

Analysing MaxQuant Output with R

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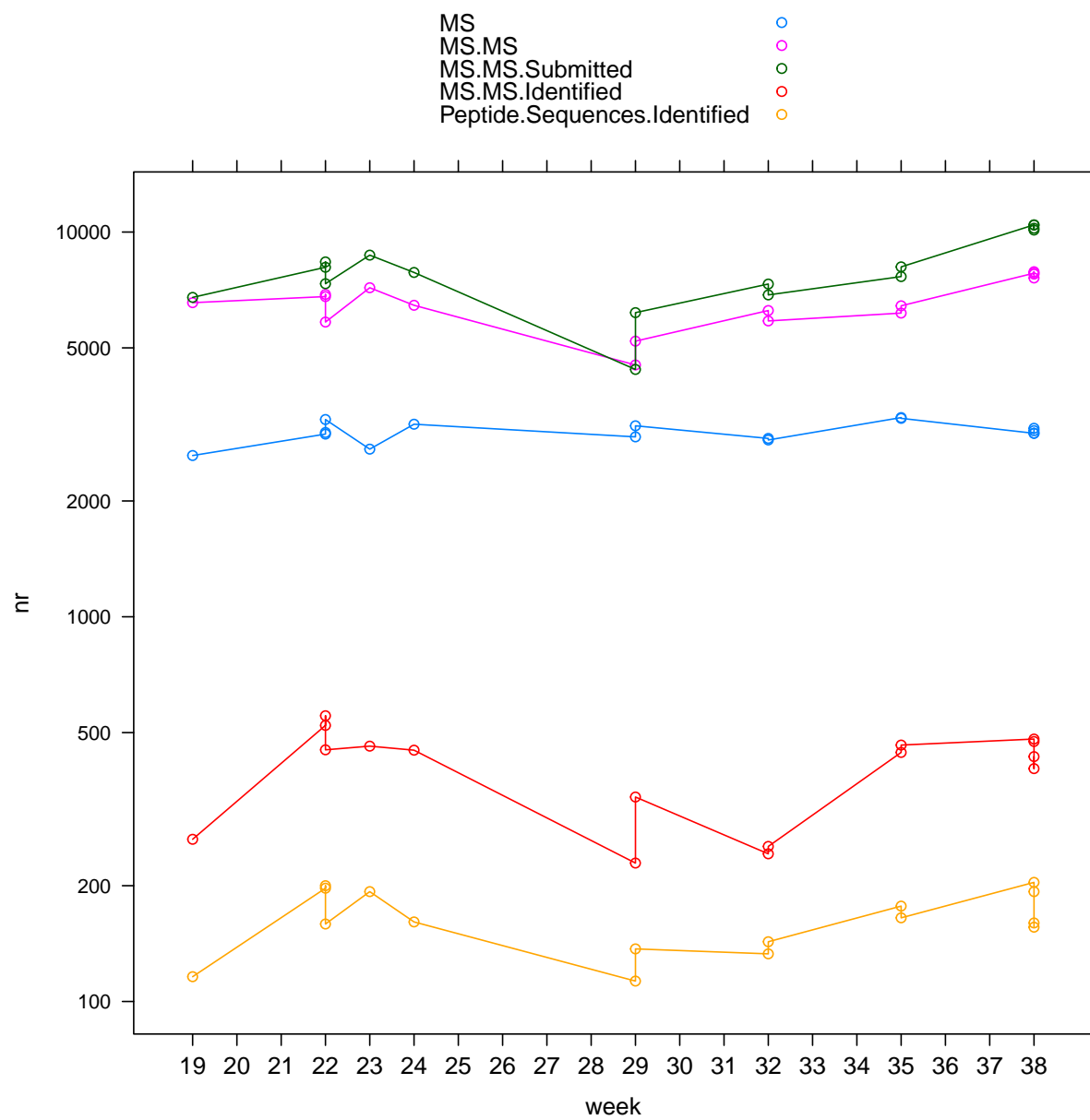
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Prepare mrm table

- nr of assigned spectra (MS2) / versus total spectra
- How many H/L target peptides are identified
- Ratio among H/L of the target peptides
- Intensity of heavy or light over the runs

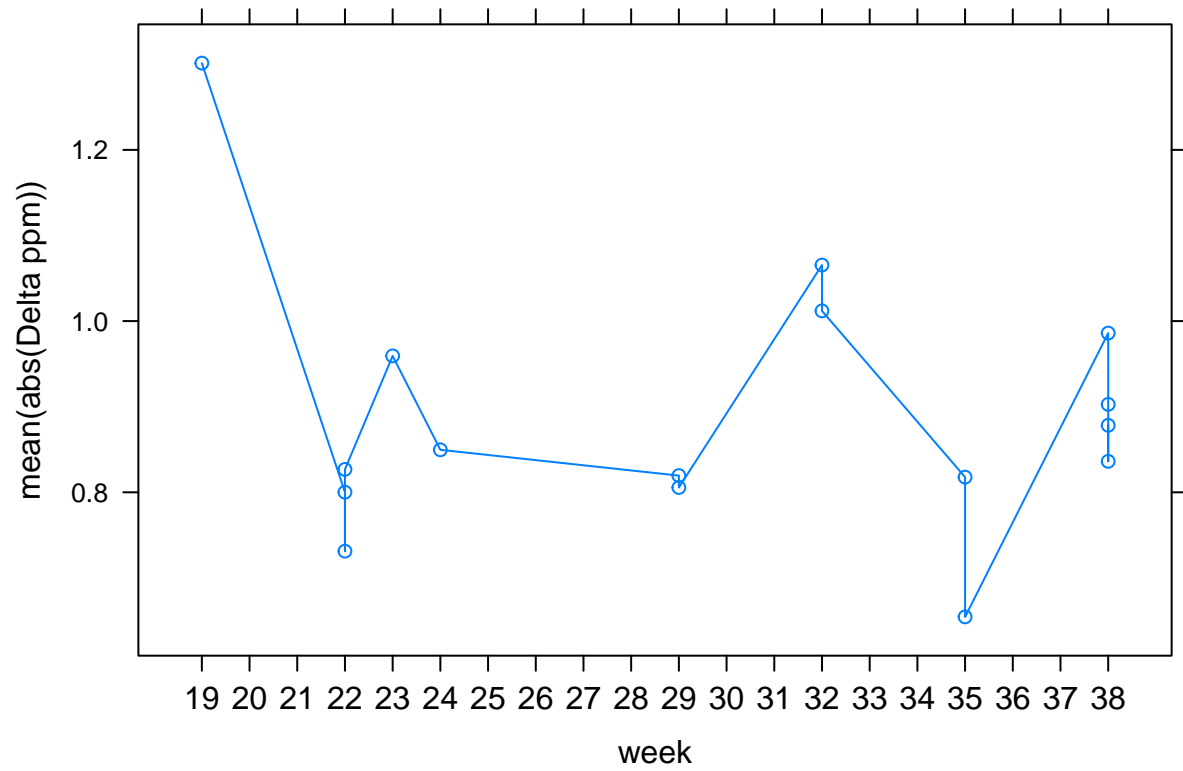
Dump maxquant txt files into sqlite database

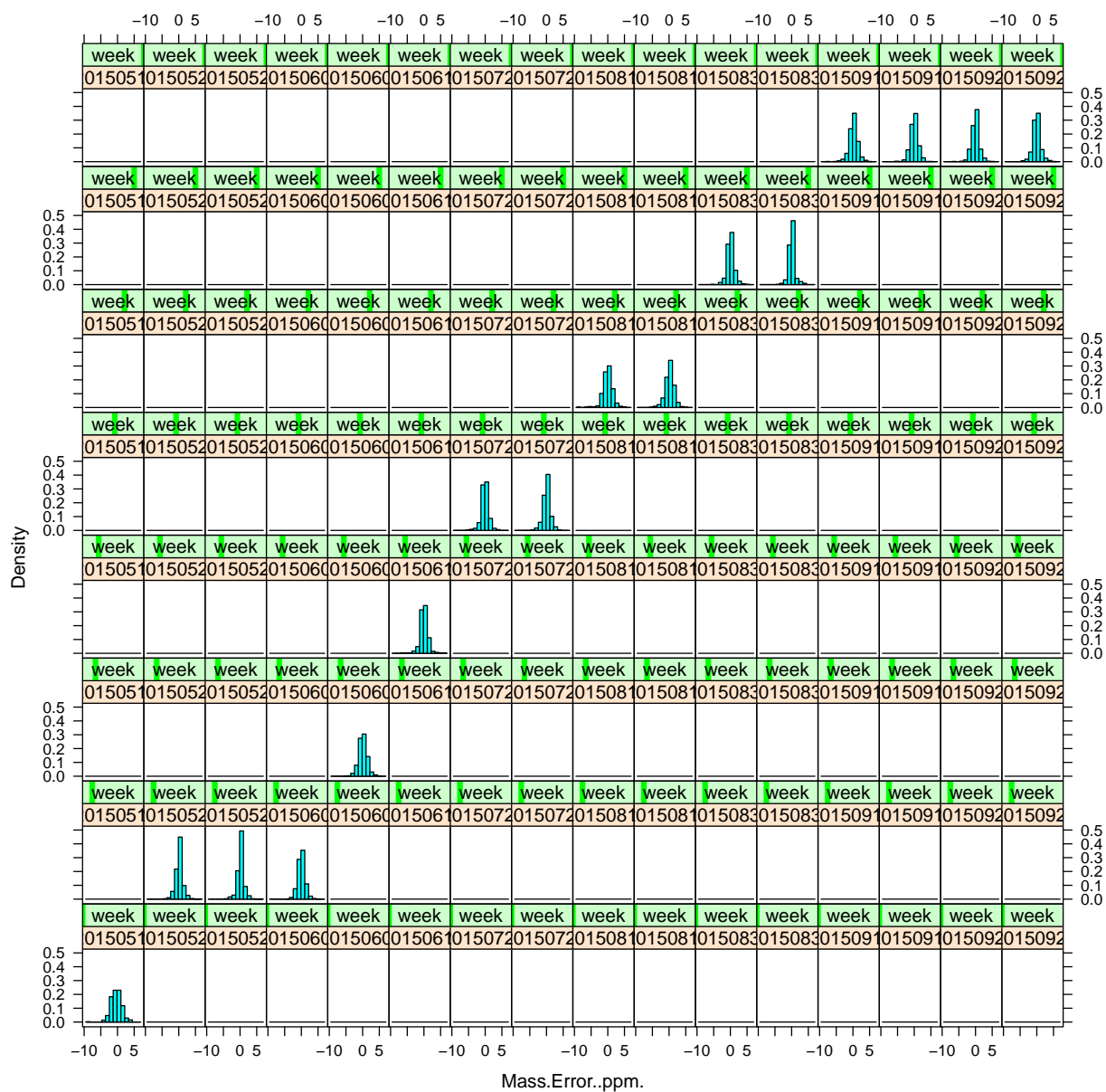
Take a look at the summary table



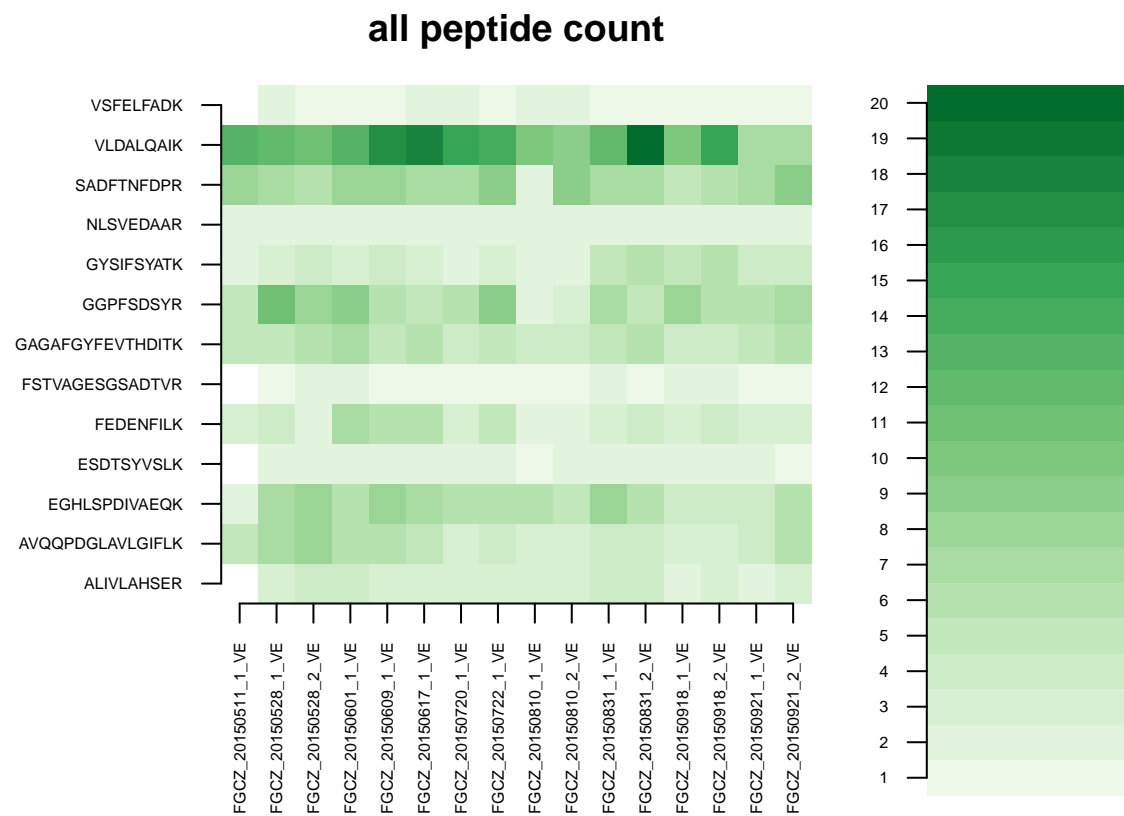
Peptide Evidence

Looking at measurement error

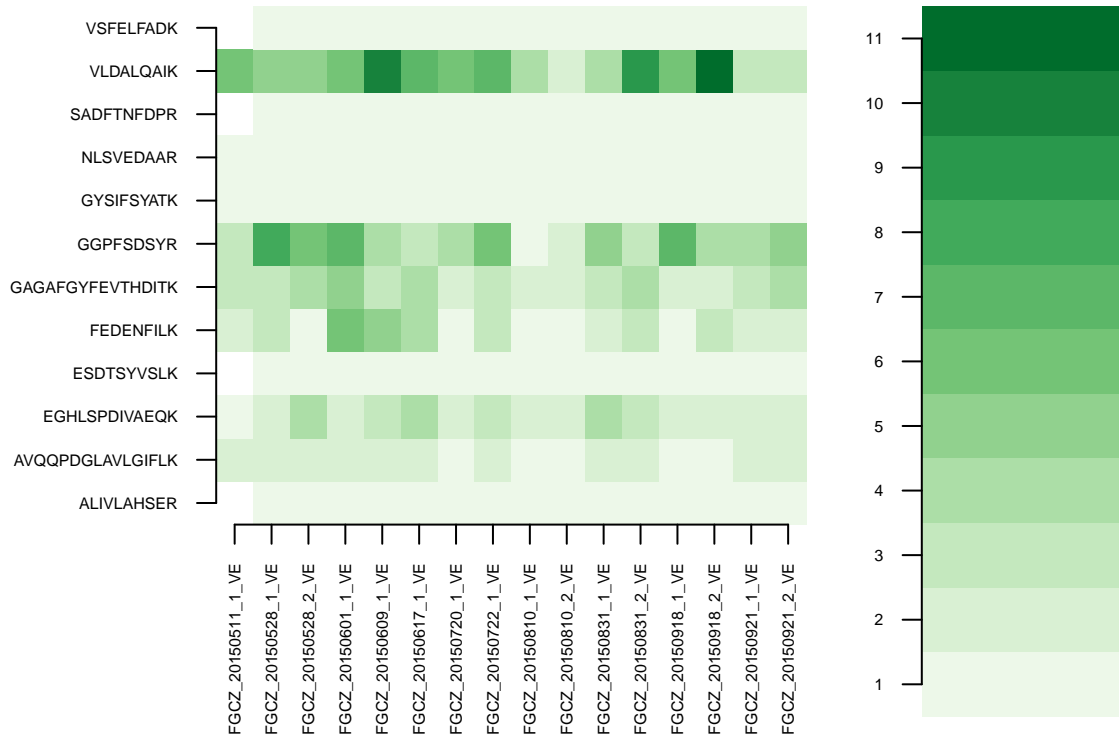




Looking at fold changes



labeled peptide count



not labeled peptide count

