

Analysing MaxQuant Output with R

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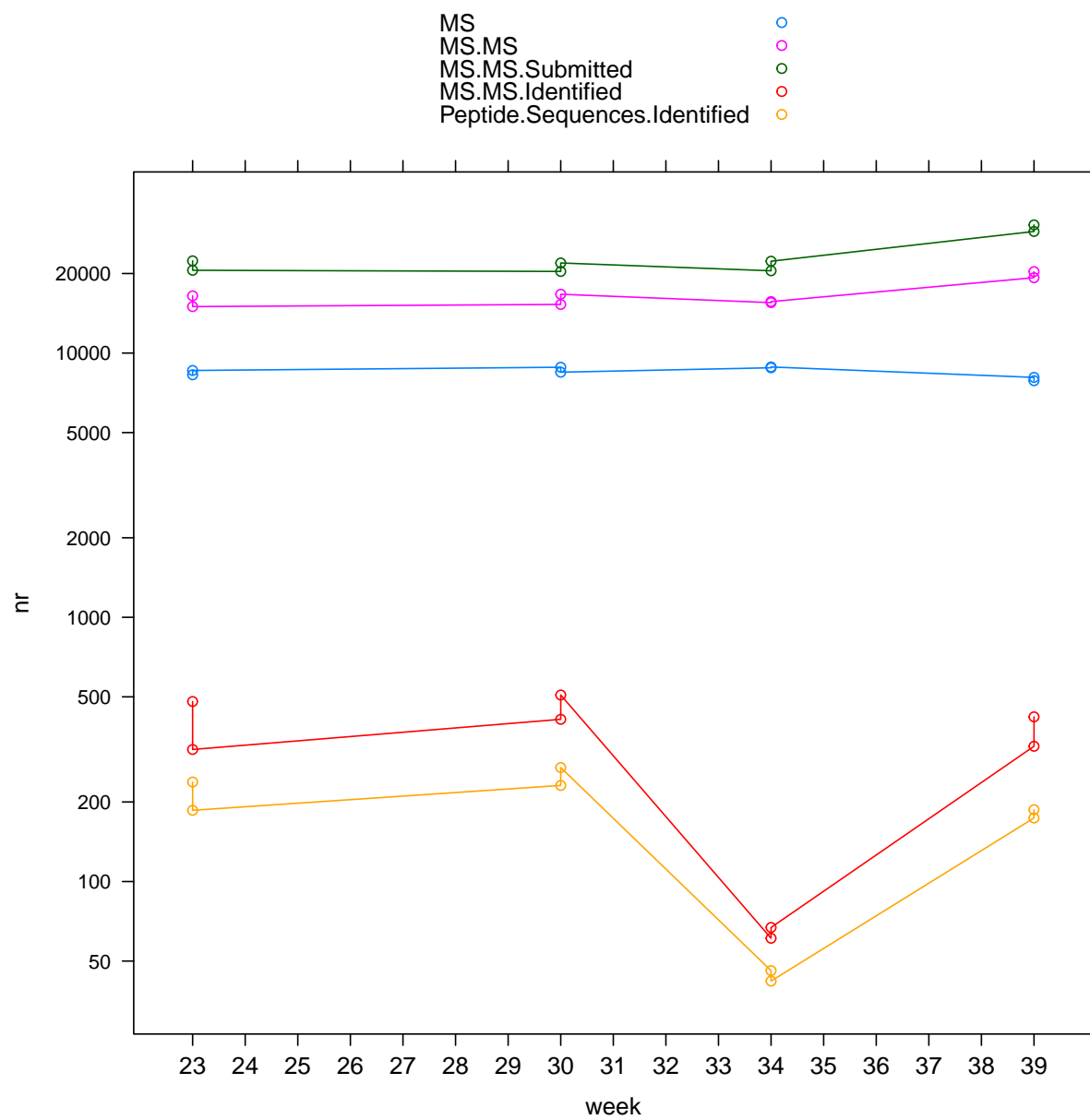
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Prepare mrm table

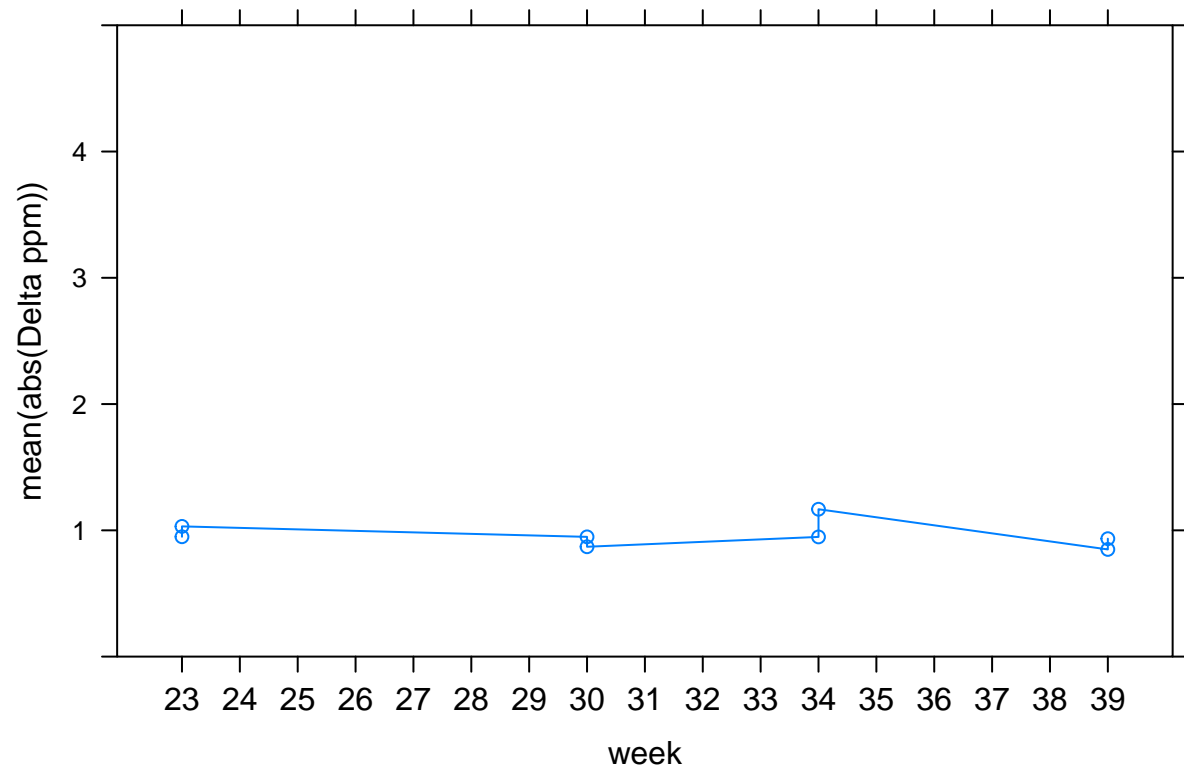
- nr of assigned spectra (MS2) / versus total spectra
- How many H/L target peptides are identified
- Ratio among H/L of the target peptides
- Intensity of heavy or light over the runs

Analysed Dataset is evytimmerman_20150929.sqlite3

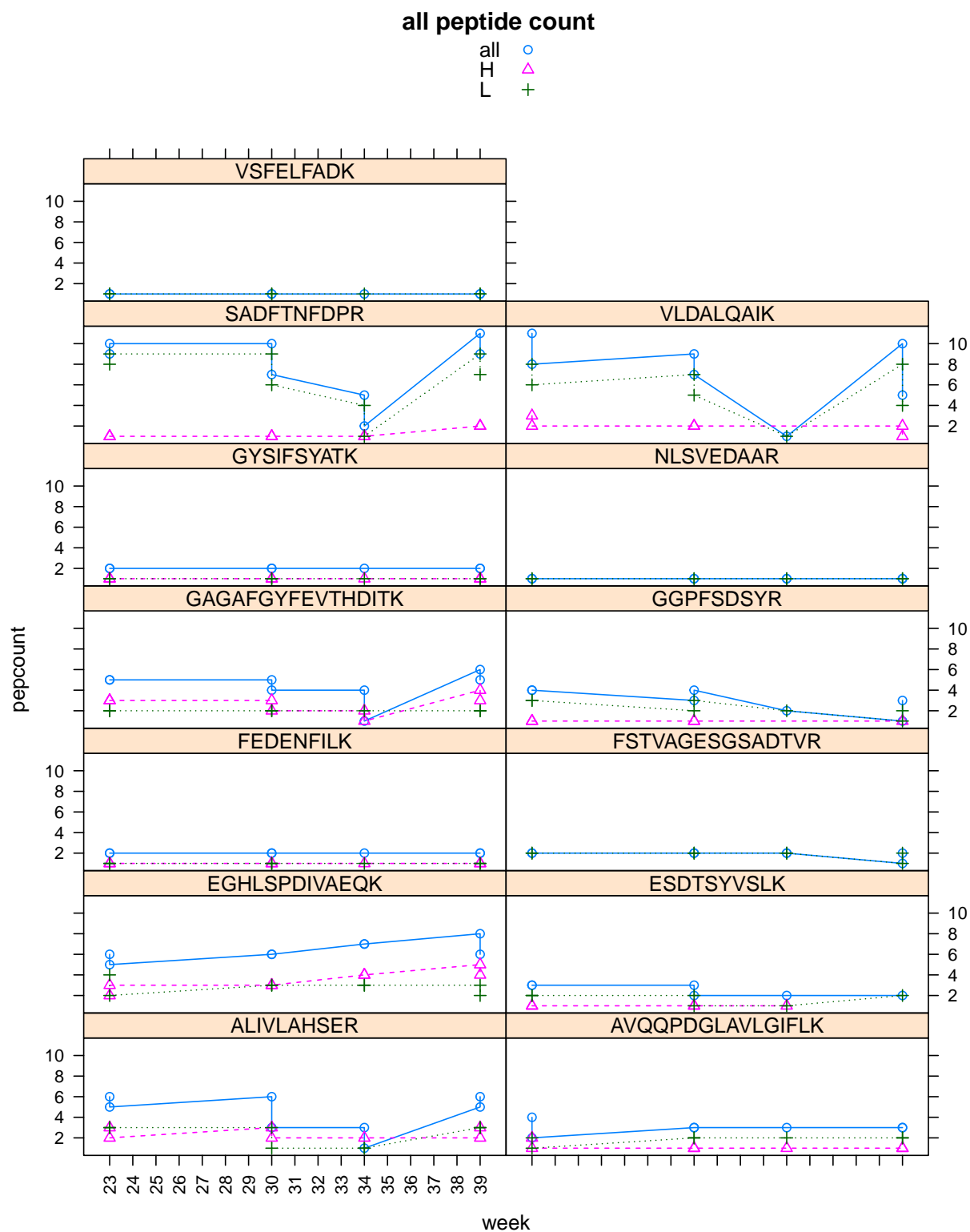
Number of spectra, spectra peptide matches, and unique peptides



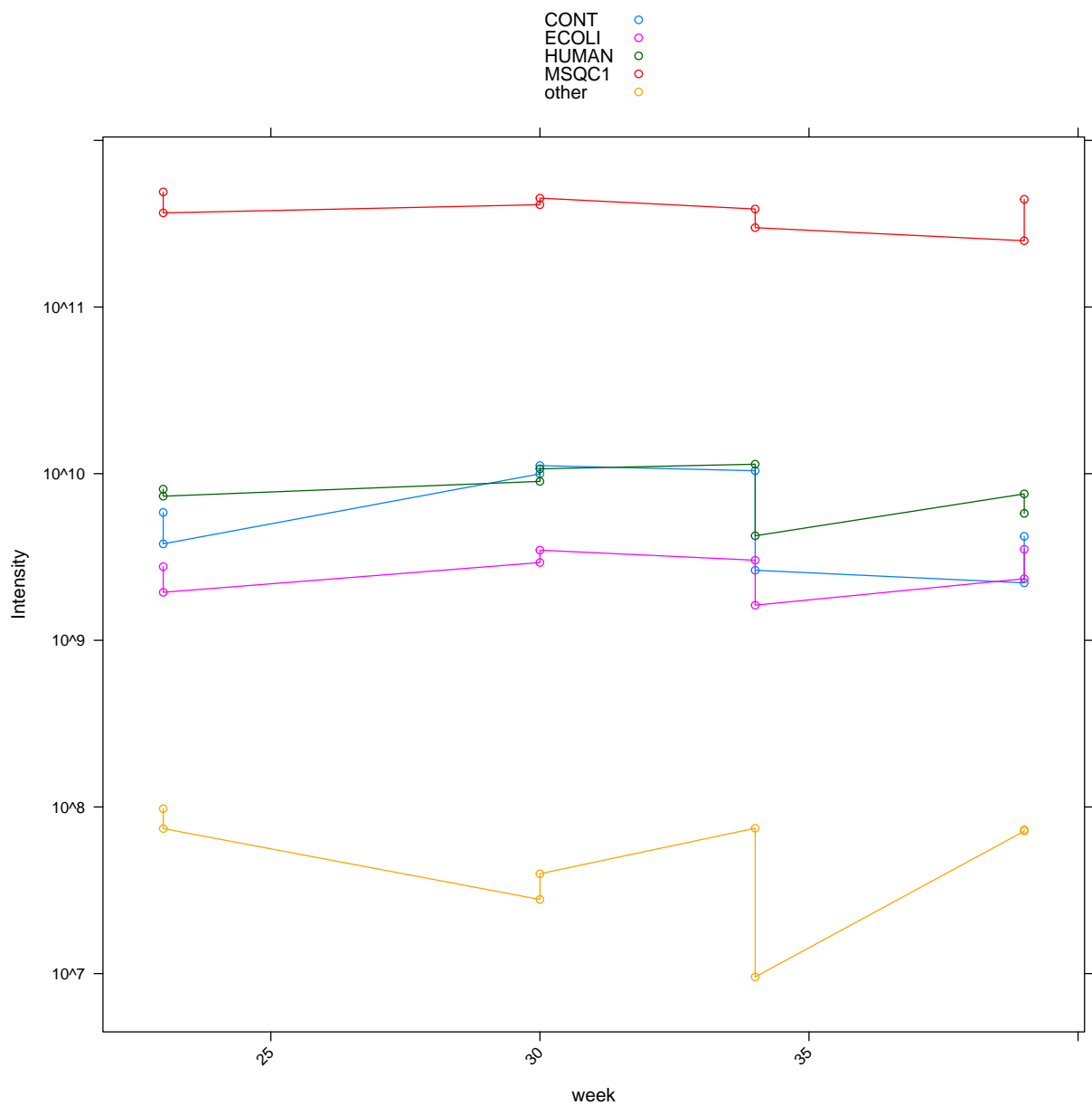
Looking at measurement error



Looking at MSQC 1 peptide counts

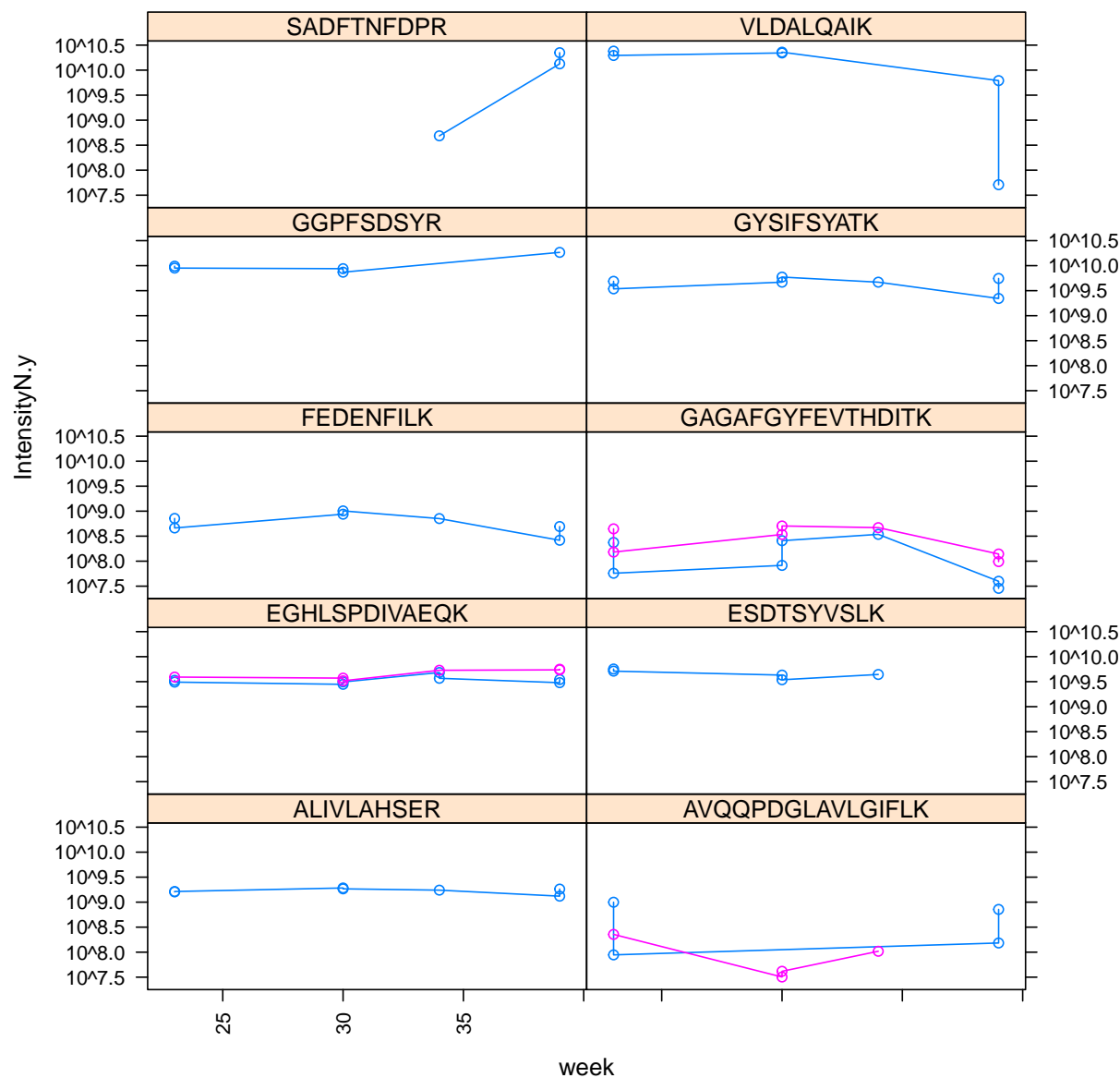


Look at Intensities (by species)



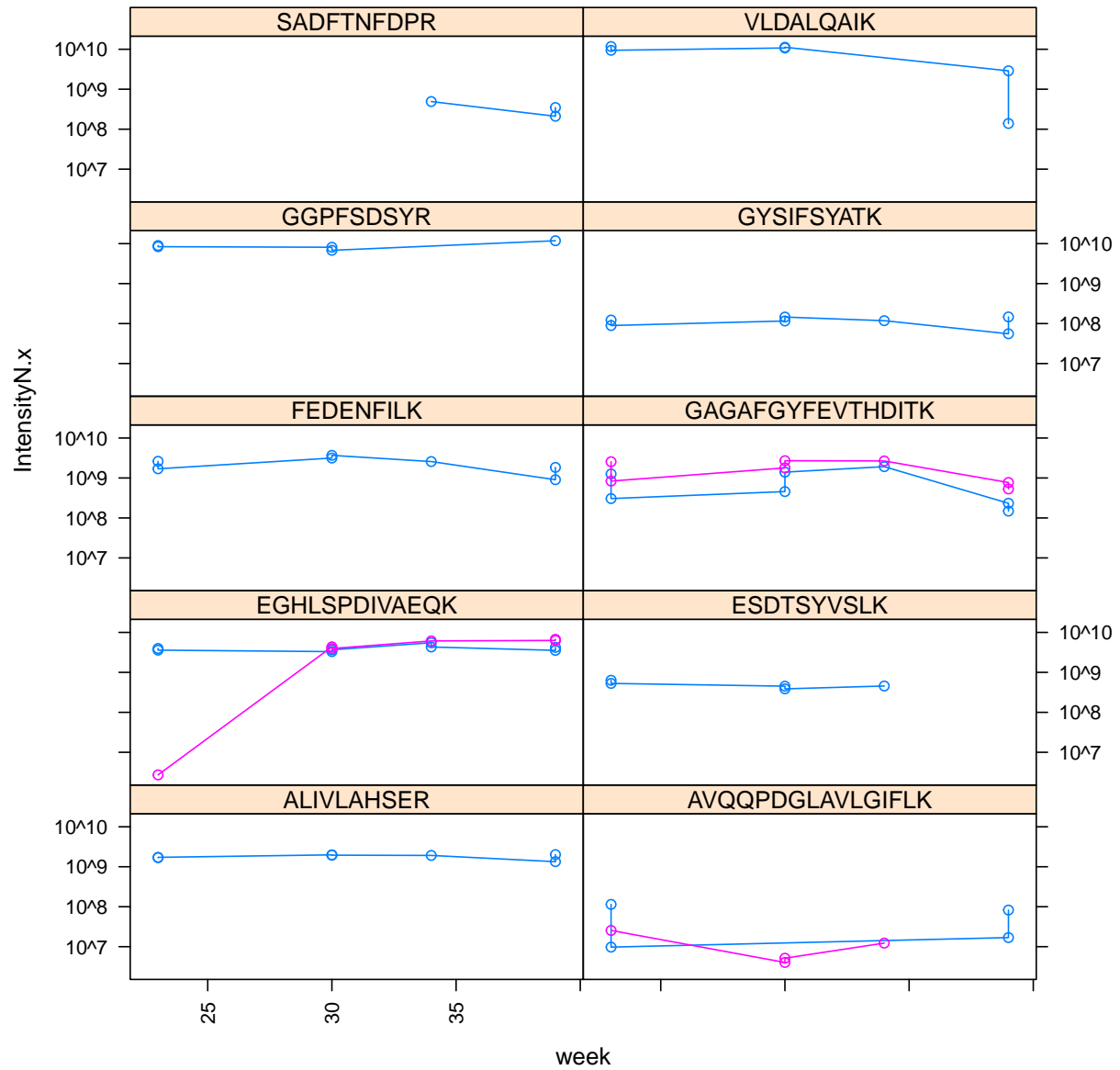
Looking at intensities msqc1

light
2 ○
3 ○



heavy

2 ○
3 ○



Fold change

H/L
2 ○
3 ○

