

# Analysing MaxQuant Output with R

*FGC Zurich*

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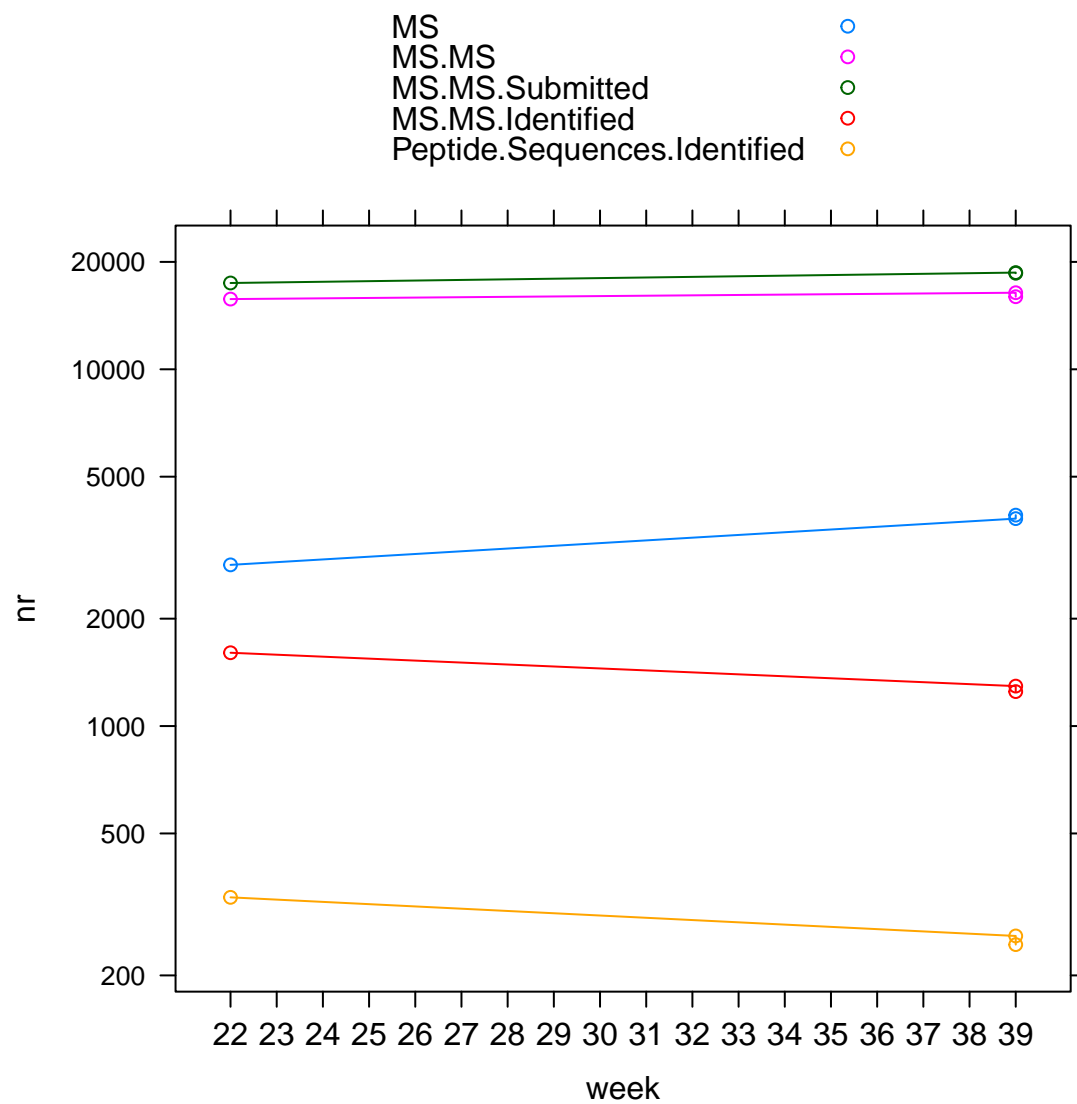
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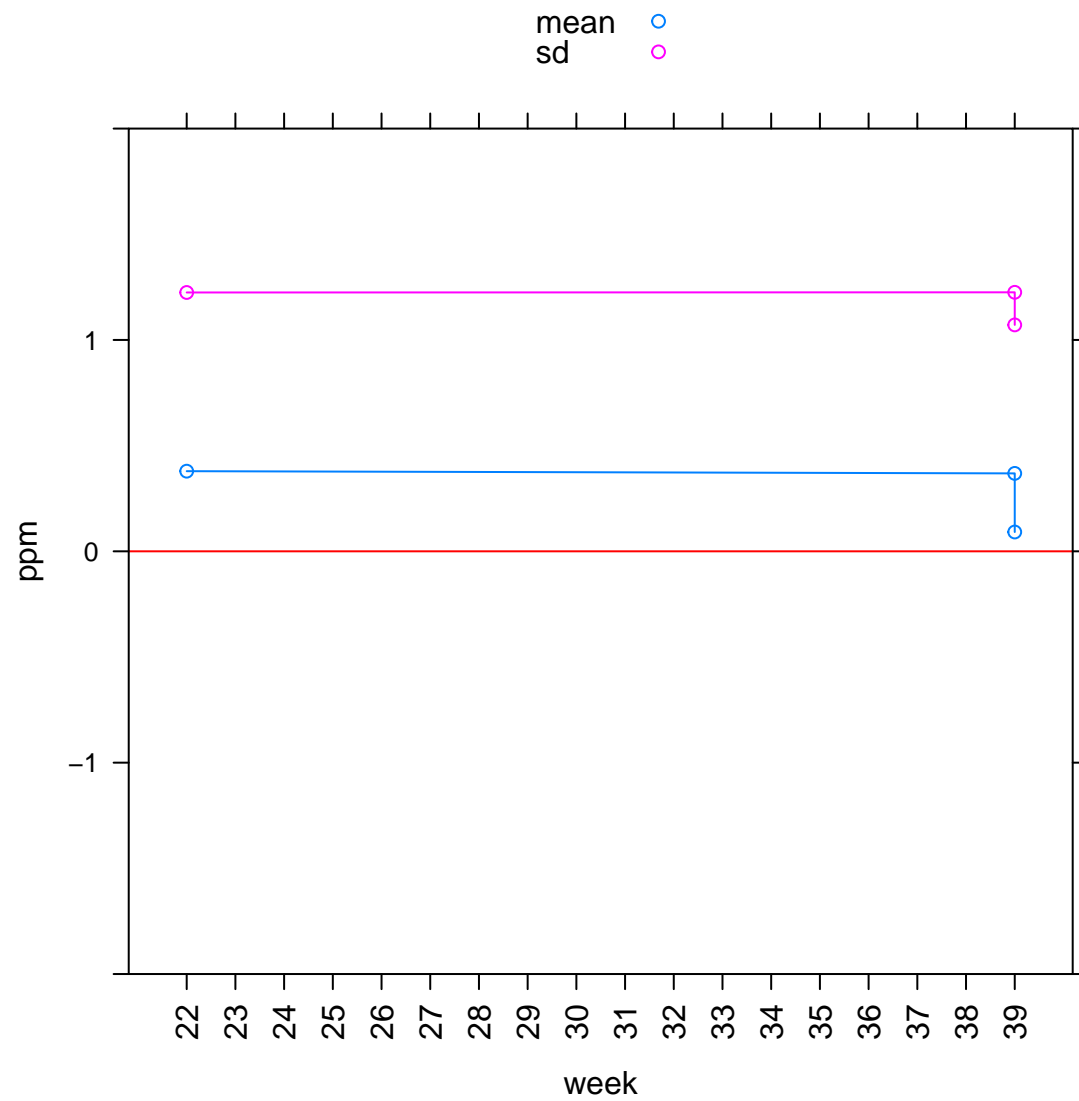
## Prepare mrm table

- 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

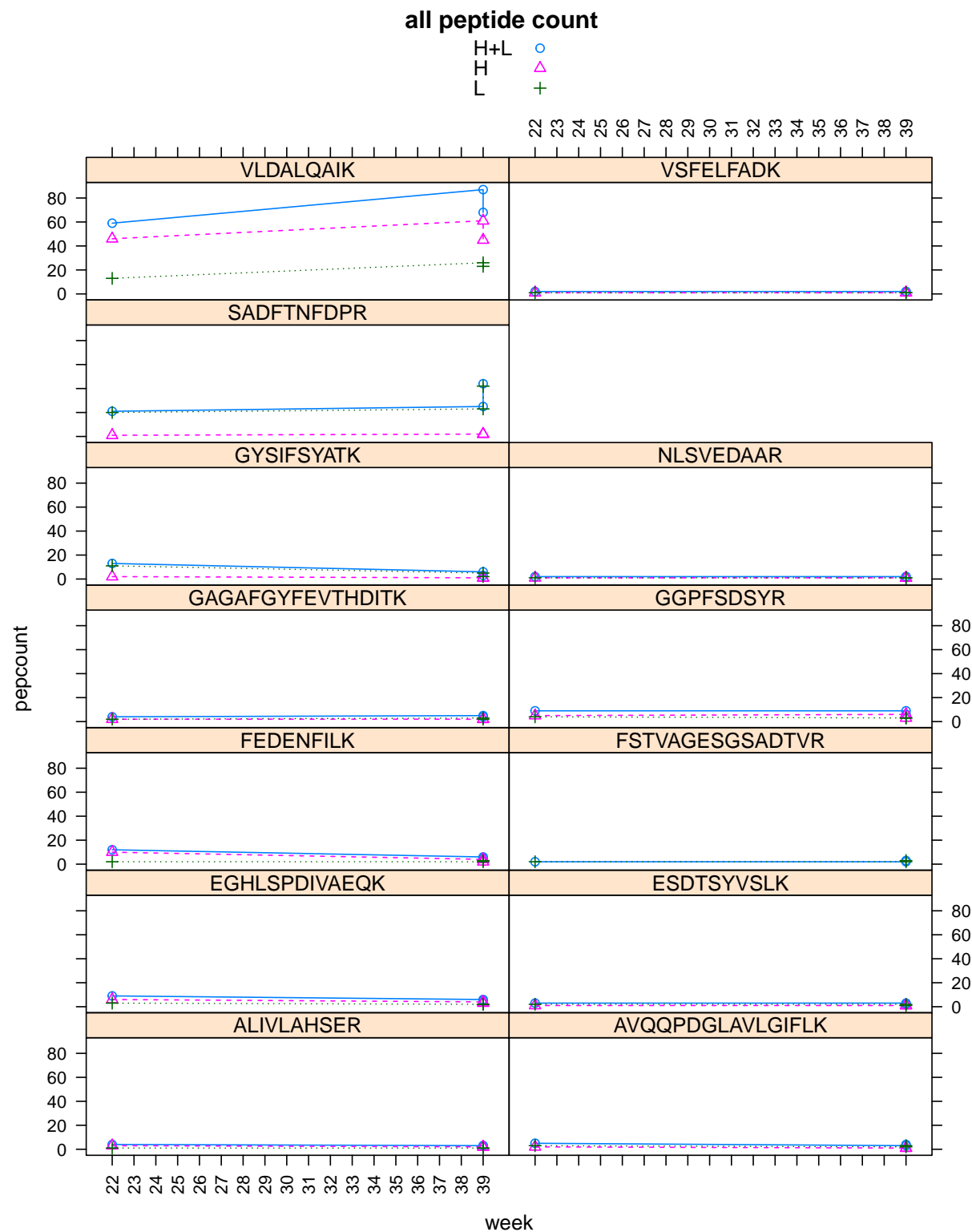
## Analysed Dataset is IMP\_DIV



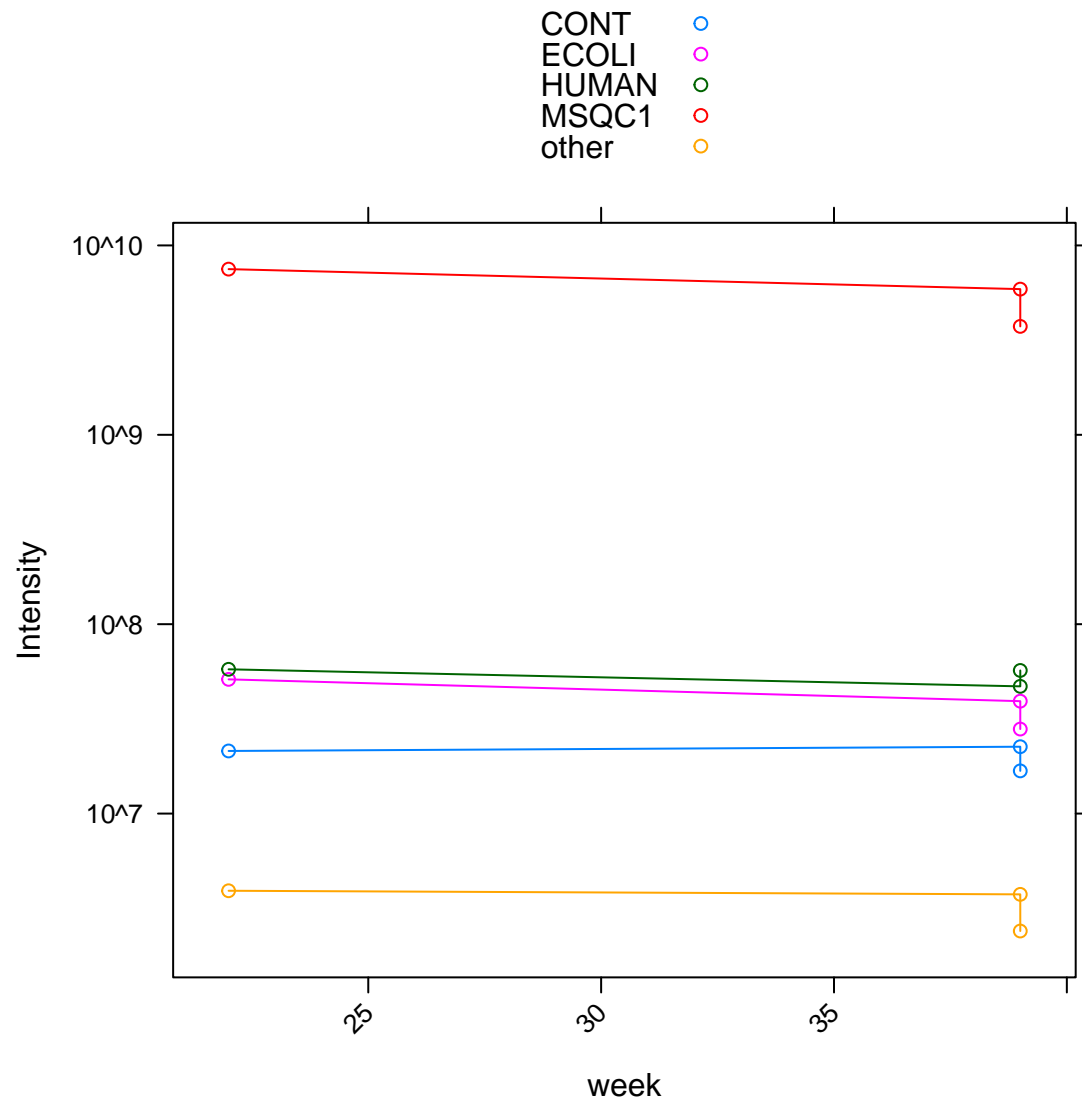
## Looking at measurement error



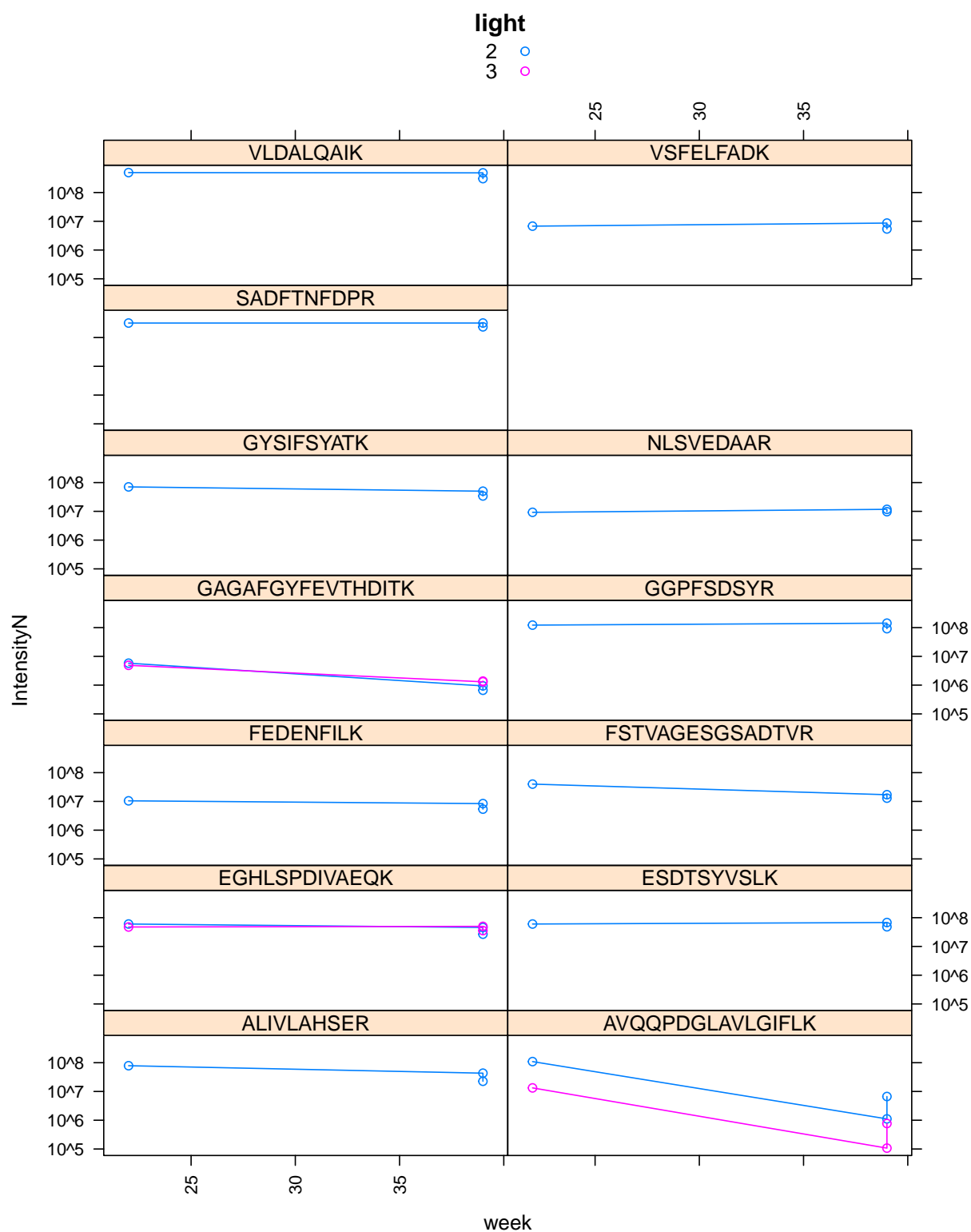
Looking at MSQC 1 peptide counts

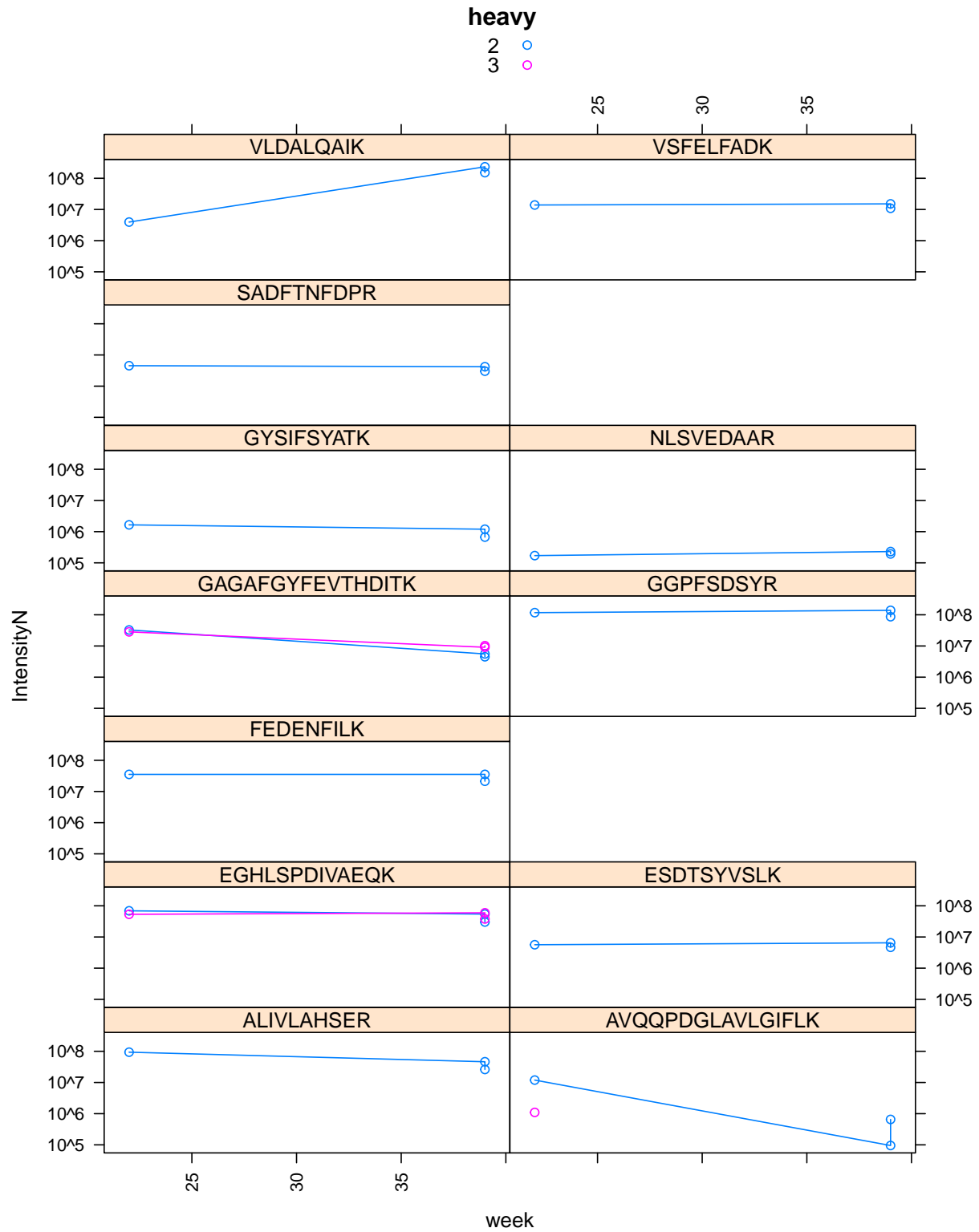


## Look at Intensities (by species)

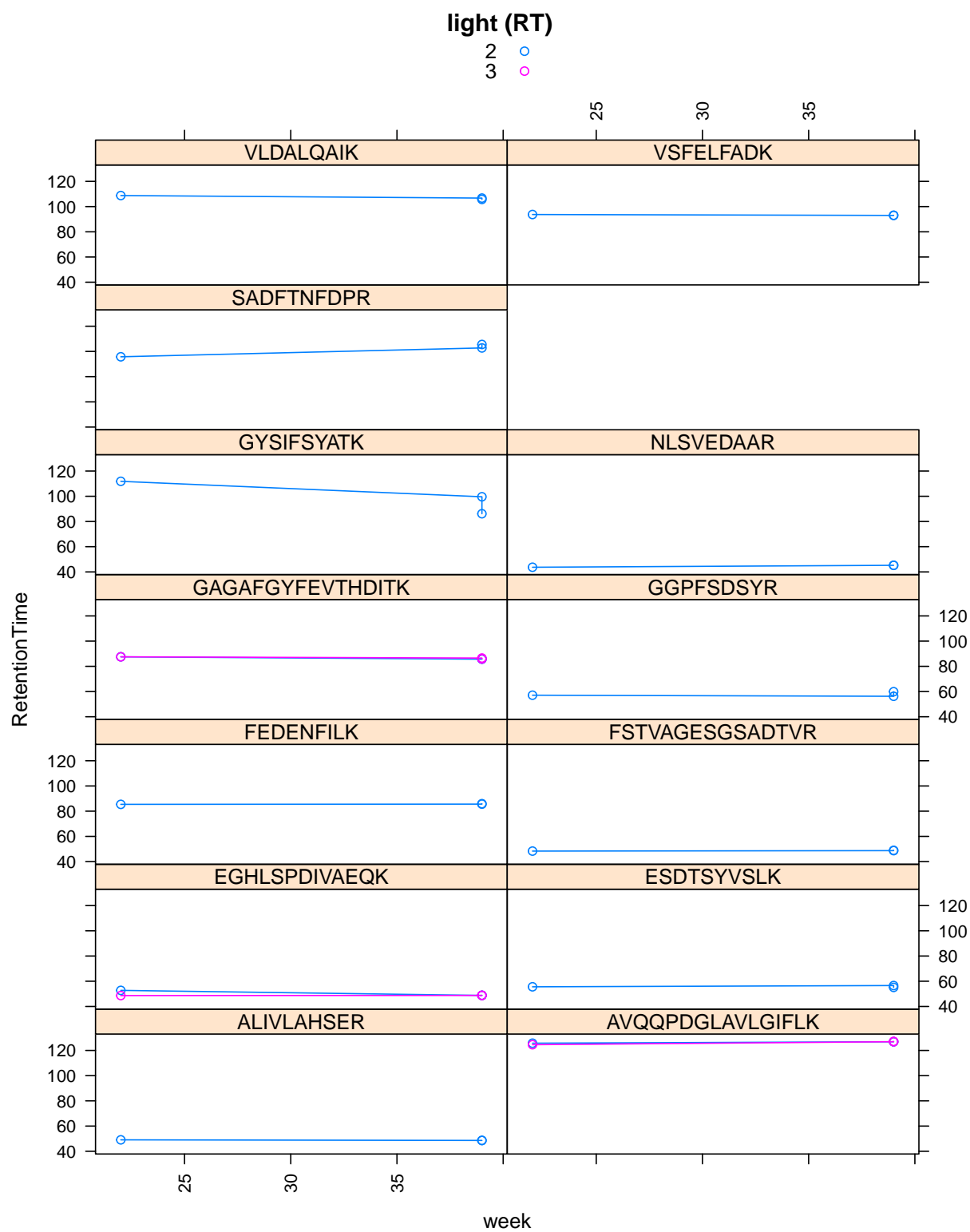


# Looking at intensities msqc1

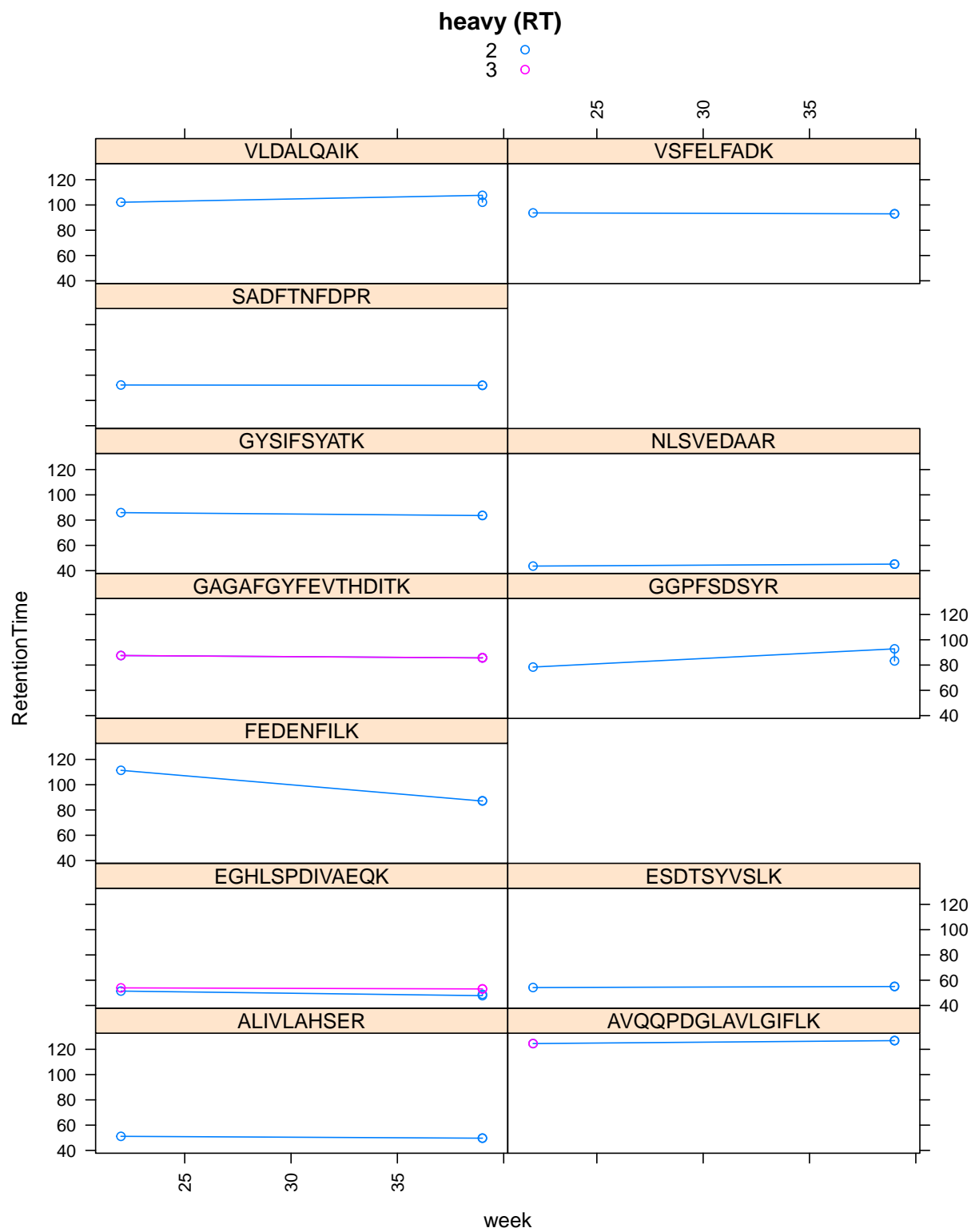




## Looking at retention time







## Log fold change

```
## Warning in inner_join_impl(x, y, by$x, by$y): joining factors with
## different levels, coercing to character vector
```

