Analysing MaxQuant Output with R

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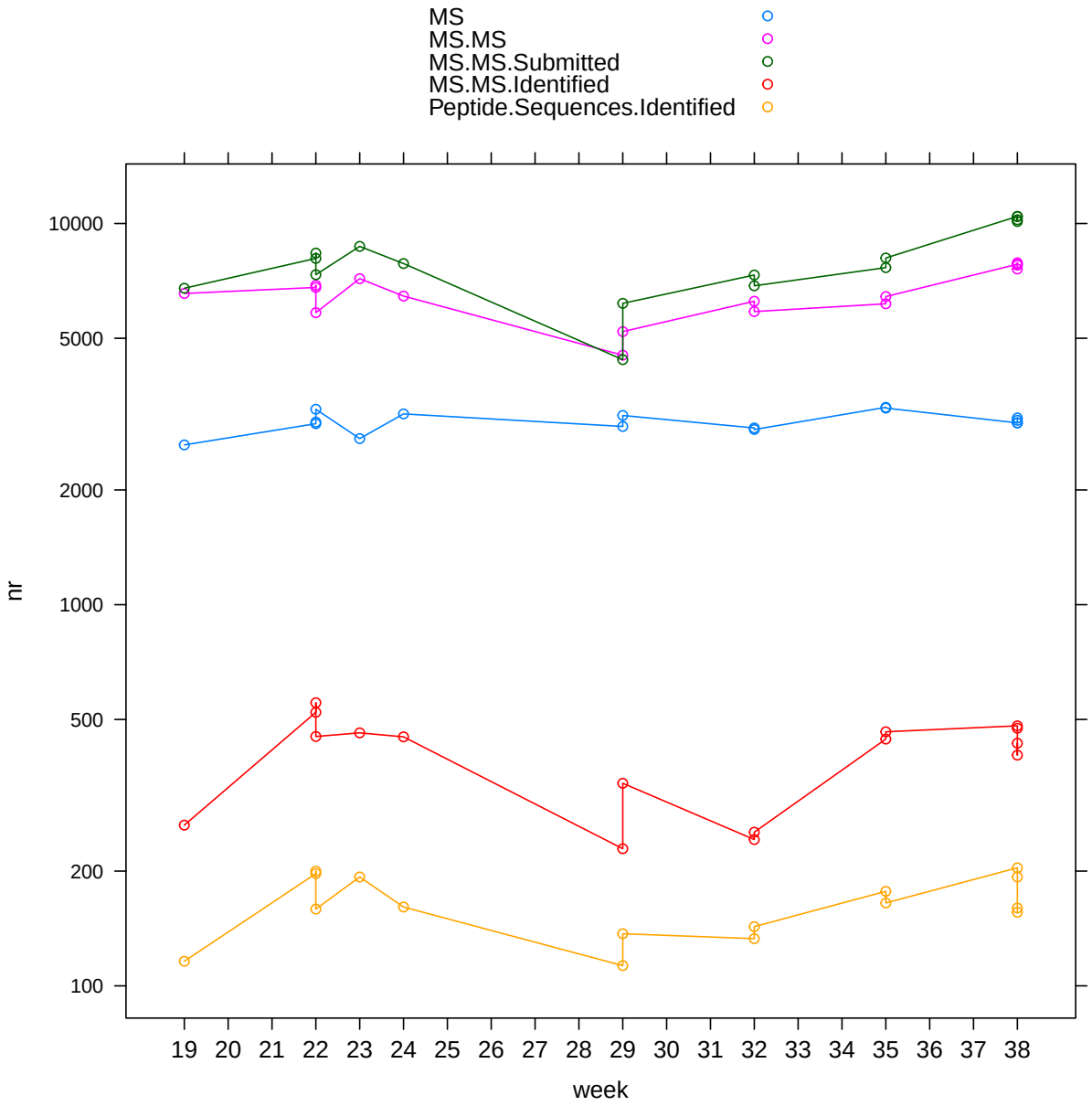
Prepare mrm table

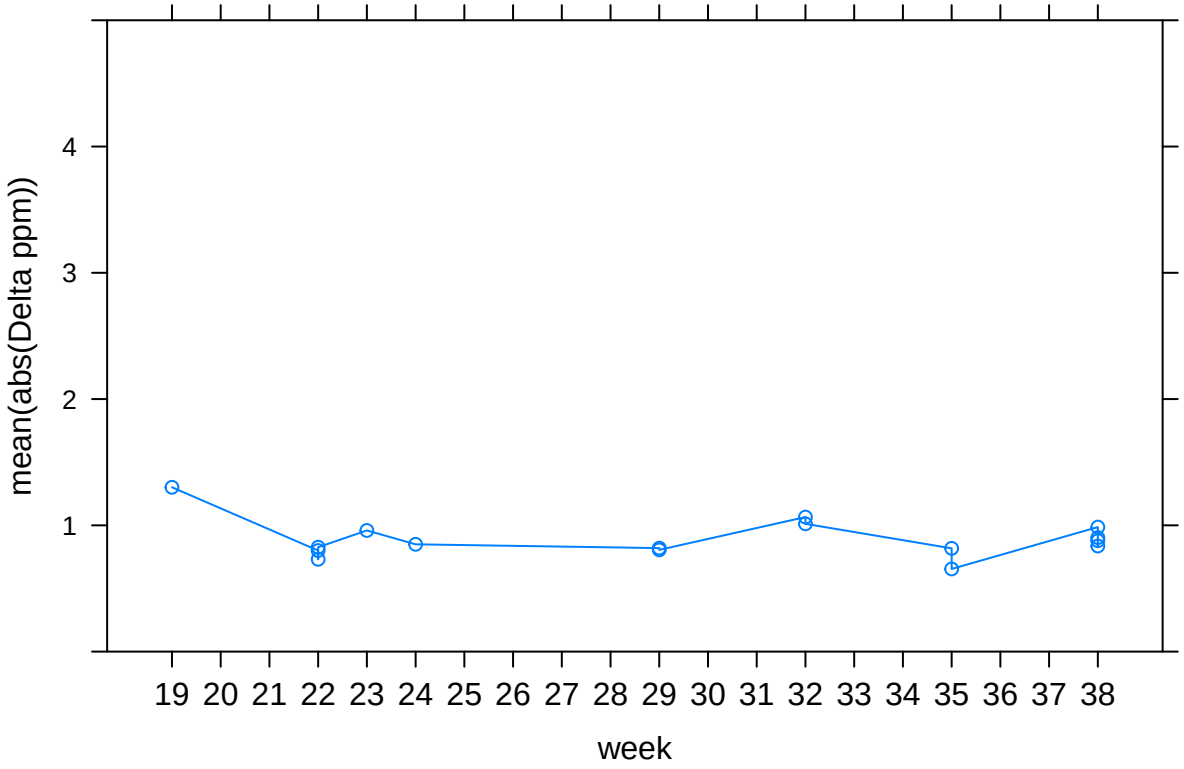
- nr of assigned spectra (MS2) / versus total spectra
- How many H/L target peptides are identified
- Ratio among H/L of the target peptides
- Intensity of heavy or light over the runs

Analysed Dataset is paolo_20151029_MSQC1.sqlite3

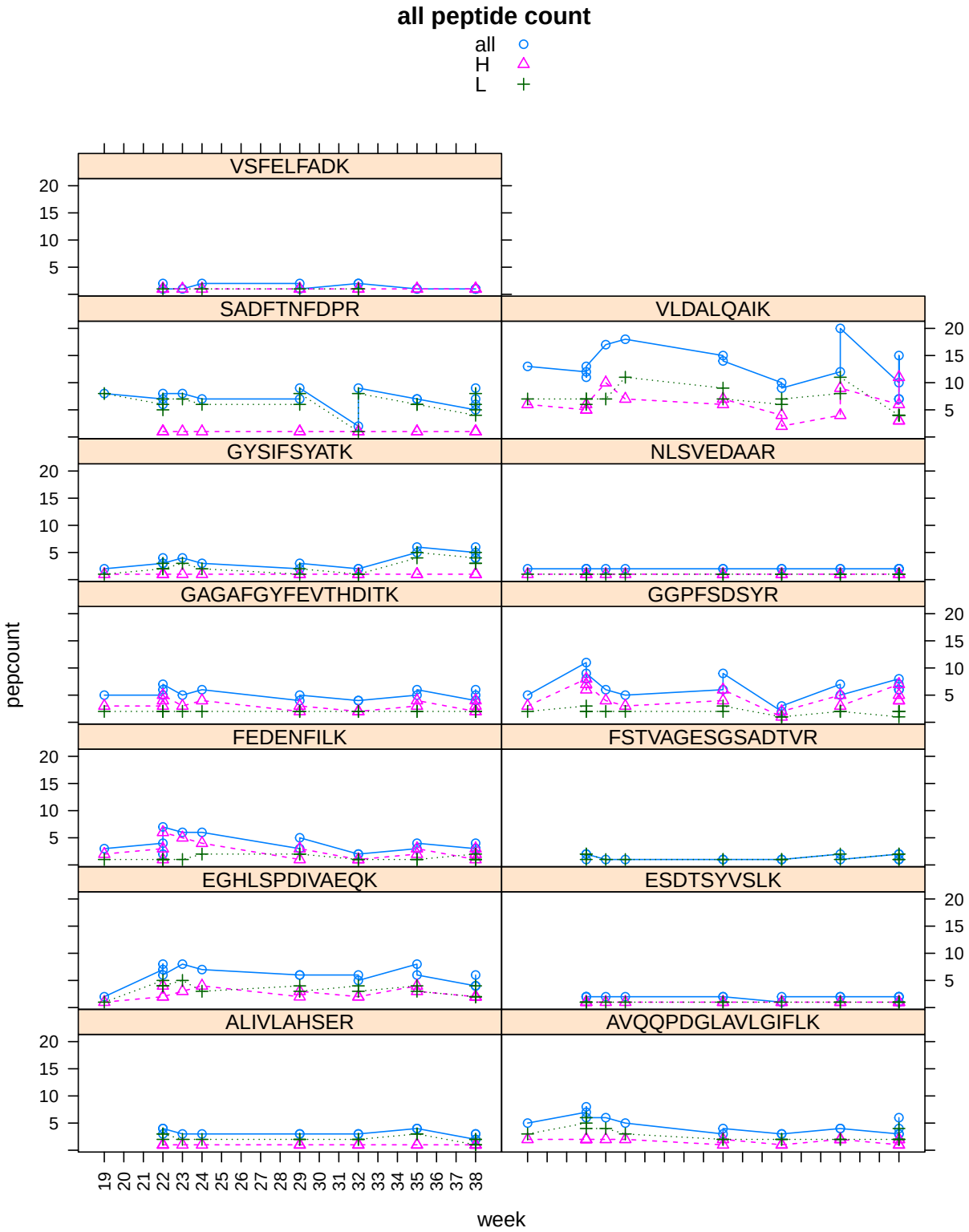
Number of spectra, spectra peptide matches, and unique peptides



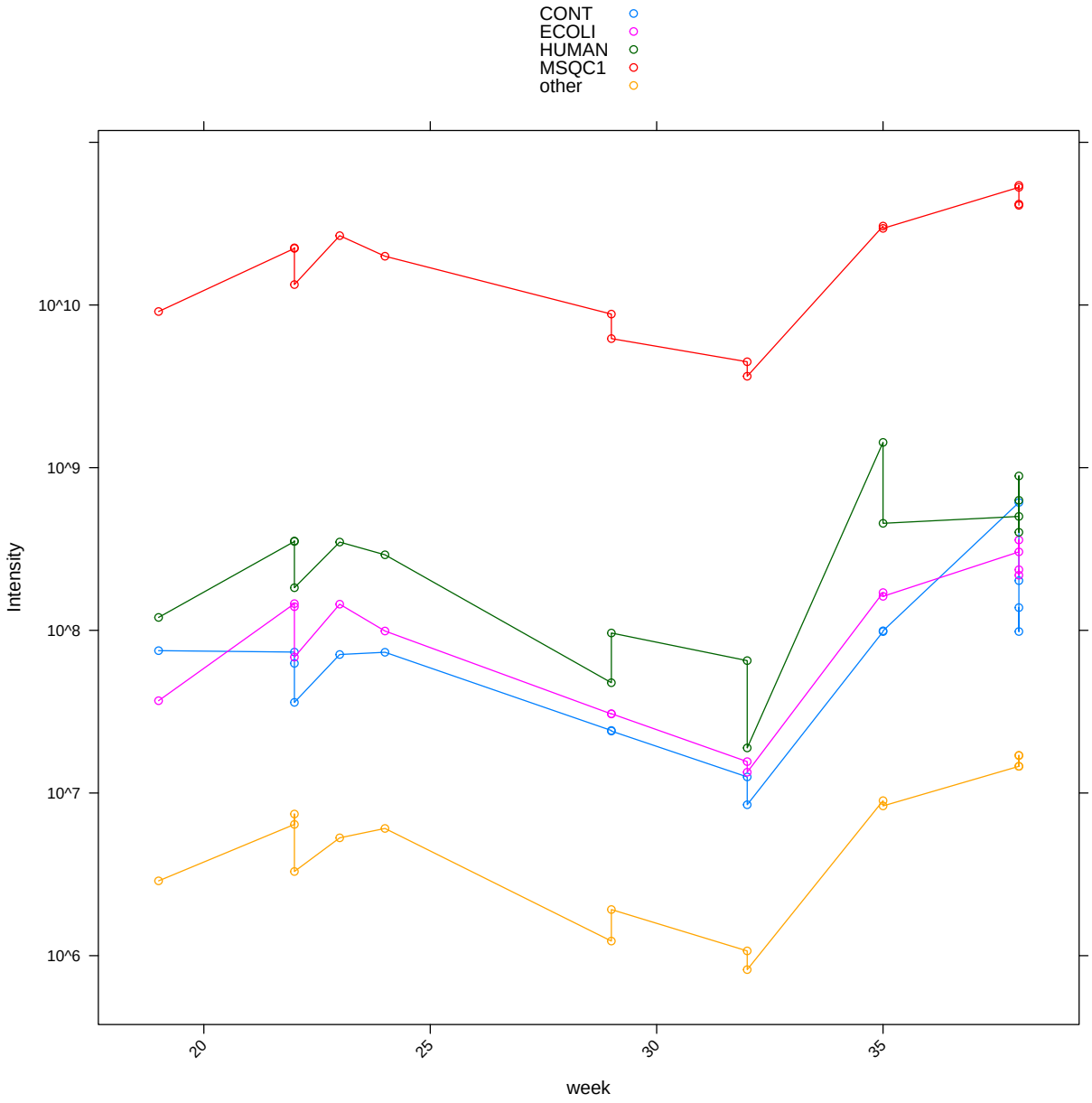
Looking at measurement error



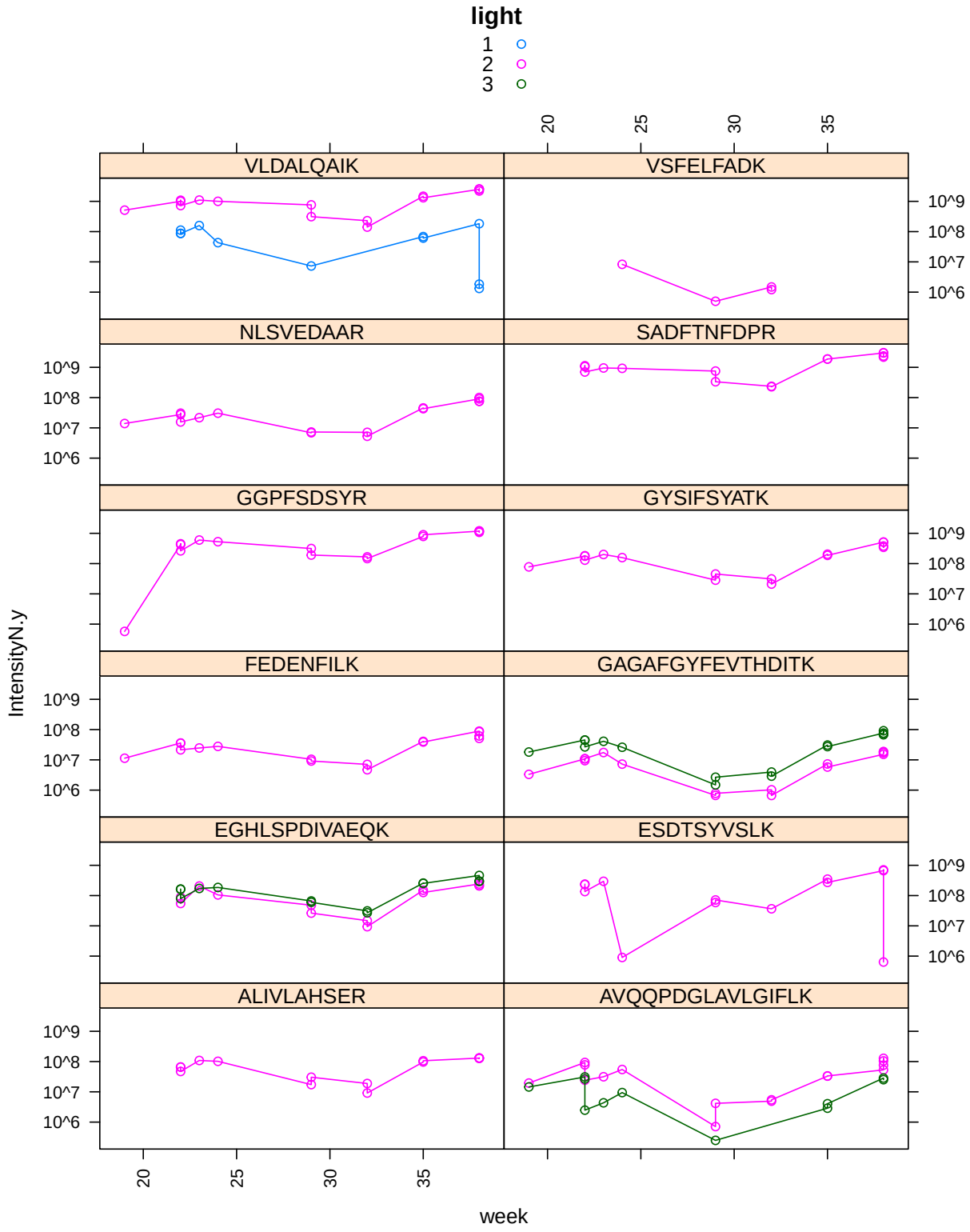
Looking at MSQC 1 peptide counts

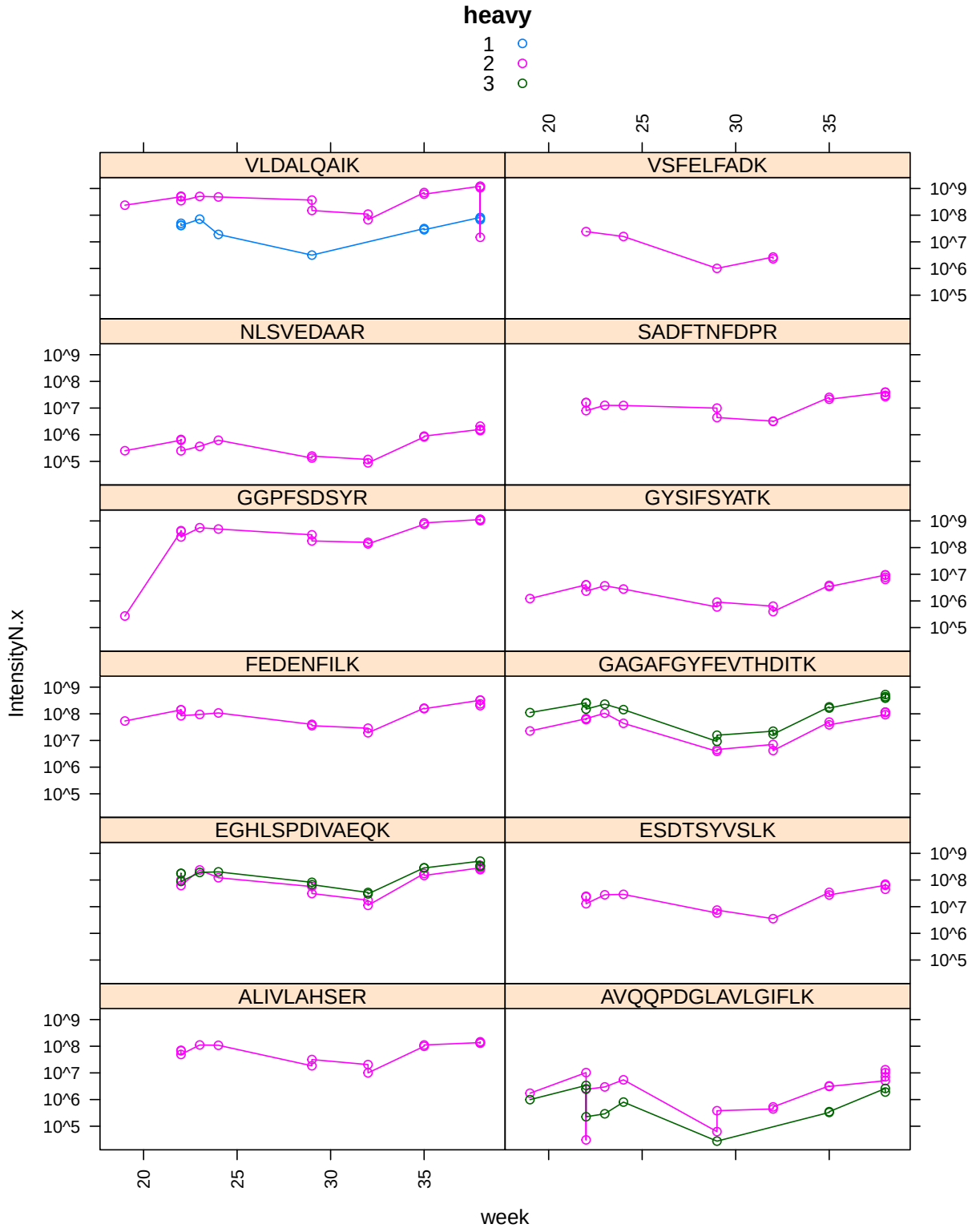


Look at Intensities (by species)

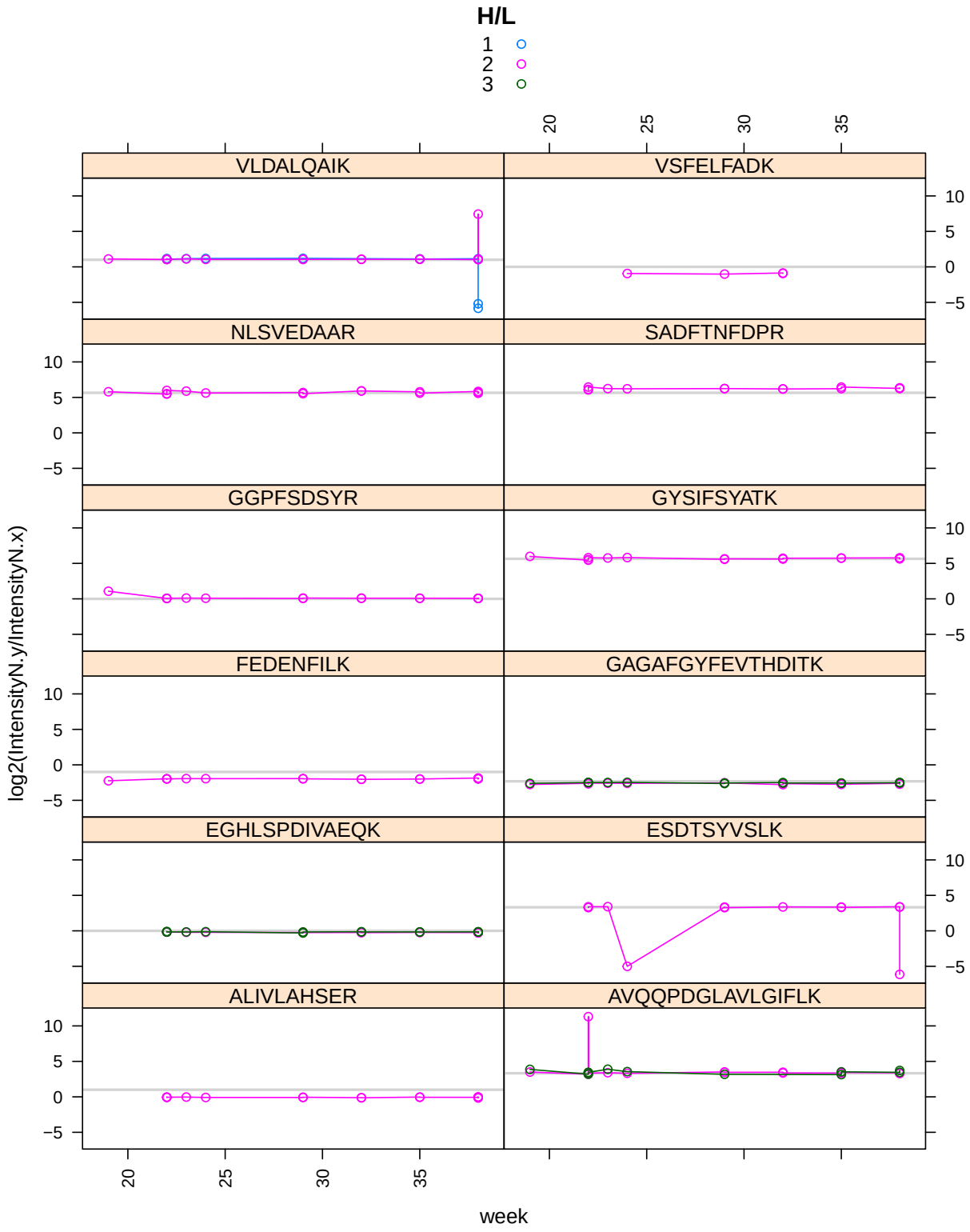


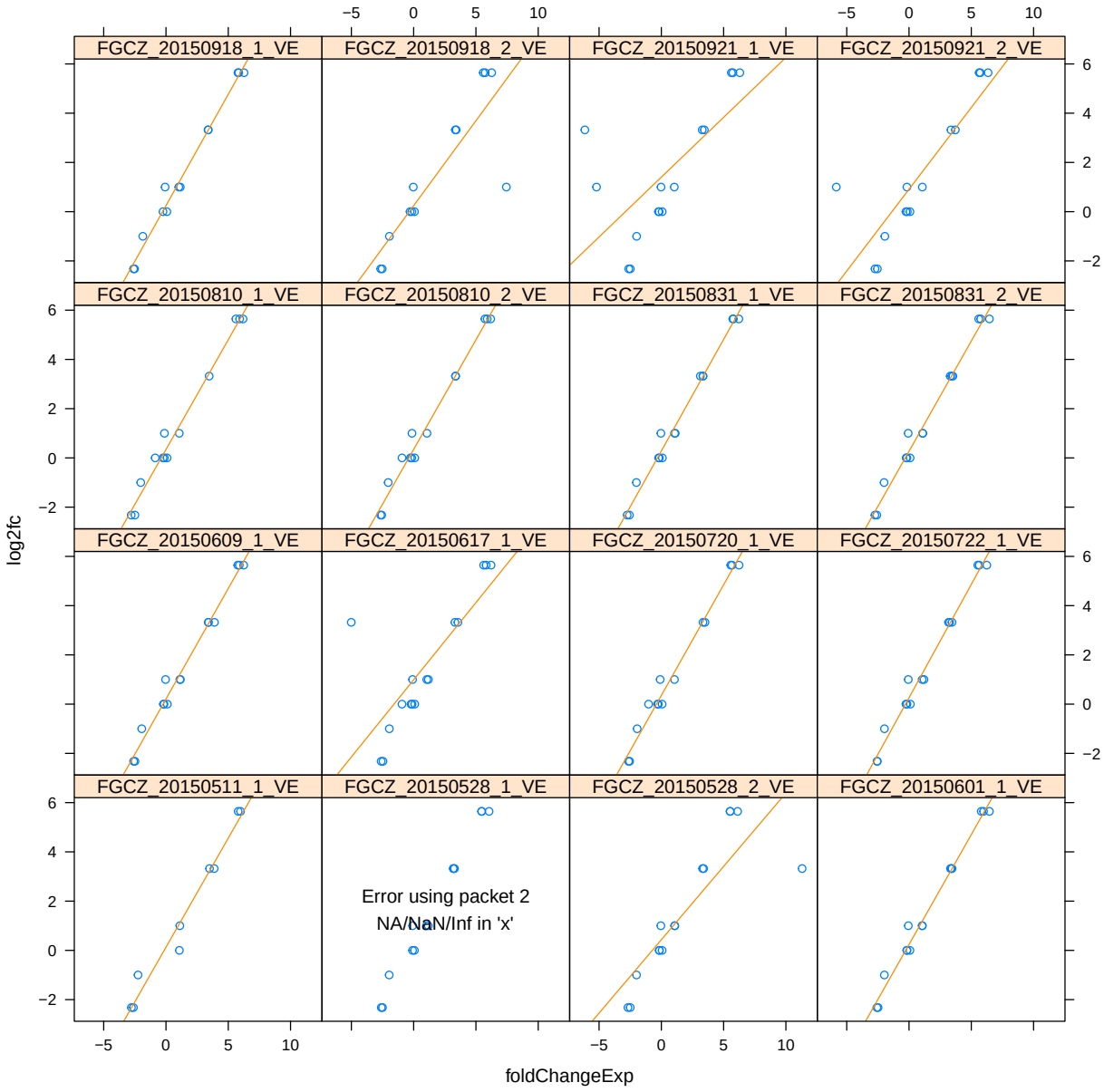
Looking at intensities msqc1

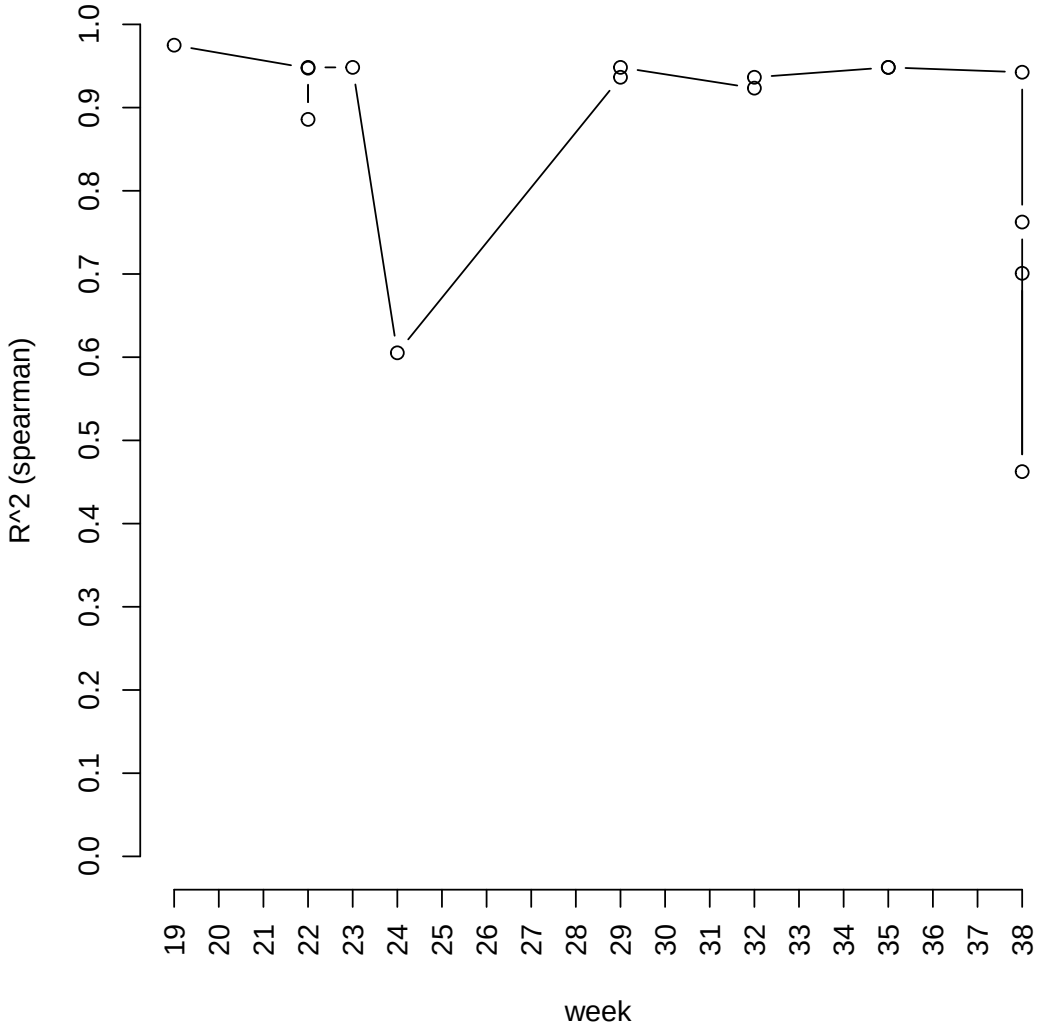



heavy
1
2
3
VLDALQAIK
VSFELFADK
NLSVEDAAR
SADFTNFDPR
GGPFSDSYR
GYSIFSYATK
FEDENFILK
GAGAFGYFEVTHDITK
EGHLSPDIVAEQK
ESDTSYVSLK
ALIVLAHSER
AVQQPDGLAVLGIFLK
IntensityN.x
10^5
10^6
10^7
10^8
10^9
20
25
30
35
week

Fold change


H/L
1
2
3
VLDALQAIK
VSFELFADK
NLSVEDAAR
SADFTNFDPR
GGPFSDSYR
GYSIFSYATK
FEDENFILK
GAGAFGYFEVTHDITK
EGHLSPDIVAEQK
ESDTSYVSLK
ALIVLAHSER
AVQQPDGLAVLGIFLK
log2(IntensityN.y/IntensityN.x)
week


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
Error using packet 2
NA/NaN/Inf in 'x'
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
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
week