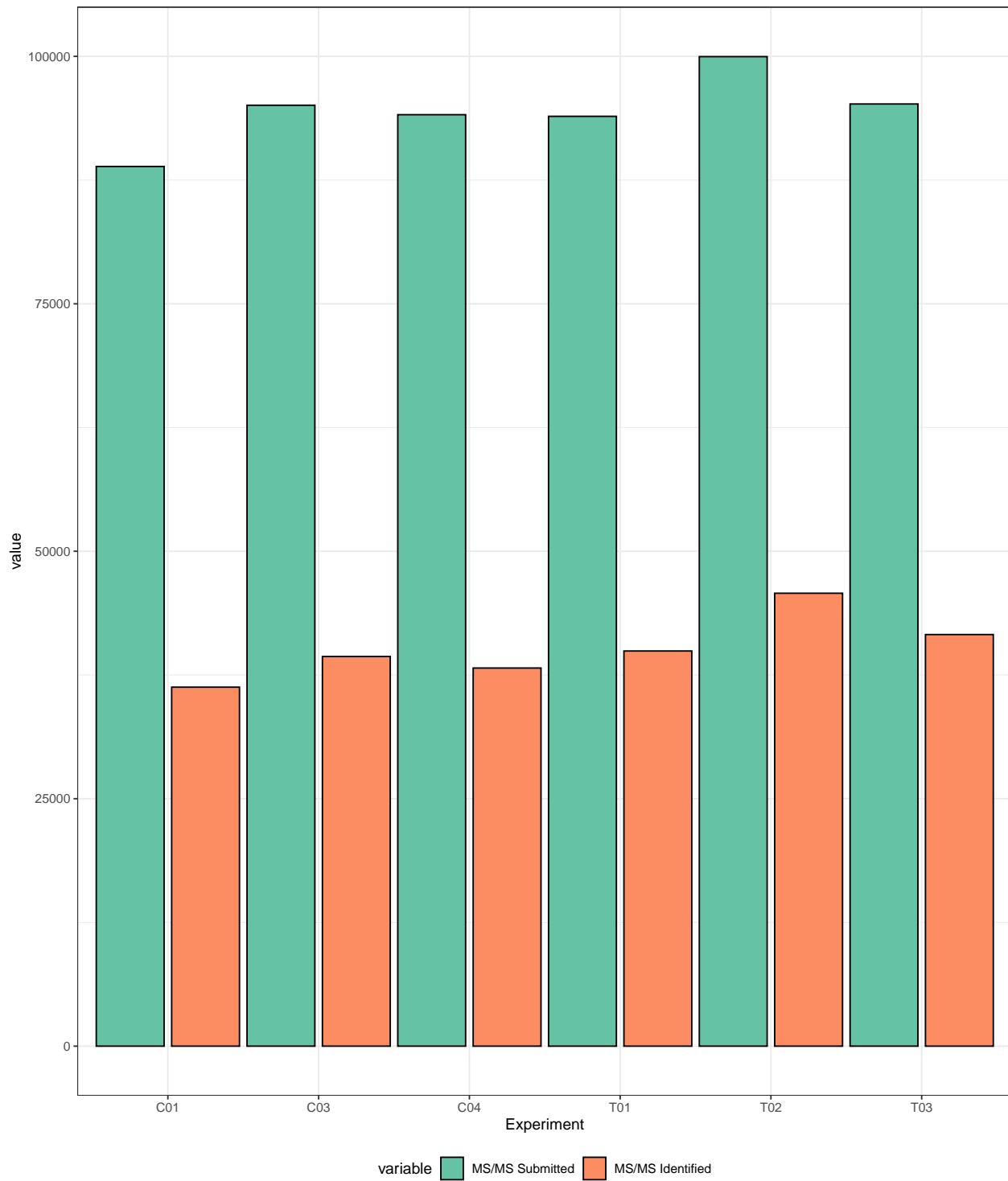




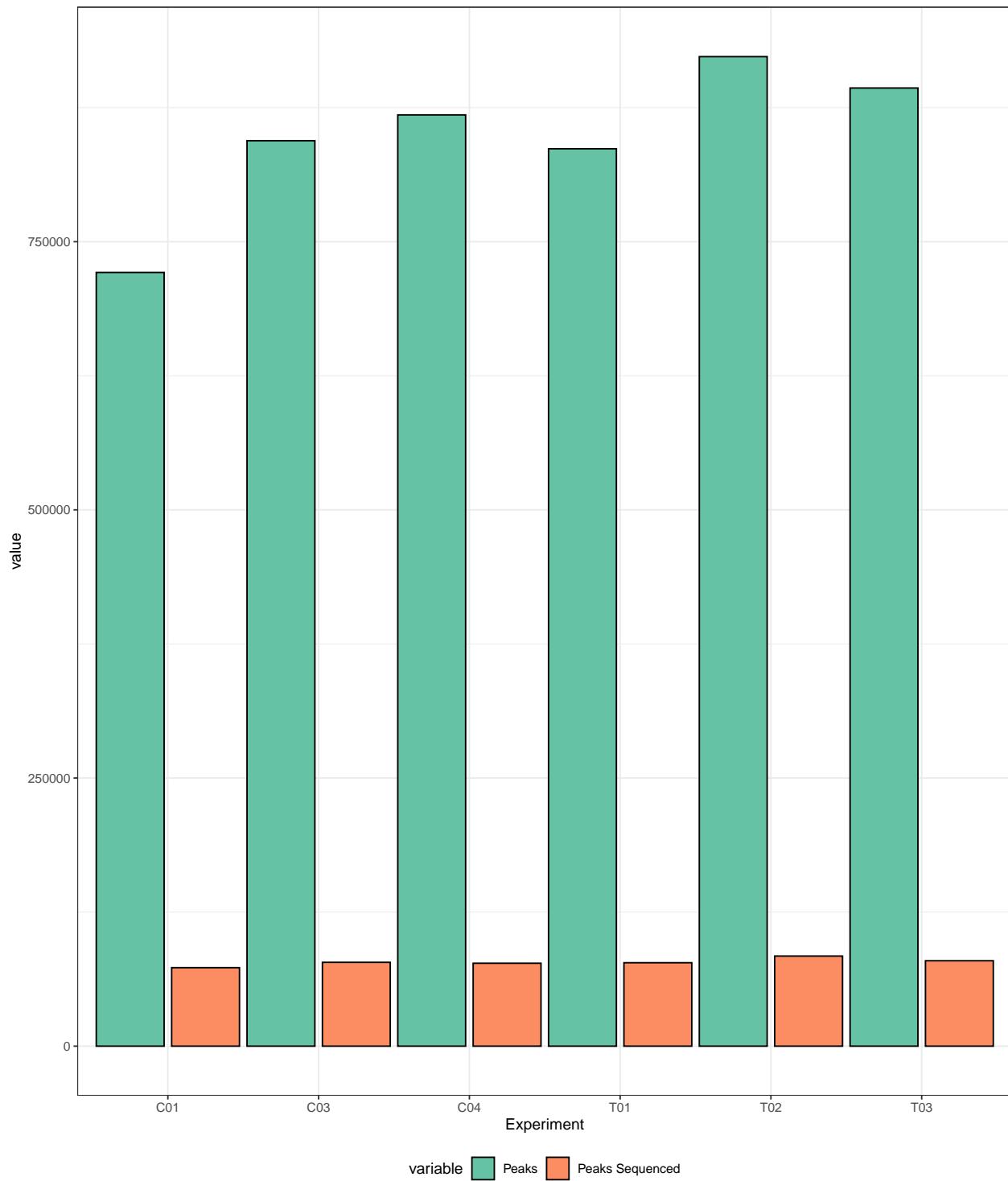
Peptides Sequences Identified

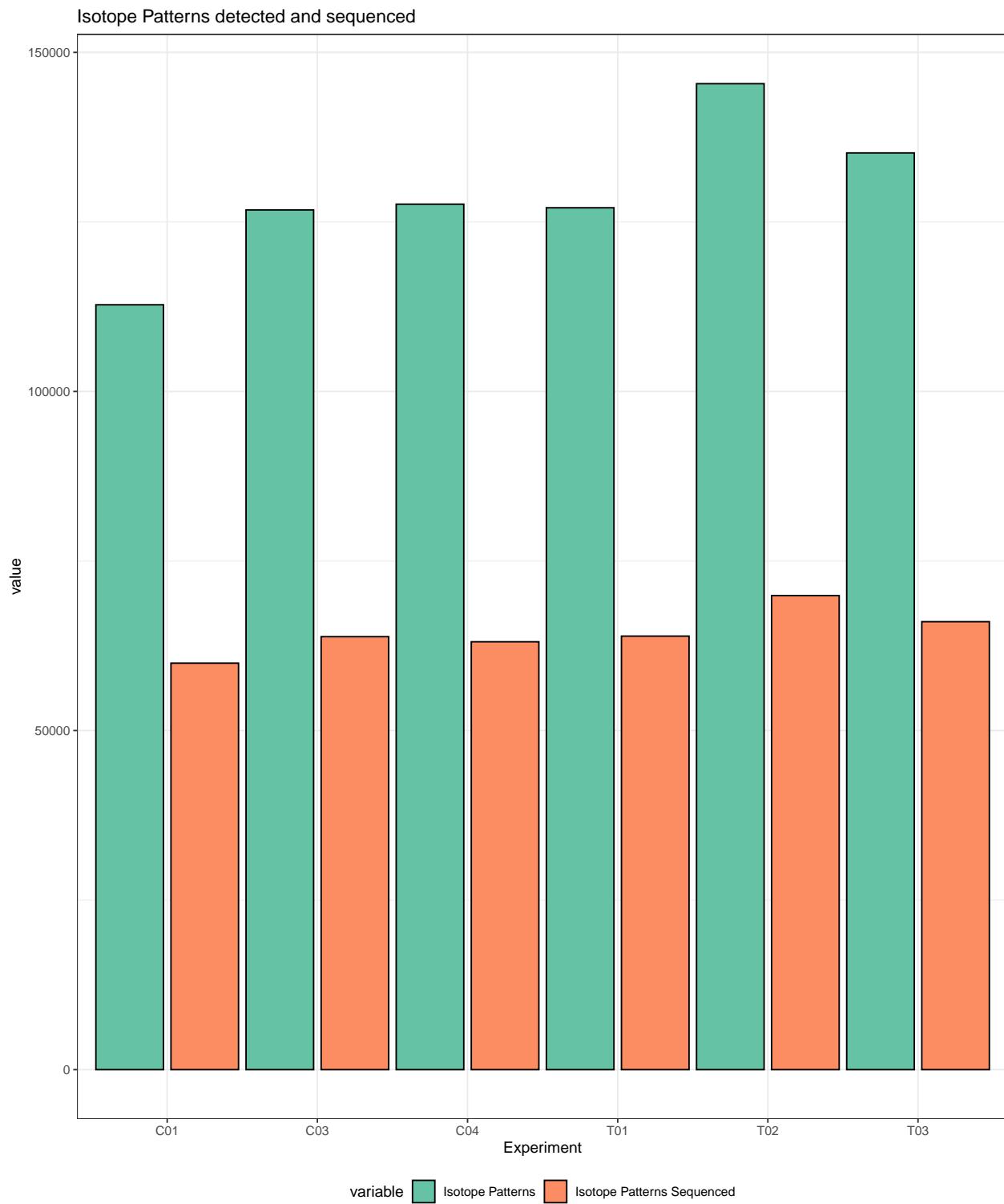


MS/MS Submitted and Identified

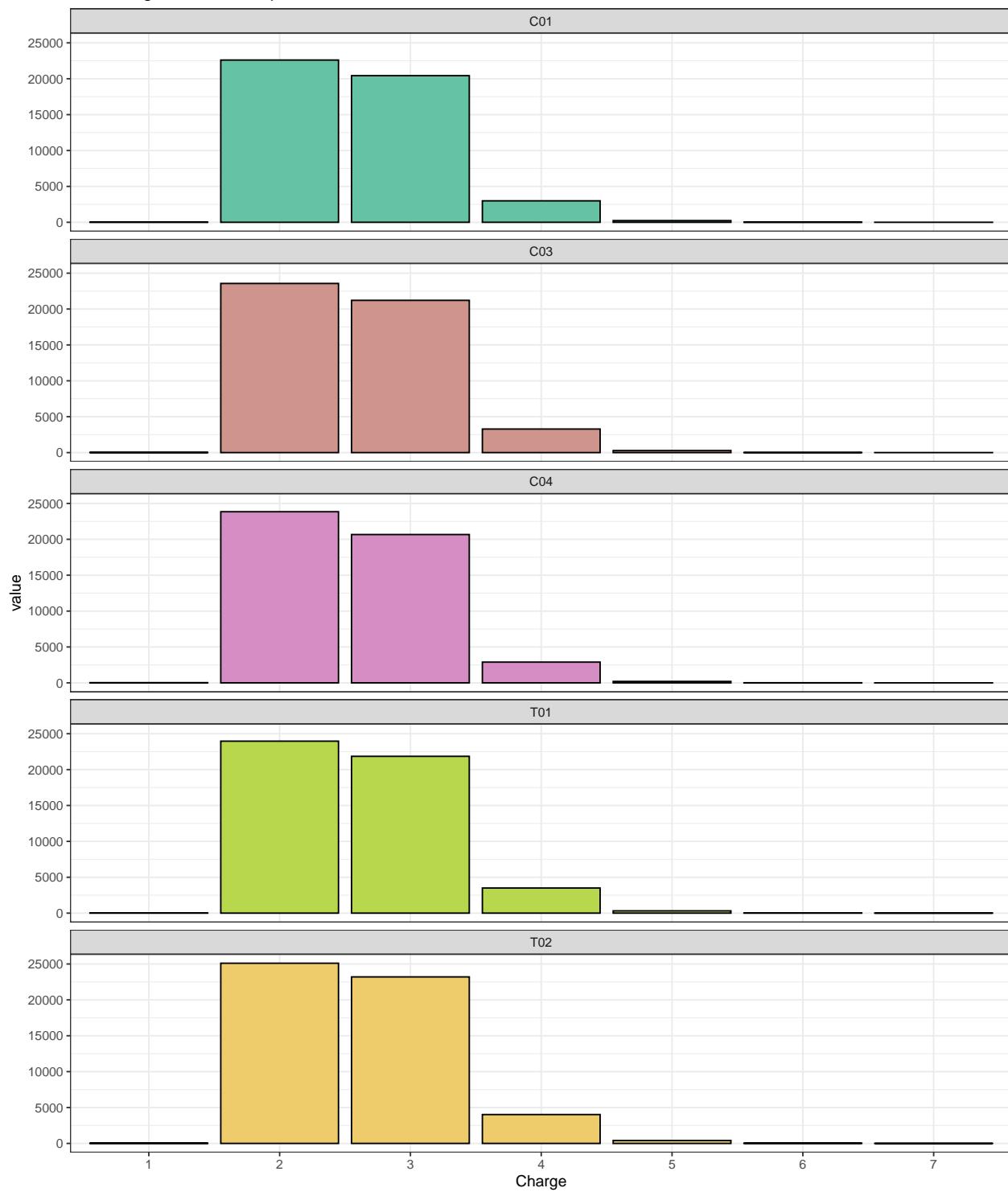


Peaks detected and sequenced in the full scans

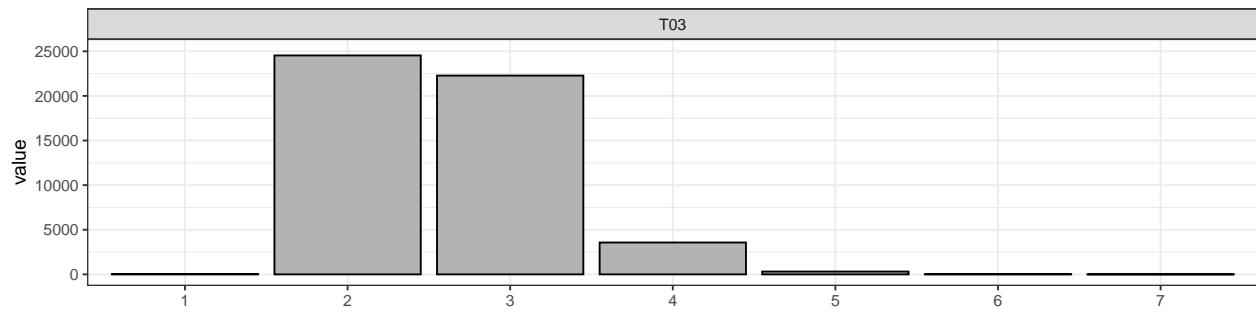




The charge-state of the precursor ion.

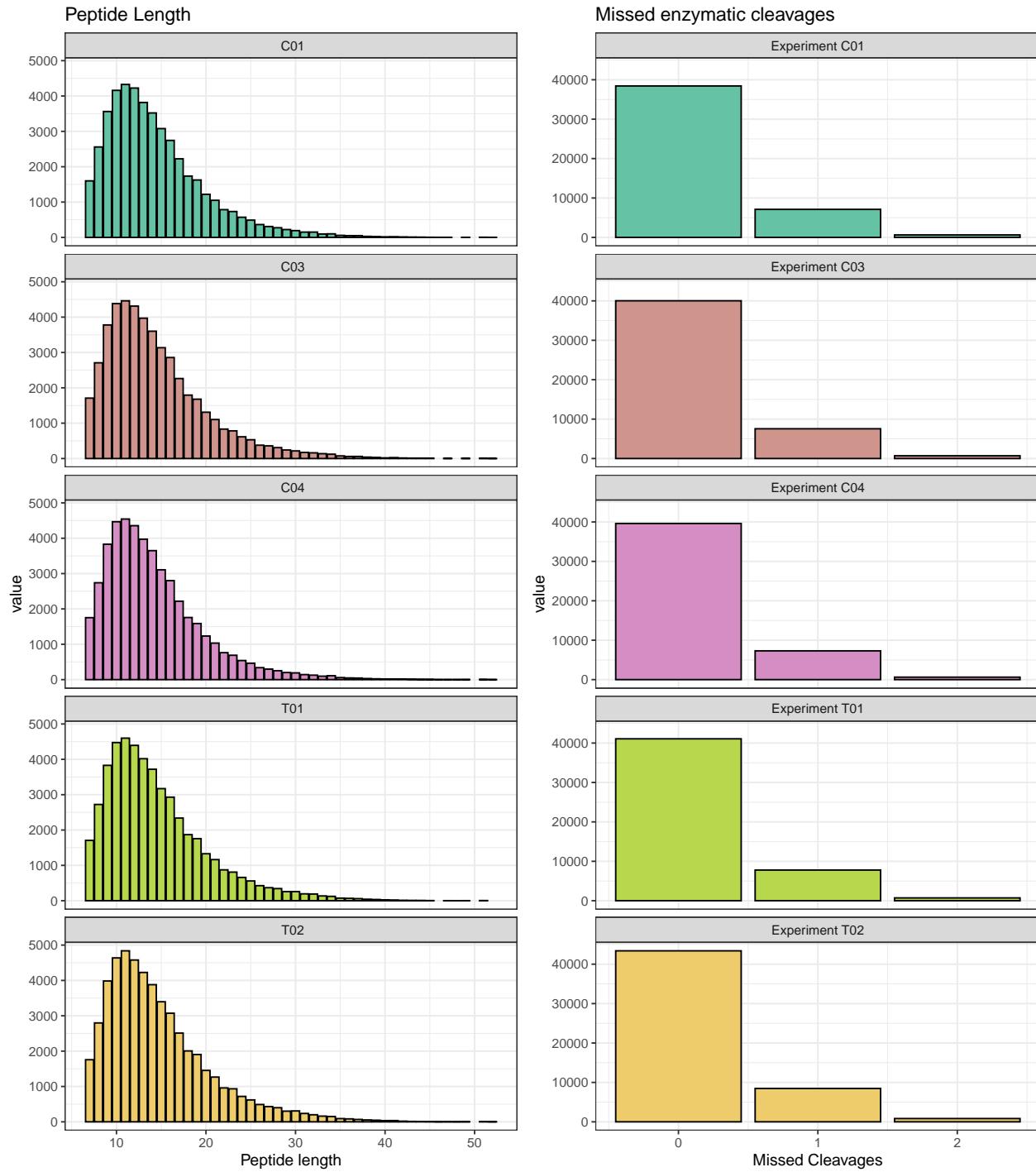


The charge-state of the precursor ion.

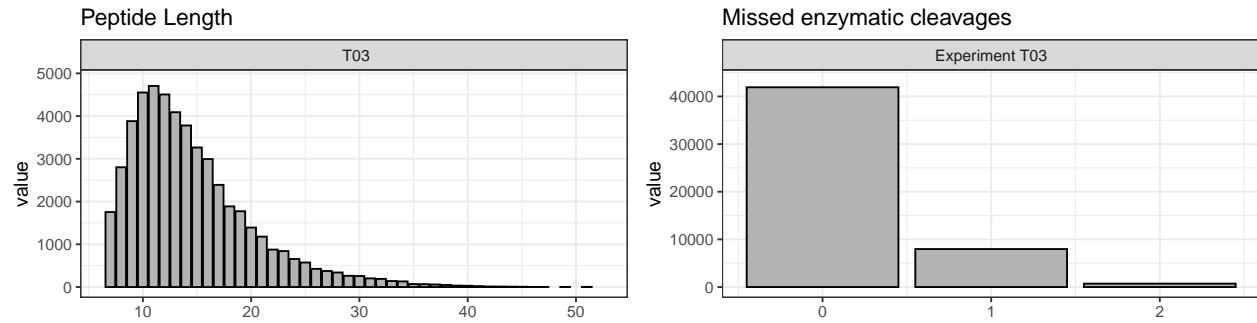


Charge

Protease Specificity

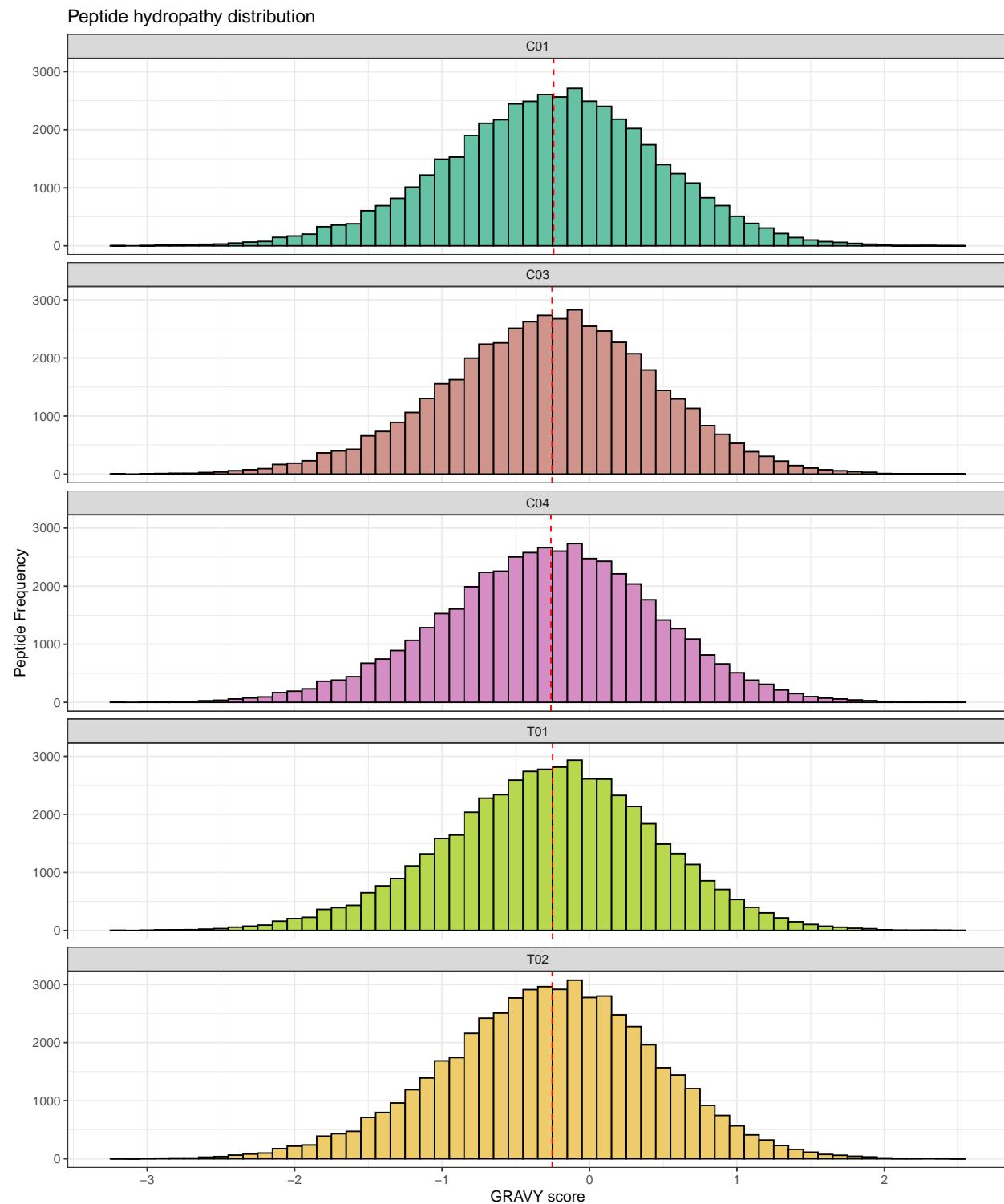


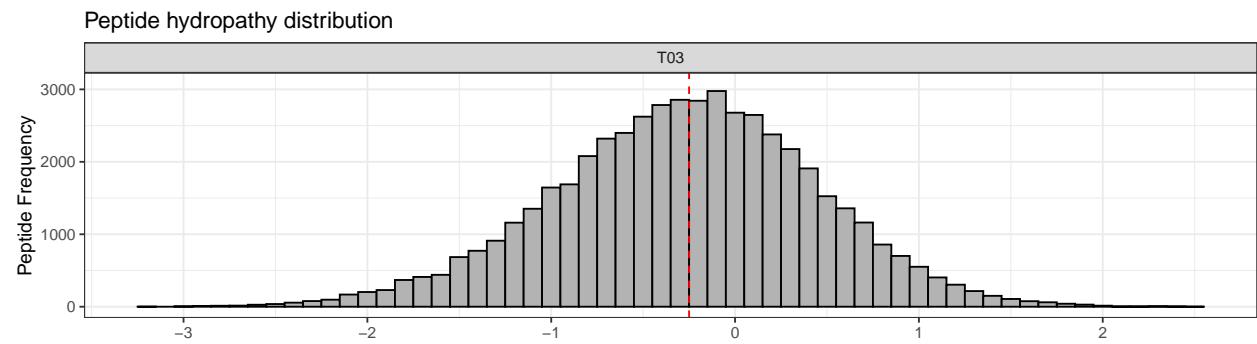
Protease Specificity



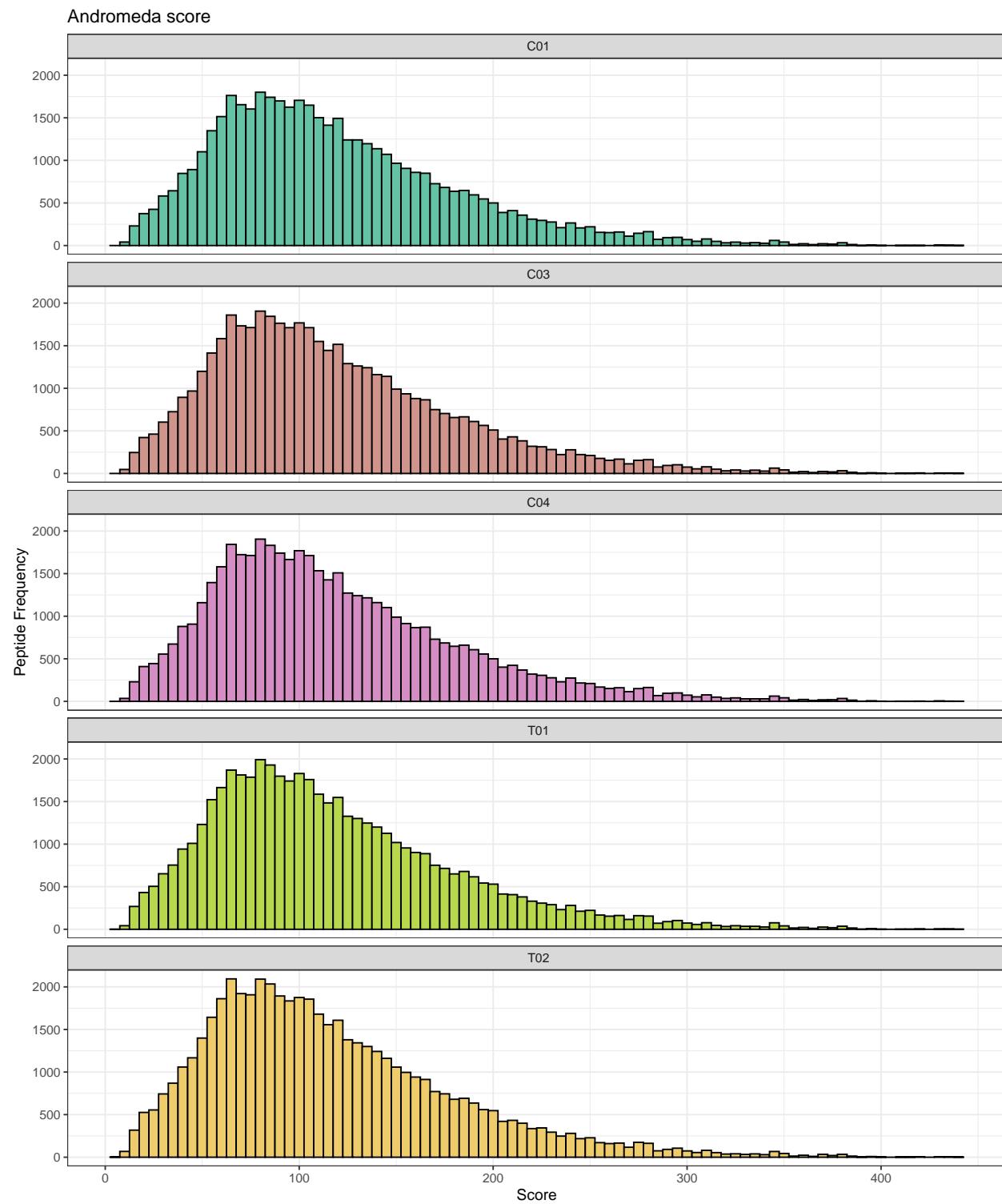
Peptide length

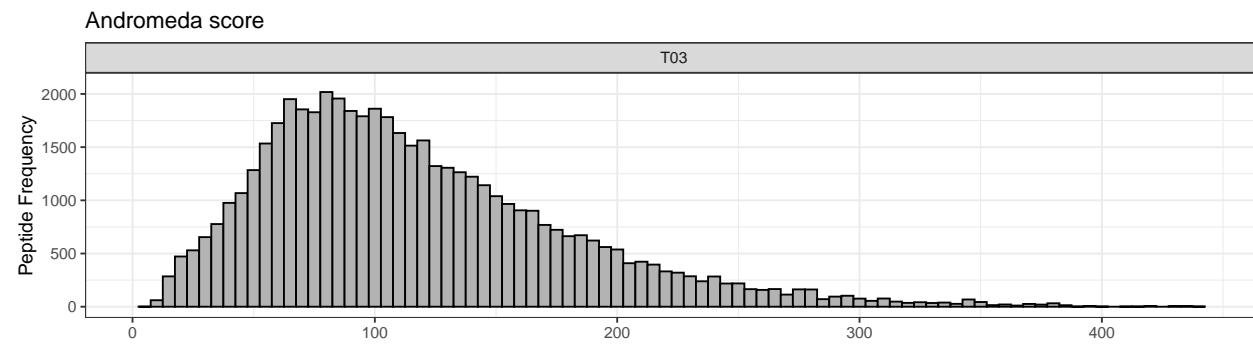
Missed Cleavages



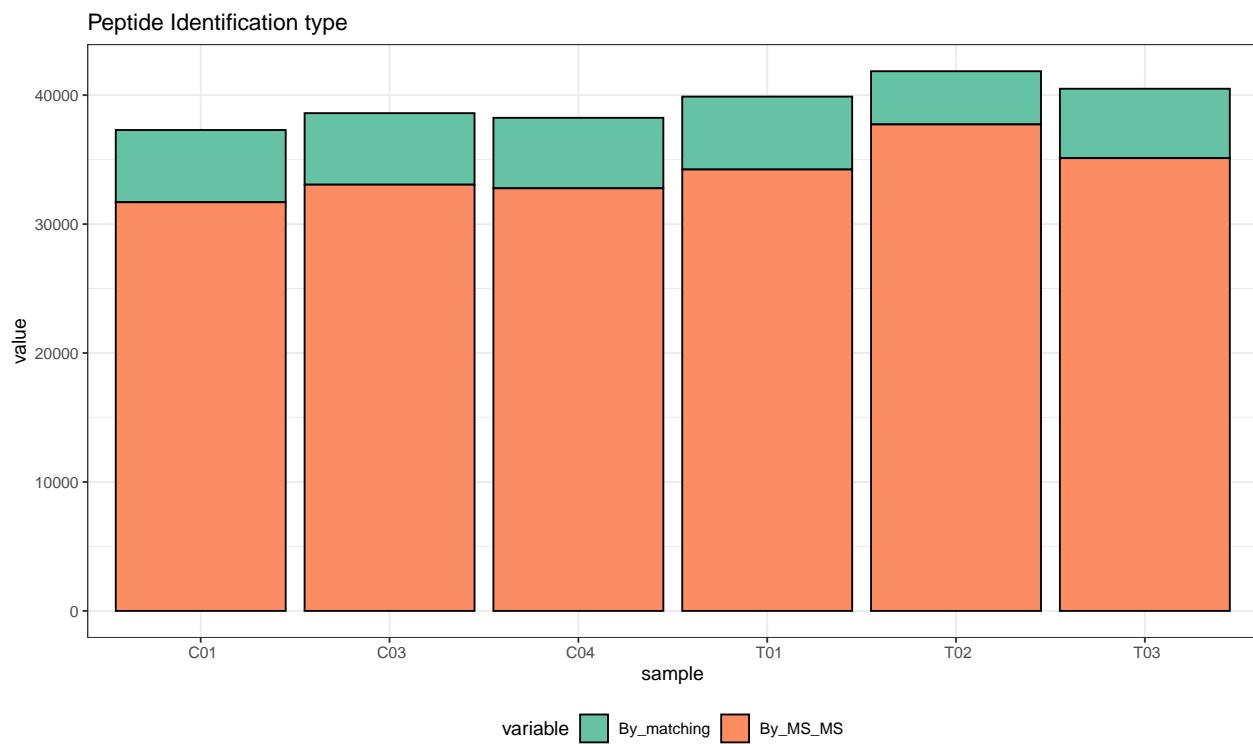
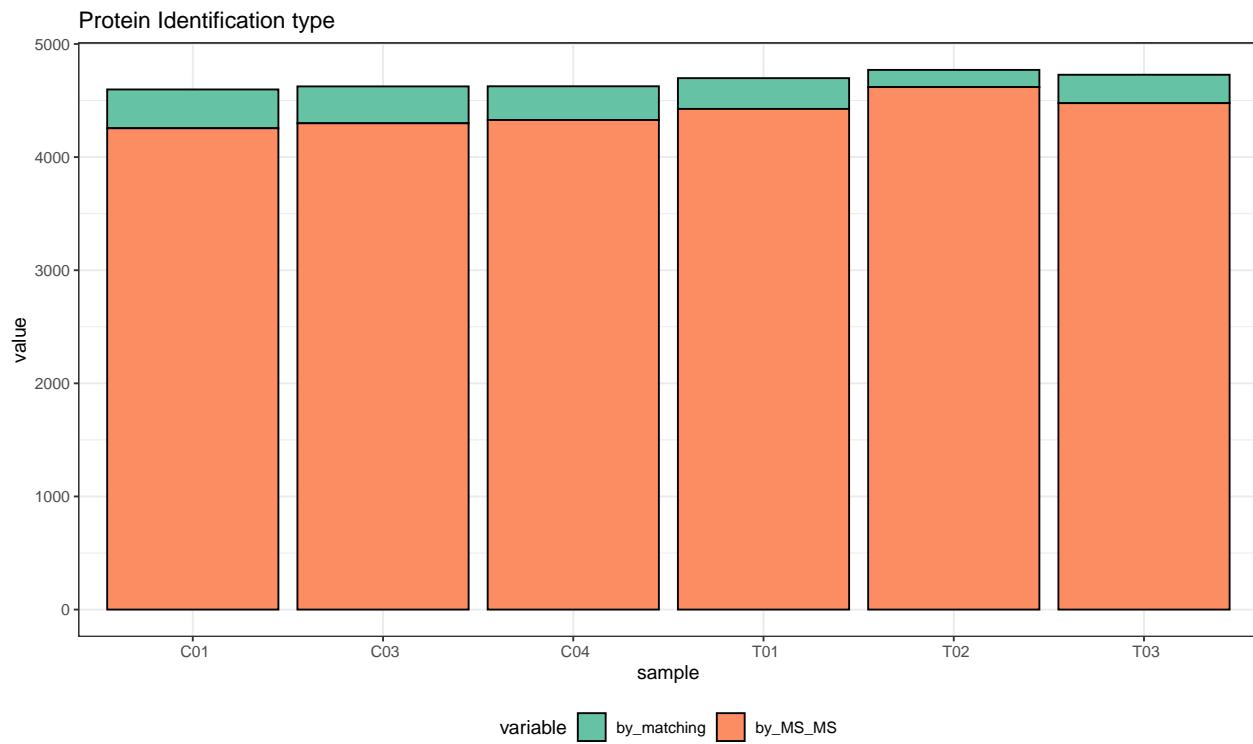


GRAYV score

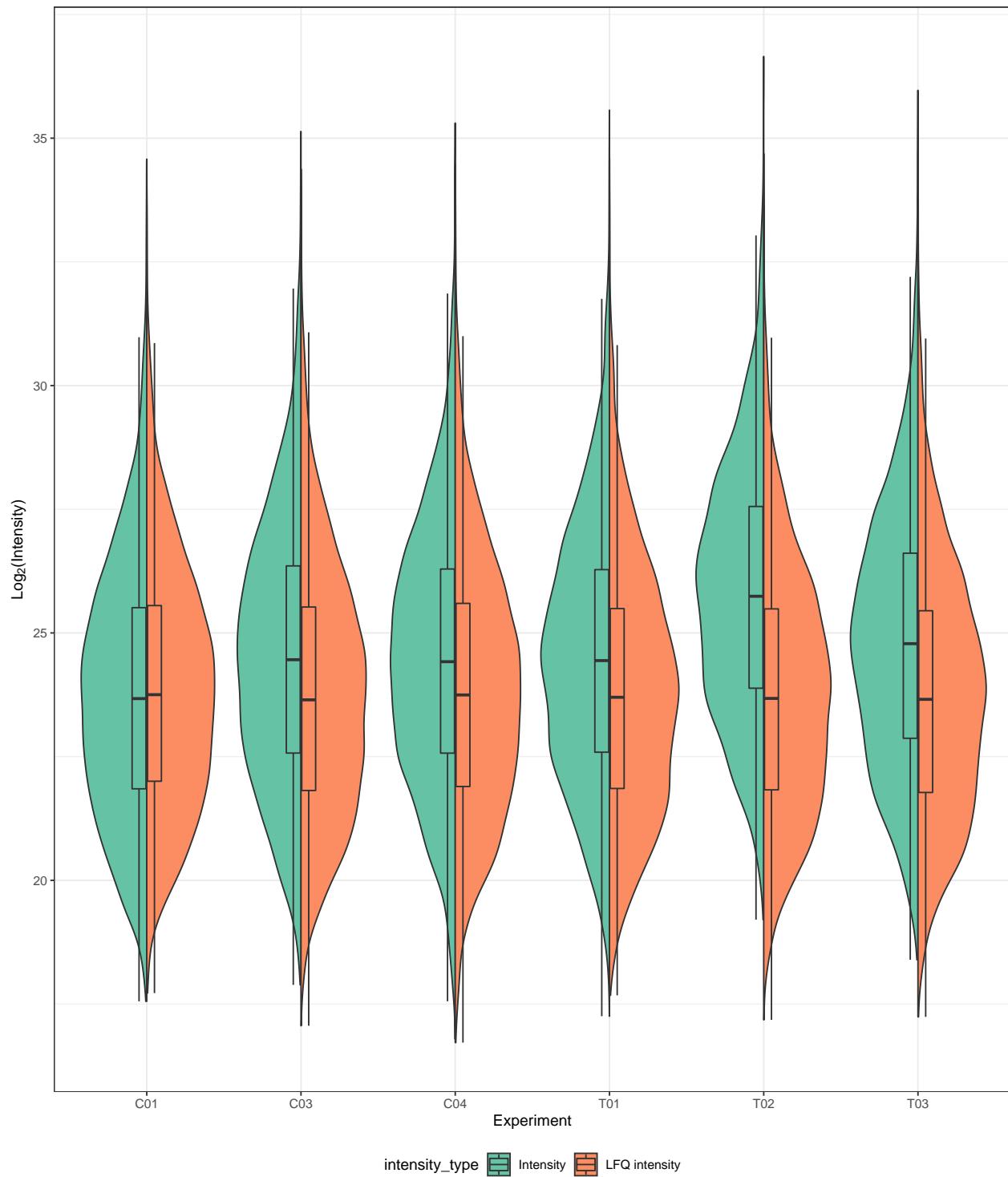




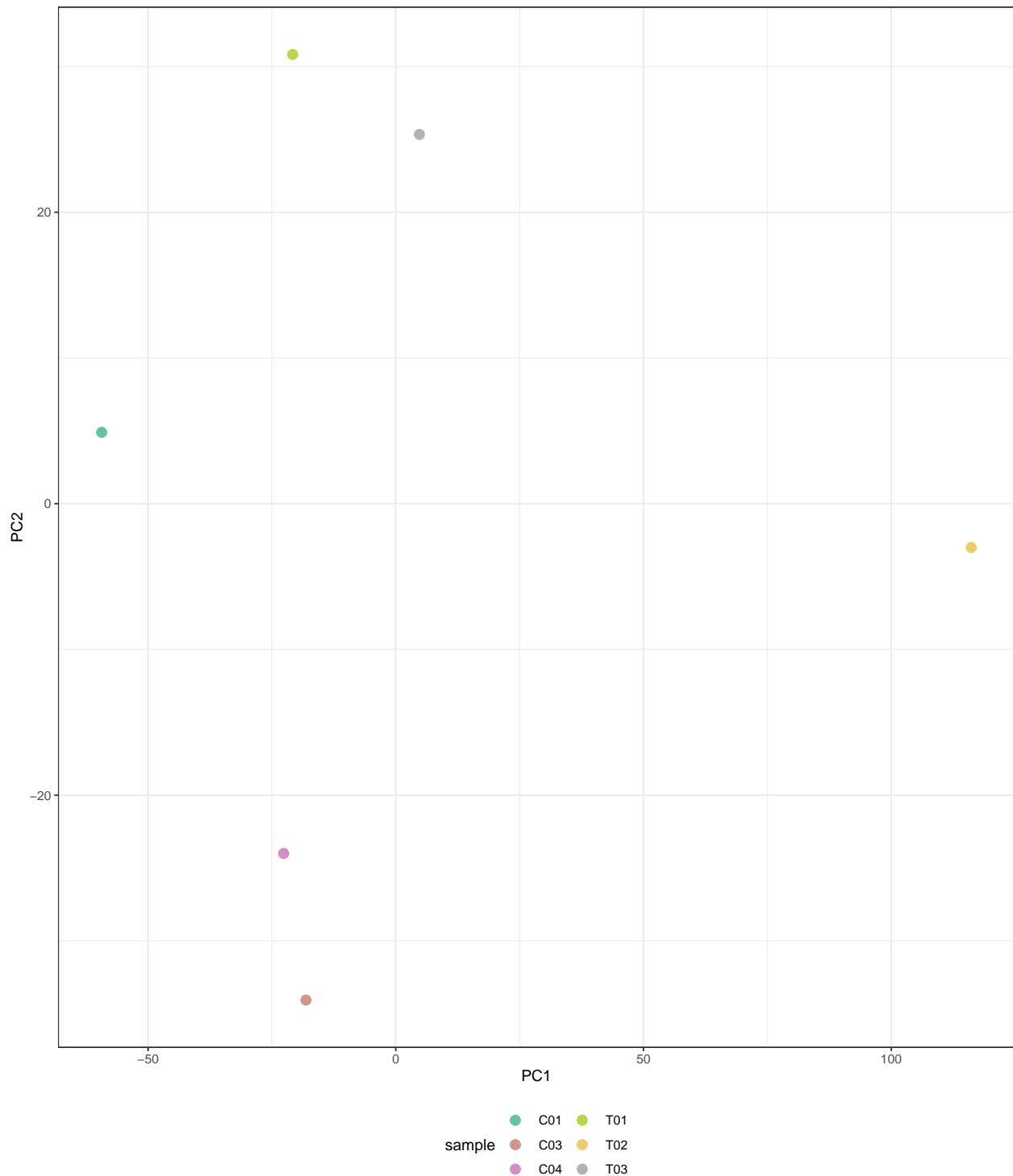
Score



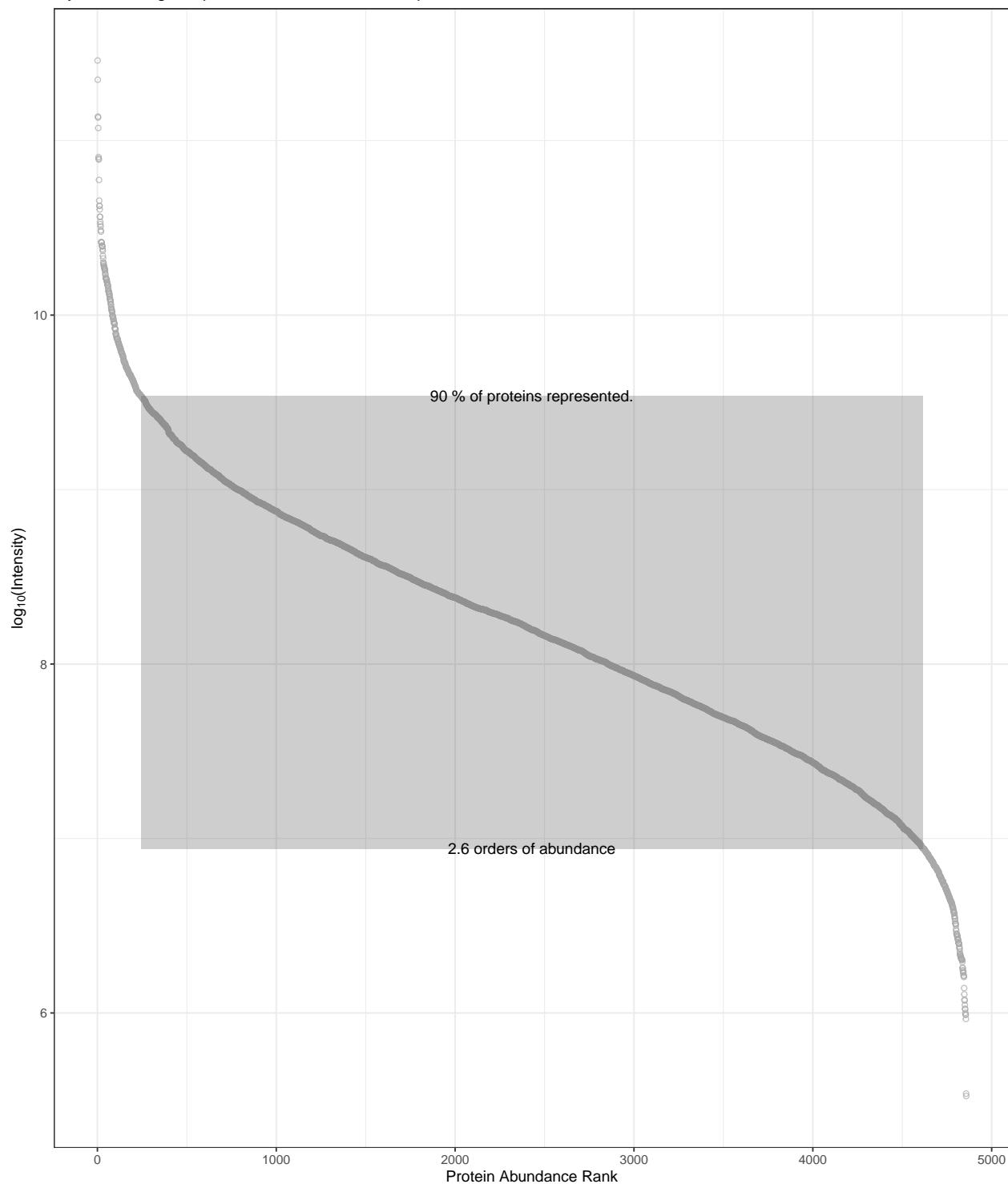
Protein Intensity & LFQ intensity

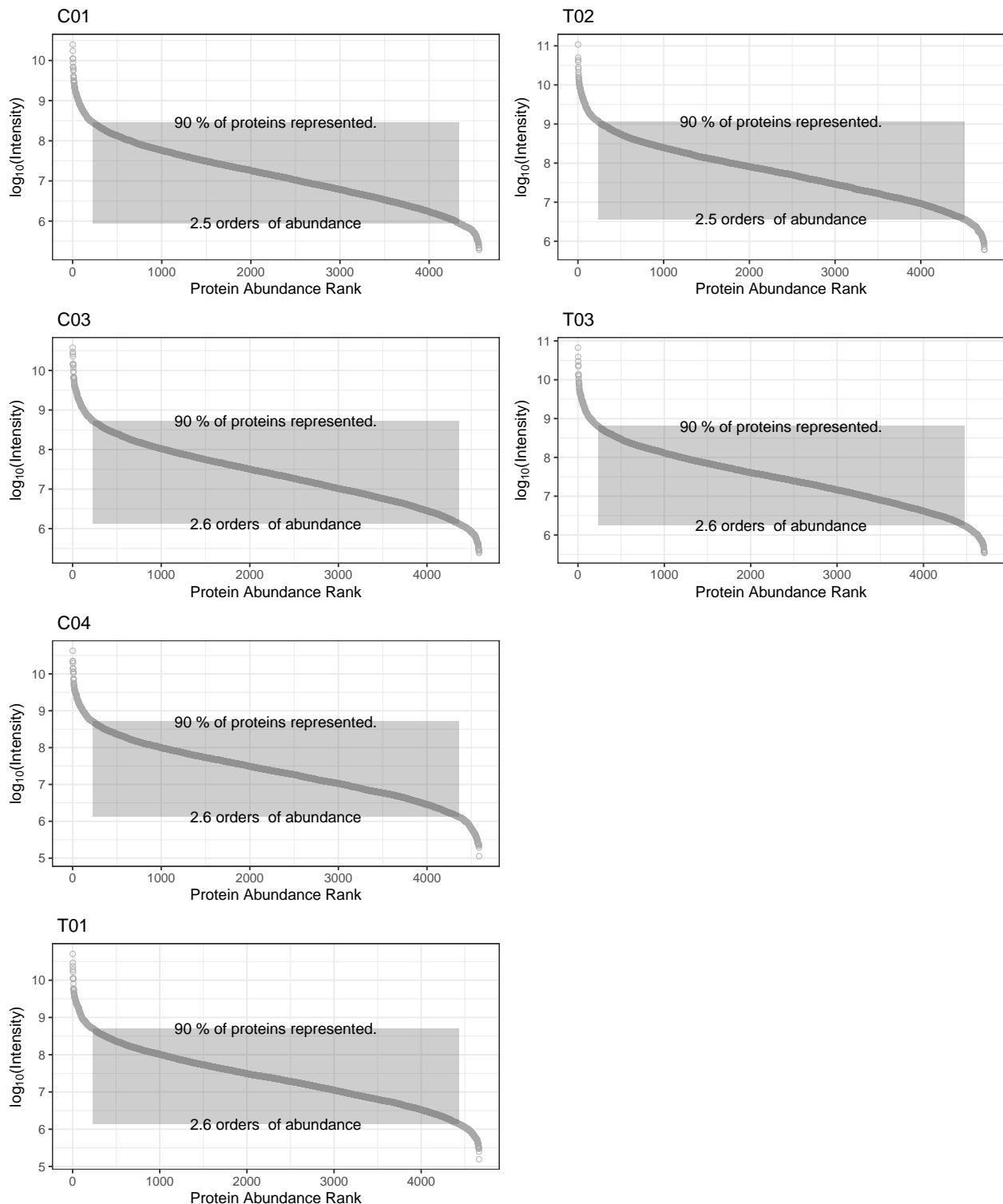


PCA of intensity



Dynamic range of protein abundance all samples

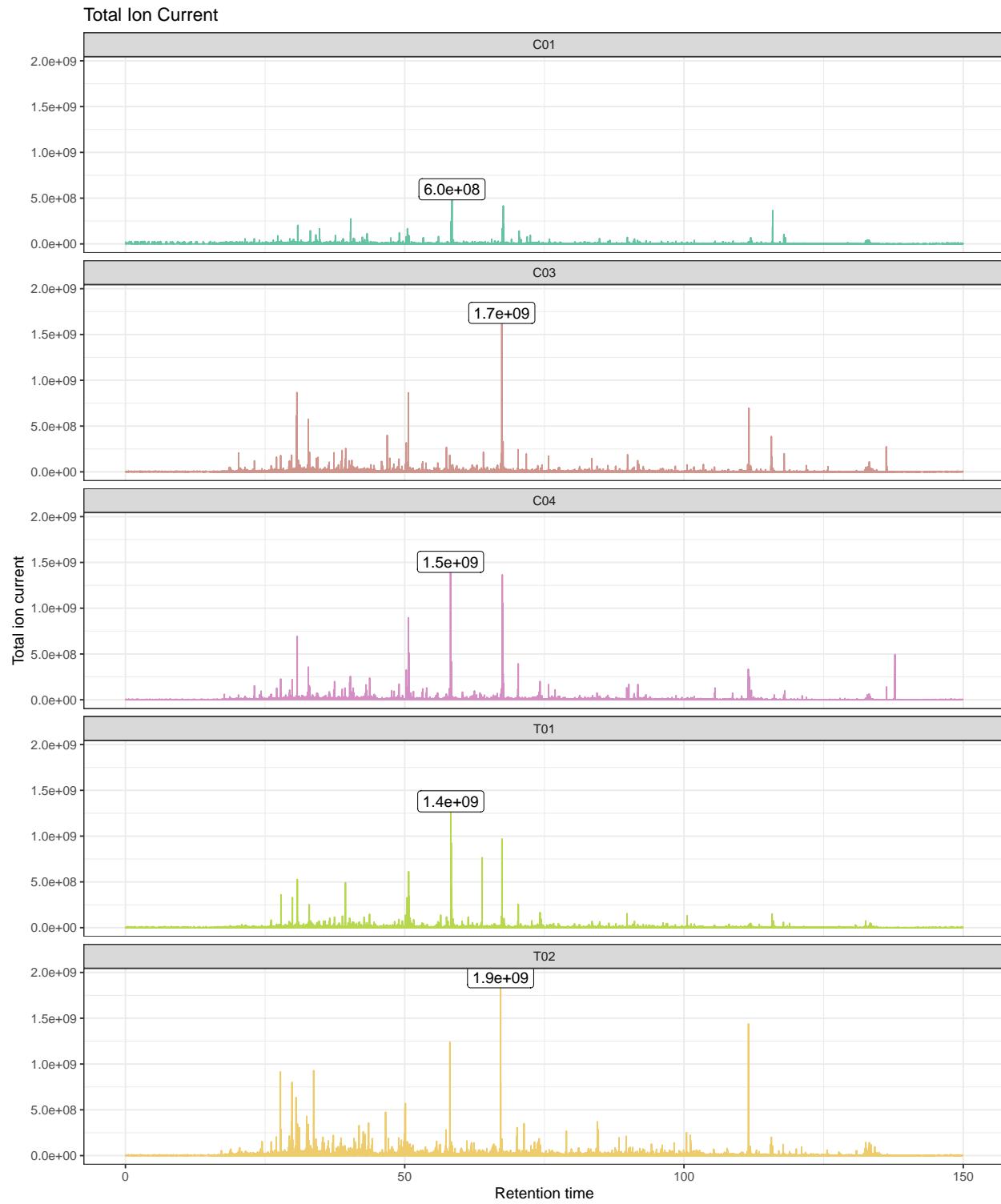


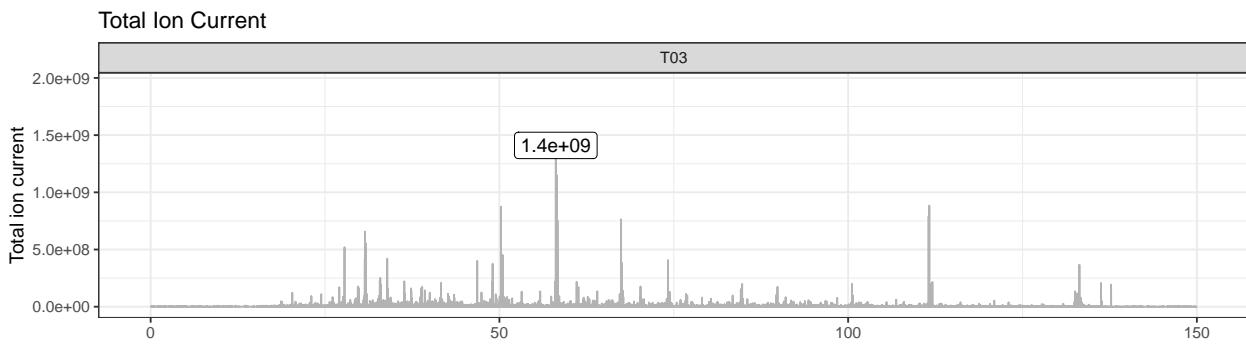


```
## [1] "No UniprotID provided."
```

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

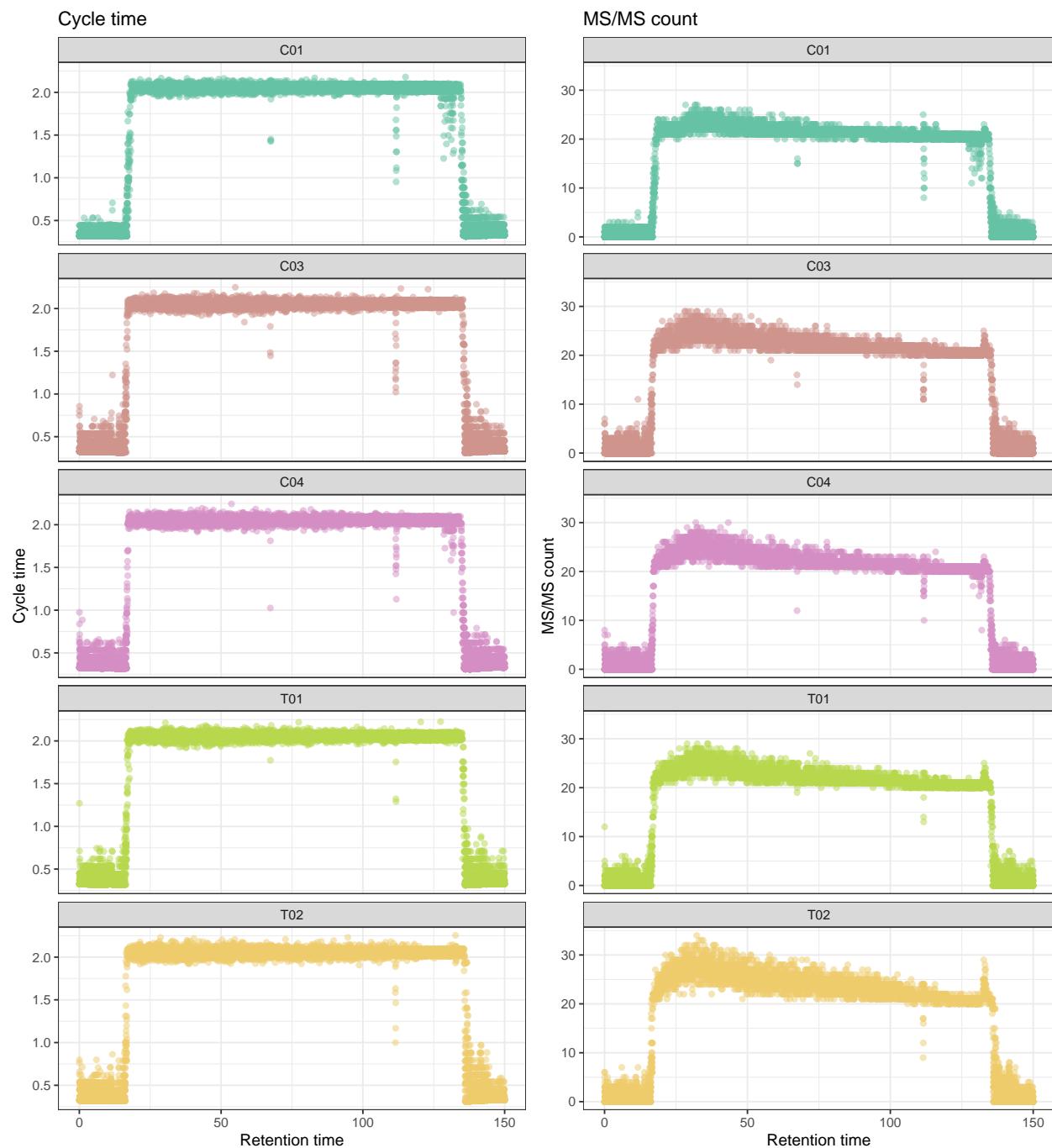
```
## [1] "No iRT peptides found in the MaxQuant output."
```





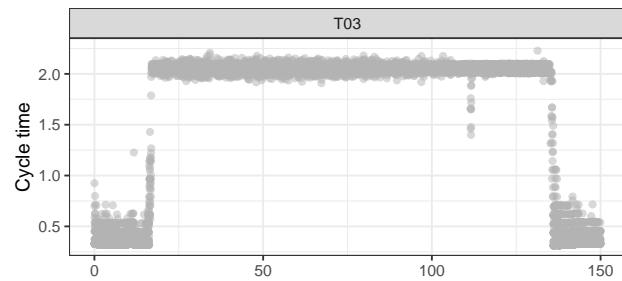
Retention time

Acquisition Cycle

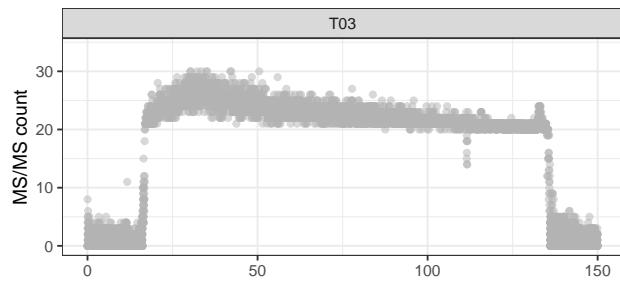


Acquisition Cycle

Cycle time



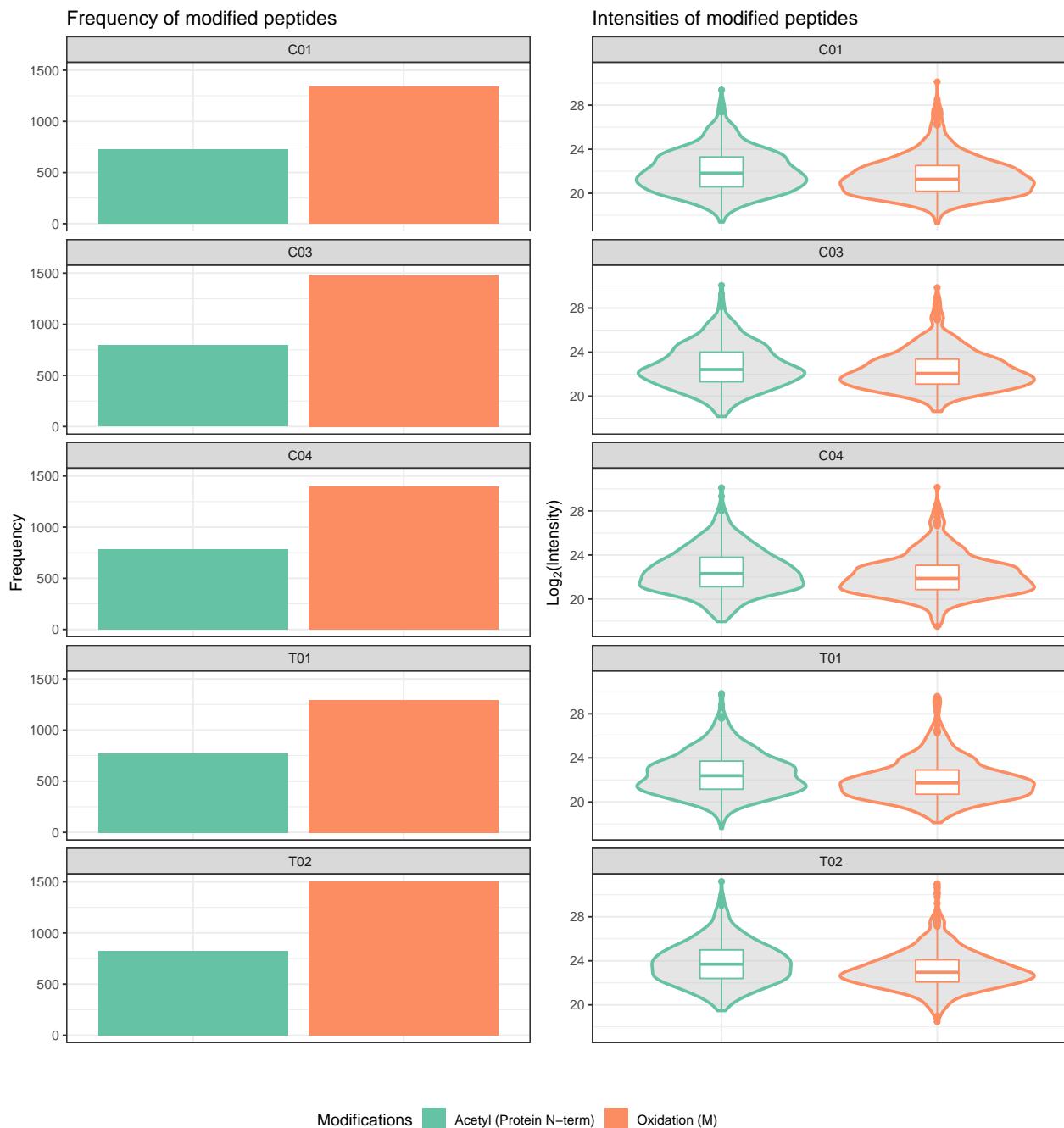
MS/MS count



Retention time

Retention time

Post–Translational Modifications



Post-Translational Modifications

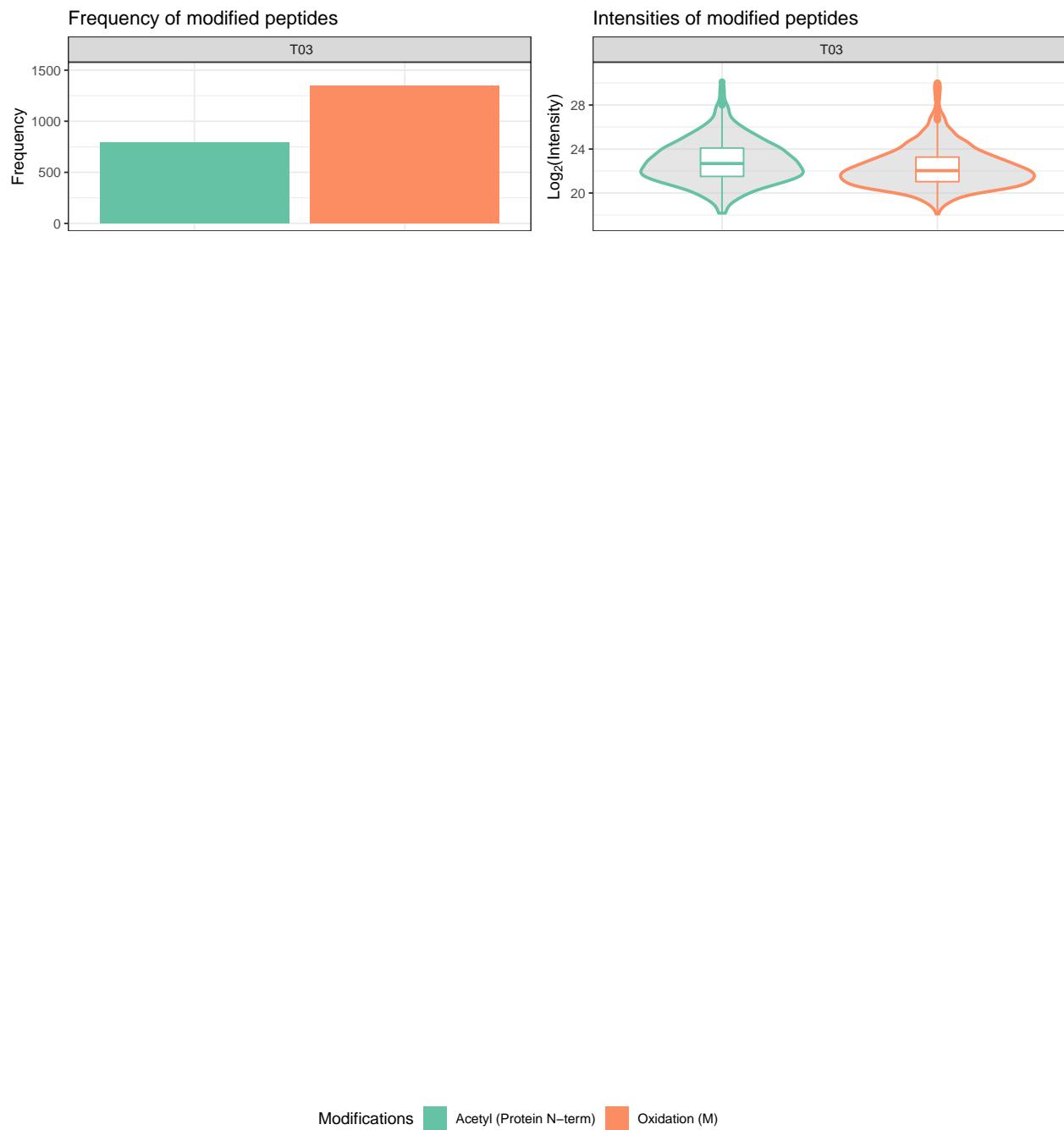


Table 1: Protein Information

| Experiment | Proteins_Identified | Missing_values | Potential_contaminants | Reverse | Only.identified.by.site |
|------------|---------------------|----------------|------------------------|---------|-------------------------|
| C01 | 4608 | 324 | 42 | 0 | 7 |
| C03 | 4642 | 290 | 42 | 0 | 12 |
| C04 | 4644 | 288 | 43 | 0 | 14 |
| T01 | 4709 | 223 | 36 | 0 | 10 |
| T02 | 4796 | 136 | 41 | 0 | 14 |
| T03 | 4762 | 170 | 45 | 0 | 14 |

Table 2: Intensity Information

| Experiment | mean | sd | median | min | max | n |
|--------------------|-------|-------|--------|-------|-------|------|
| Log2 Intensity C01 | 26.48 | 29.16 | 23.67 | 17.55 | 34.54 | 4608 |
| Log2 Intensity C03 | 27.39 | 29.99 | 24.45 | 17.89 | 35.13 | 4642 |
| Log2 Intensity C04 | 27.28 | 29.91 | 24.42 | 16.79 | 35.31 | 4644 |
| Log2 Intensity T01 | 27.27 | 30.05 | 24.43 | 17.25 | 35.57 | 4709 |
| Log2 Intensity T02 | 28.43 | 31.07 | 25.74 | 19.21 | 36.65 | 4796 |
| Log2 Intensity T03 | 27.63 | 30.43 | 24.78 | 18.40 | 35.97 | 4762 |

Table 3: Charge Information

| Experiment | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|------------|-----|------|------|-----|-----|-----|-----|
| C01 | 0.1 | 48.8 | 44.1 | 6.5 | 0.5 | 0.0 | 0.0 |
| C03 | 0.1 | 48.7 | 43.8 | 6.8 | 0.6 | 0.0 | 0.0 |
| C04 | 0.1 | 50.1 | 43.4 | 6.1 | 0.4 | 0.0 | 0.0 |
| T01 | 0.1 | 48.2 | 44.0 | 7.0 | 0.6 | 0.0 | 0.0 |
| T02 | 0.1 | 47.5 | 43.9 | 7.6 | 0.8 | 0.1 | 0.0 |
| T03 | 0.1 | 48.3 | 43.9 | 7.0 | 0.6 | 0.0 | 0.0 |

Table 4: Peptide hydrophobicity (GRAVY)

| Experiment | Mean | Max | Min | Median |
|------------|-------|------|-------|--------|
| C01 | -0.26 | 2.54 | -3.19 | -0.24 |
| C03 | -0.27 | 2.54 | -3.19 | -0.25 |
| C04 | -0.28 | 2.54 | -3.19 | -0.26 |
| T01 | -0.27 | 2.54 | -3.19 | -0.25 |
| T02 | -0.27 | 2.54 | -3.19 | -0.25 |
| T03 | -0.27 | 2.54 | -3.17 | -0.25 |