Analysing MaxQuant Output with R

FGC Zurich

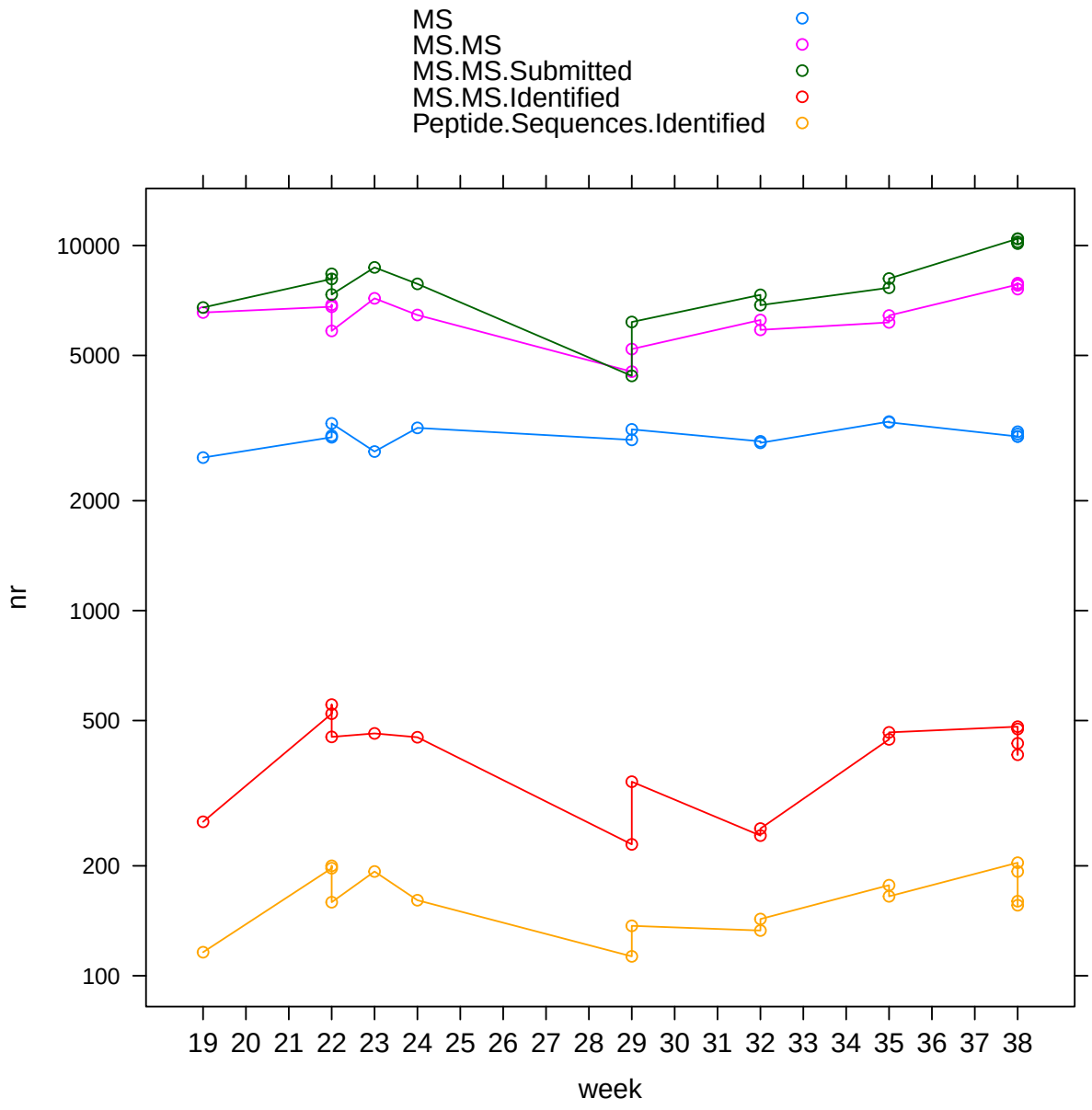
30 September 2015

Contents

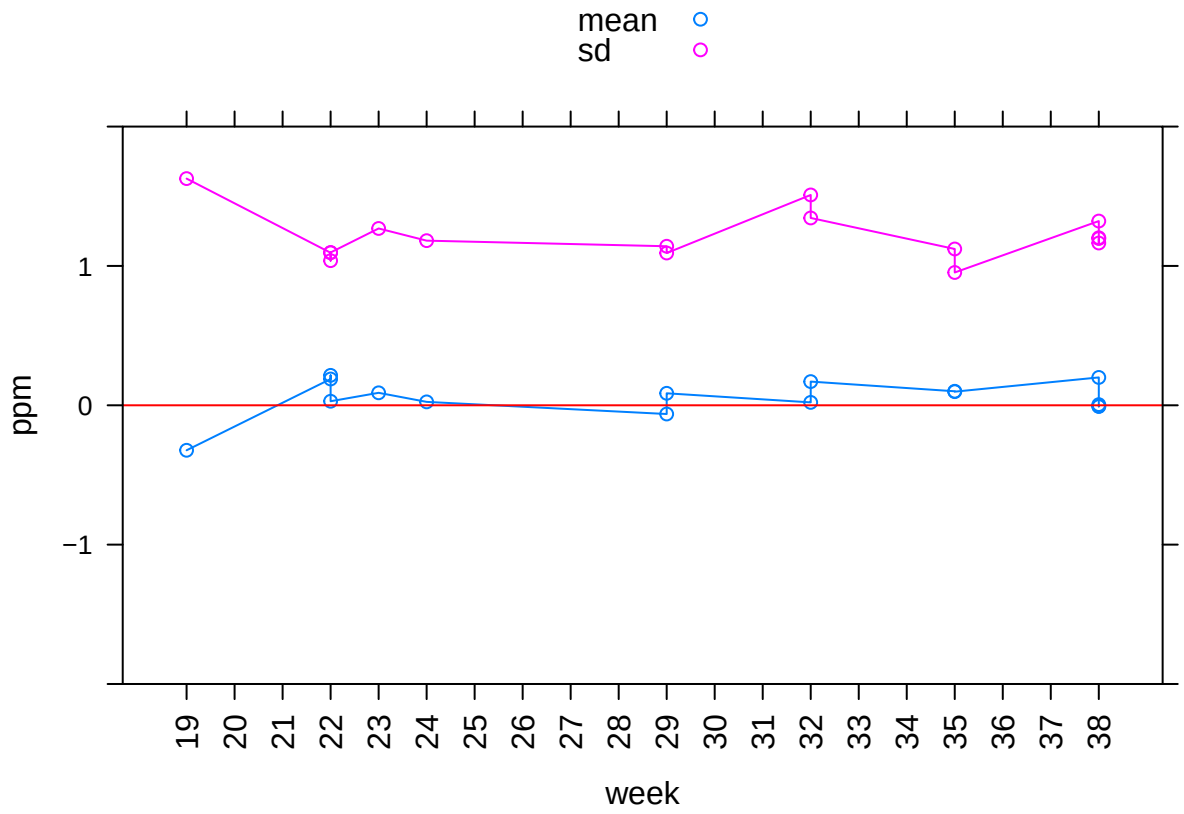
Prepare mrm table

- 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

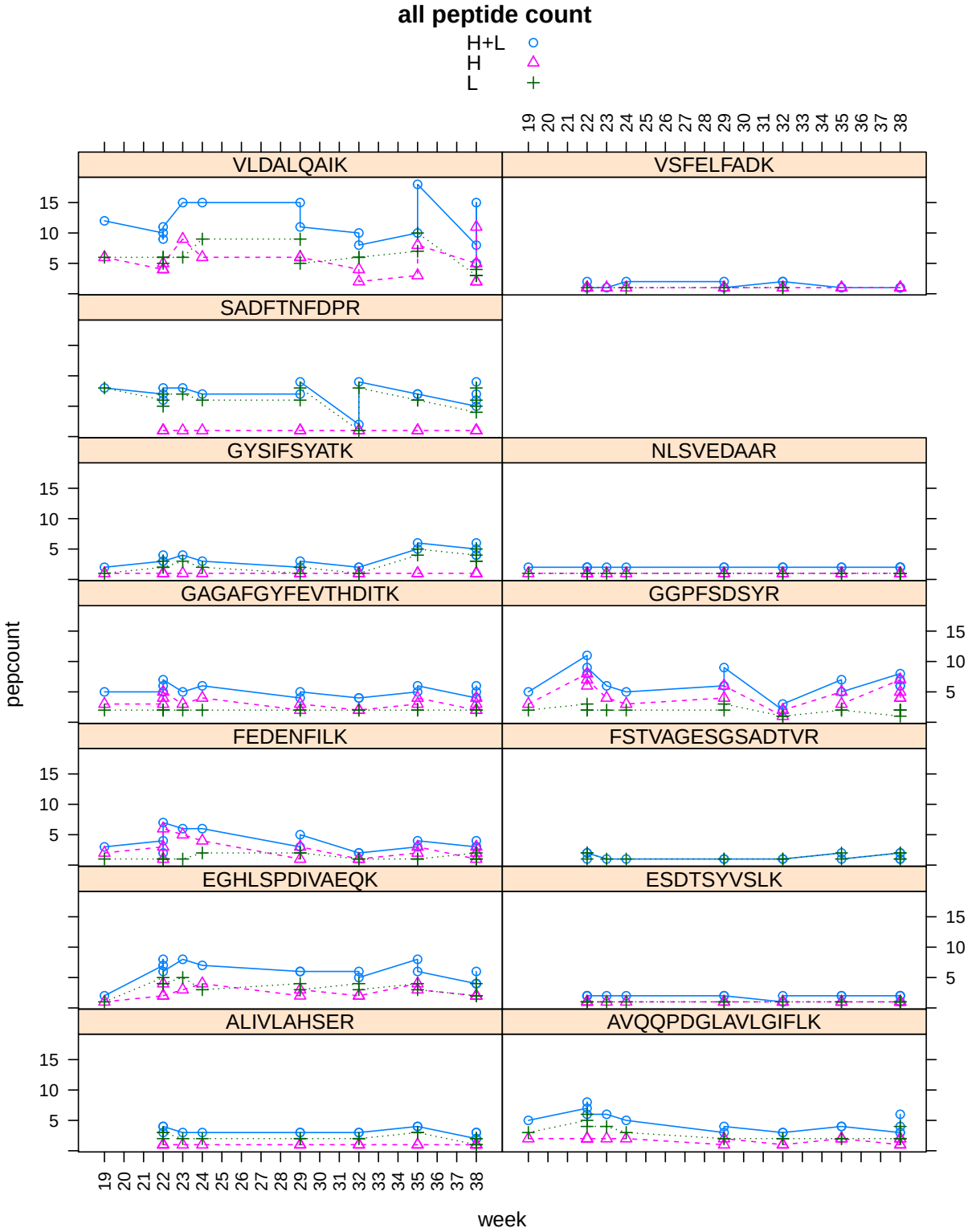
Analysed Dataset is FGCZ_VE



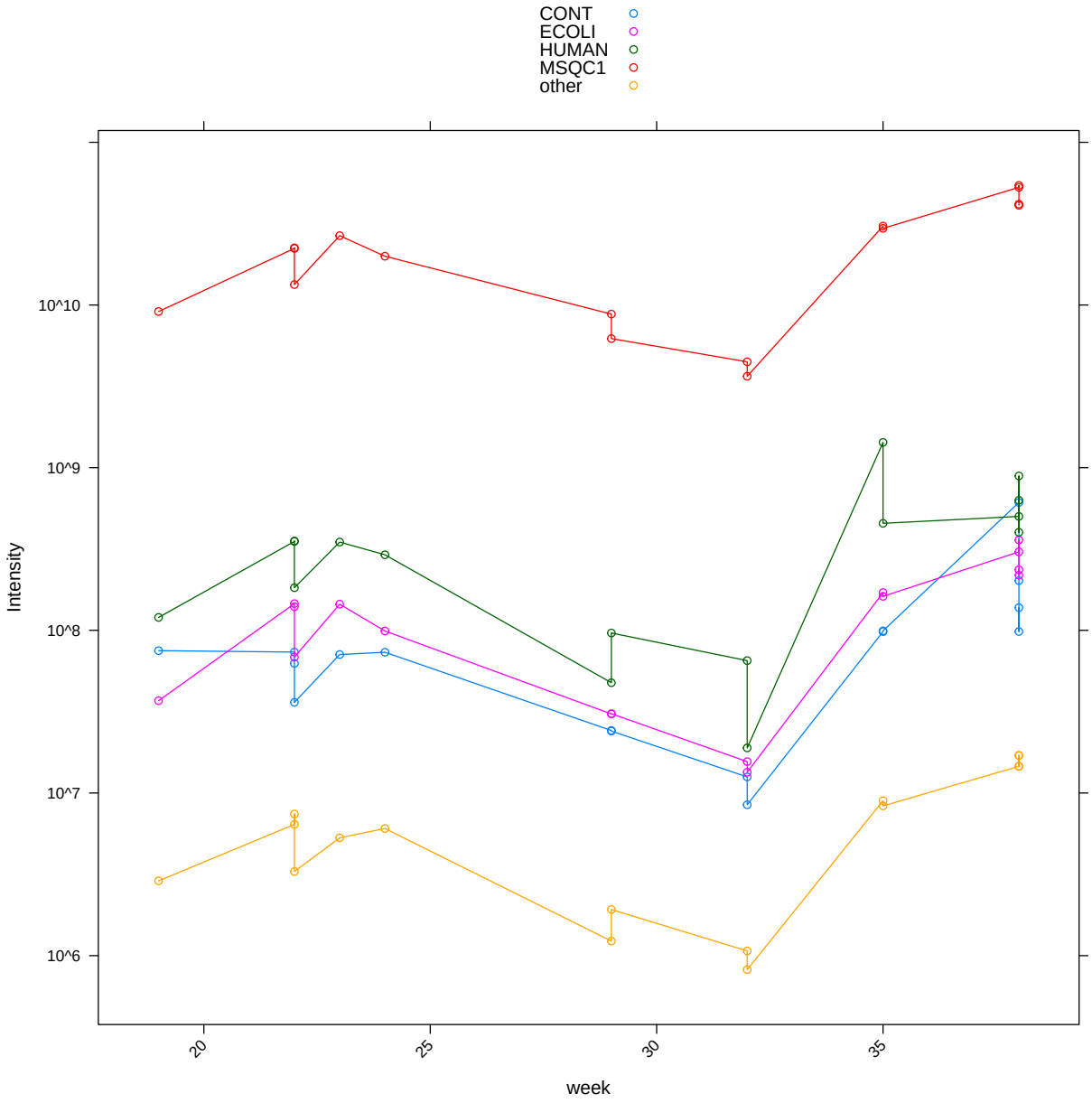
Looking at measurement error



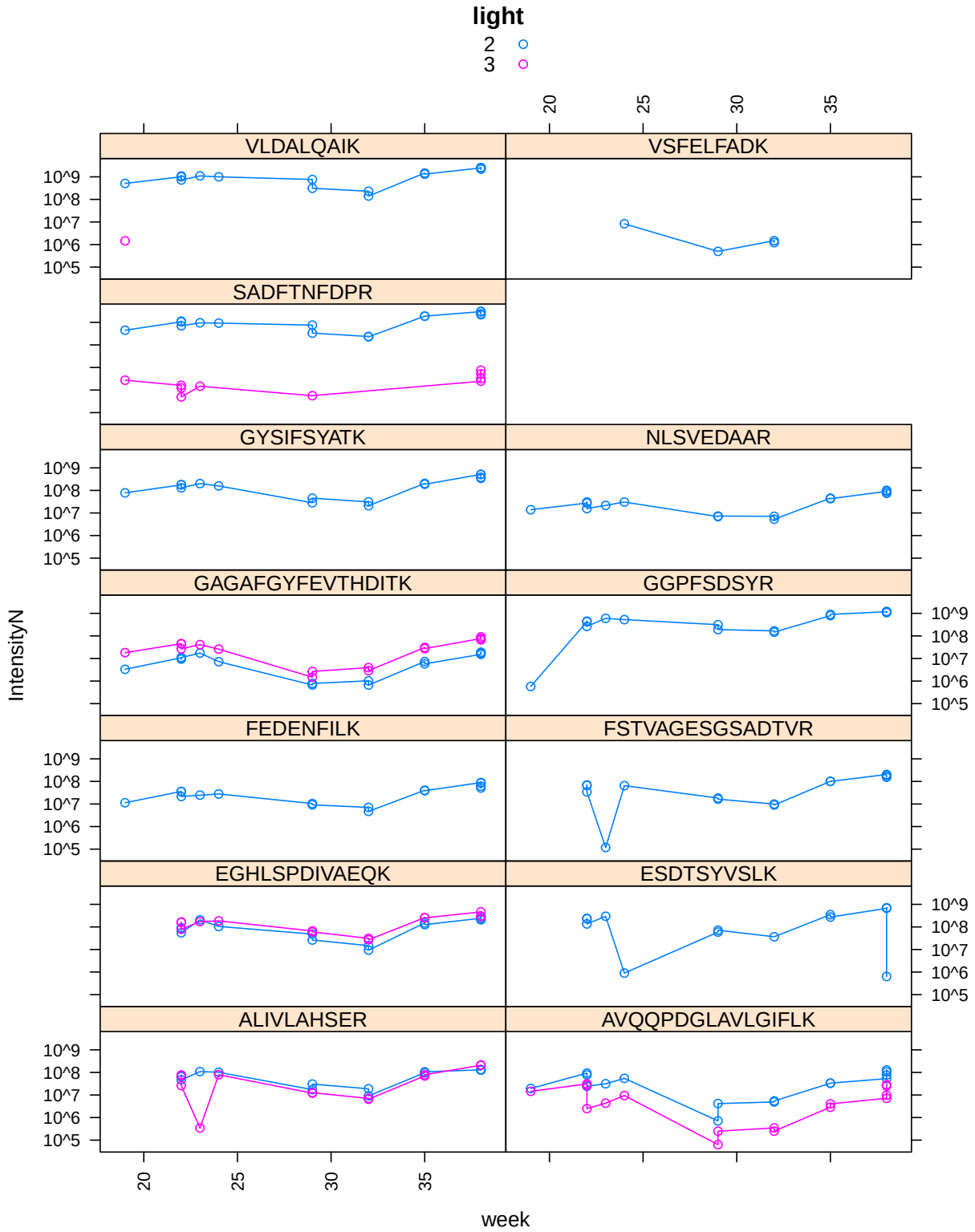
Looking at MSQC 1 peptide counts

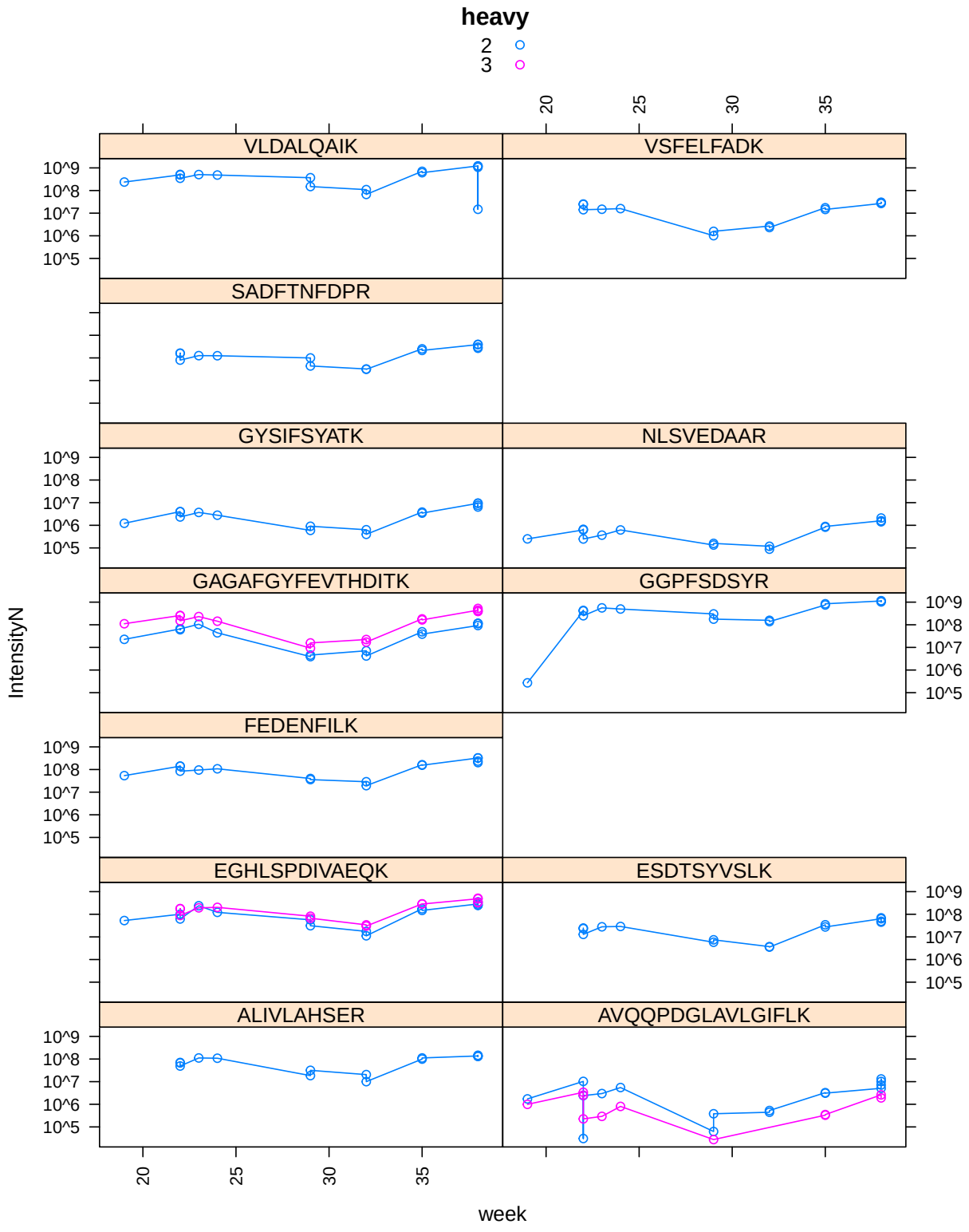


Look at Intensities (by species)

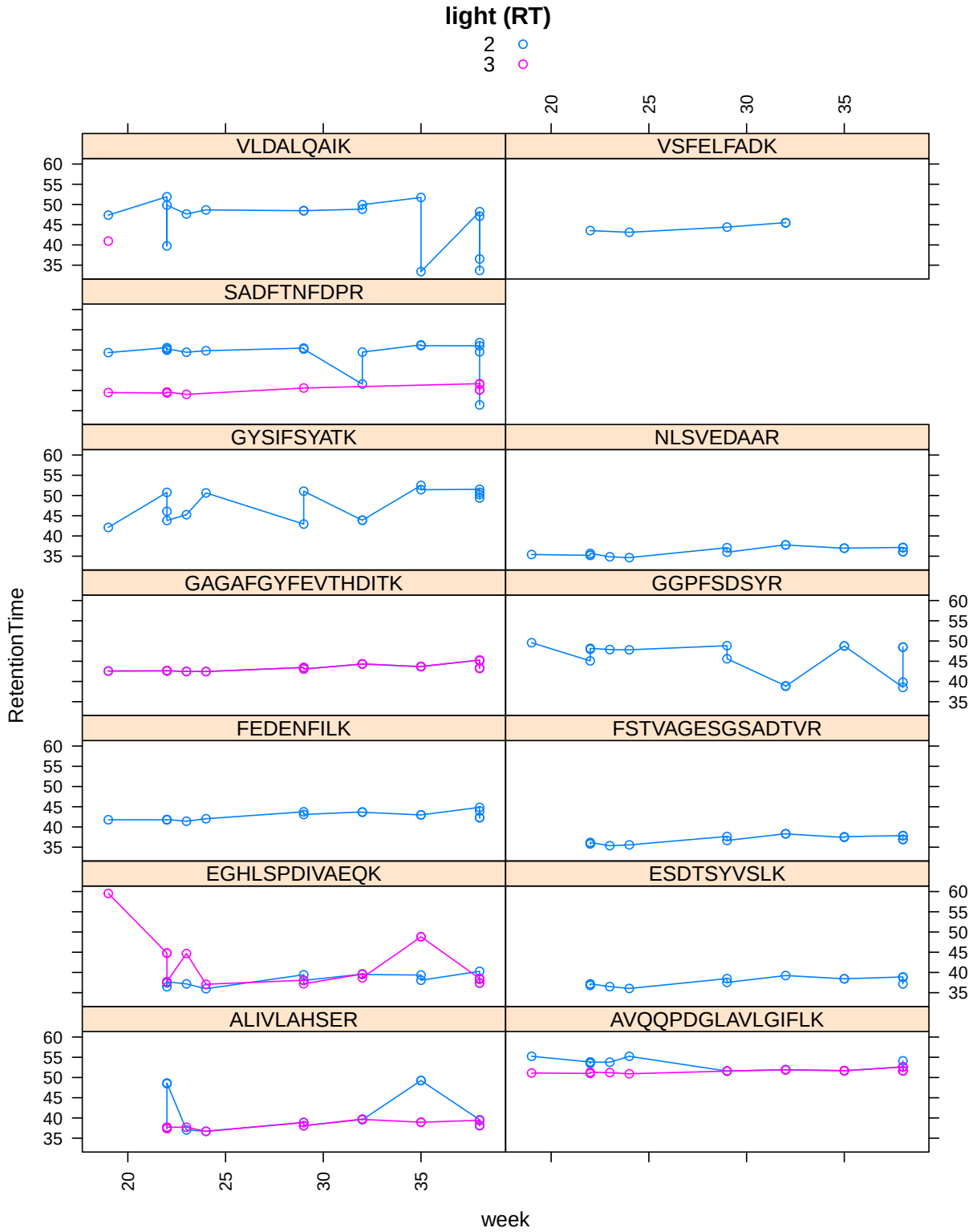


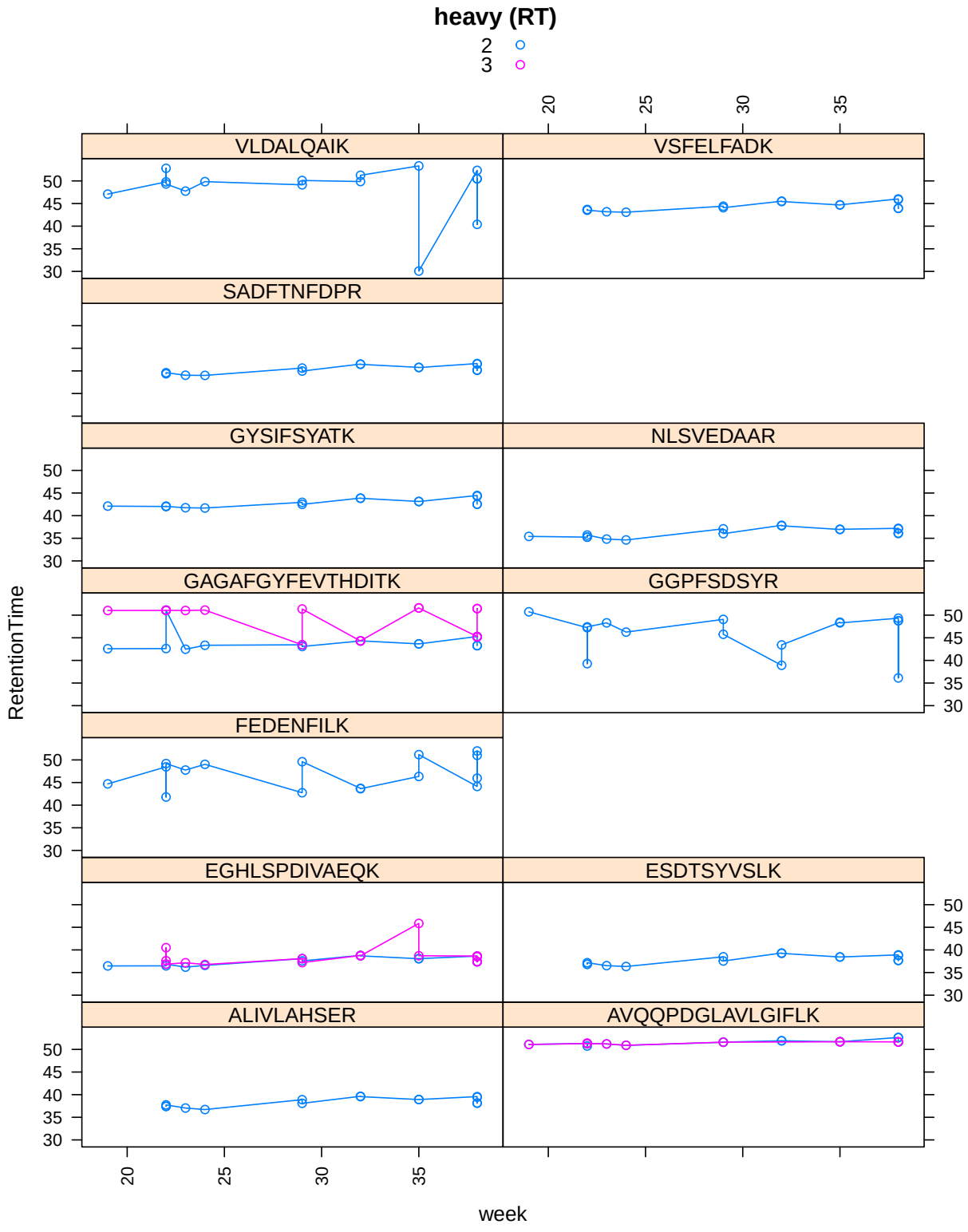
Looking at intensities msqc1




heavy
2
3
VLDALQAIK
VSFELFADK
SADFTNFDPR
GYSIFSYATK
NLSVEDAAR
GAGAFGYFEVTHDITK
GGPFSDSYR
FEDENFILK
EGHLSPDIVAEQK
ESDTSYVSLK
ALIVLAHSER
AVQQPDGLAVLGIFLK
IntensityN
10^9
10^8
10^7
10^6
10^5
20
25
30
35
week

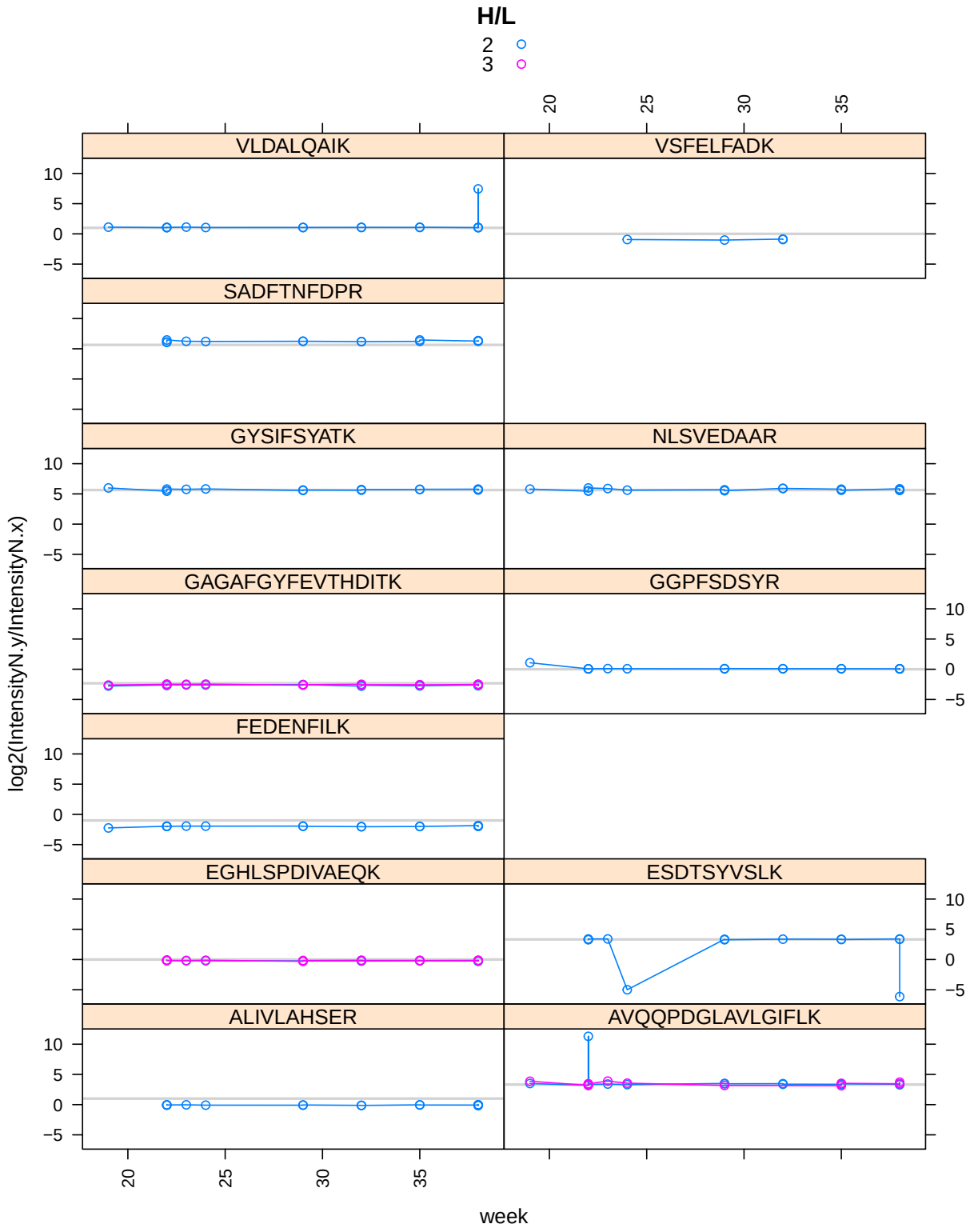
Looking at retention time

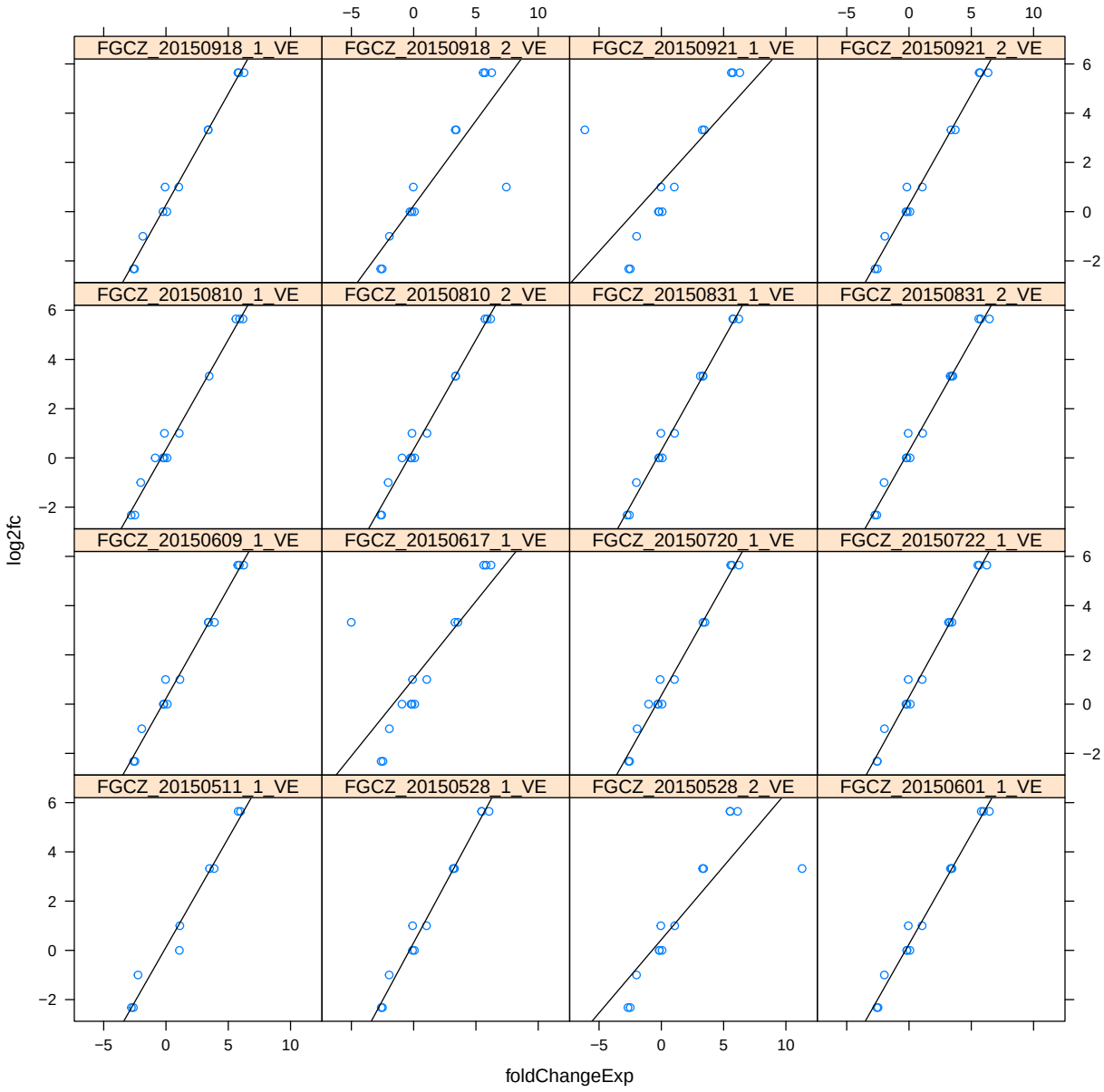


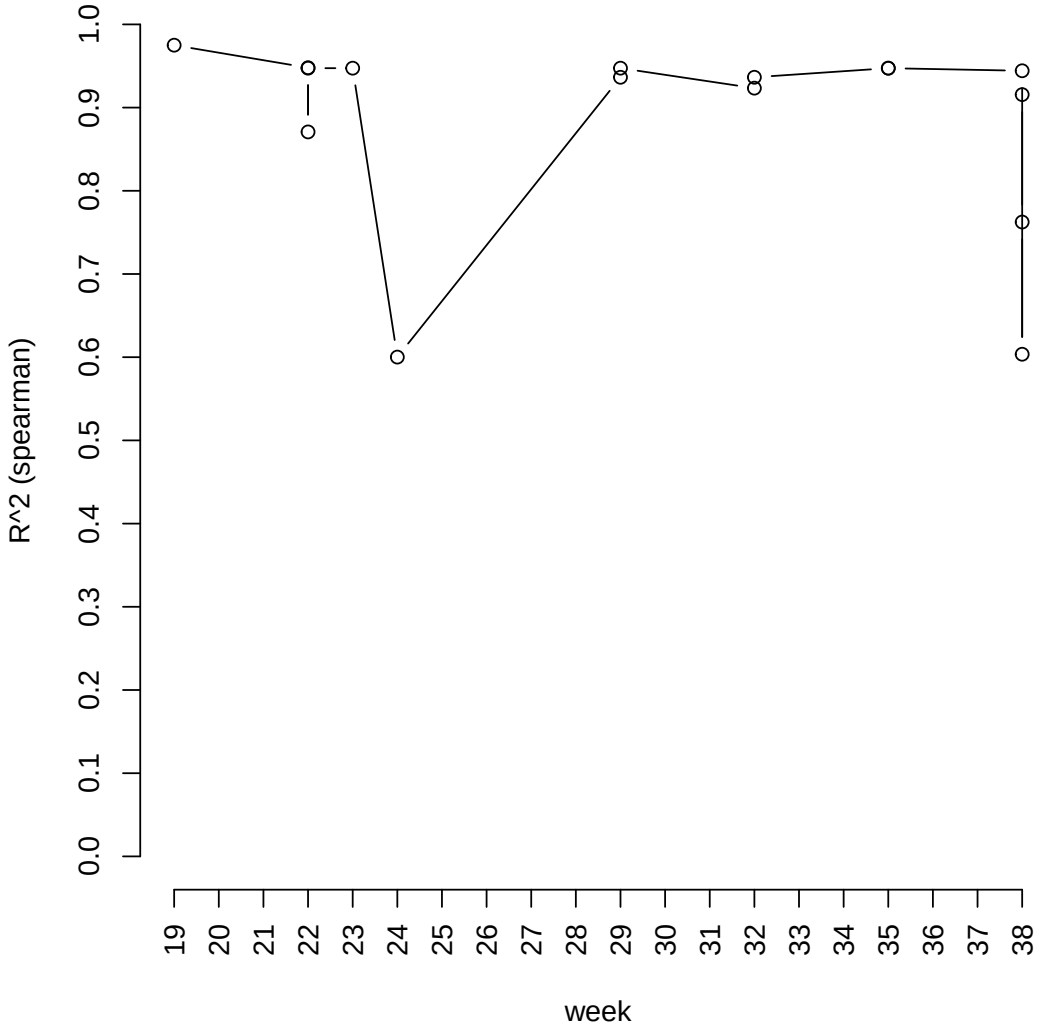

heavy (RT)
2
3
VLDALQAIK
VSFELFADK
SADFTNFDPR
GYSIFSYATK
NLSVEDAAR
GAGAFGYFEVTHDITK
GGPFSDSYR
FEDENFILK
EGHLSPDIVAEQK
ESDTSYVSLK
ALIVLAHSER
AVQQPDGLAVLGIFLK
RetentionTime
week

Log fold change

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




FGCZ_20150918_1_VE
FGCZ_20150918_2_VE
FGCZ_20150921_1_VE
FGCZ_20150921_2_VE
FGCZ_20150810_1_VE
FGCZ_20150810_2_VE
FGCZ_20150831_1_VE
FGCZ_20150831_2_VE
FGCZ_20150609_1_VE
FGCZ_20150617_1_VE
FGCZ_20150720_1_VE
FGCZ_20150722_1_VE
FGCZ_20150511_1_VE
FGCZ_20150528_1_VE
FGCZ_20150528_2_VE
FGCZ_20150601_1_VE
log2fc
foldChangeExp
−5
0
5
10
−2
0
2
4
6


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
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
week