

MS Fragger / Philosopher QC output

Lumos_H0027_PH_T_R1

Scans: 689367

PSMs: 247236

PSMs (quantified): 125976

Precursors (ions): 164501

Modified Peptides: 122813

Peptides: 110351

Protein Groups: 9057

Protein Groups (quantified – qupm > 0): 7916

Protein Groups (qupm > 1): 6786

Protein Groups (qupm == 0): 1130

Folder: D:\MS_PerDoubleKO

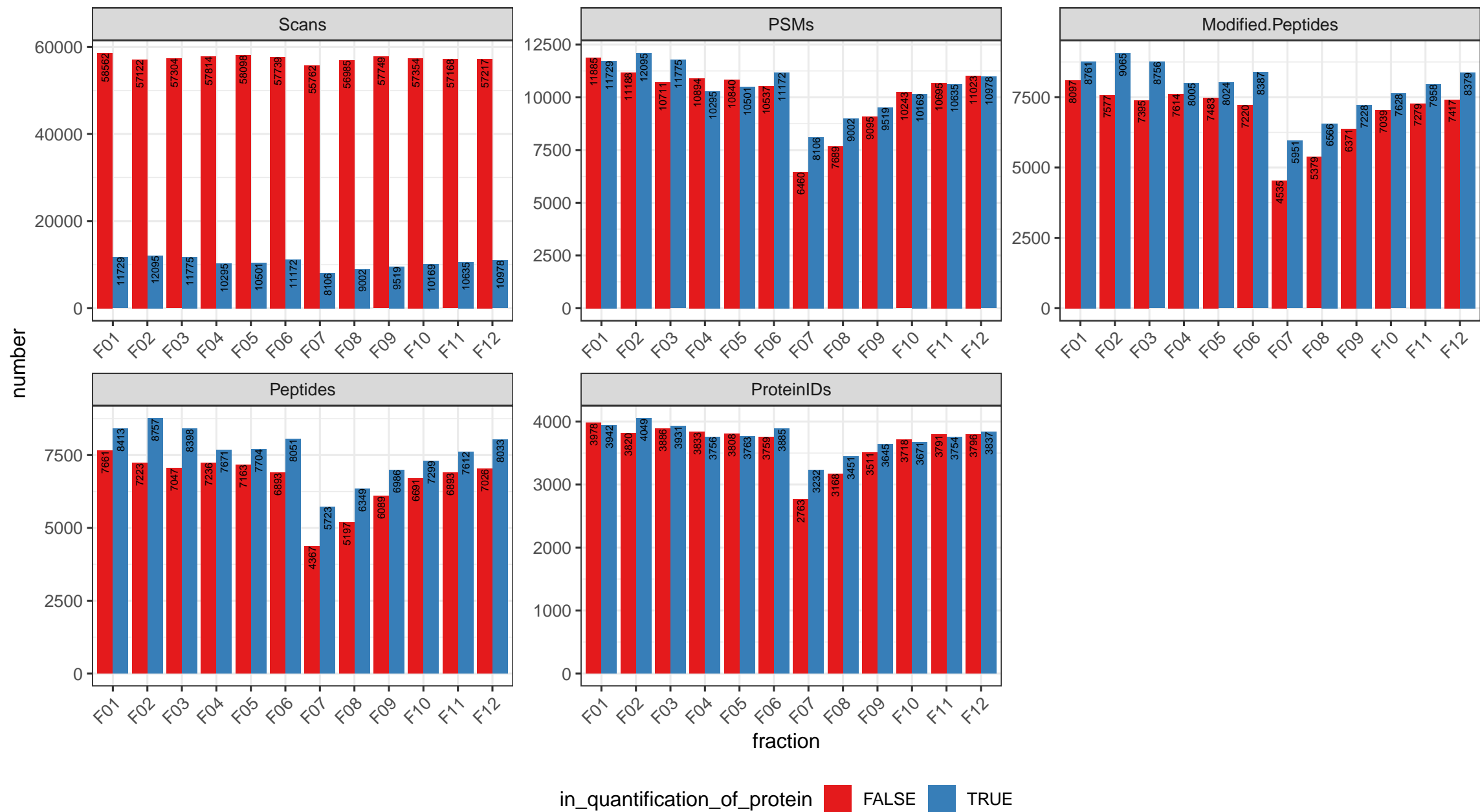
Fractions: 12

F01|F02|F03|F04|F05|F06|F07|F08|F09|F10|F11|F12

Date of QC analysis: 2023–04–24

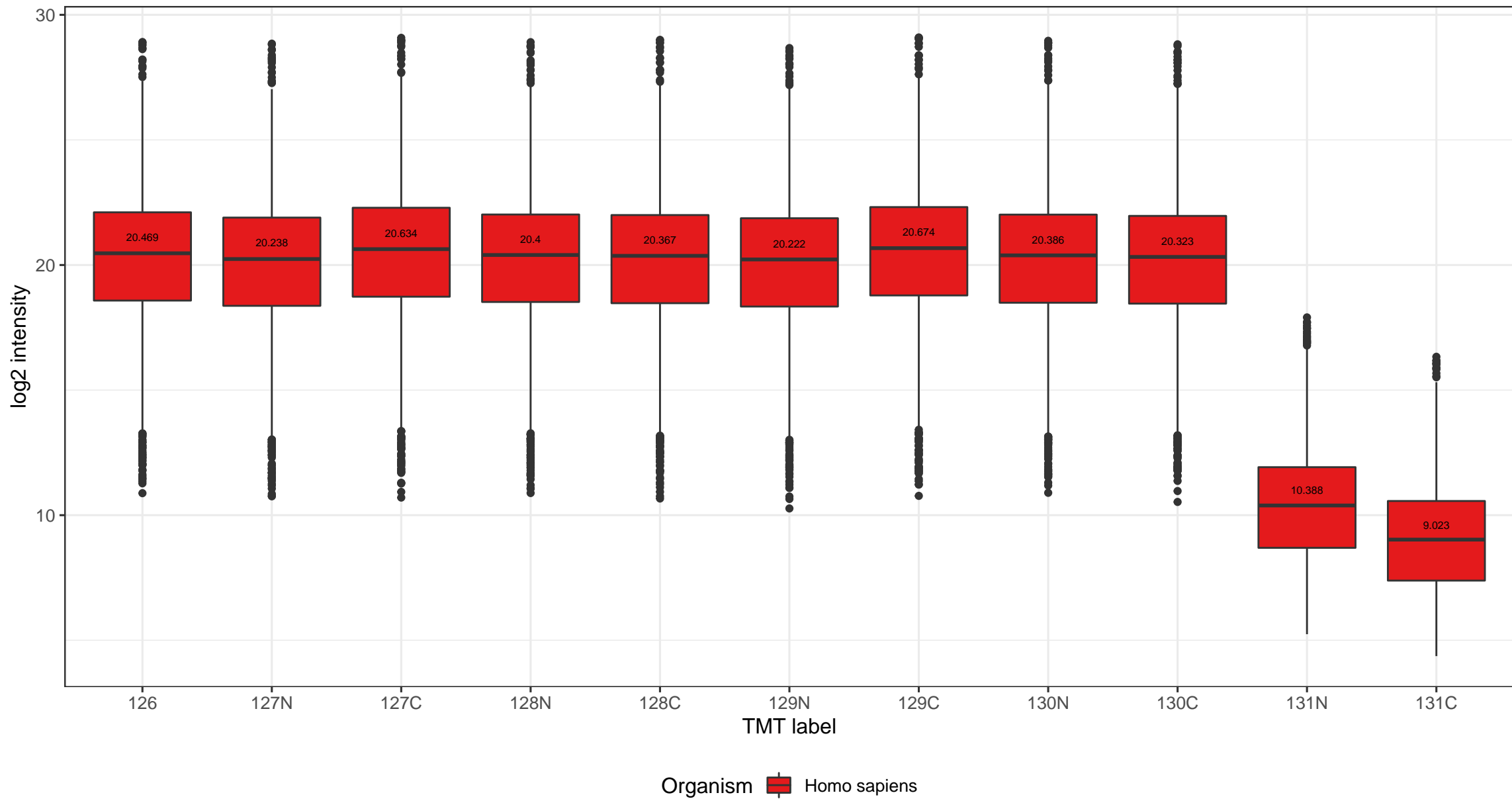
QC script version: V1

Scans: 689367 | PSMs: 247236 | Ions: 164501 | Peptides: 110351 | Proteins: 9057

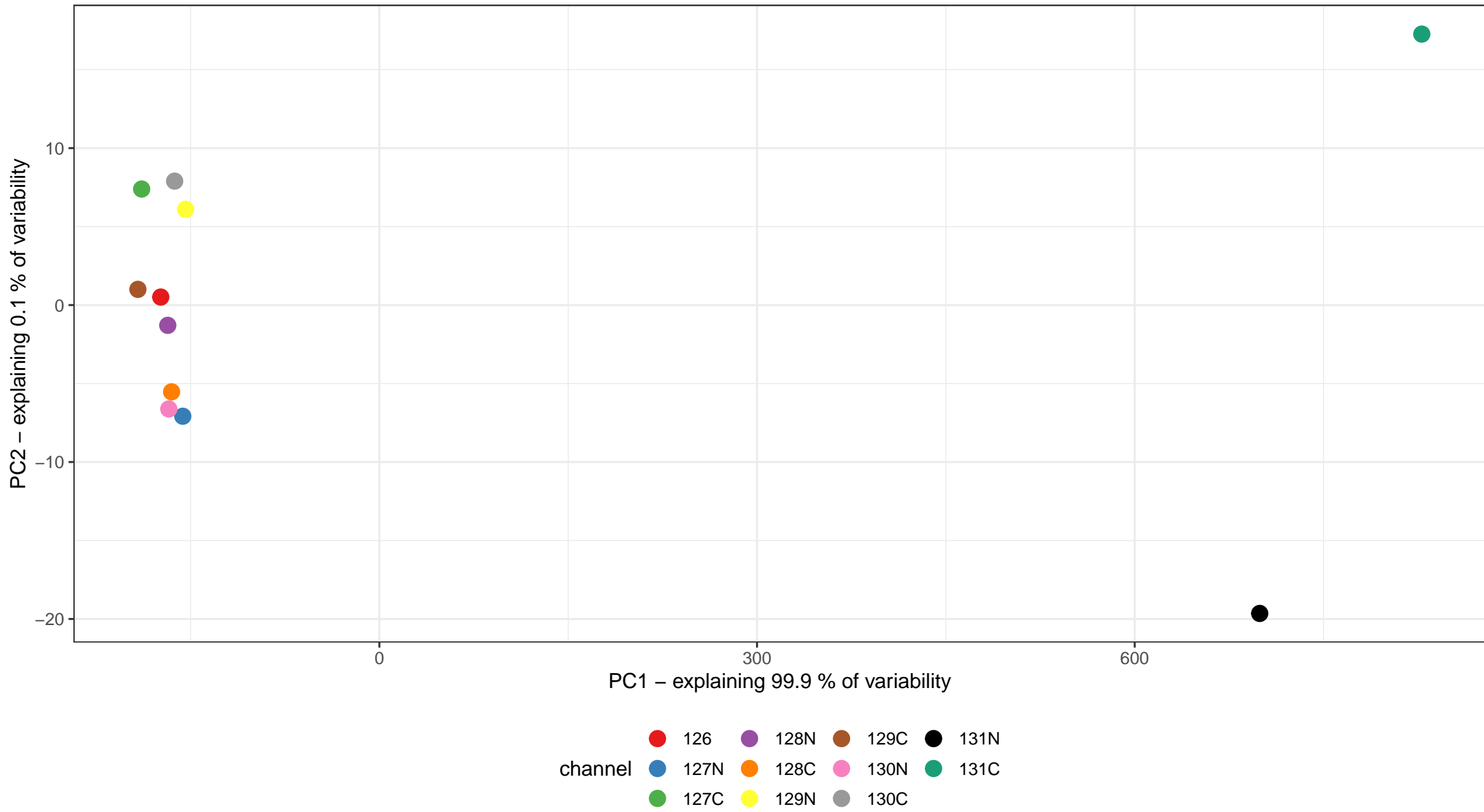


Intensity per channel

based on protein.tsv

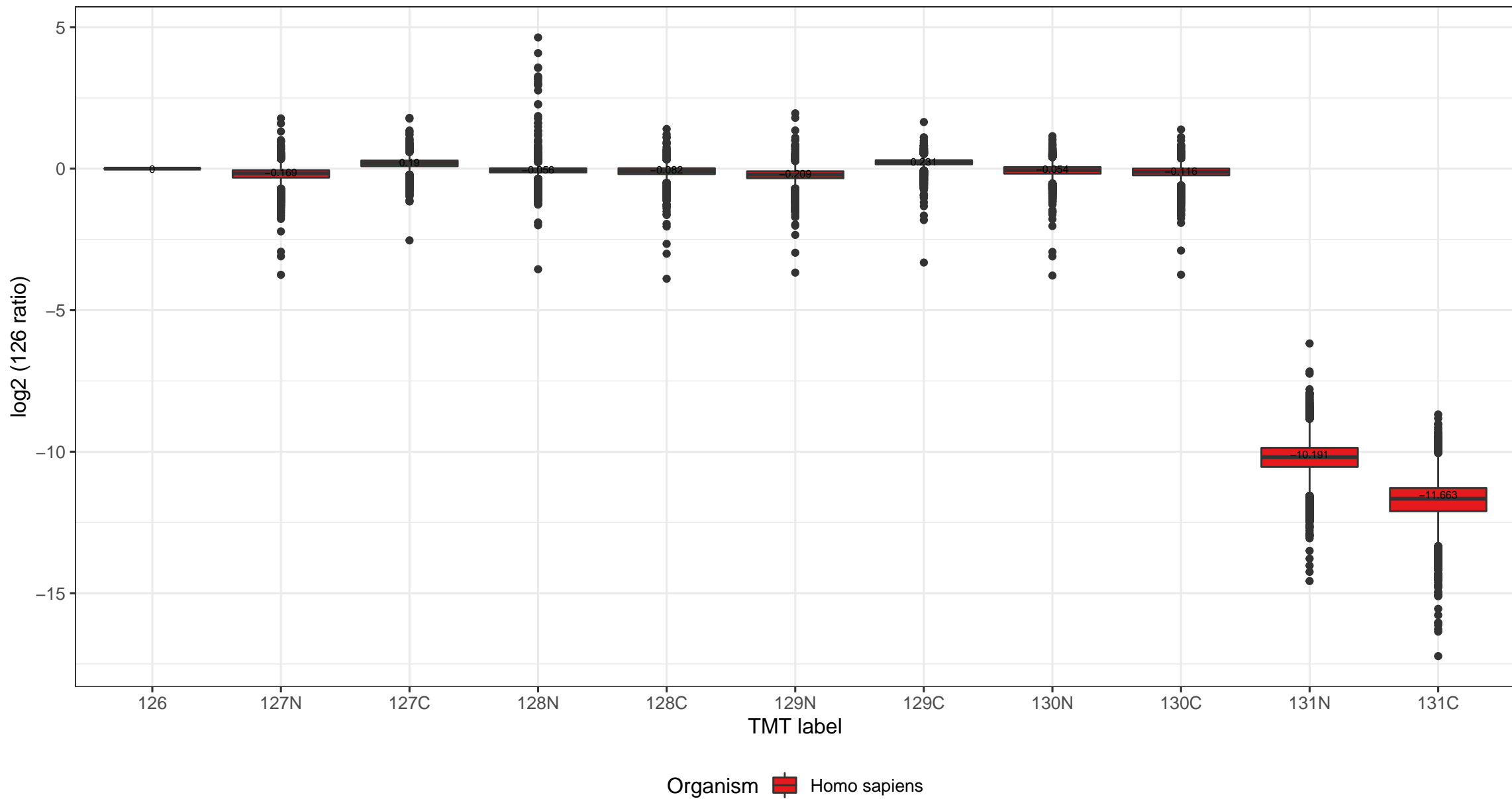


PCA of TMT intensities

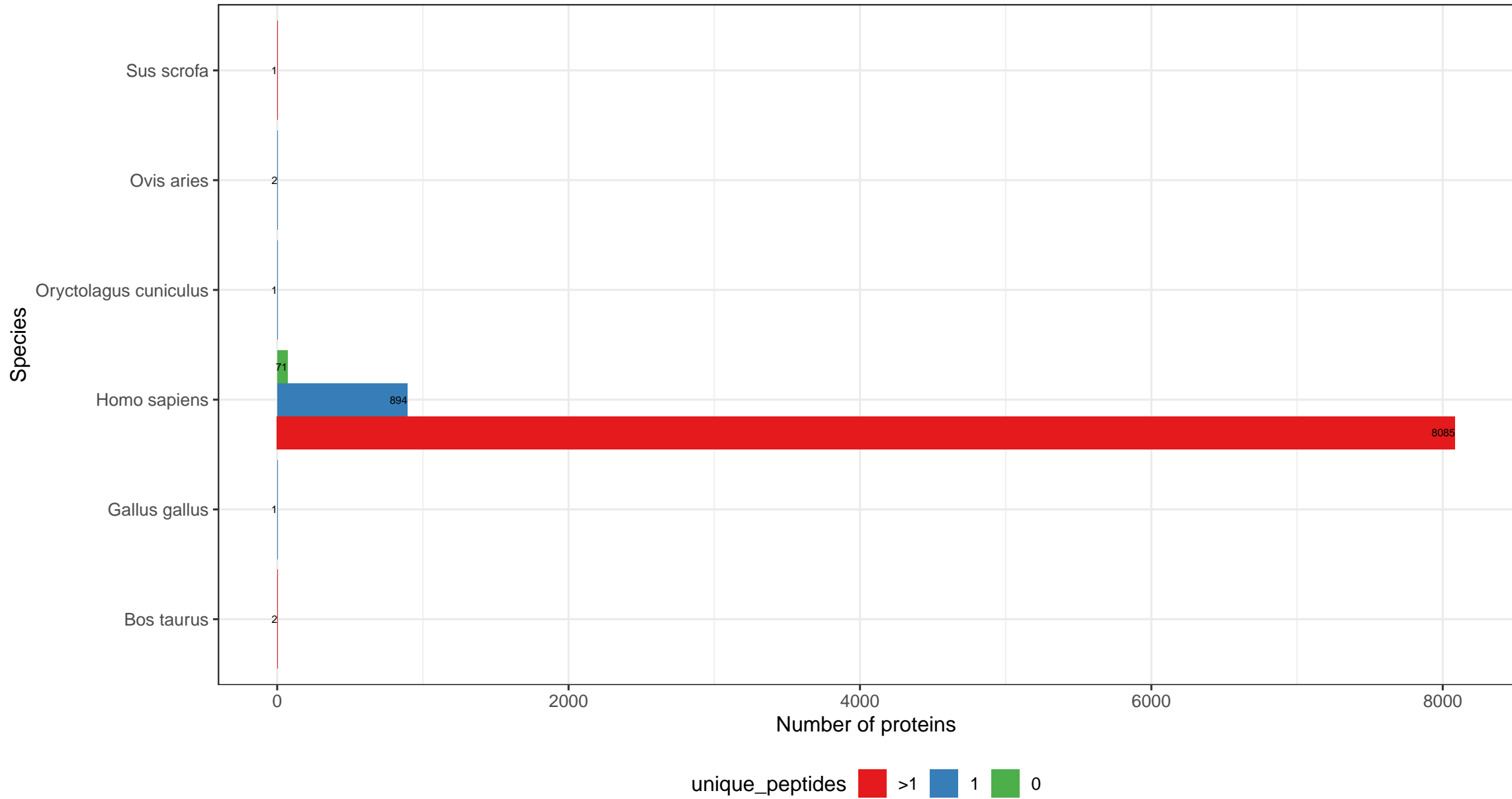


Relative intensity per channel

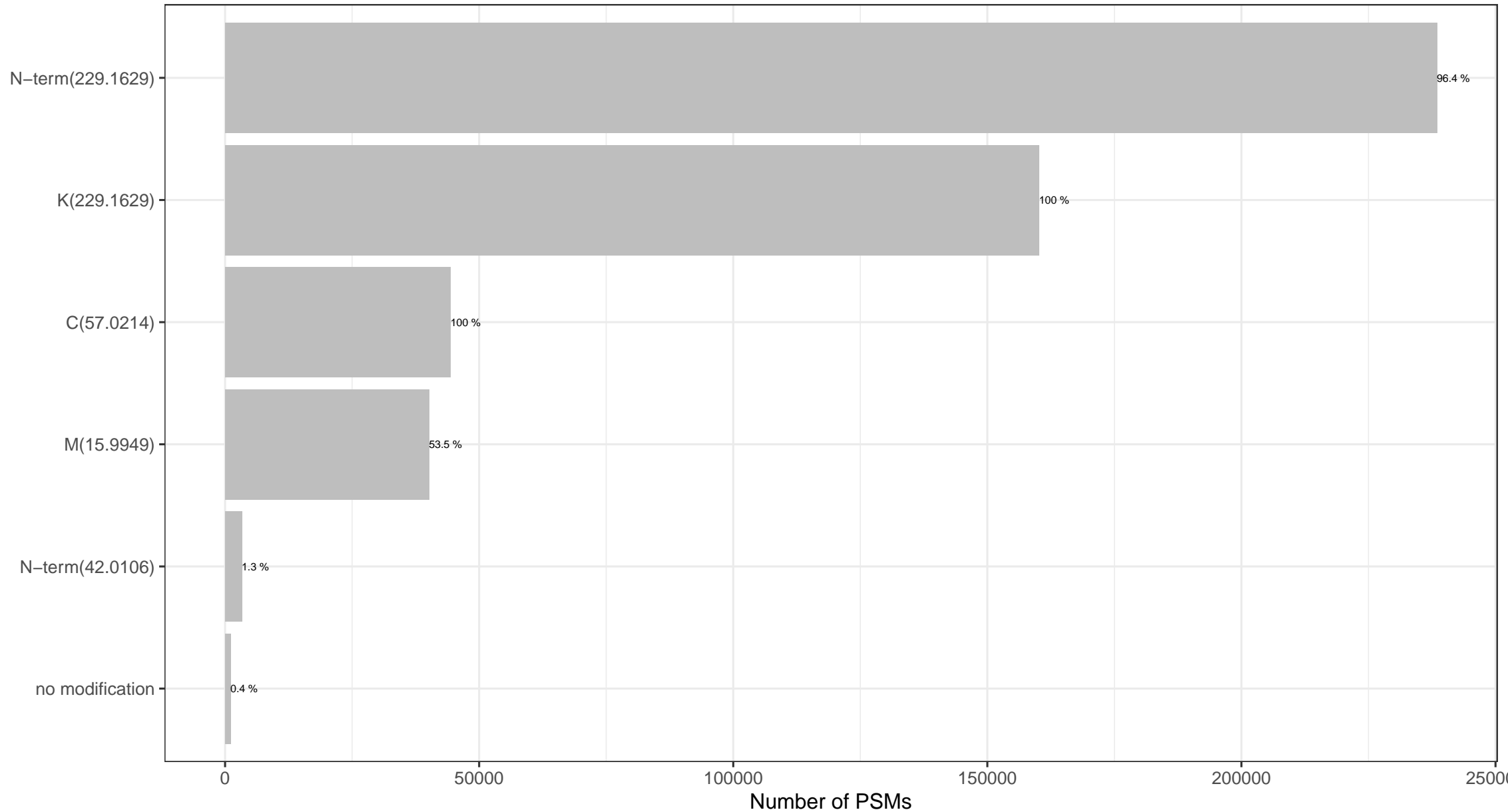
based on protein.tsv



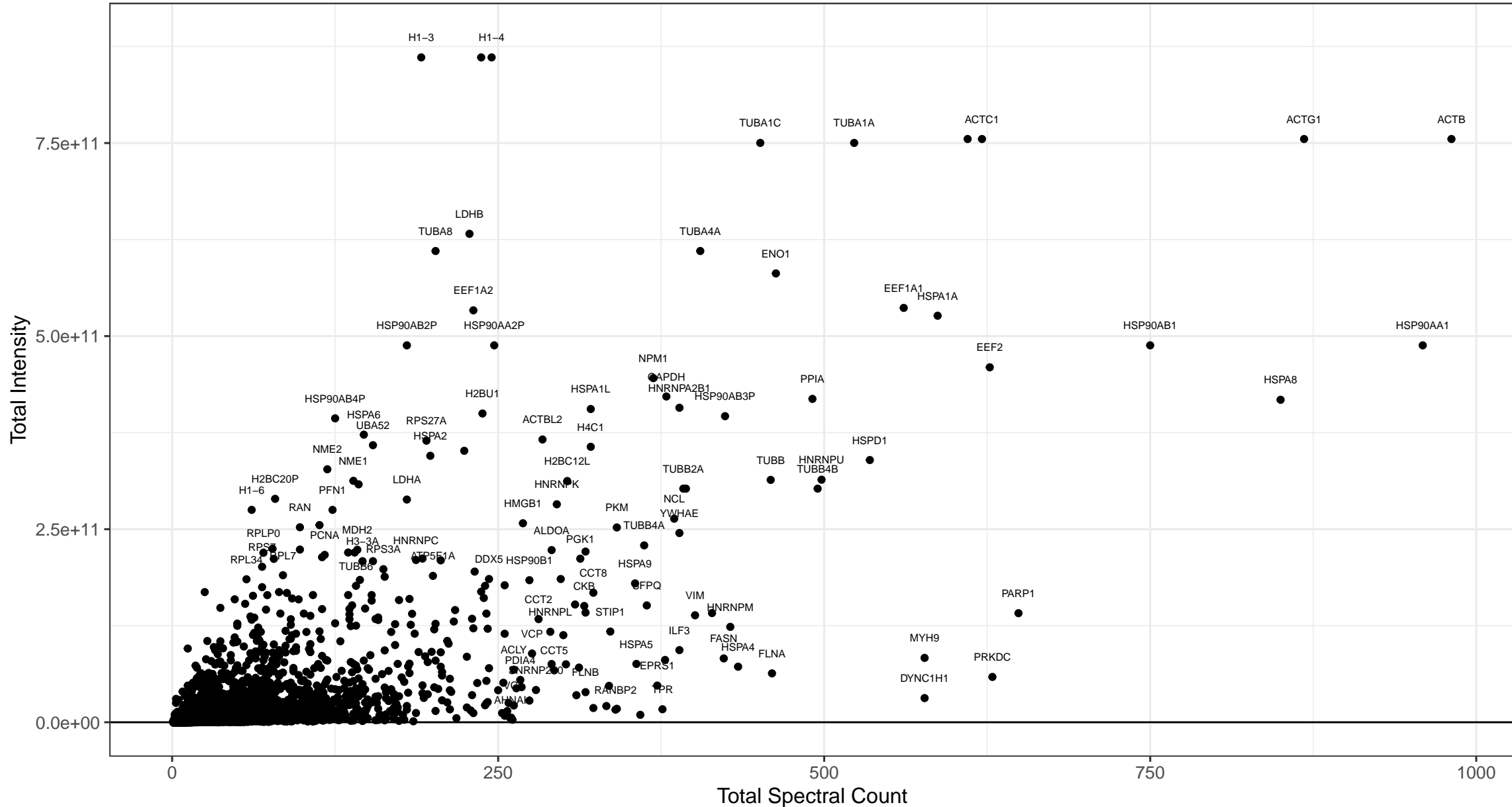
Species identified based on protein.tsv



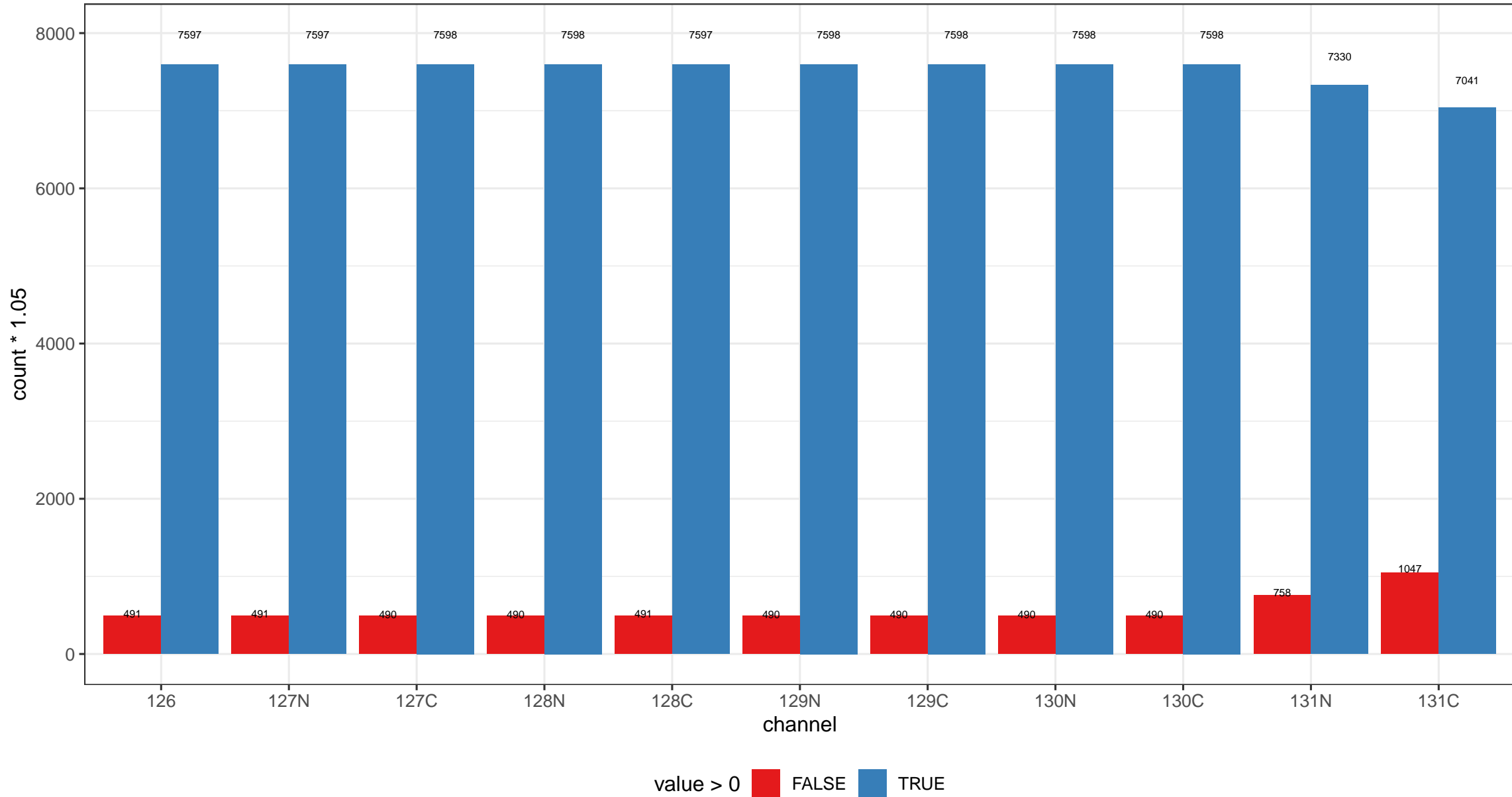
Modifications based on psm.tsv



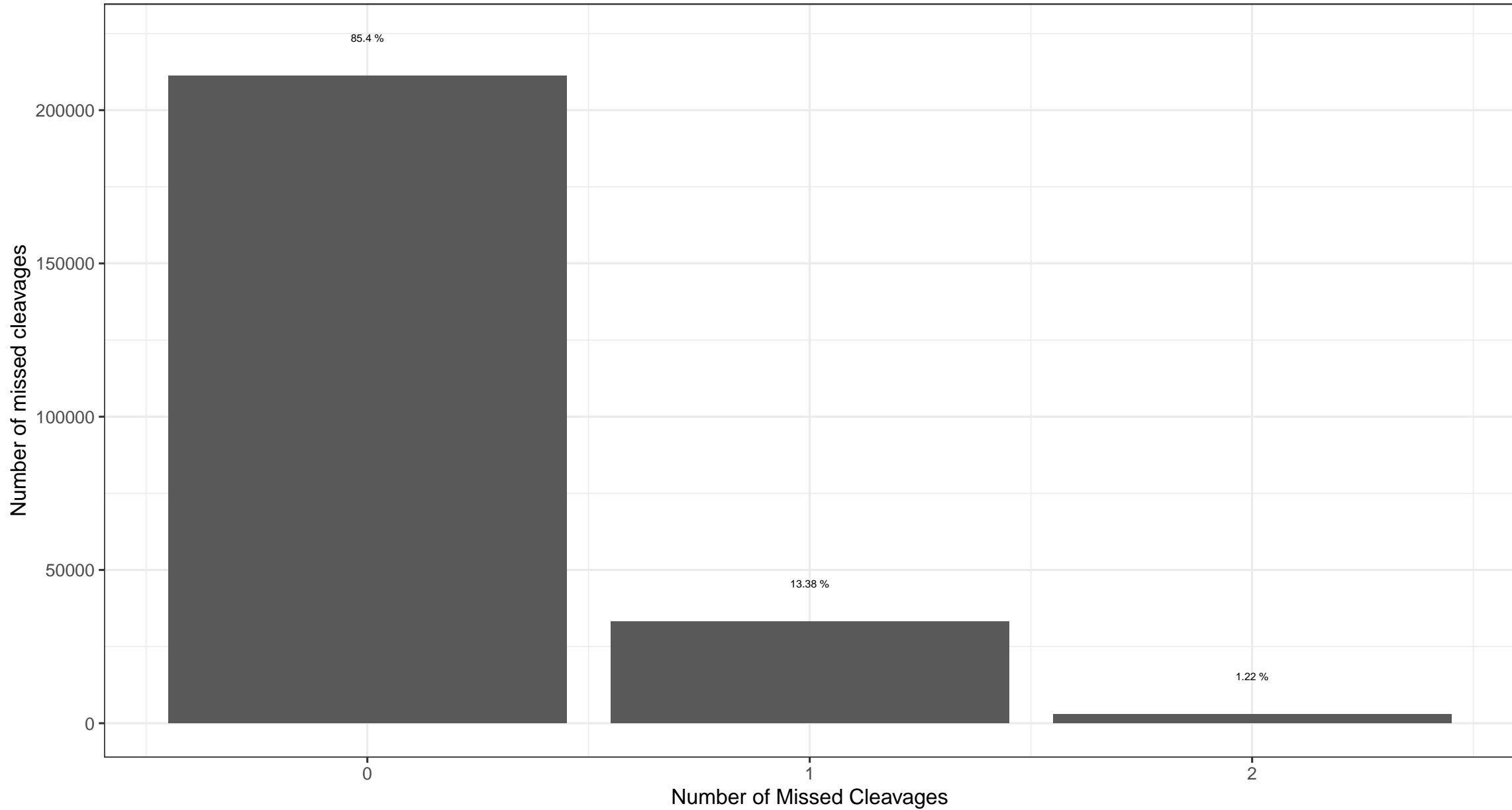
Most abundant proteins
based on protein.tsv



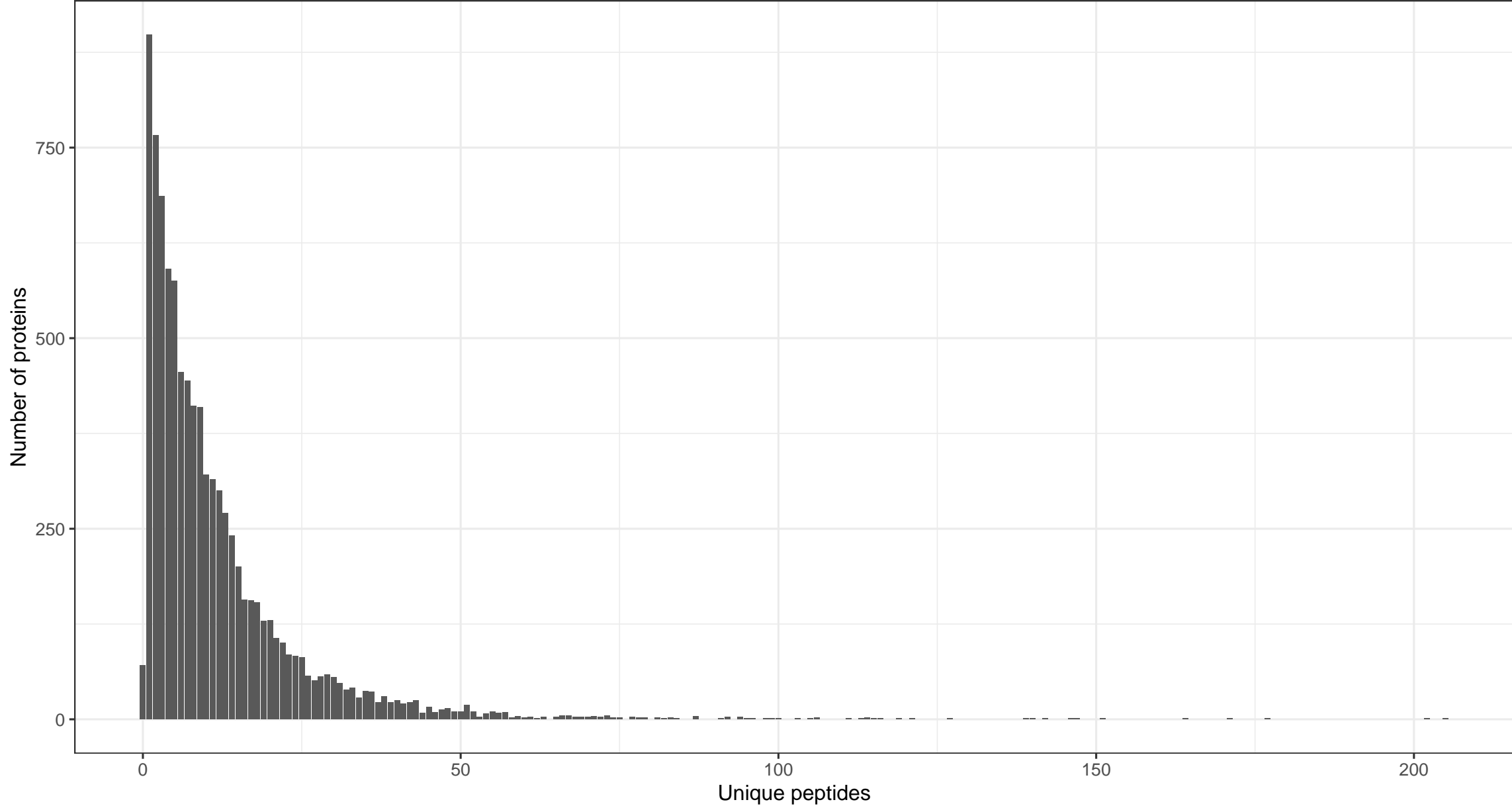
TMT signal intensity > 0 distribution
based on protein.tsv



Number of missed cleavages
based on psm.tsv

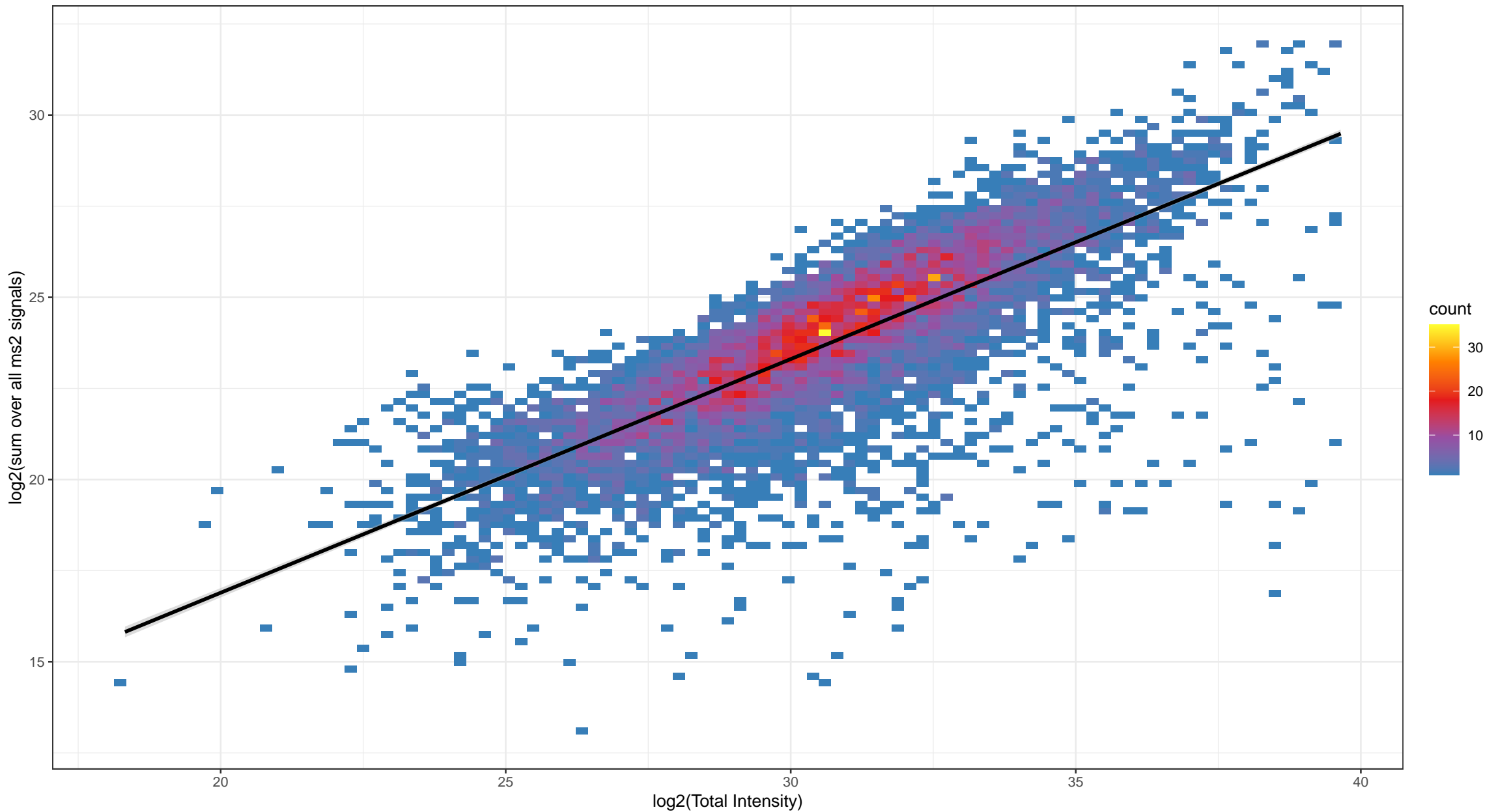


Proteins >1 unique pept.: 8088
based on protein.tsv



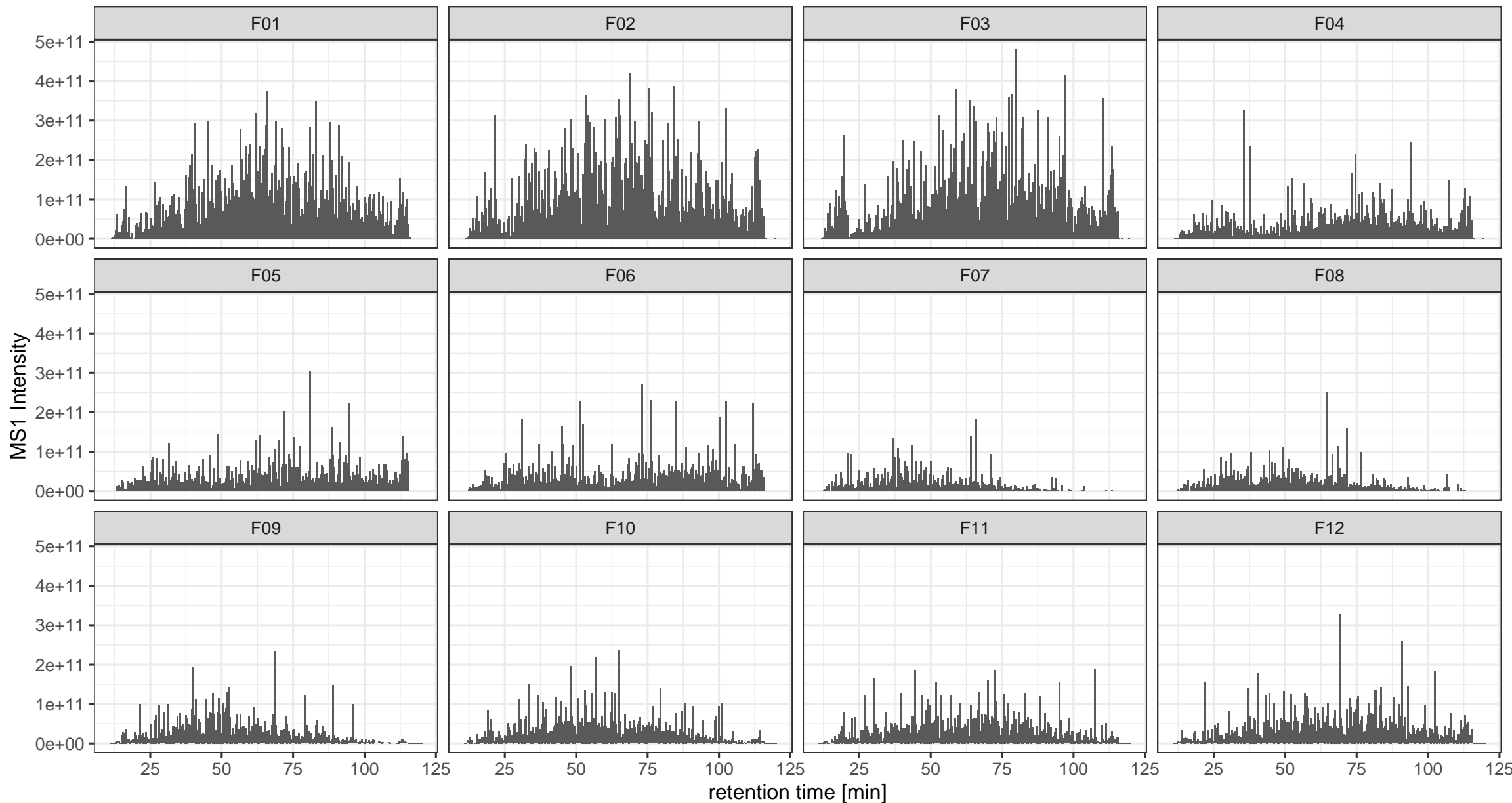
Total Intensity vs sum of TMT signal

based on protein.tsv



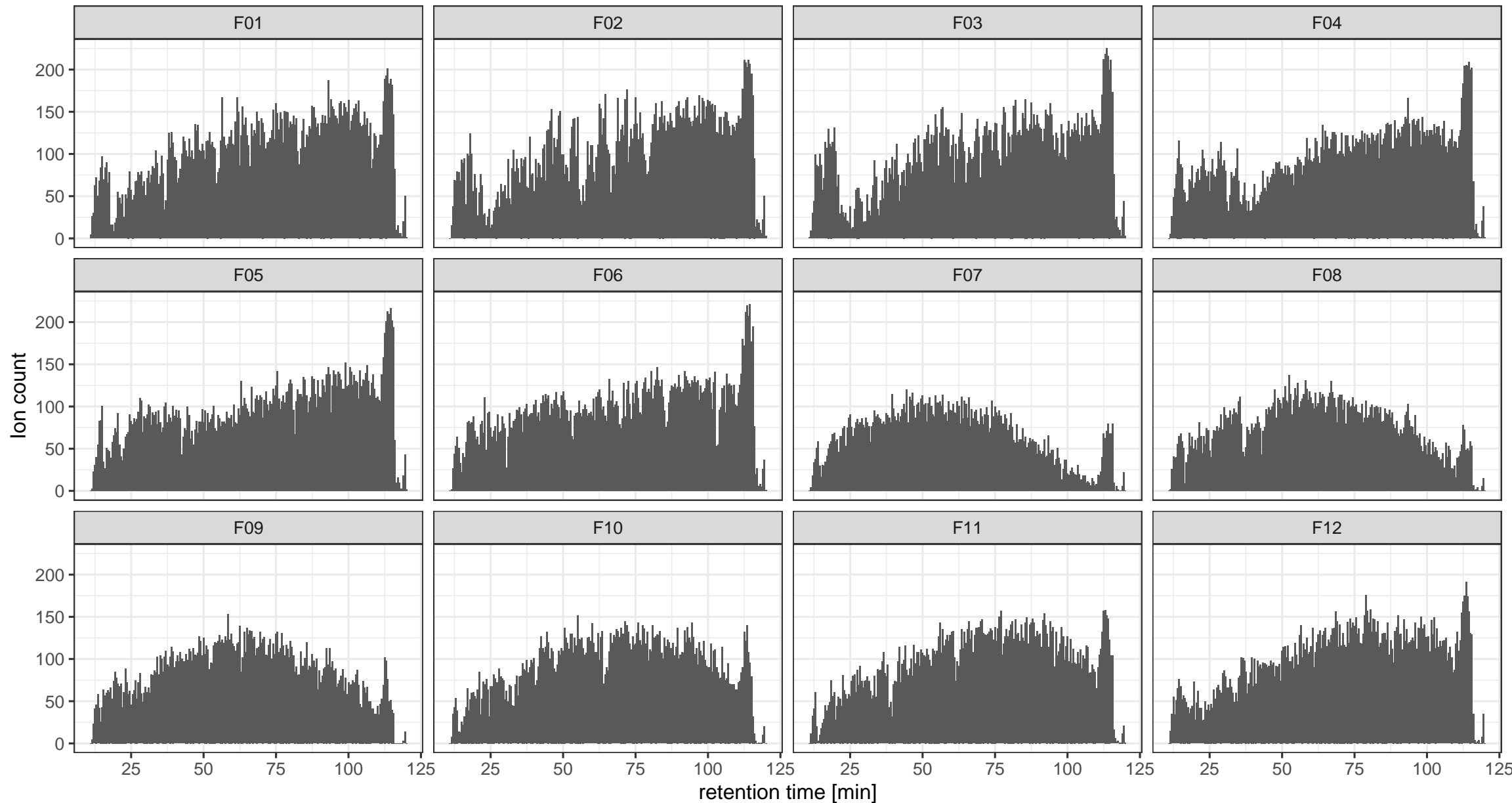
LC chromatogram

based on psm.tsv



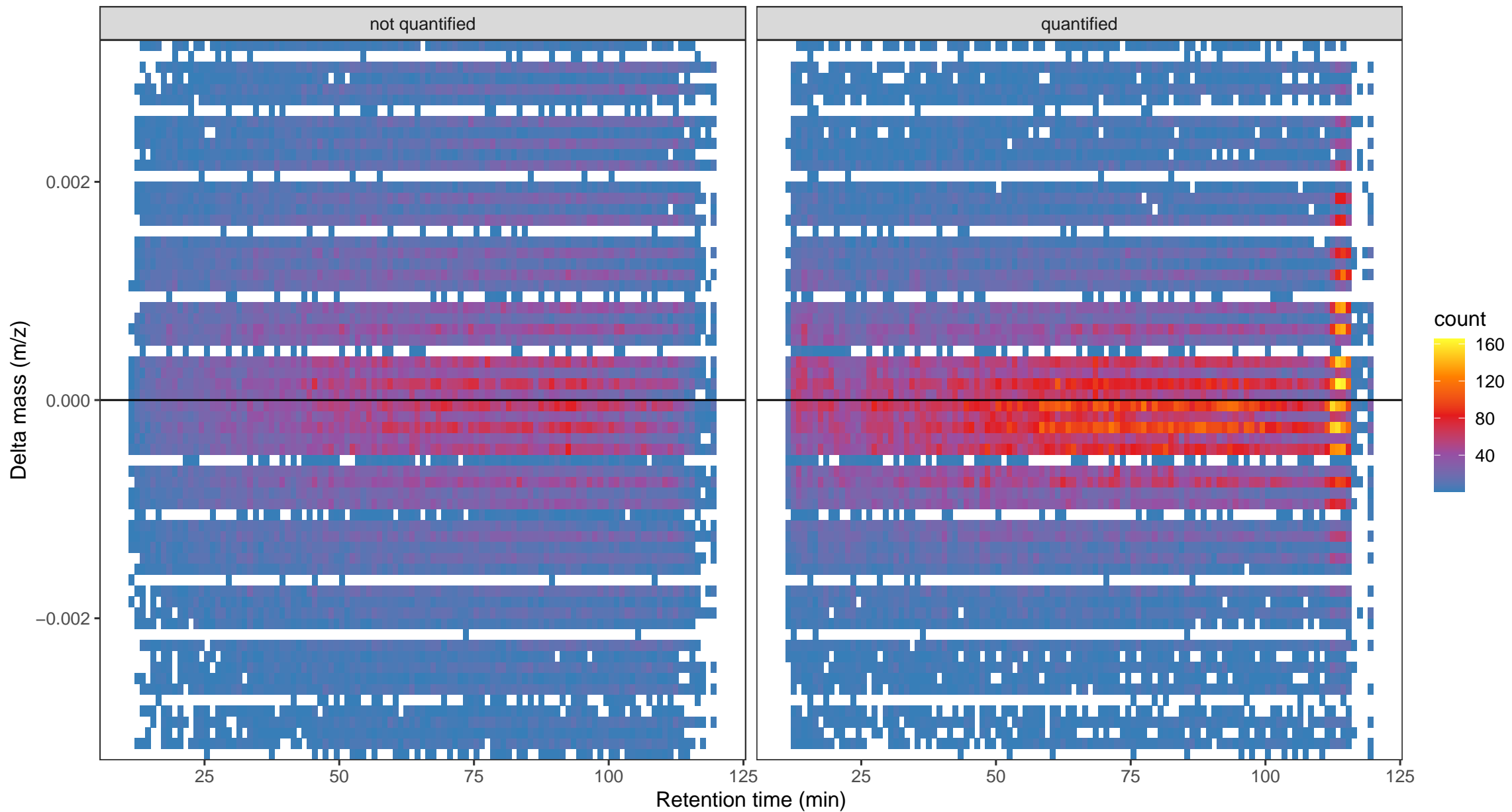
TIC chromatogram

based on psm.tsv



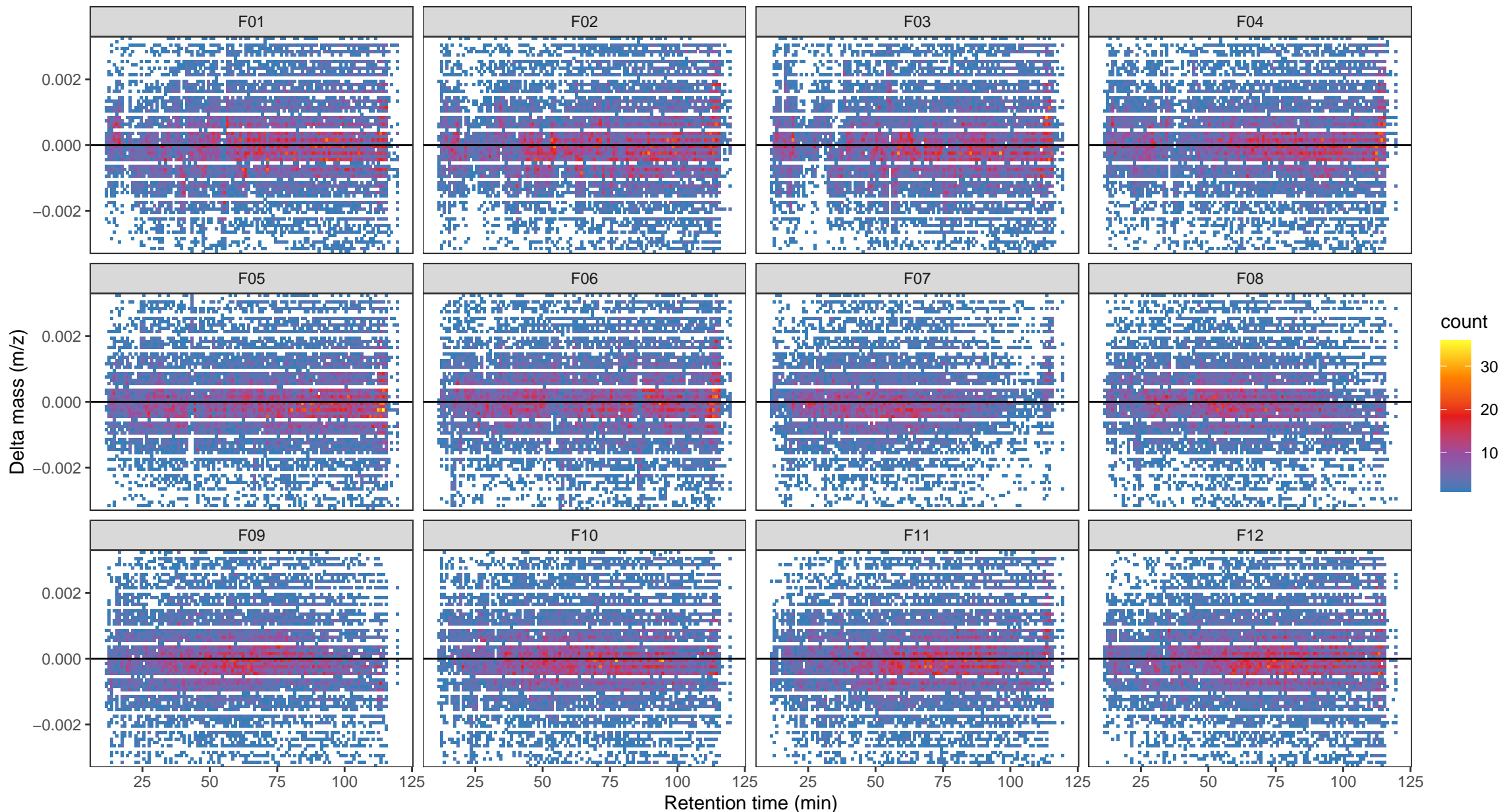
Delta mass histogram

based on psm.tsv

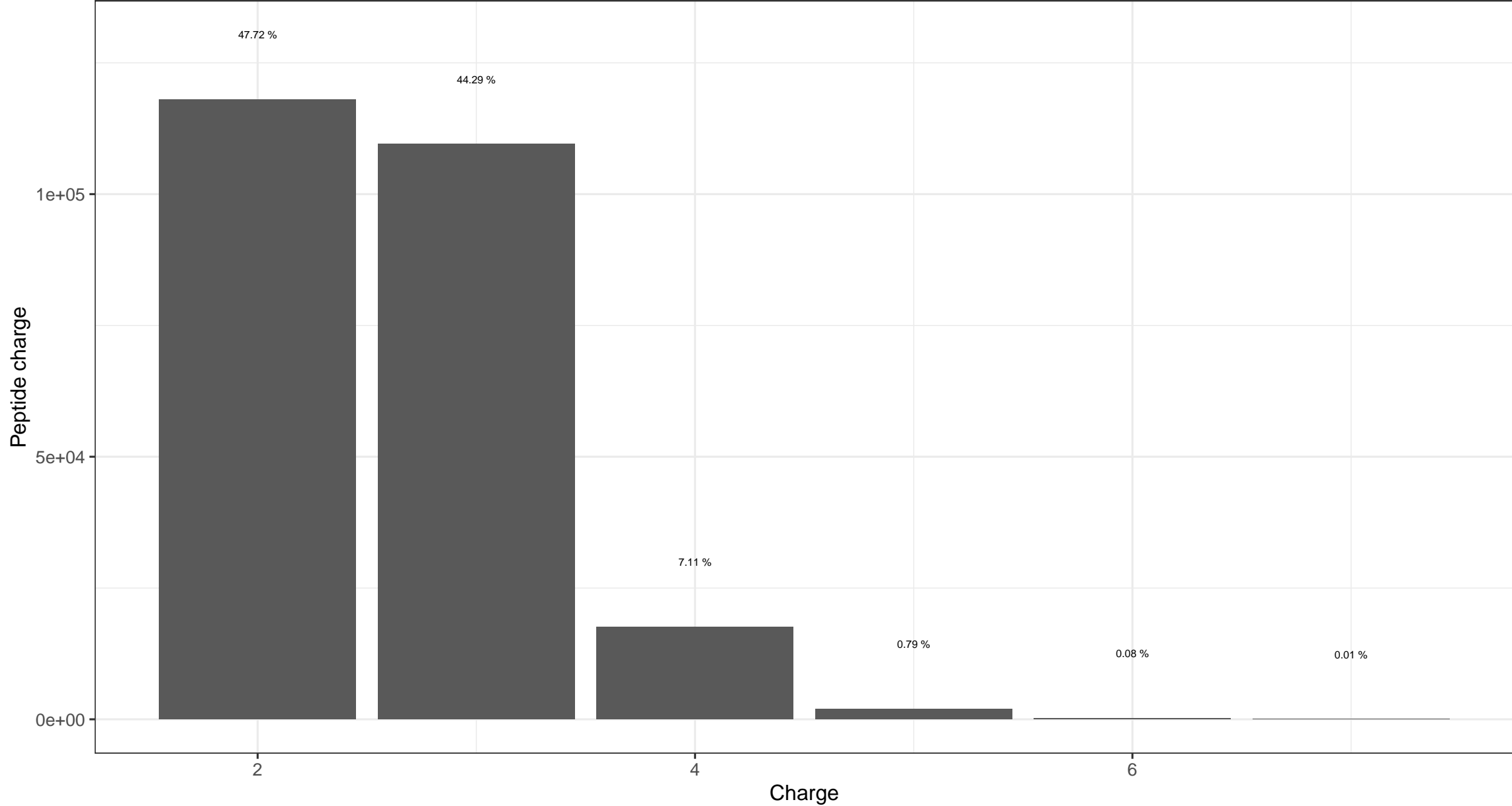


Delta mass histogram

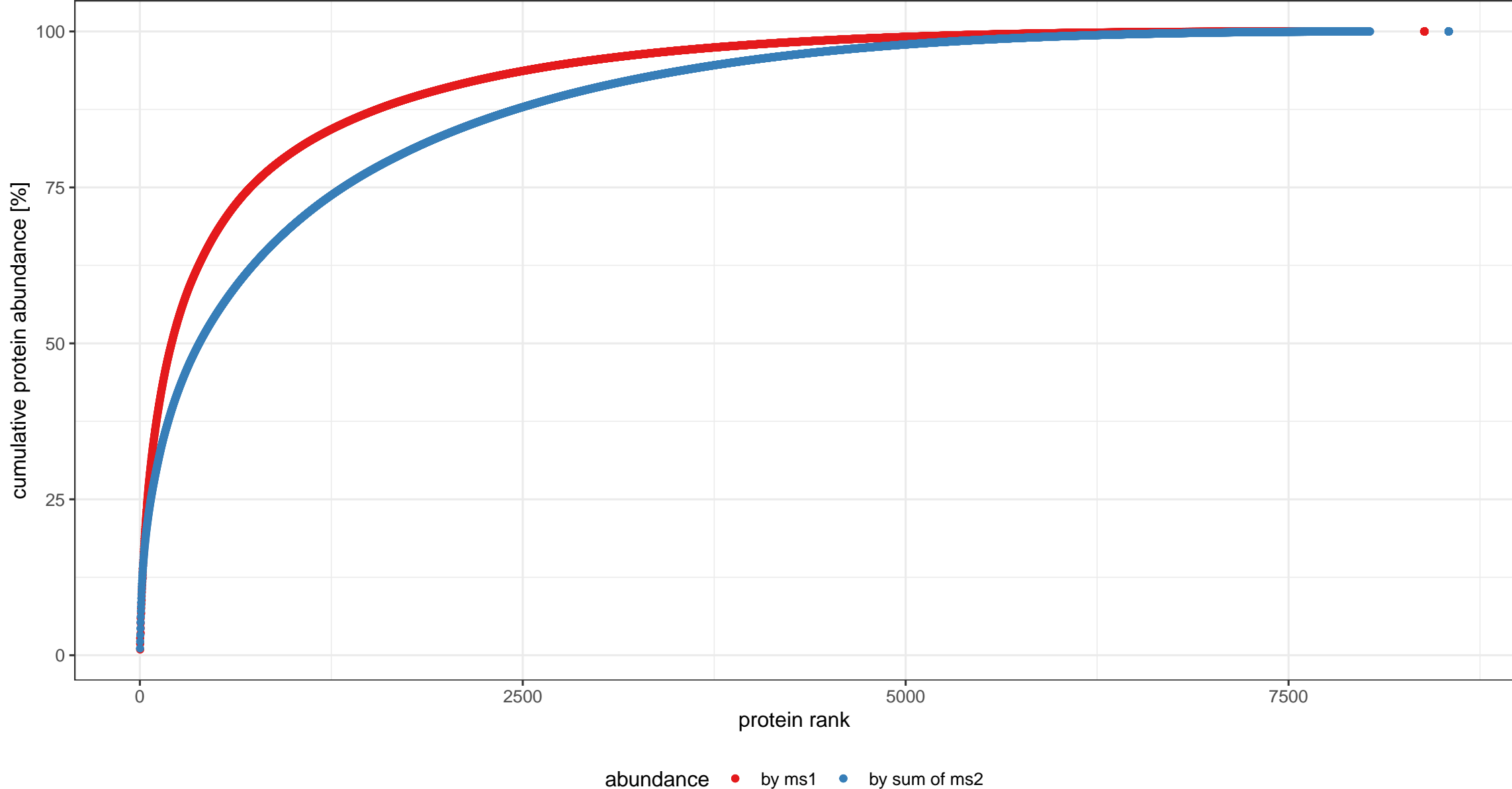
based on psm.tsv



Charge distribution
based on psm.tsv

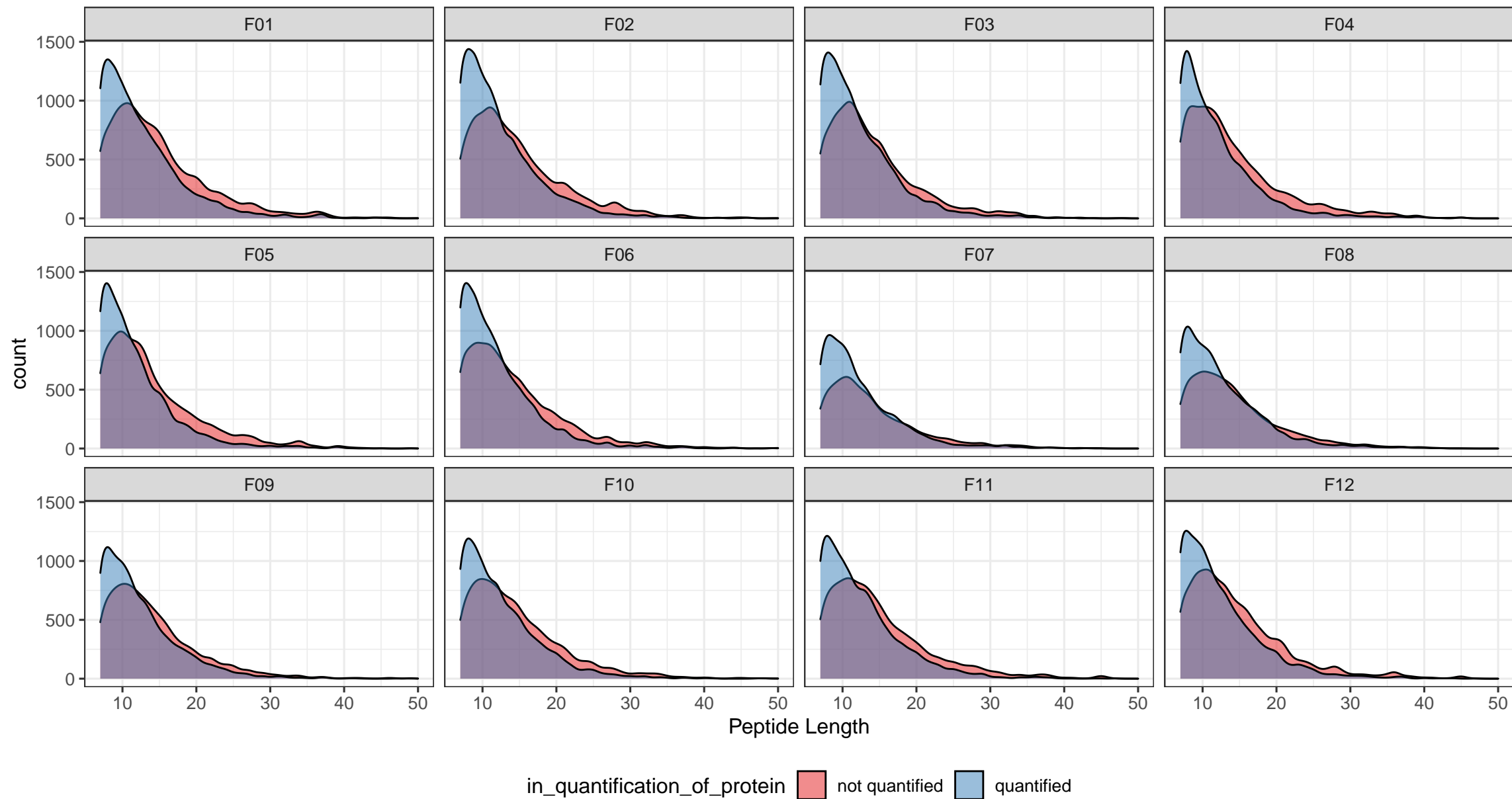


cumulative sum of protein abundance vs protein ranking by abundance
most abundant protein on the left

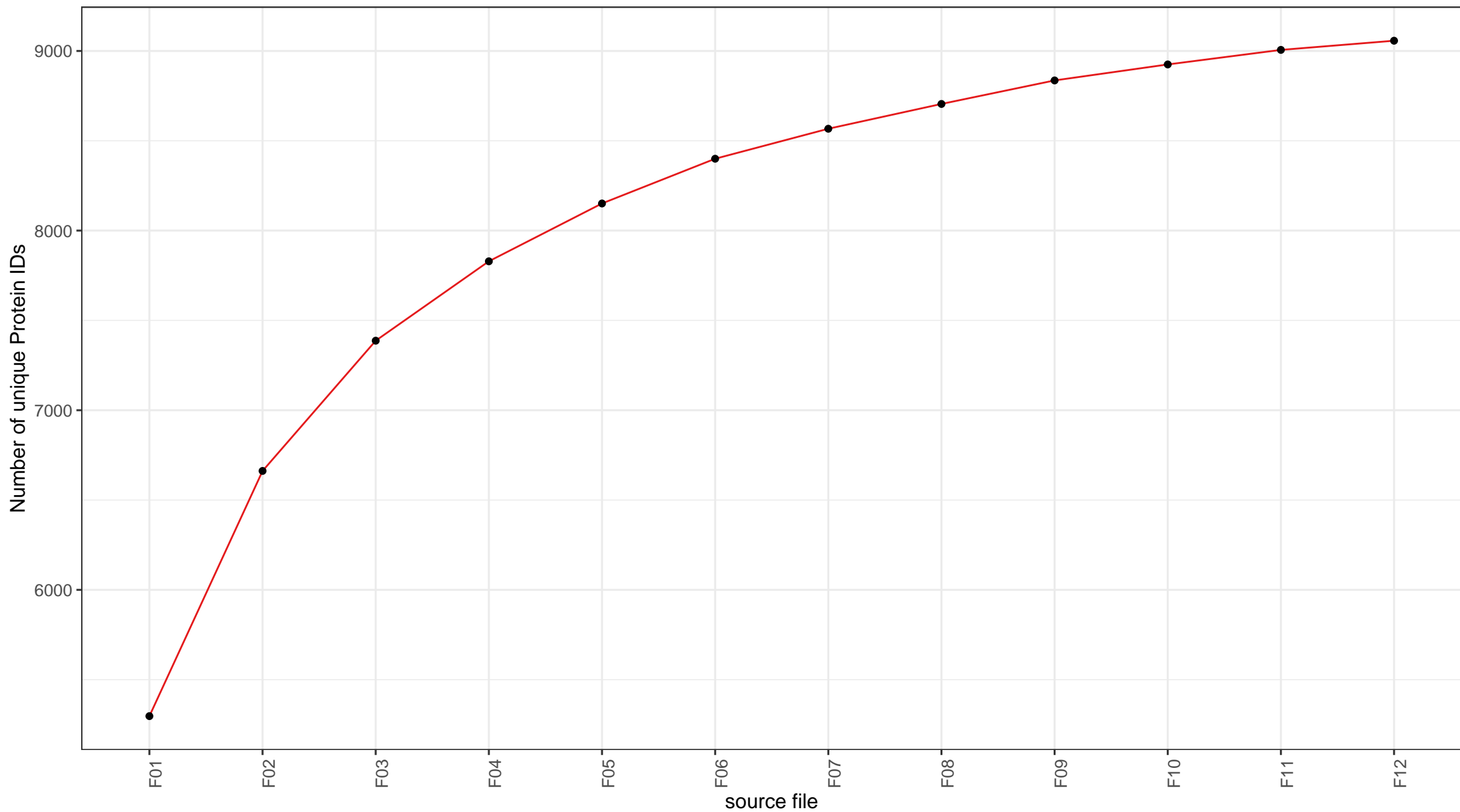


Peptide length distribution

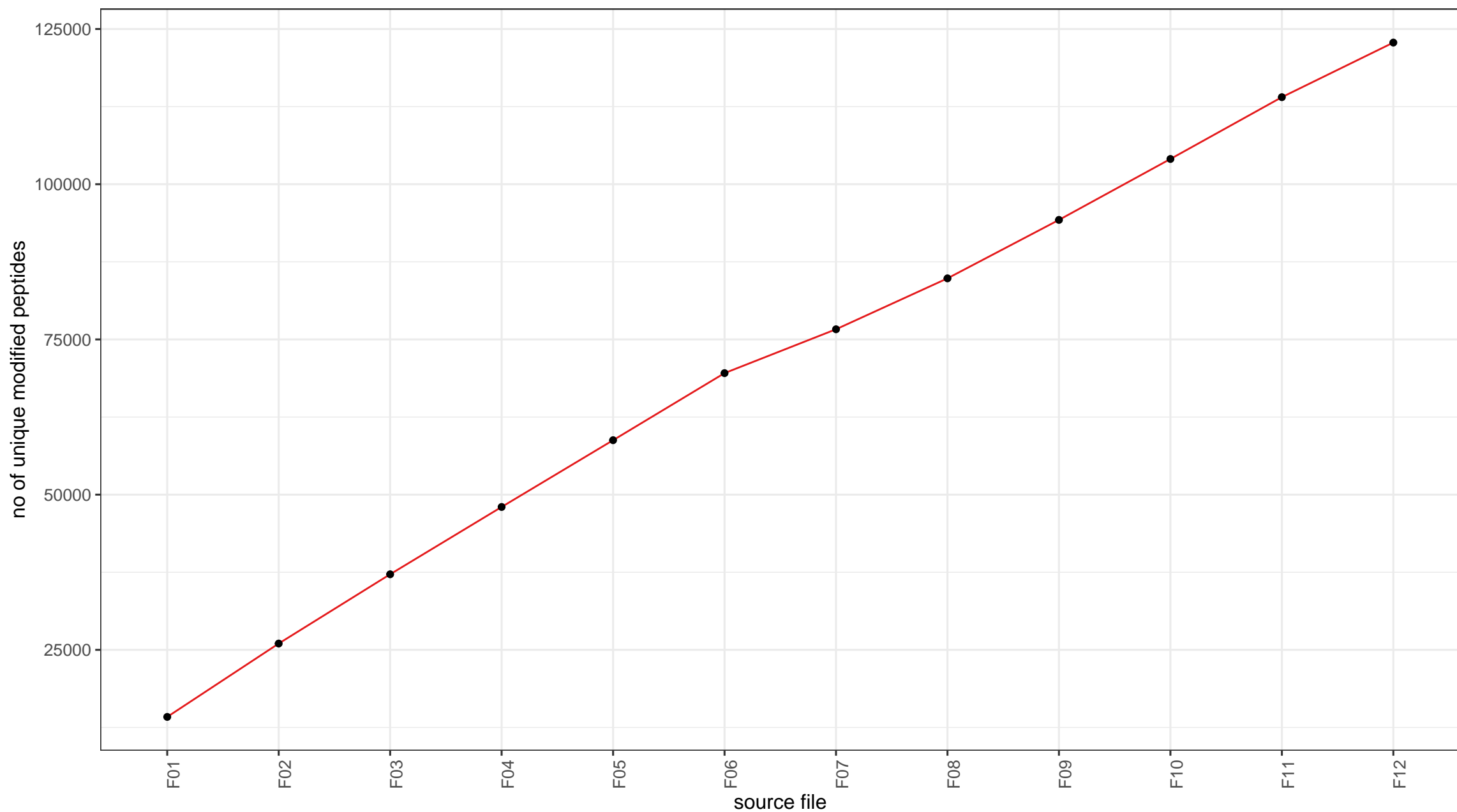
based on psm.tsv



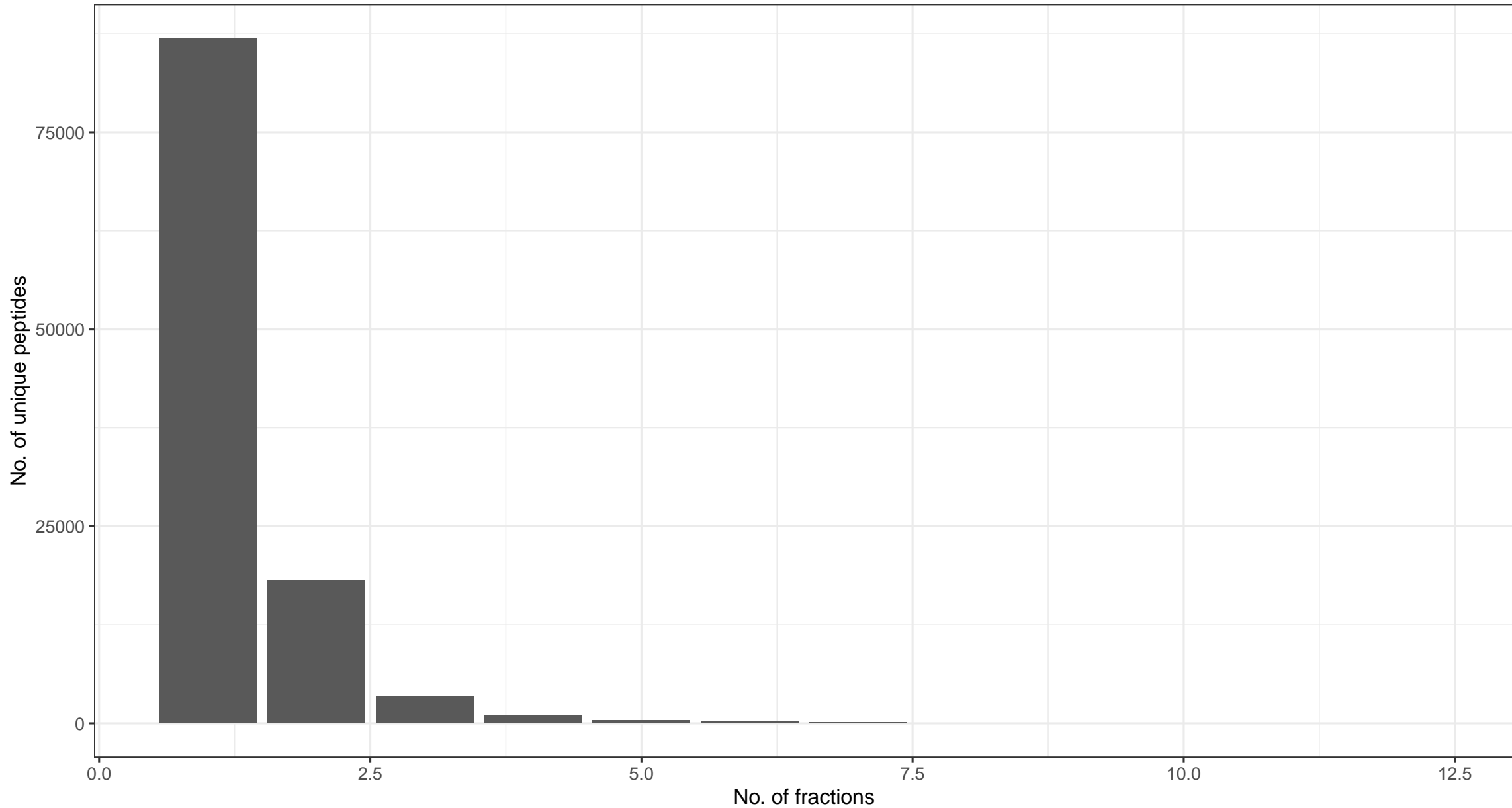
cumulative sum of unique Protein IDs



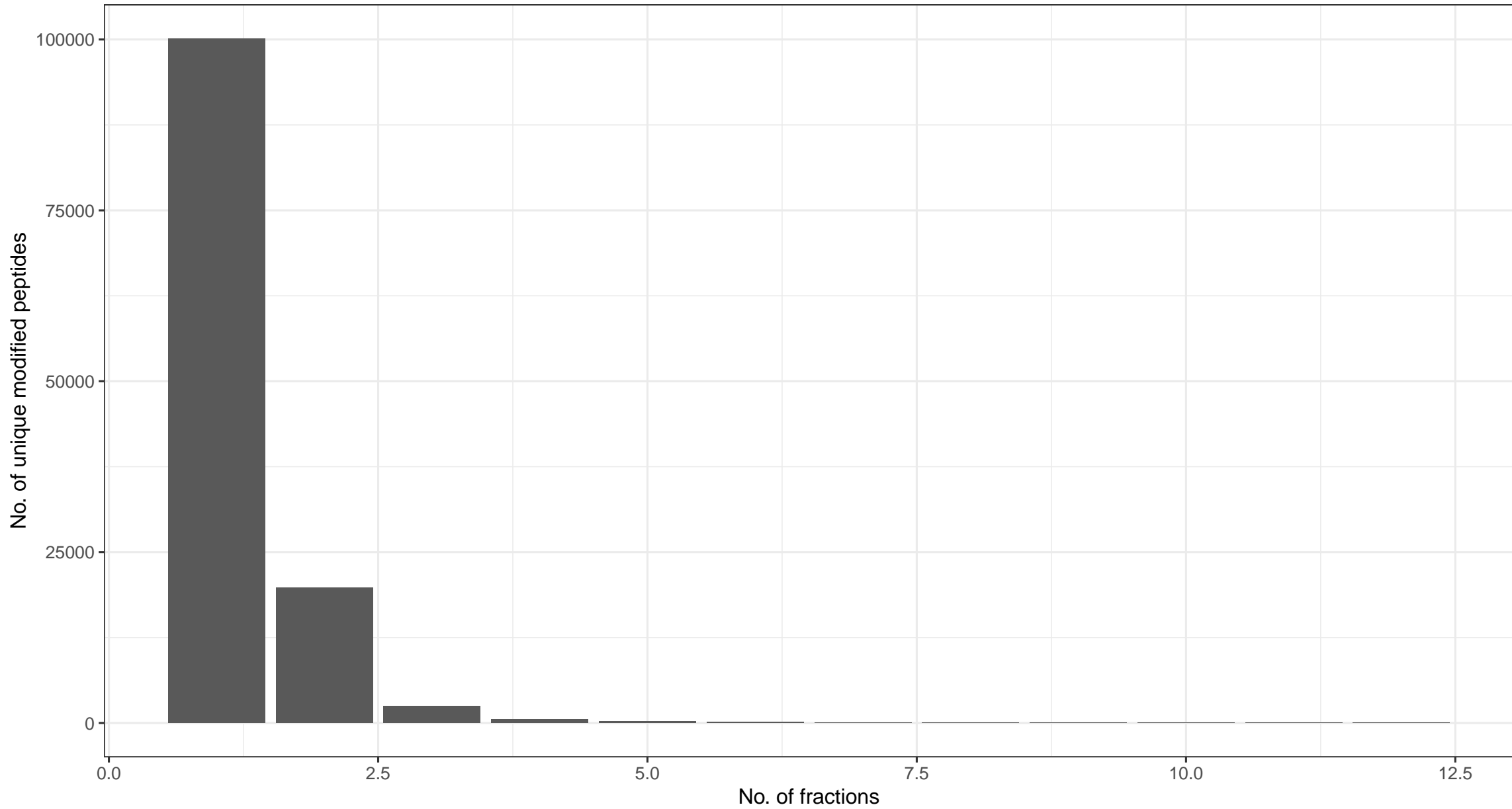
cumulative sum of unique modified peptides over number of source_files



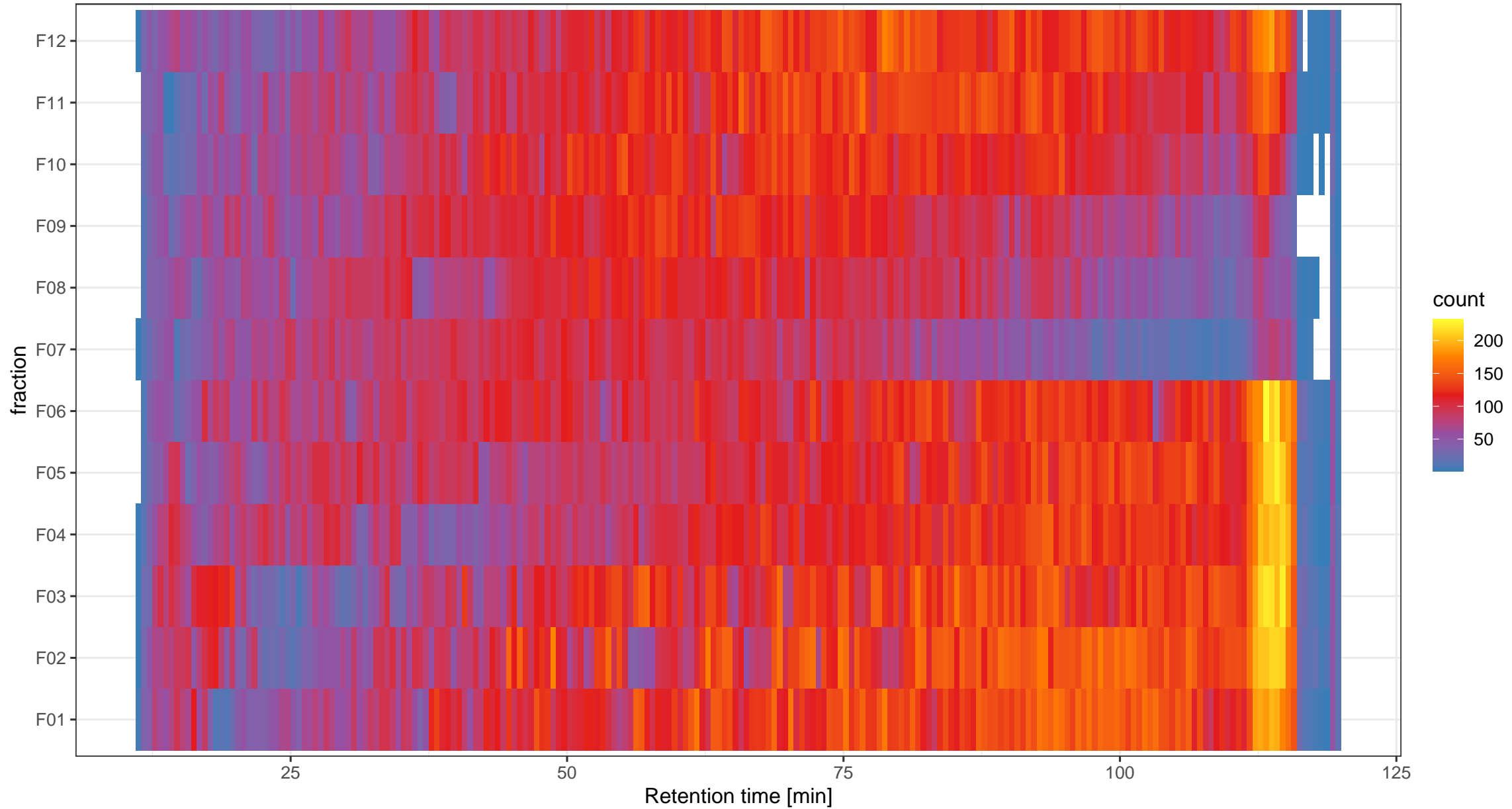
No. of fractions a unique peptide was identified in.
based on psm.tsv



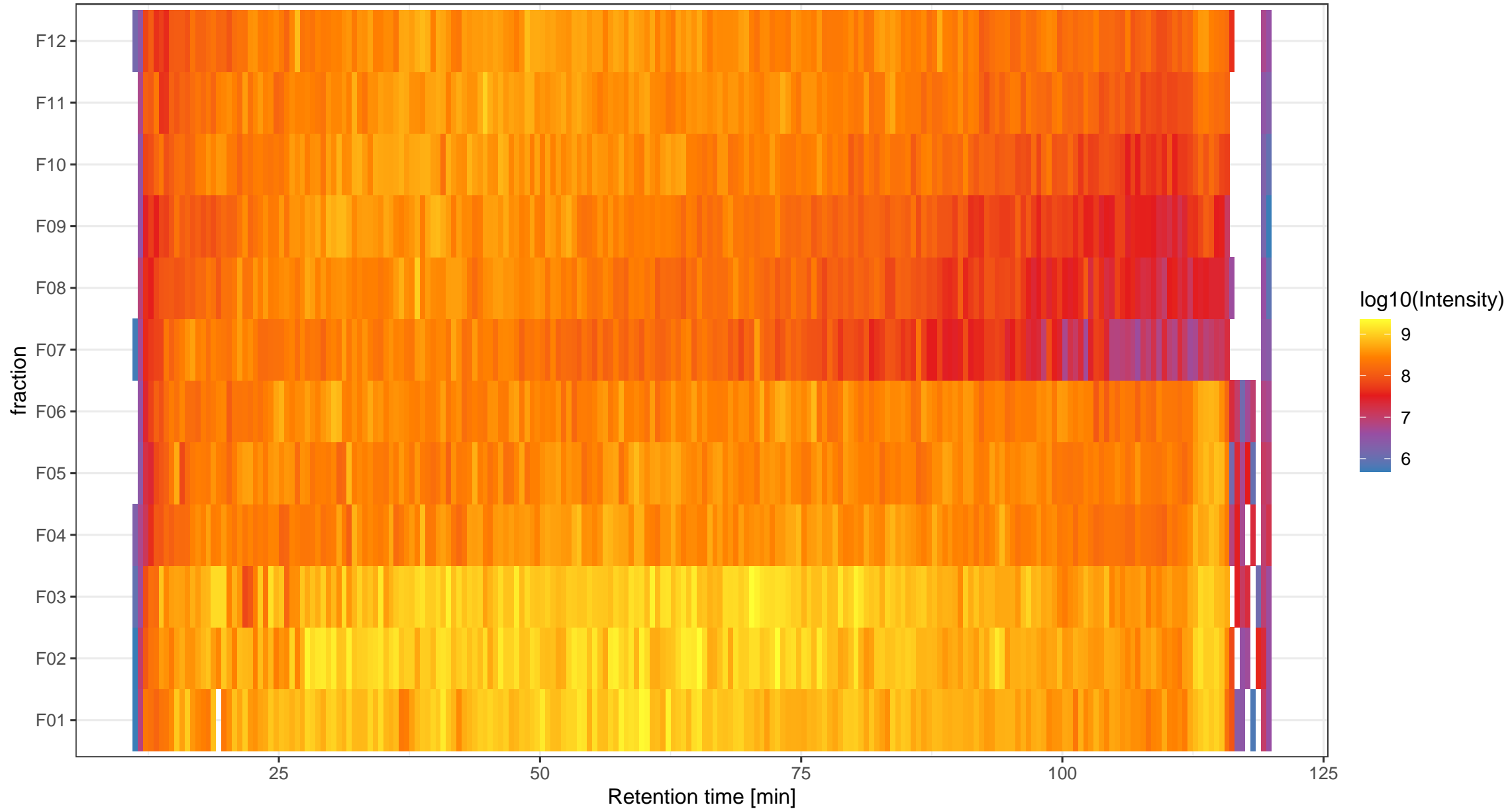
No. of fractions a unique modified peptide was identified in.
based on psm.tsv



2d histogram – PSM count per retention time
based on psm.tsv

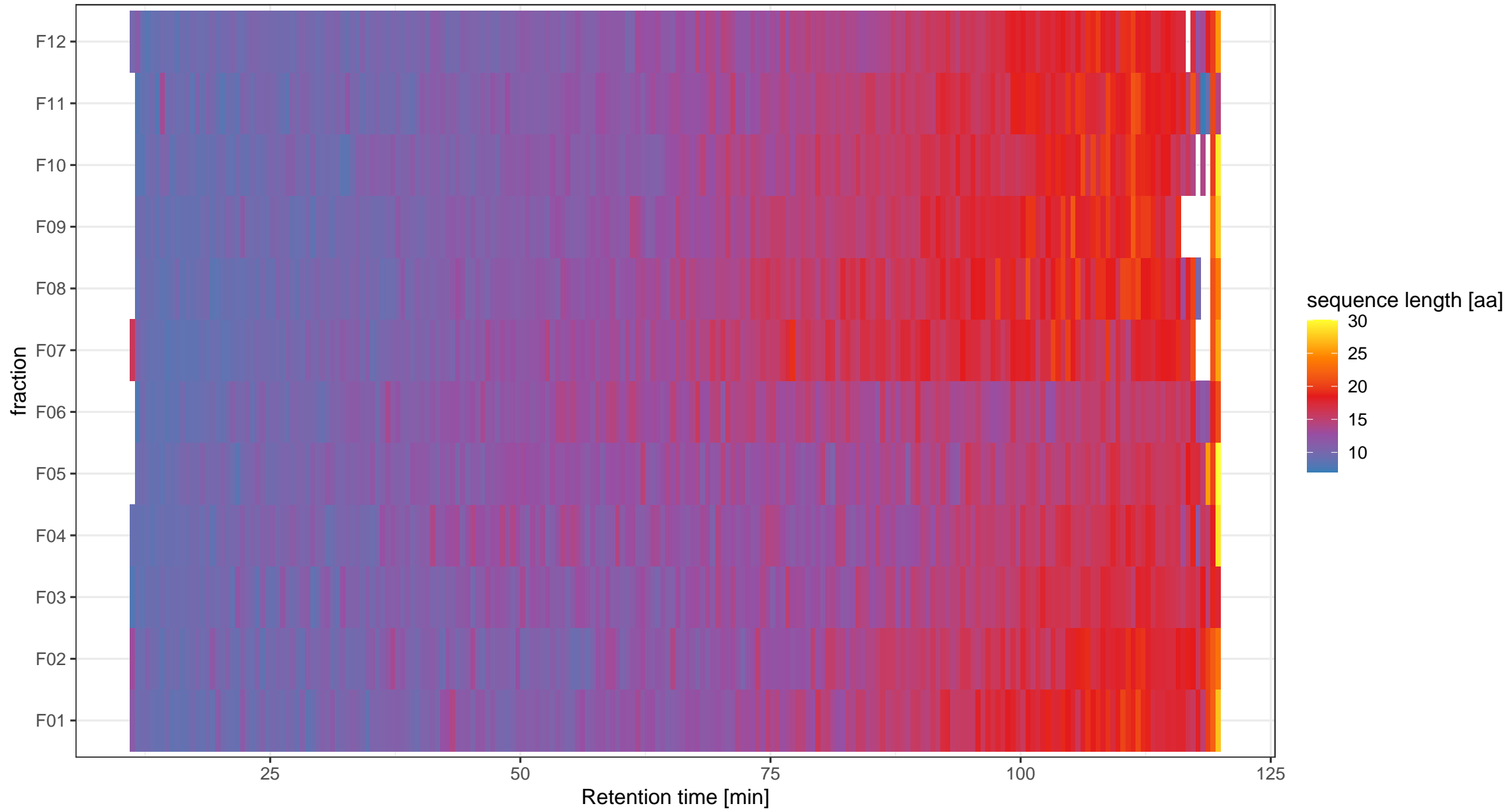


2d histogram – MS1 Intensity per retention time
based on psm.tsv



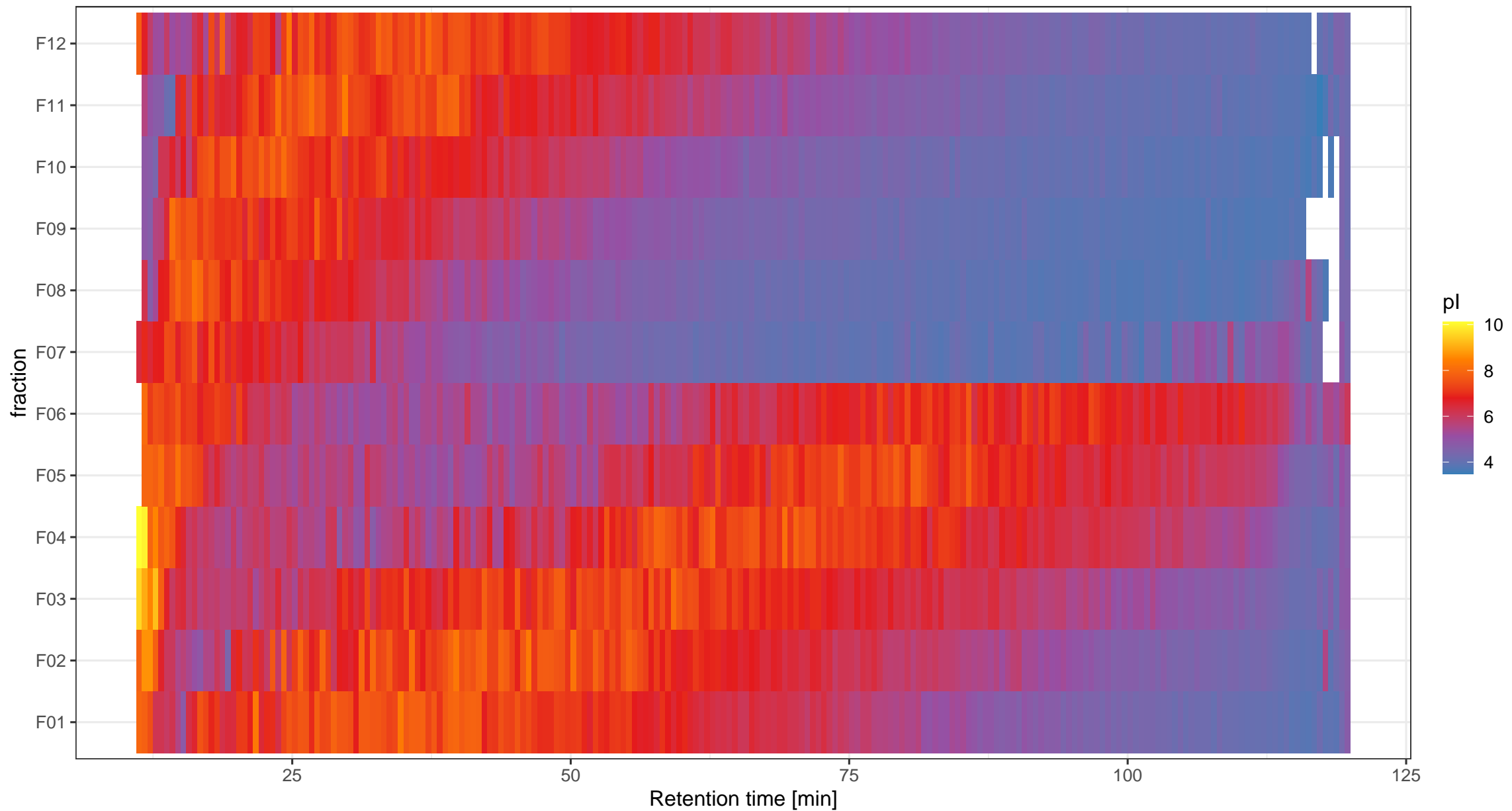
2d histogram – sequence length per retention time

based on psm.tsv

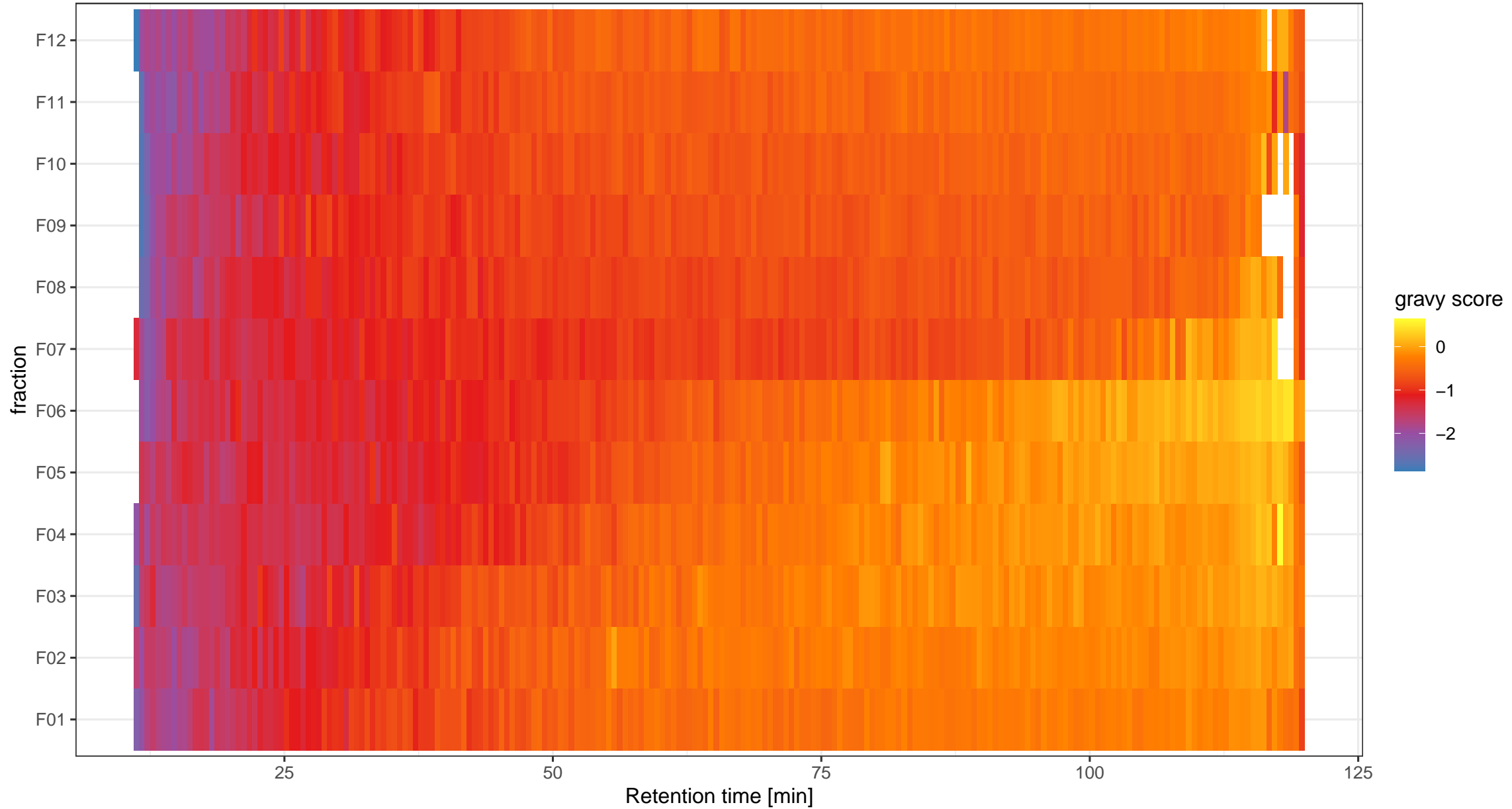


2d histogram – isoelectric point (pI) per retention time

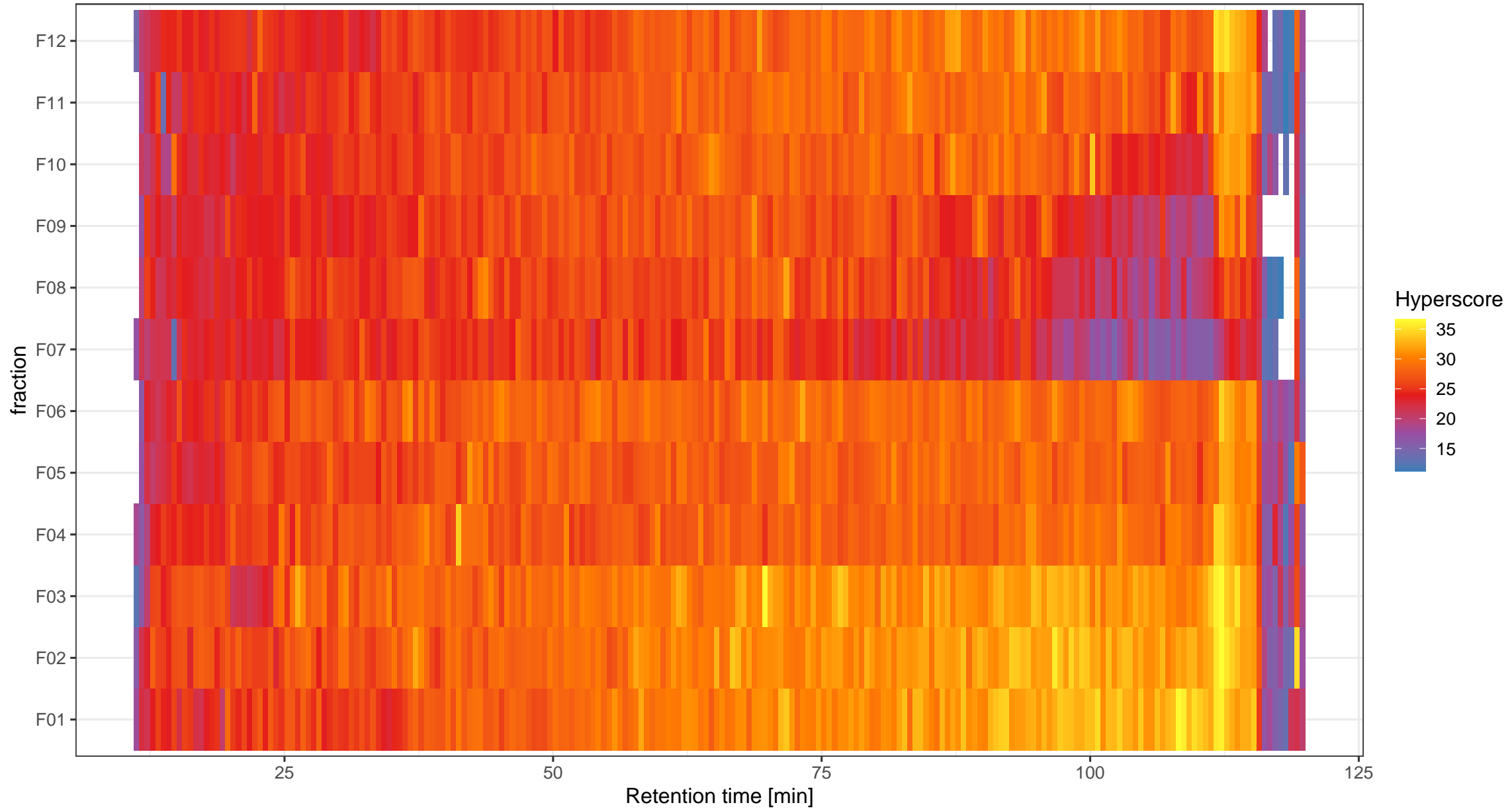
based on psm.tsv



2d histogram – hydrophobicity per retention time
based on psm.tsv



2d histogram – Hyperscore per retention time
based on psm.tsv



2d histogram – Mass error per retention time
based on psm.tsv

