

# Analysing MaxQuant Output with R

*FGC Zurich*

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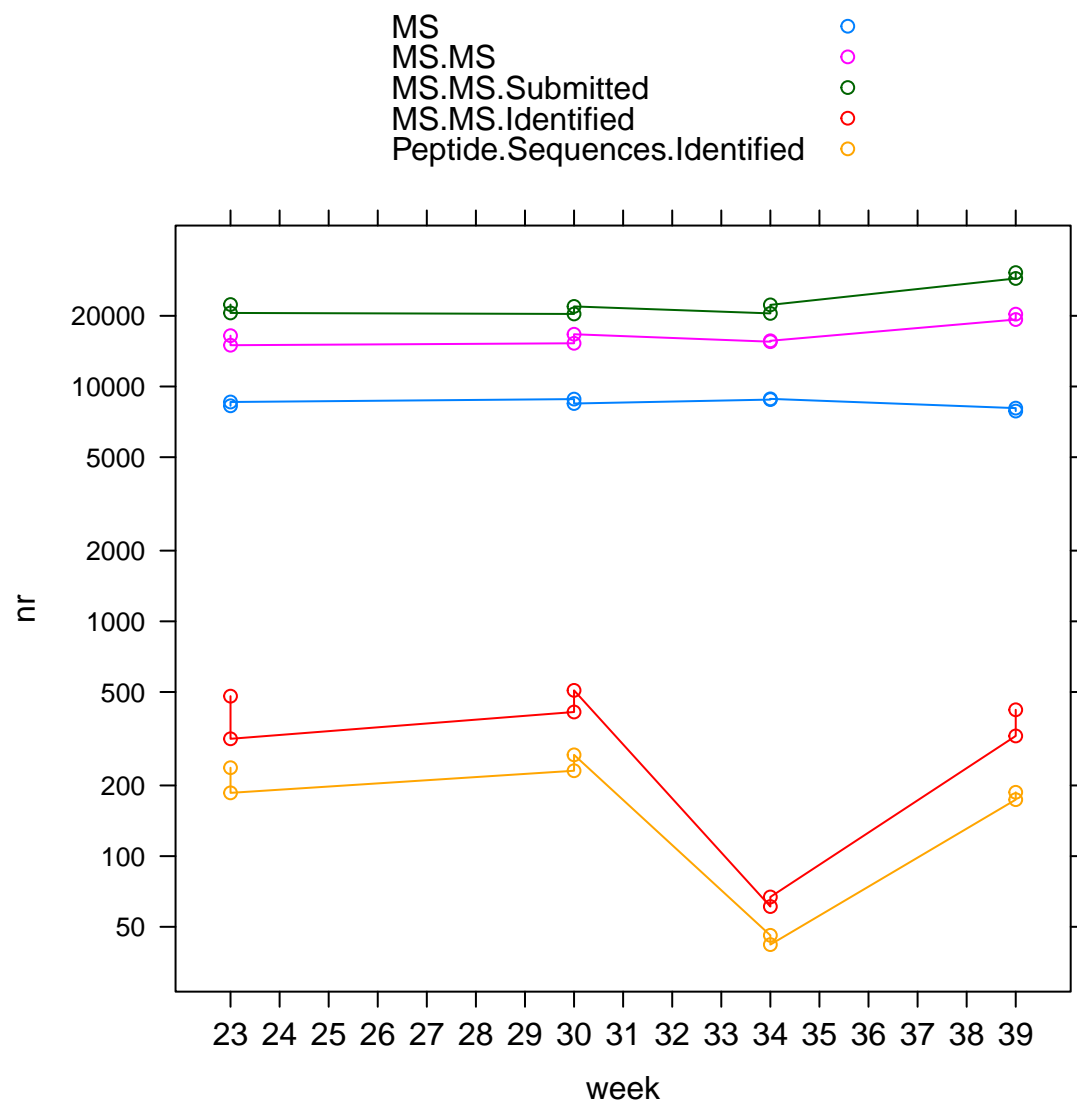
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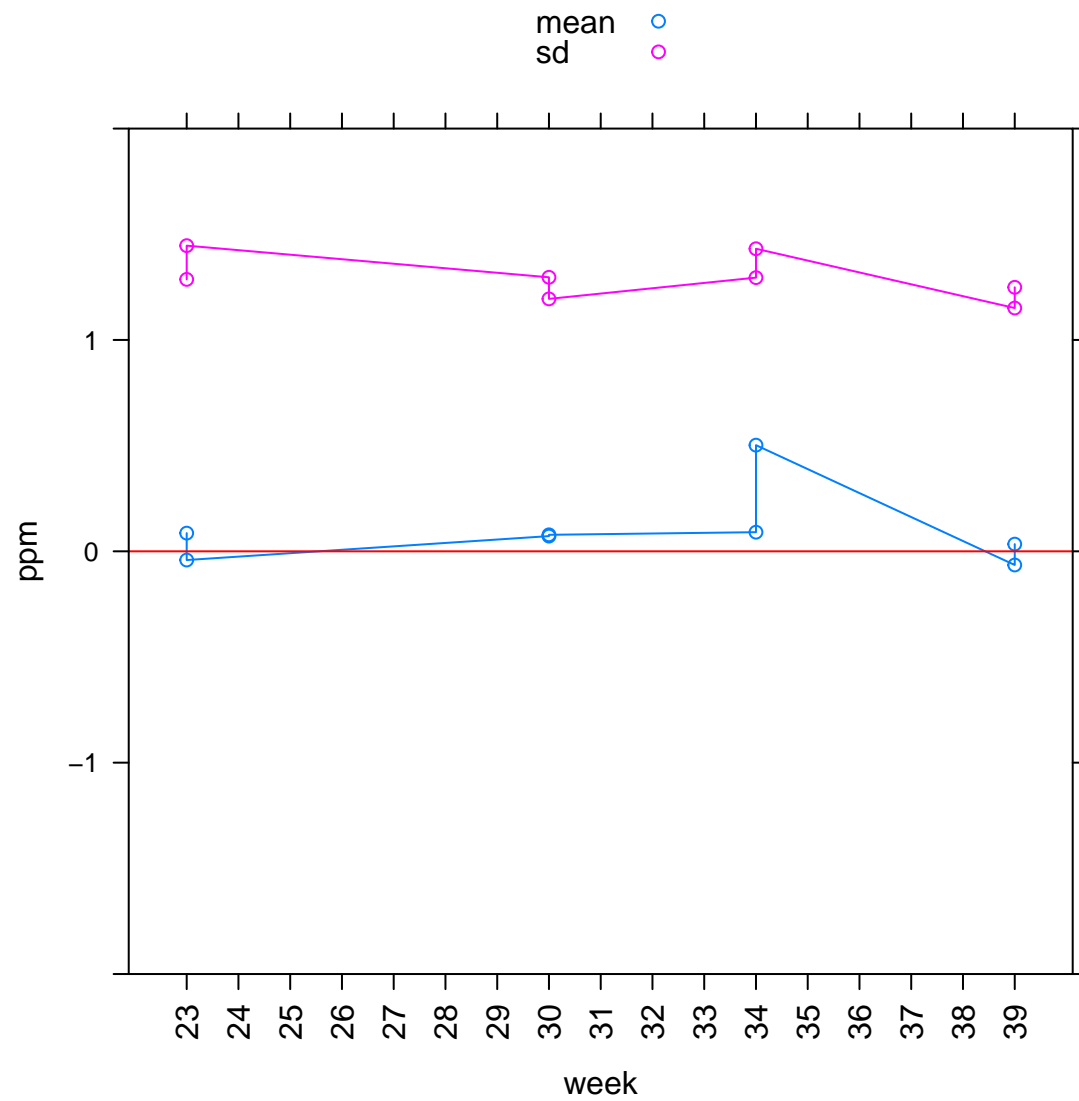
## Prepare mrm table

- 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

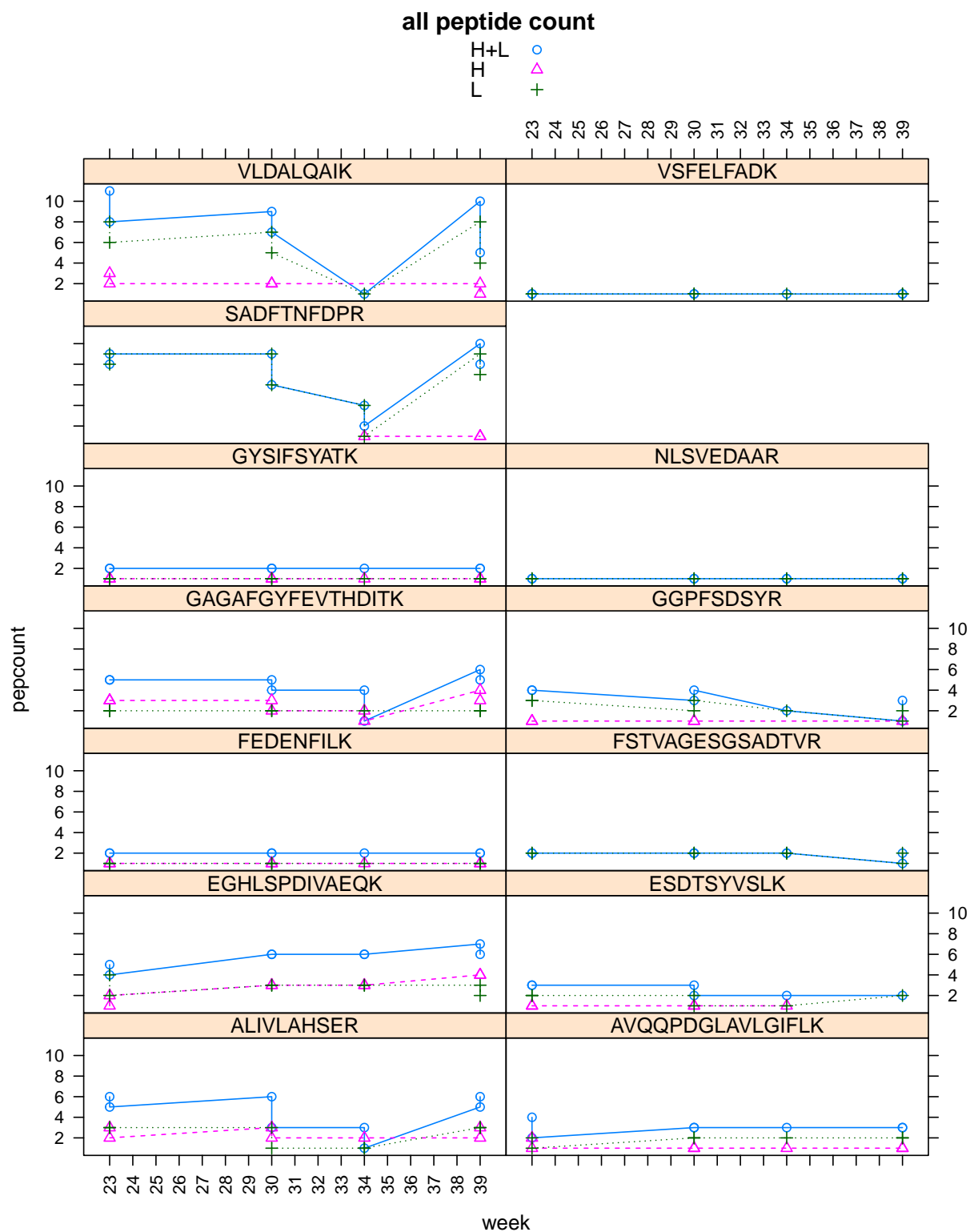
## Analysed Dataset is VIB\_QE



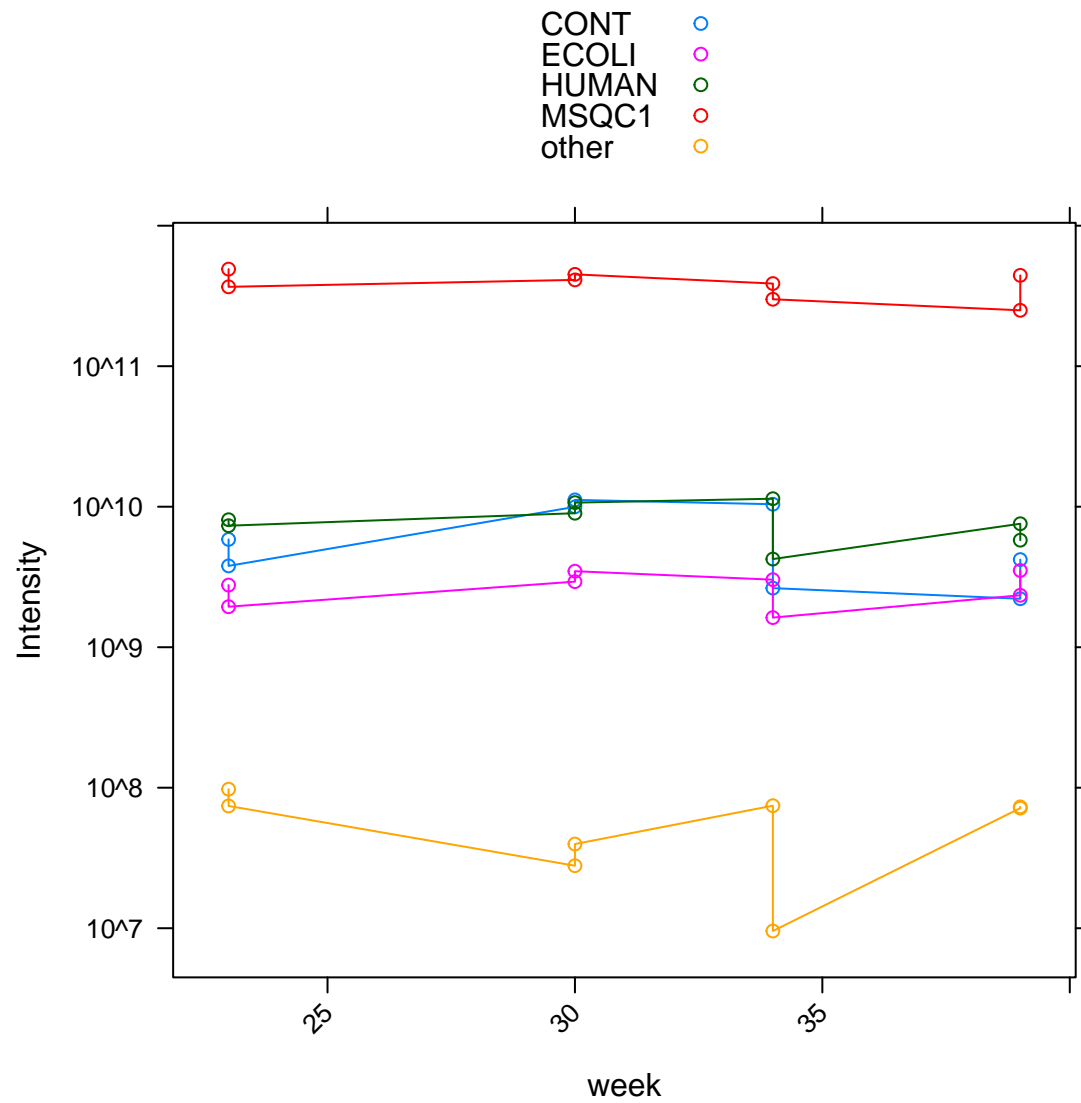
## Looking at measurement error



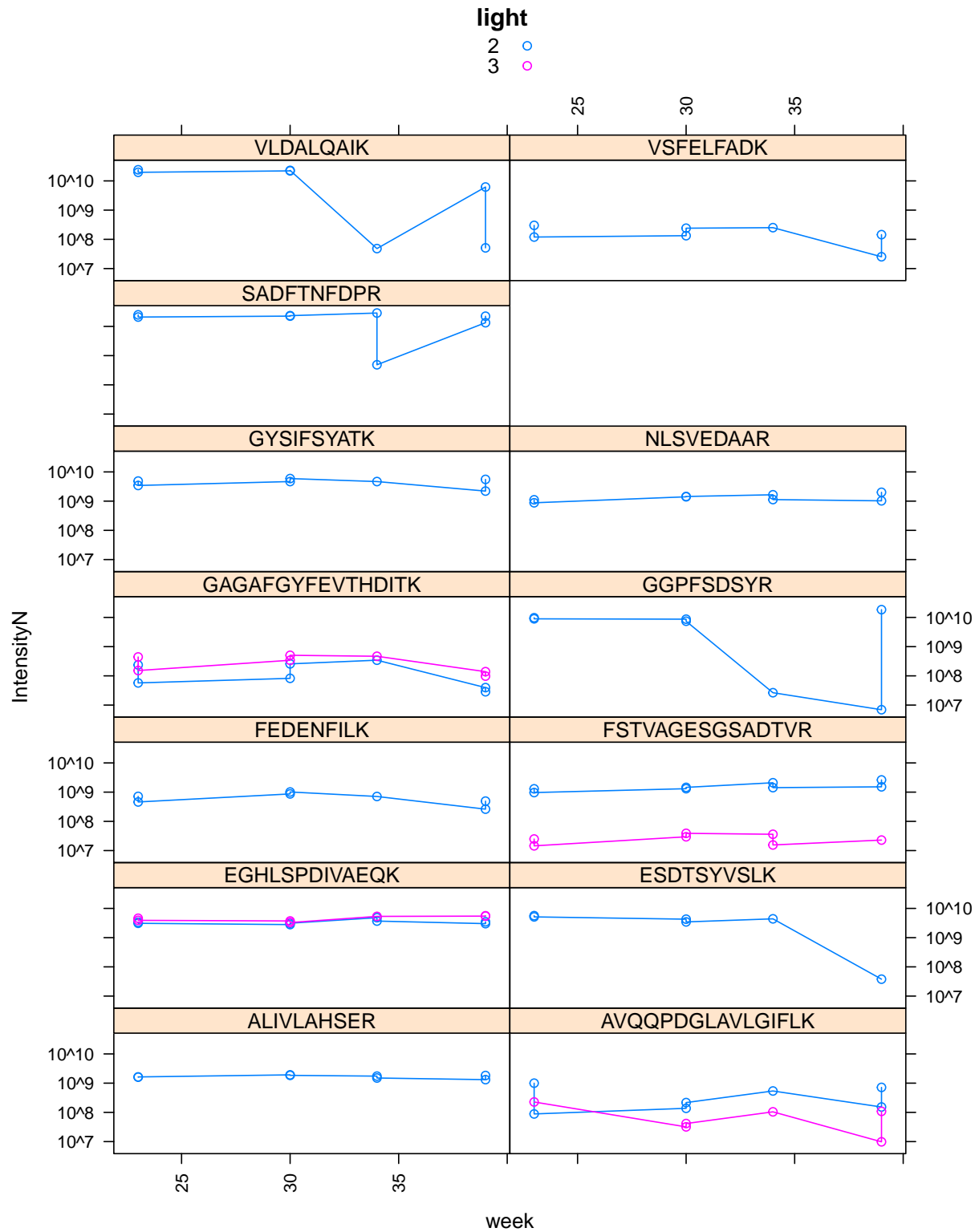
# Looking at MSQC 1 peptide counts



## Look at Intensities (by species)

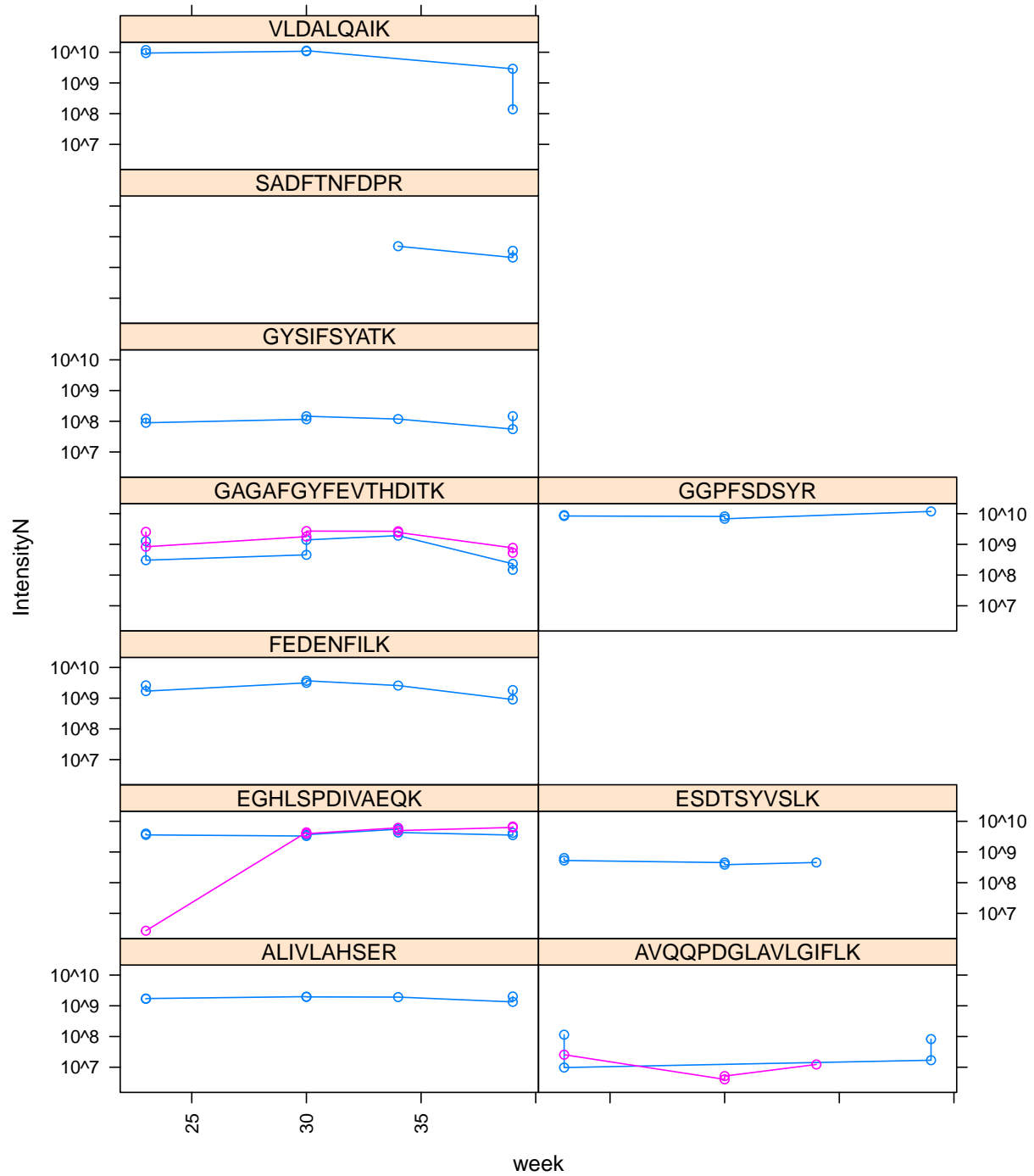


# Looking at intensities msqc1

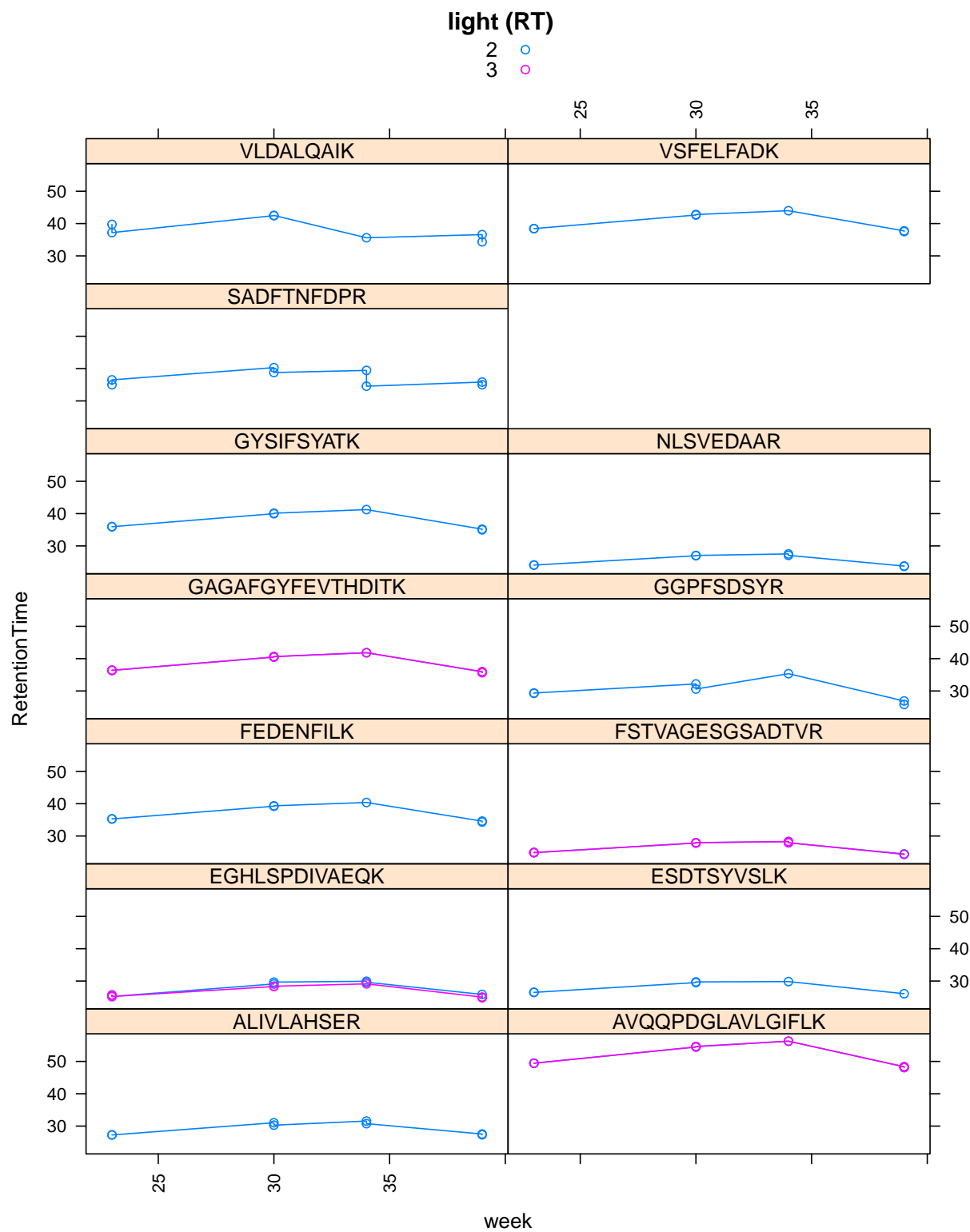


heavy

2 ○  
3 ●



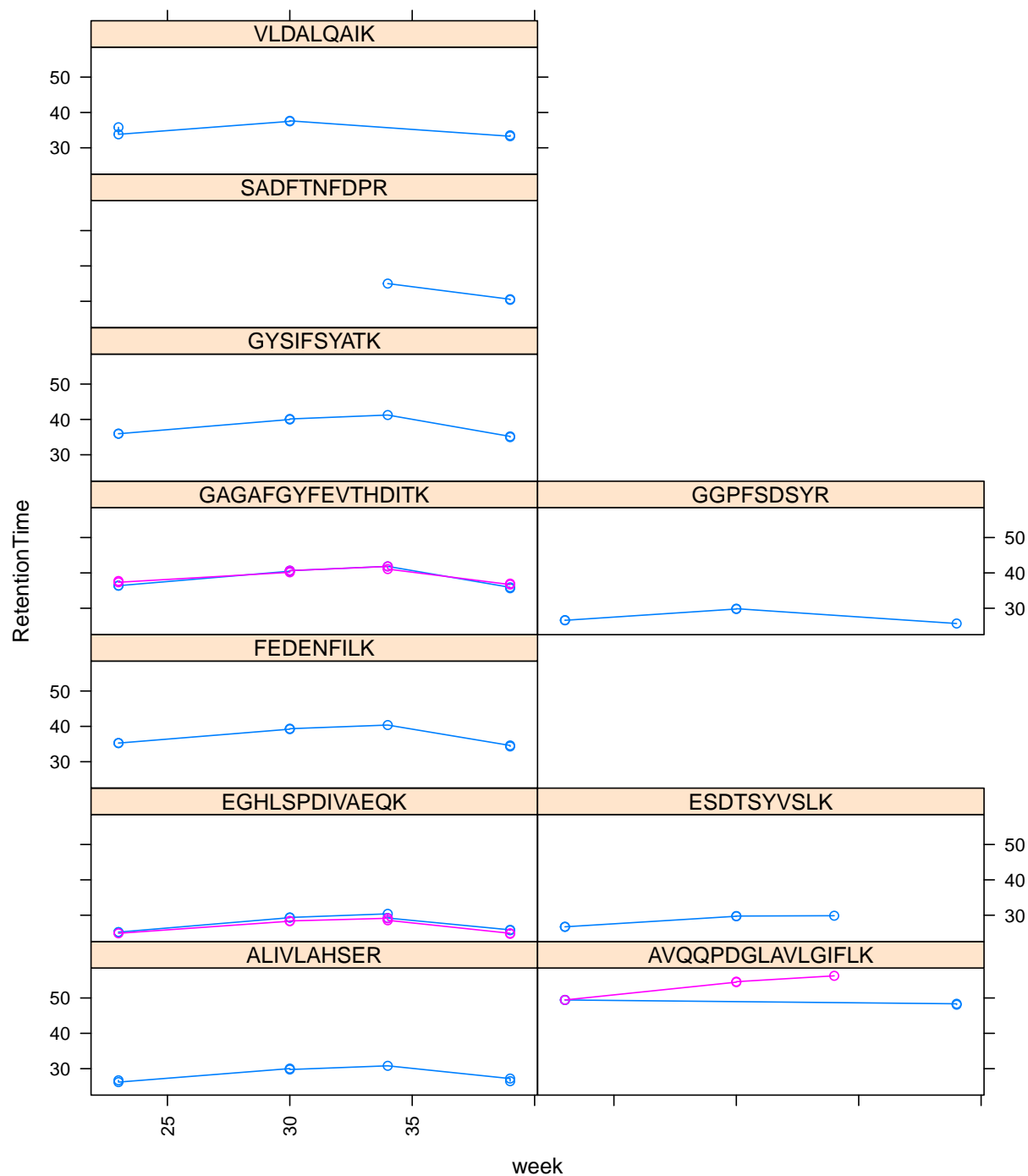
Looking at retention time





heavy (RT)

2 ○  
3 ○



Log fold change

## Warning in inner\_join\_impl(x, y, by\$x, by\$y): joining factors with  
## different levels, coercing to character vector

