Analysing MaxQuant Output with R

FGC Zurich

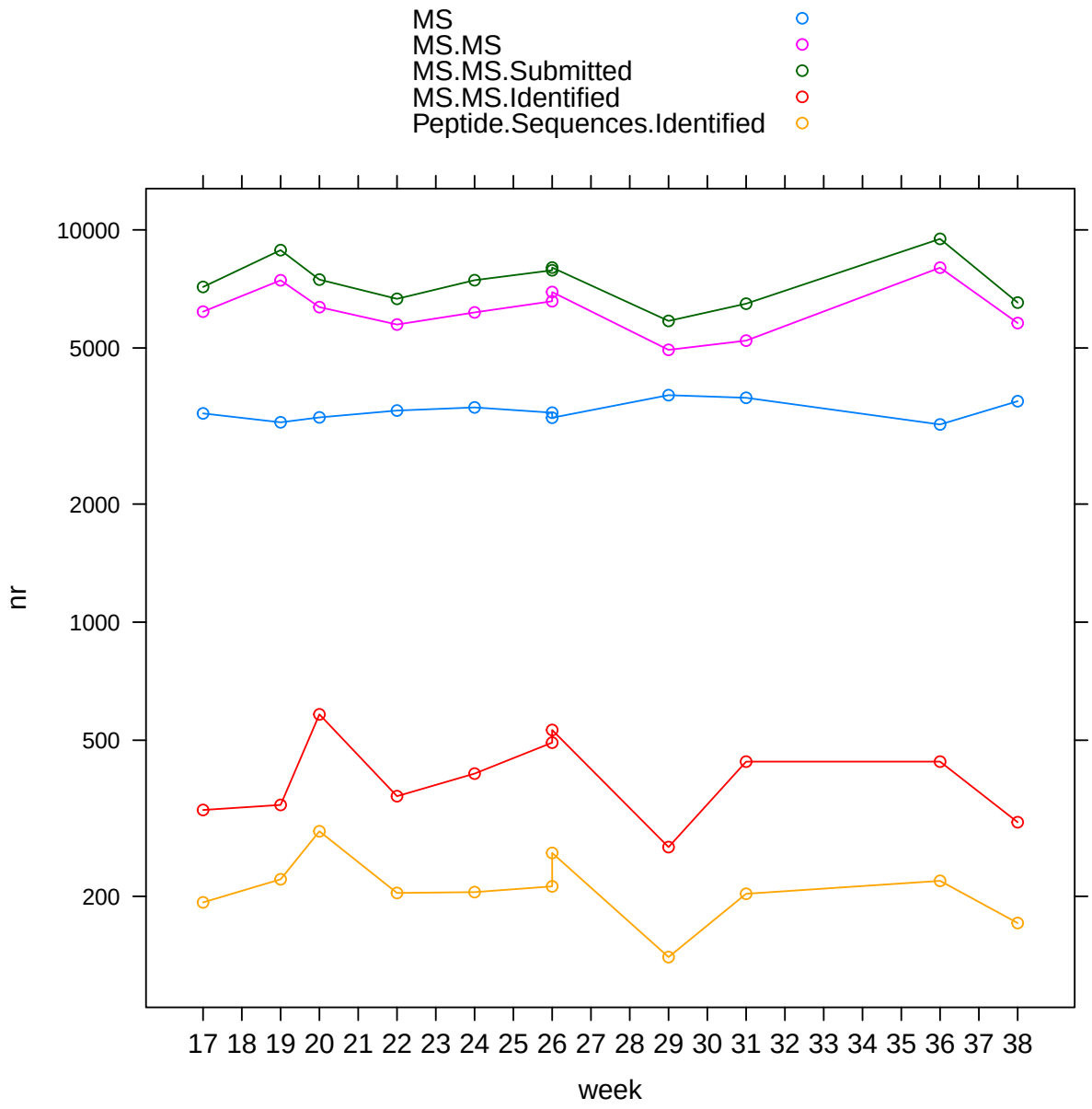
30 September 2015

Contents

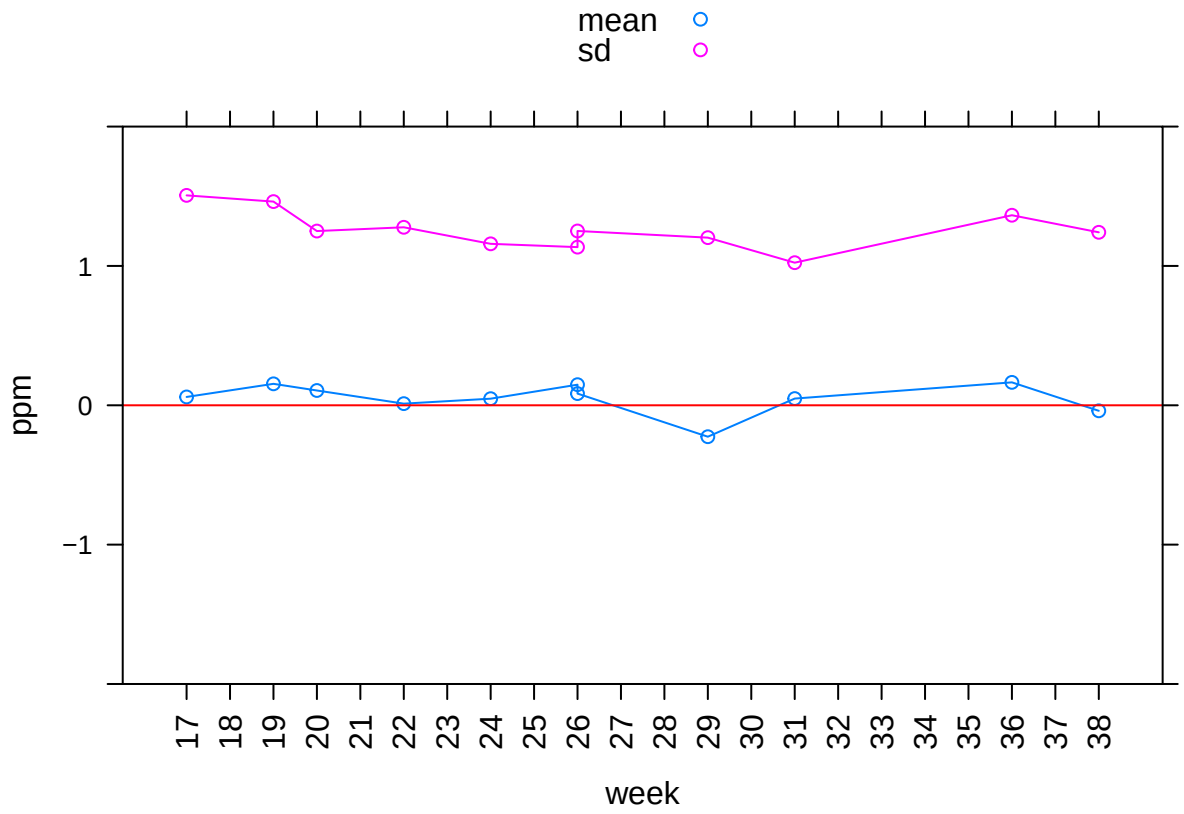
Prepare mrm table

- 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

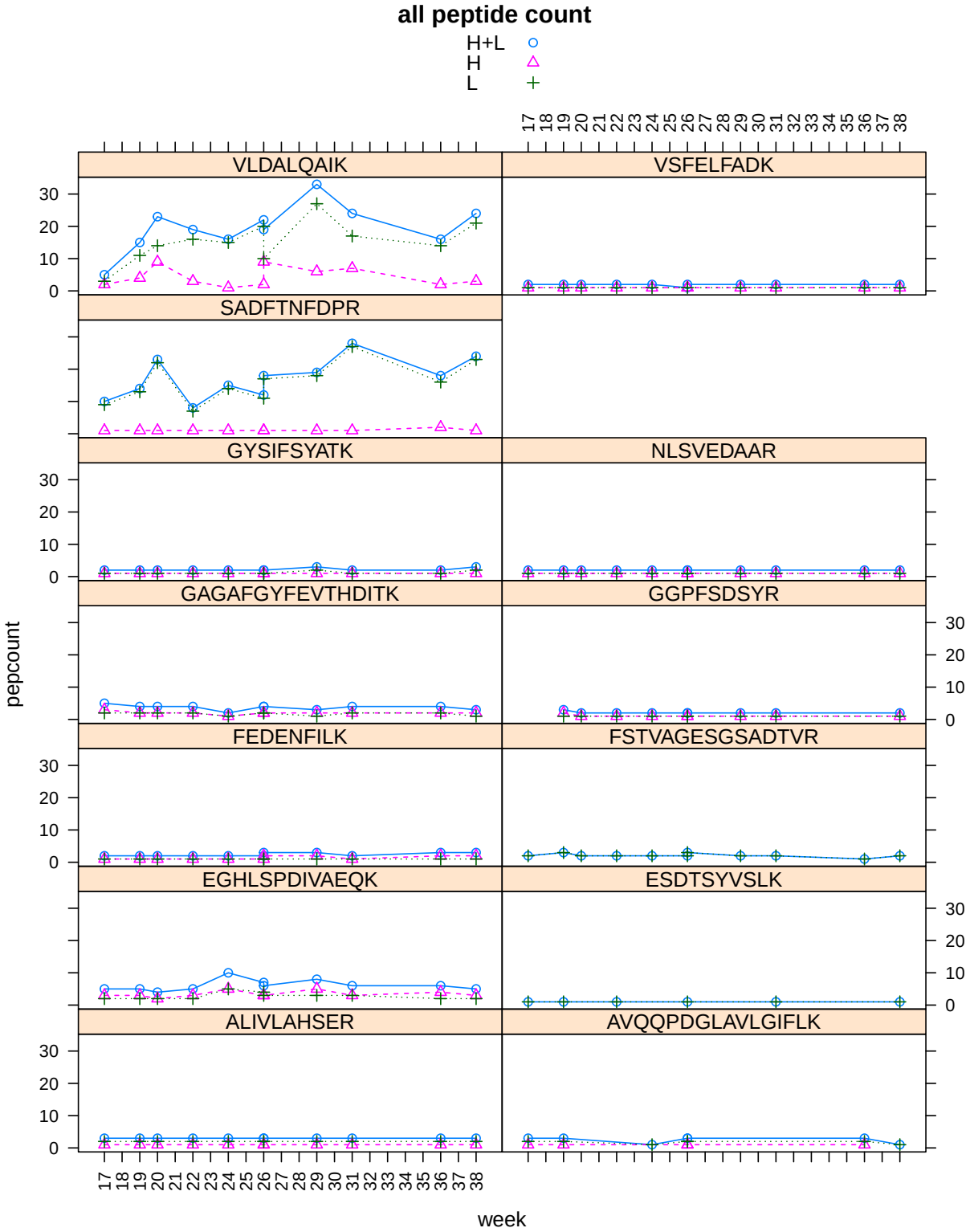
Analysed Dataset is CRG_VE



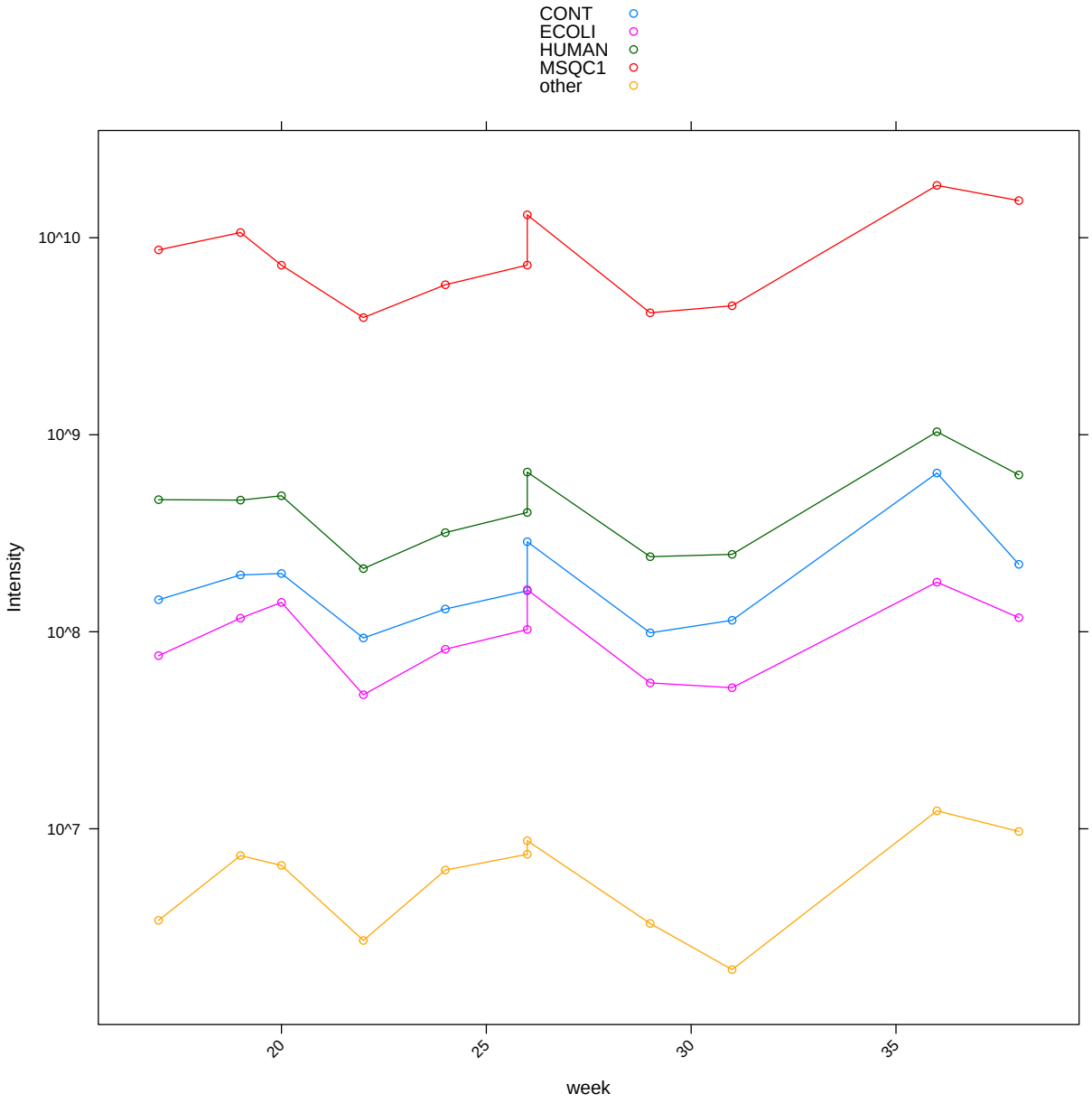
Looking at measurement error



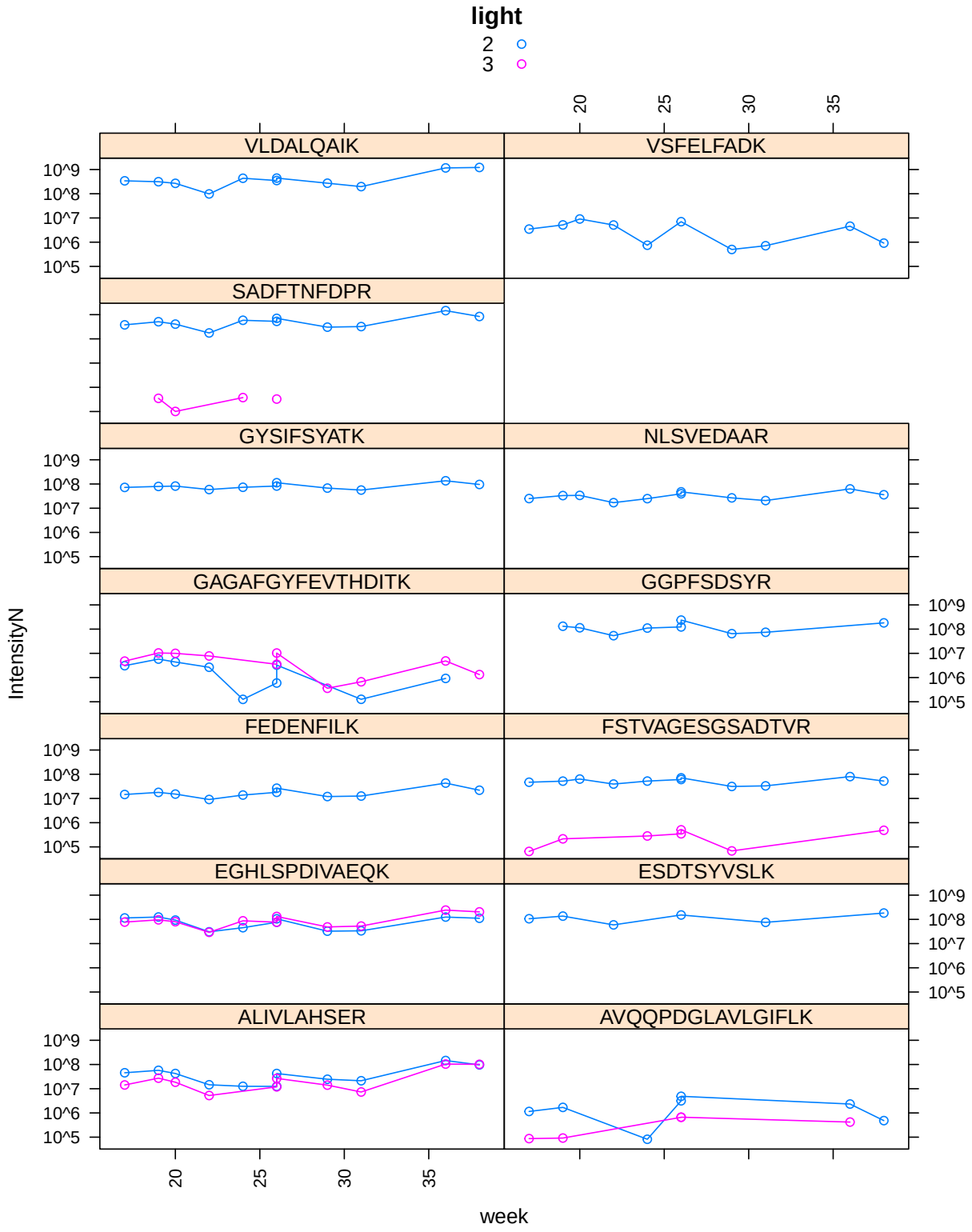
Looking at MSQC 1 peptide counts

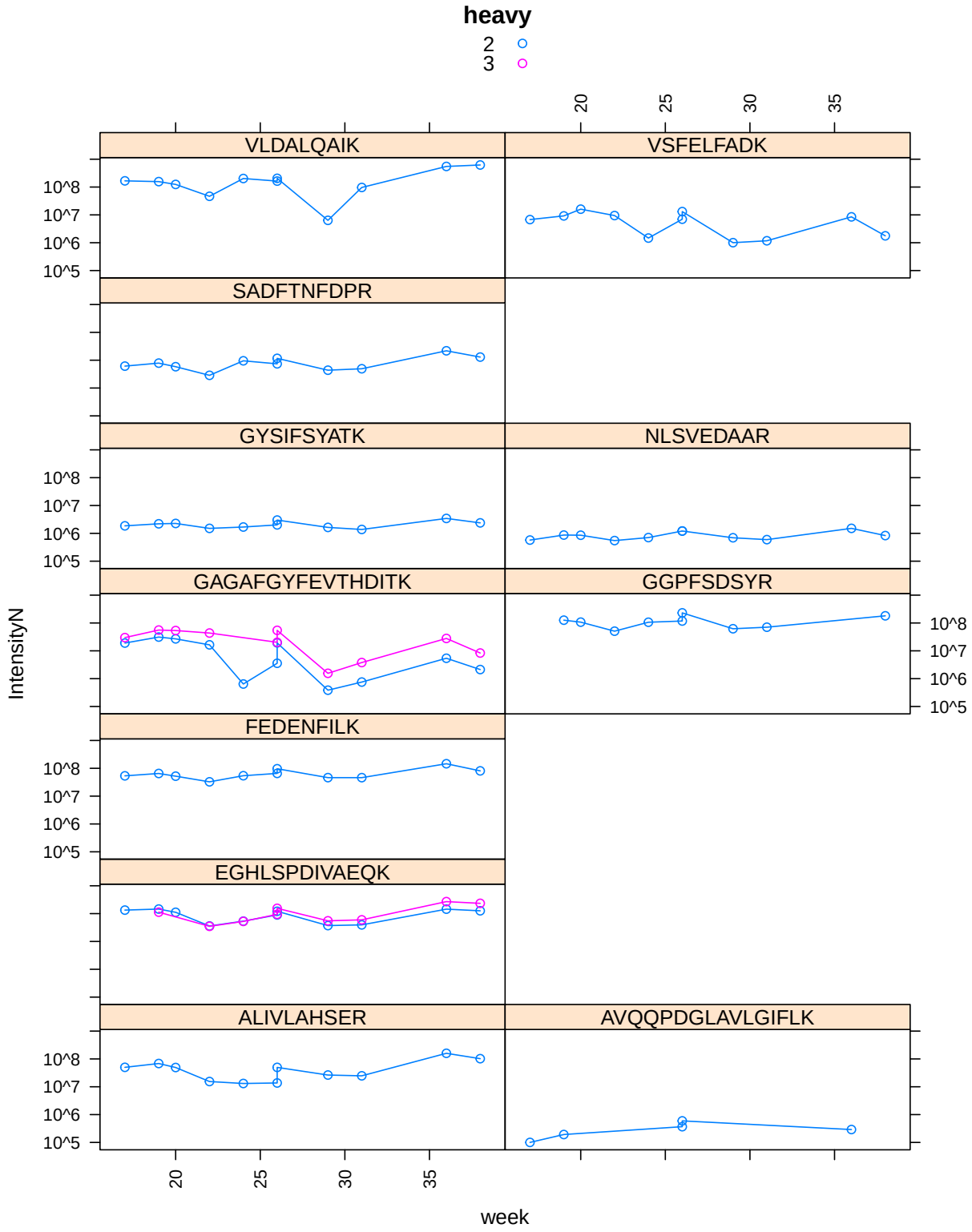


Look at Intensities (by species)

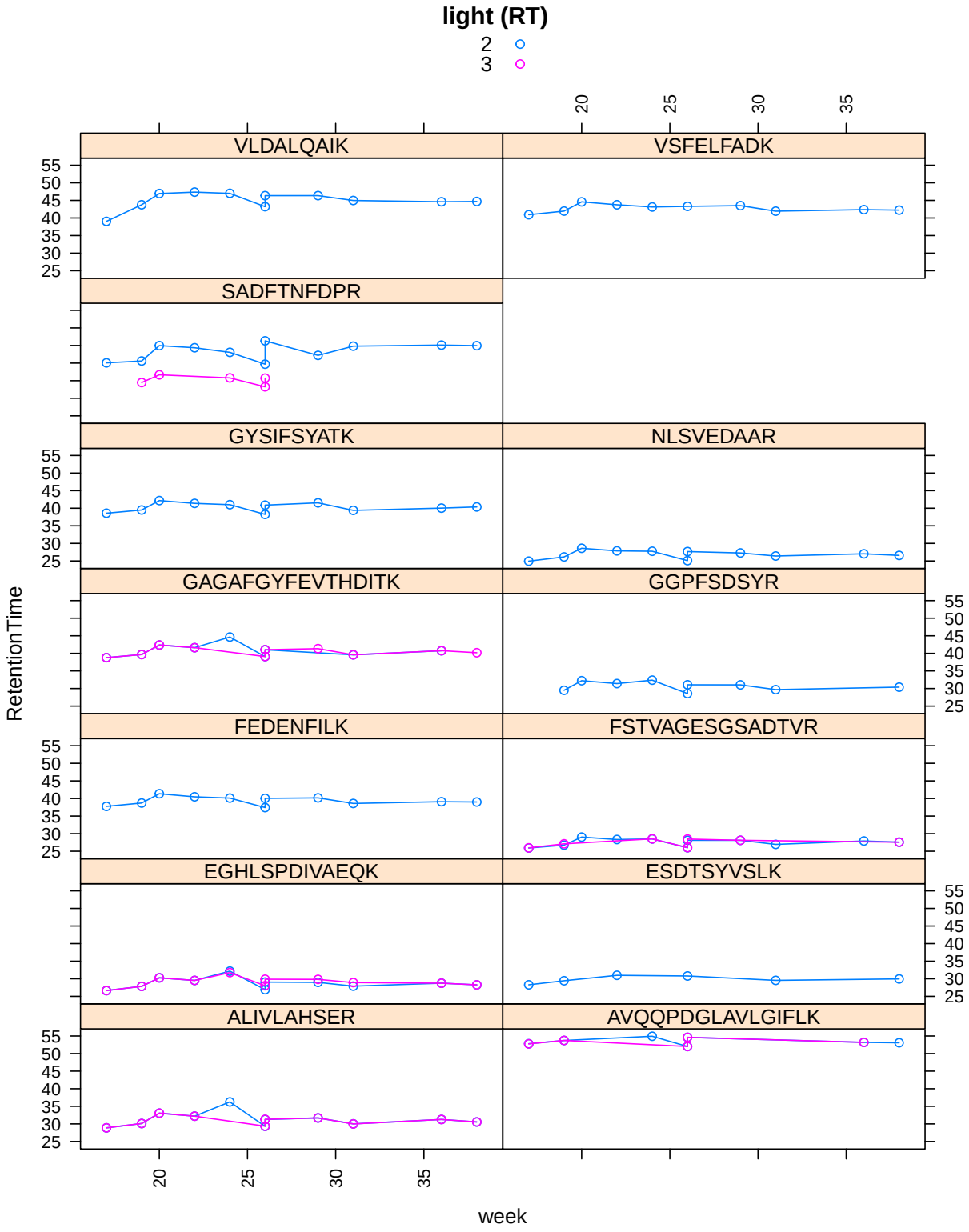


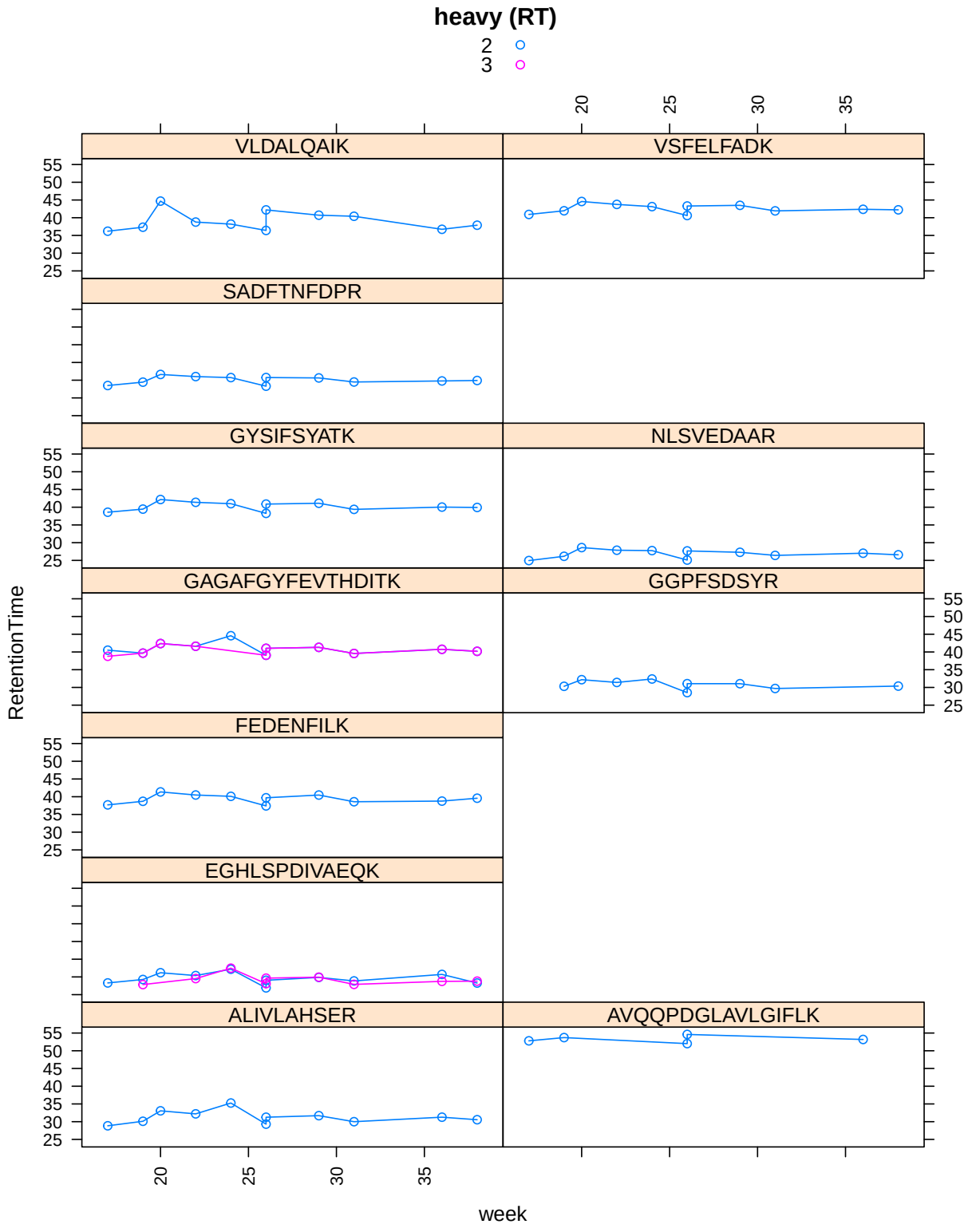
Looking at intensities msqc1




heavy
2
3
VLDALQAIK
VSFELFADK
SADFTNFDPR
GYSIFSYATK
NLSVEDAAR
GAGAFGYFEVTHDITK
GGPFSDSYR
FEDENFILK
EGHLSPDIVAEQK
ALIVLAHSER
AVQQPDGLAVLGIFLK
IntensityN
10^8
10^7
10^6
10^5
20
25
30
35
week

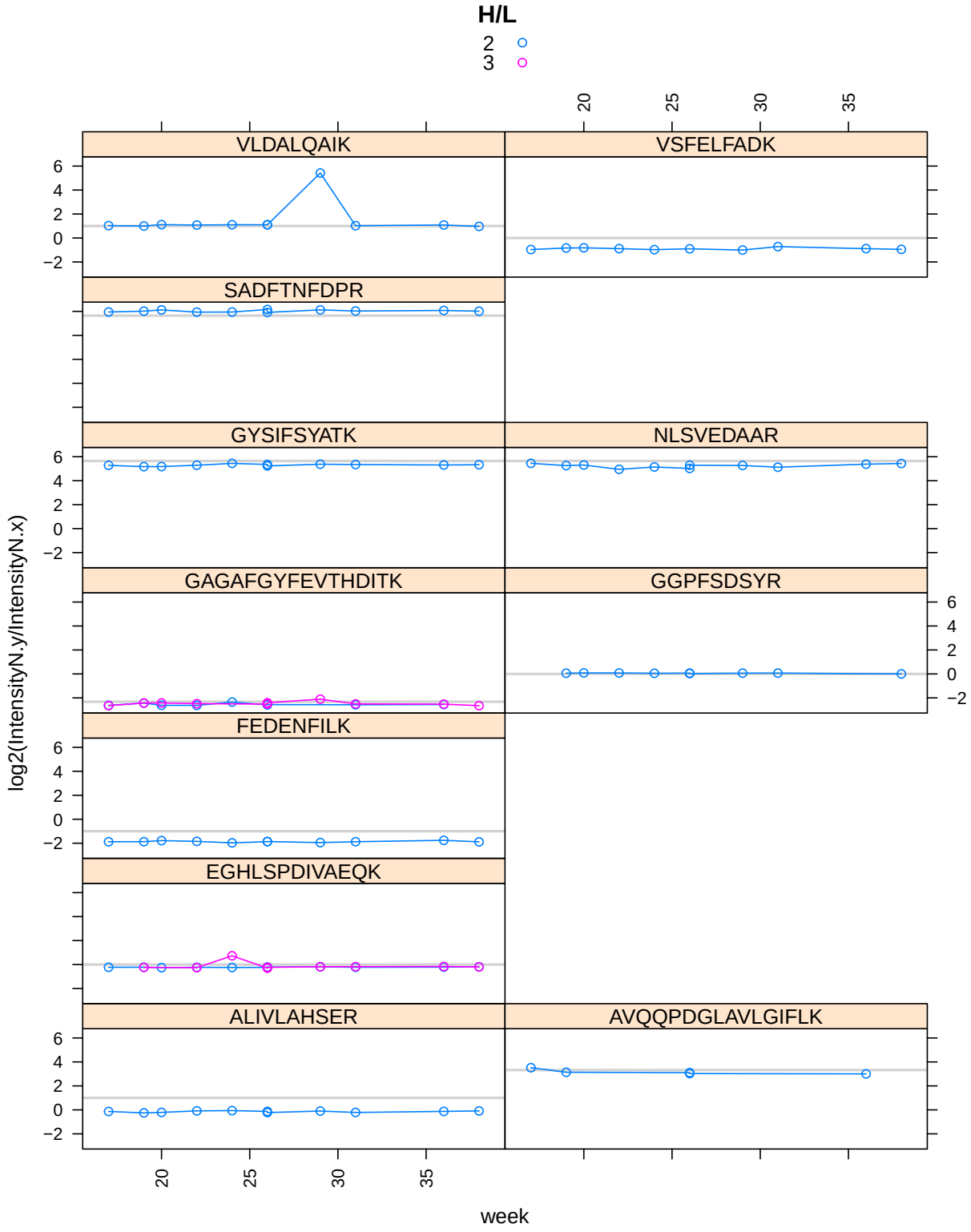
Looking at retention time

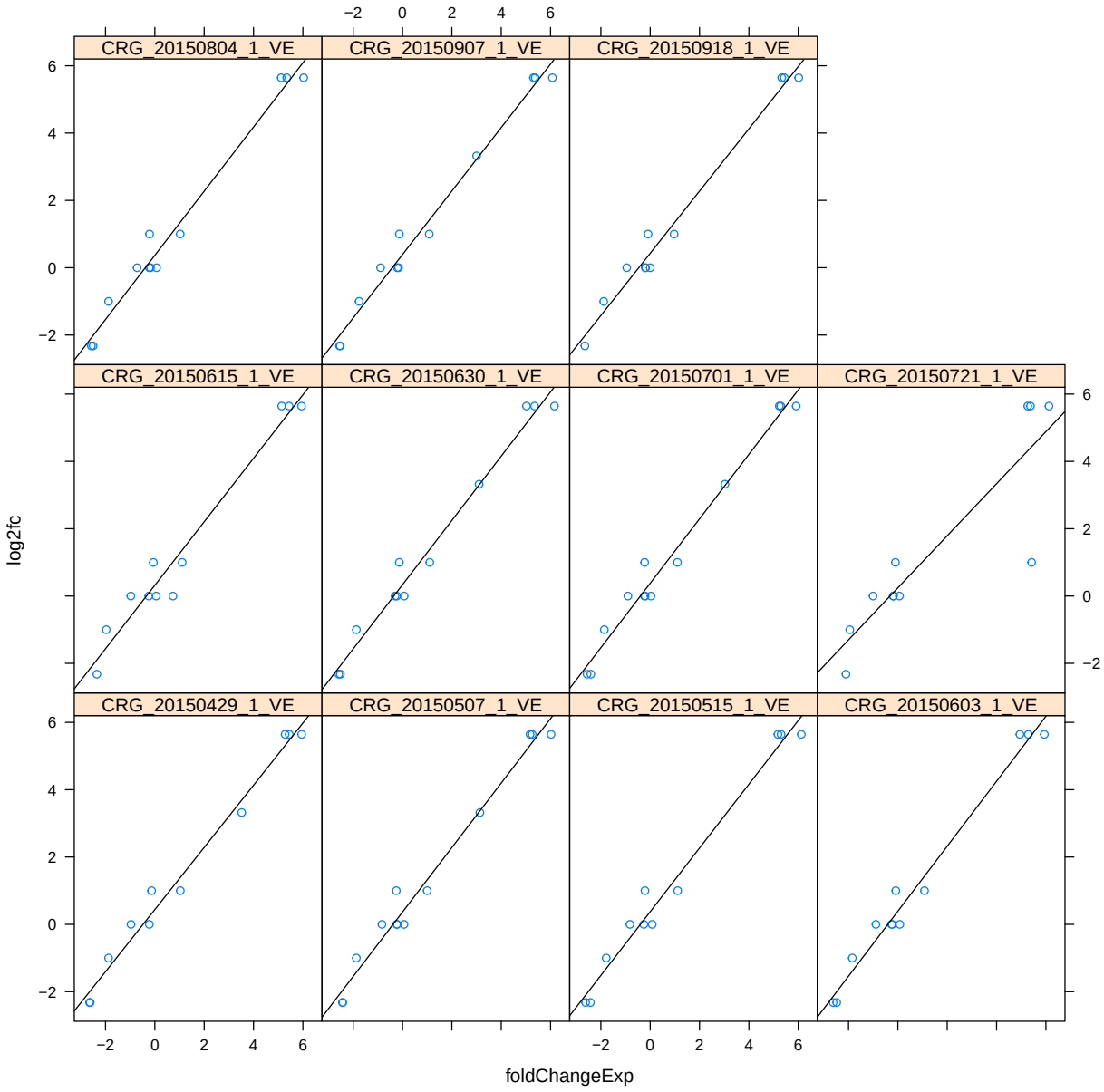


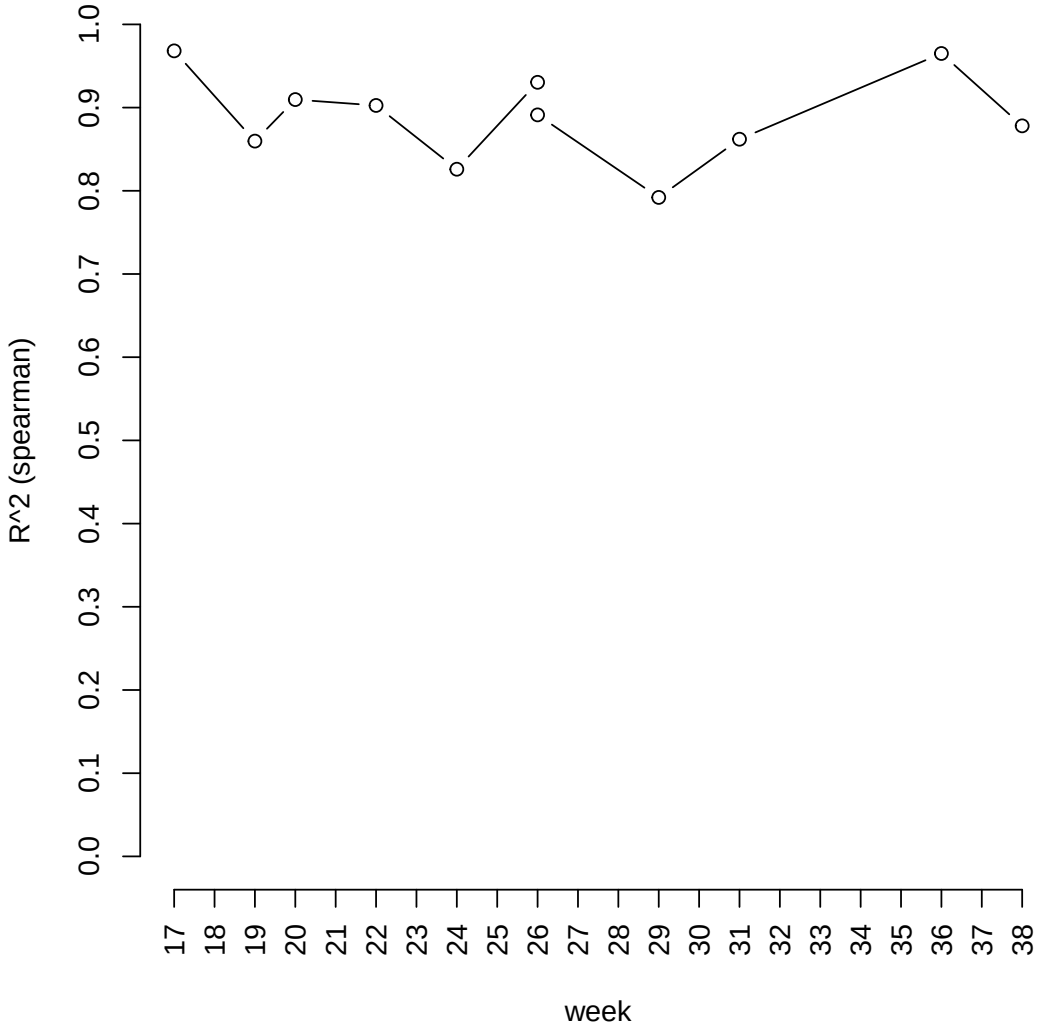

heavy (RT)
2
3
VLDALQAIK
VSFELFADK
SADFTNFDPR
GYSIFSYATK
NLSVEDAAR
GAGAFGYFEVTHDITK
GGPFSDSYR
FEDENFILK
EGHLSPDIVAEQK
ALIVLAHSER
AVQQPDGLAVLGIFLK
RetentionTime
week

Log fold change

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




CRG_20150804_1_VE
CRG_20150907_1_VE
CRG_20150918_1_VE
CRG_20150615_1_VE
CRG_20150630_1_VE
CRG_20150701_1_VE
CRG_20150721_1_VE
CRG_20150429_1_VE
CRG_20150507_1_VE
CRG_20150515_1_VE
CRG_20150603_1_VE
log2fc
foldChangeExp


R^2 (spearman)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
week