

Analysing MaxQuant Output with R

FGC Zurich

30 September 2015

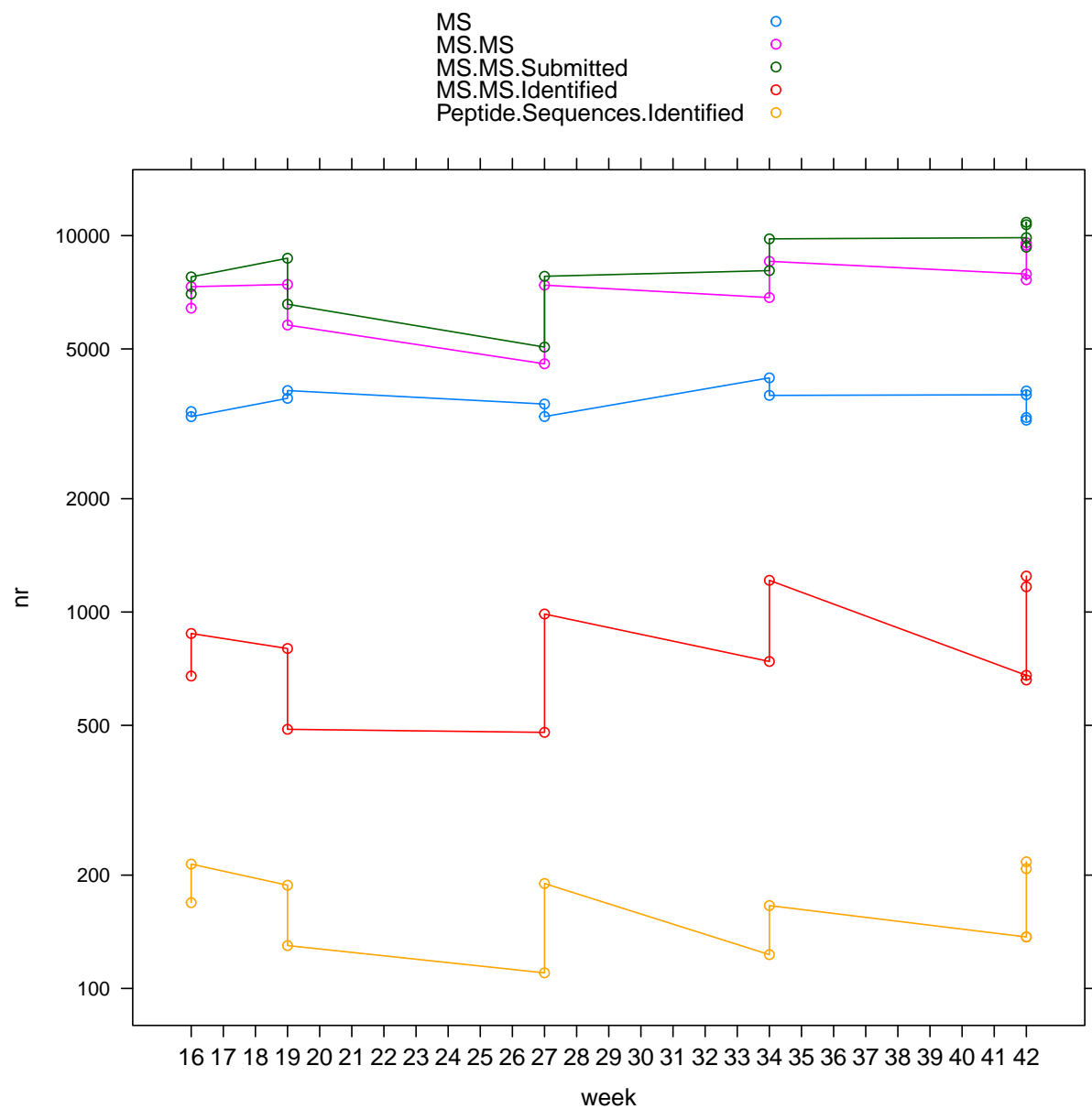
Contents

Prepare mrm table	1
Analysed Dataset is MPI_VE	2
Looking at measurement error	3
Looking at MSQC 1 peptide counts	4
Look at Intensities (by species)	5
Looking at intensities msqc1	6
Fold change	8

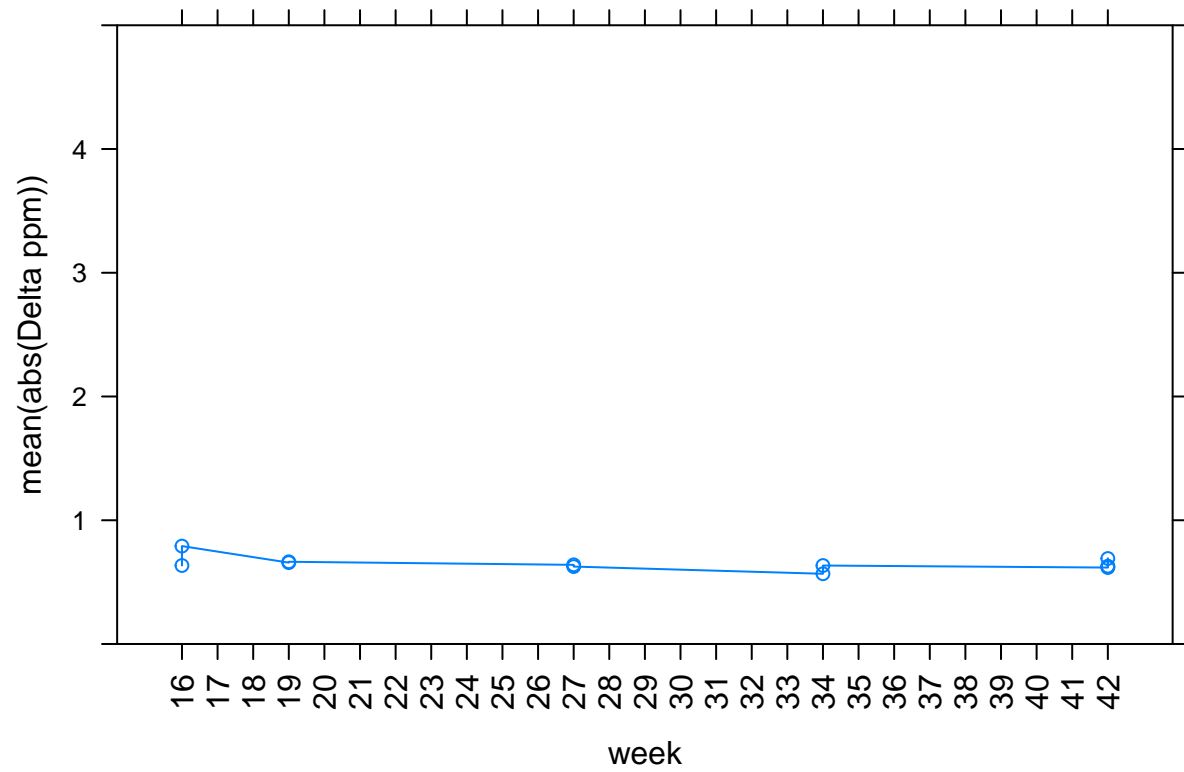
Prepare mrm table

- 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

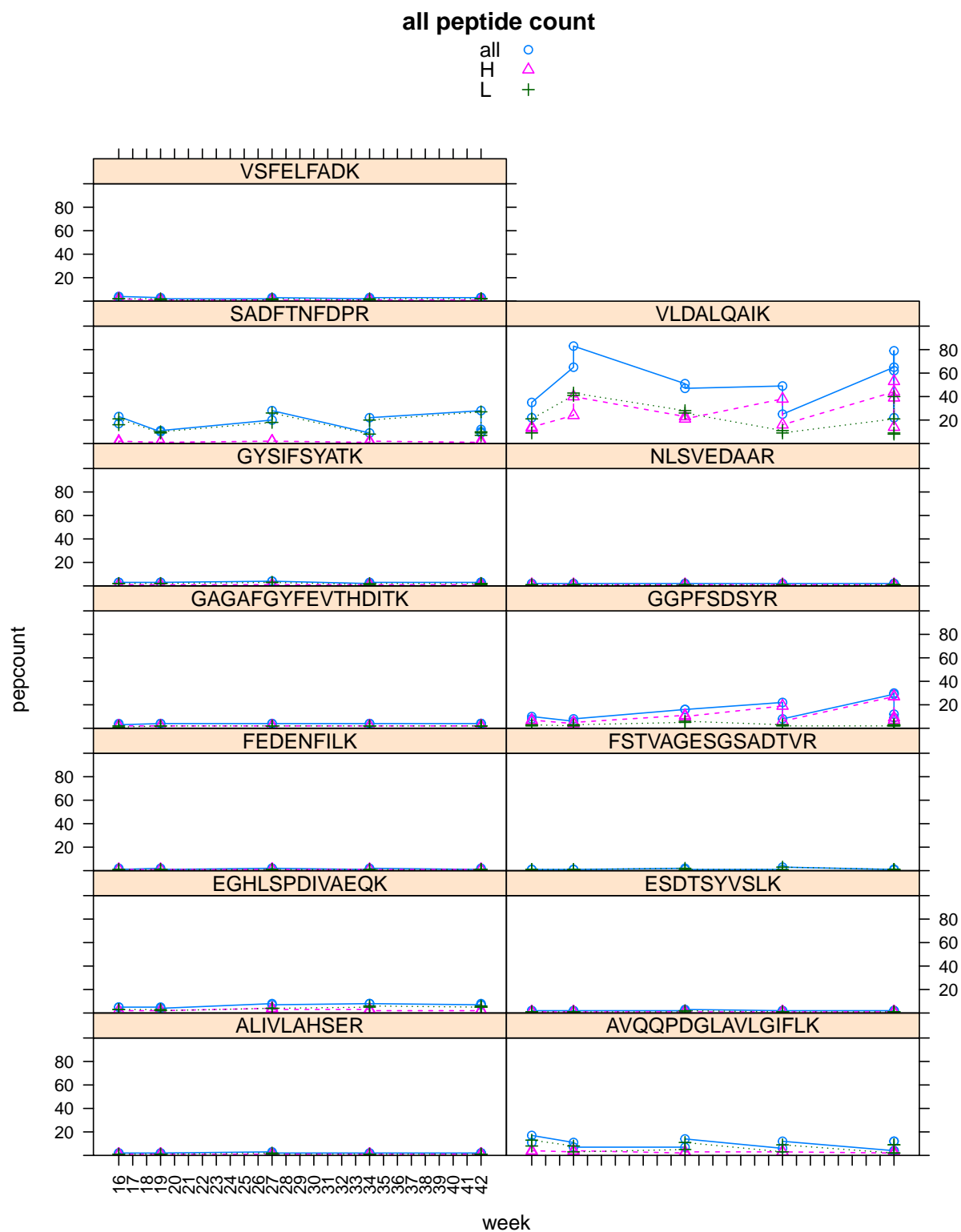
Analysed Dataset is MPI_VE



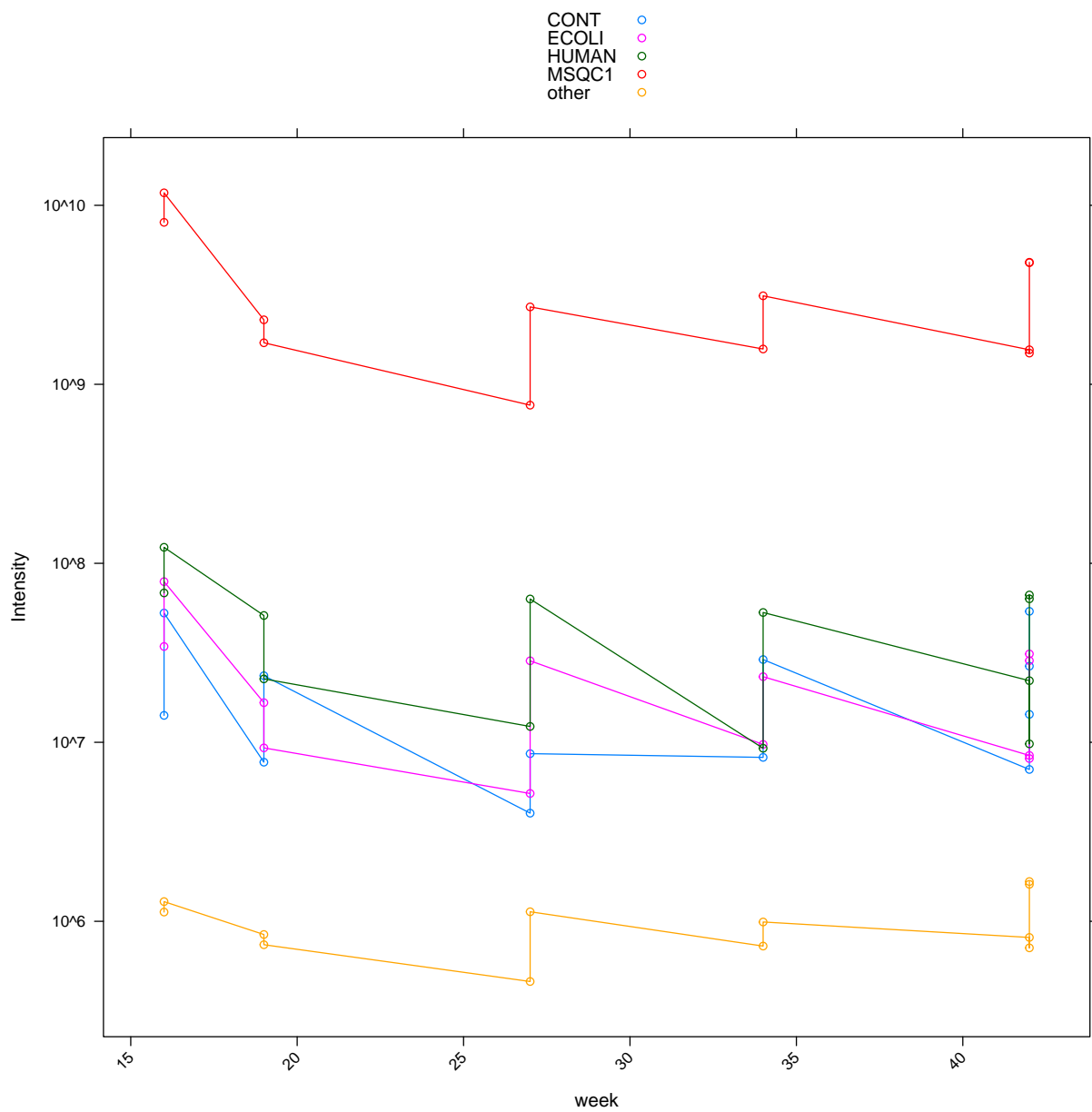
Looking at measurement error



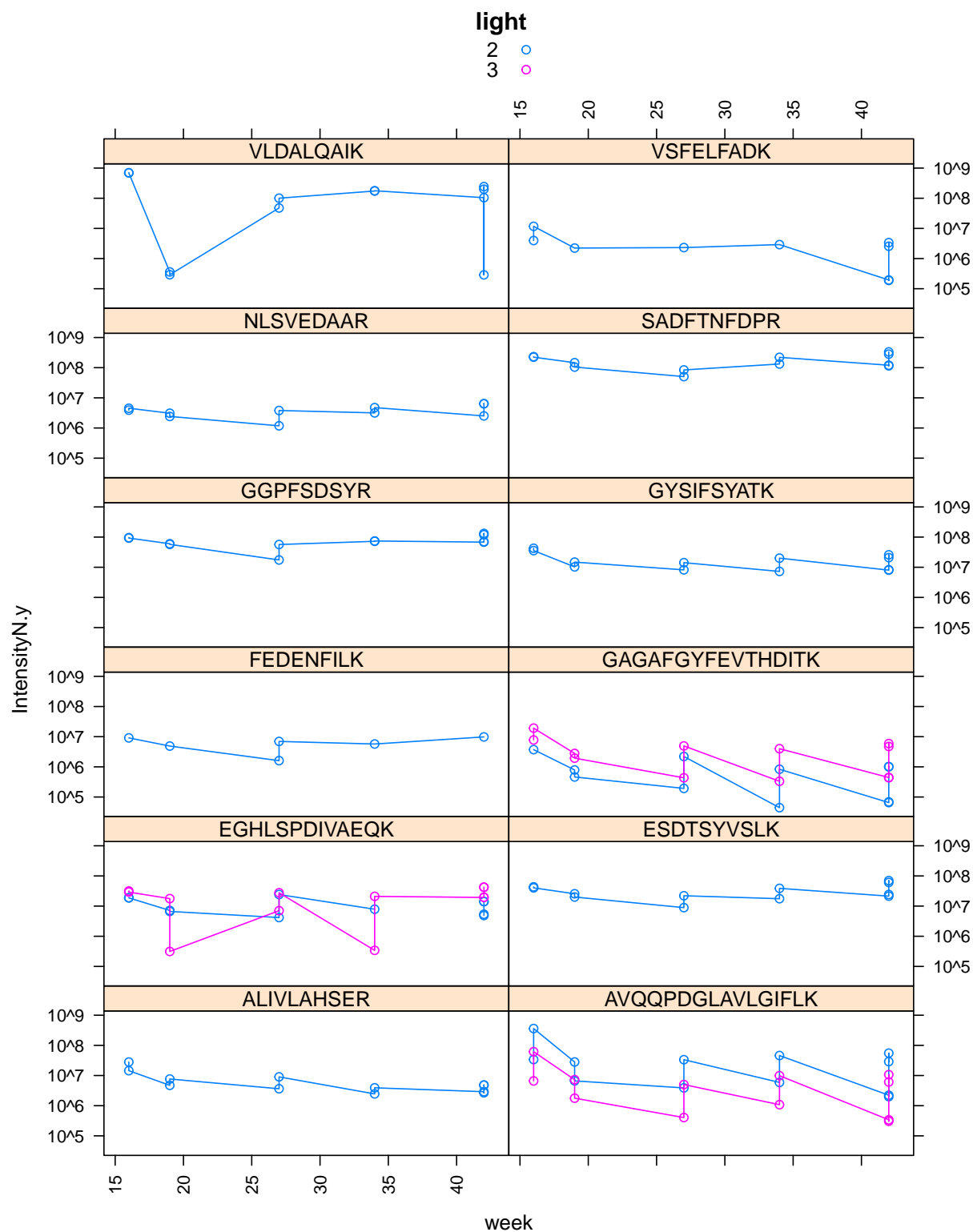
Looking at MSQC 1 peptide counts

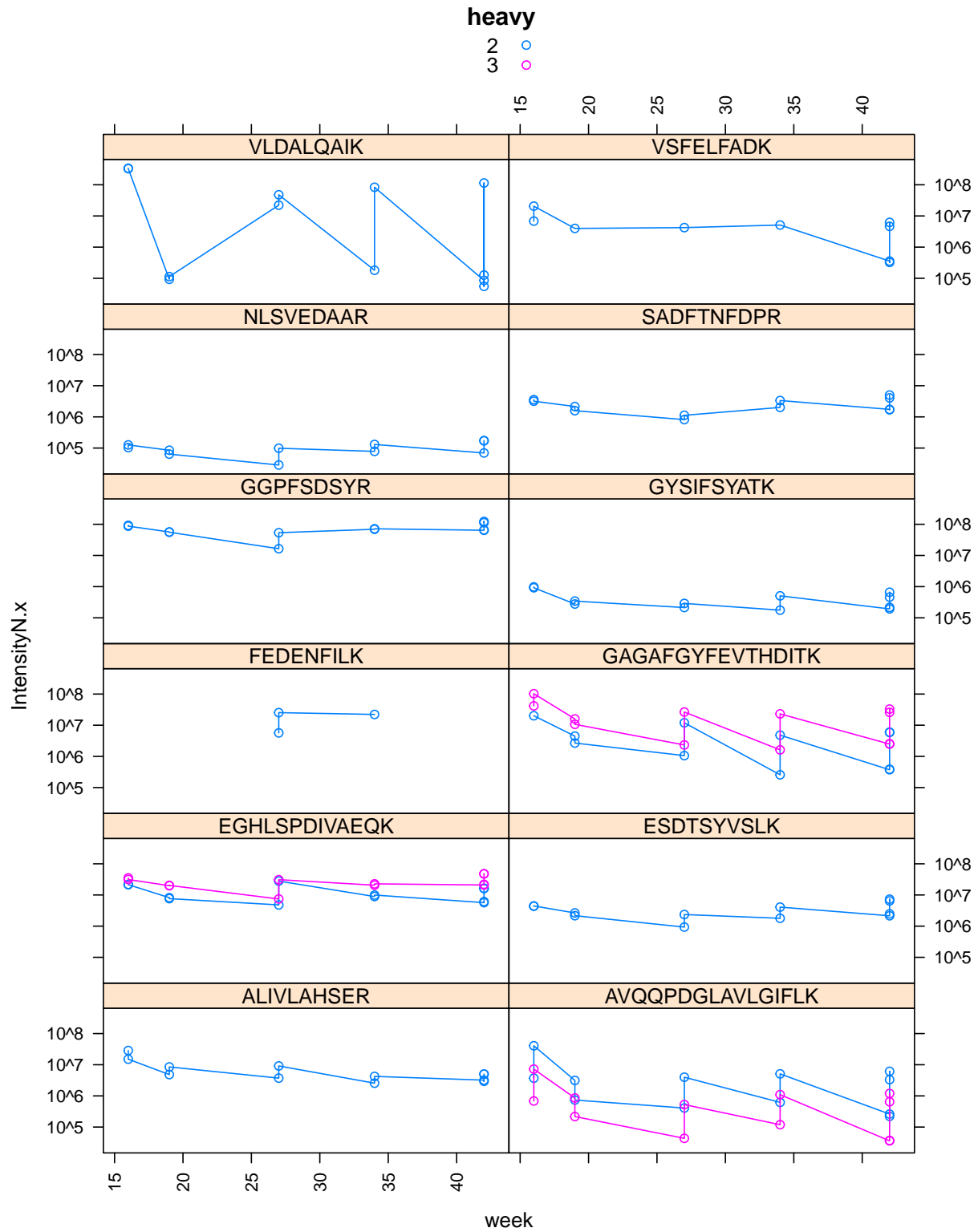


Look at Intensities (by species)



Looking at intensities msqc1





Fold change

