

# Analysing MaxQuant Output with R

*FGC Zurich*

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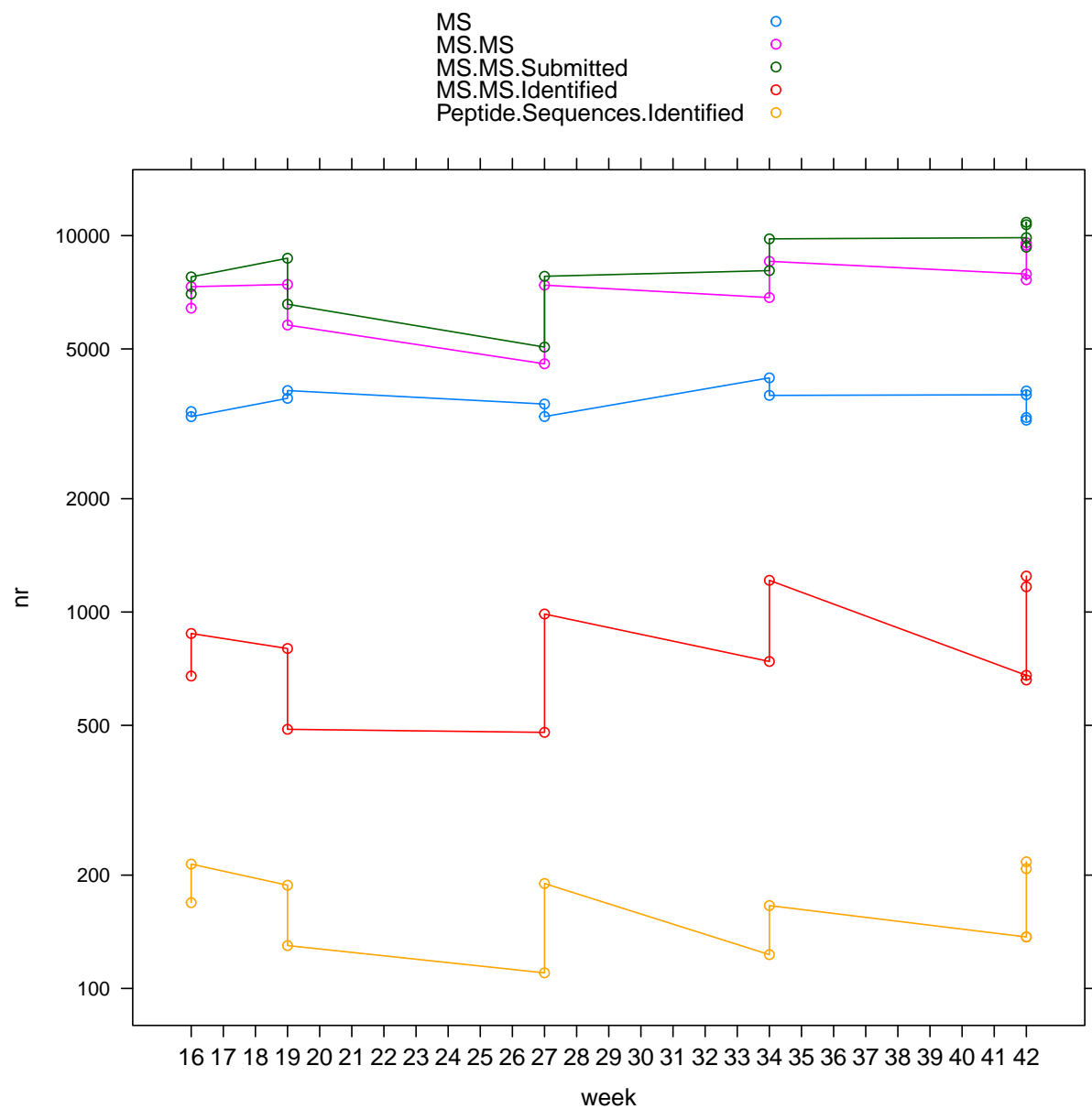
## Contents

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
Log fold change	8

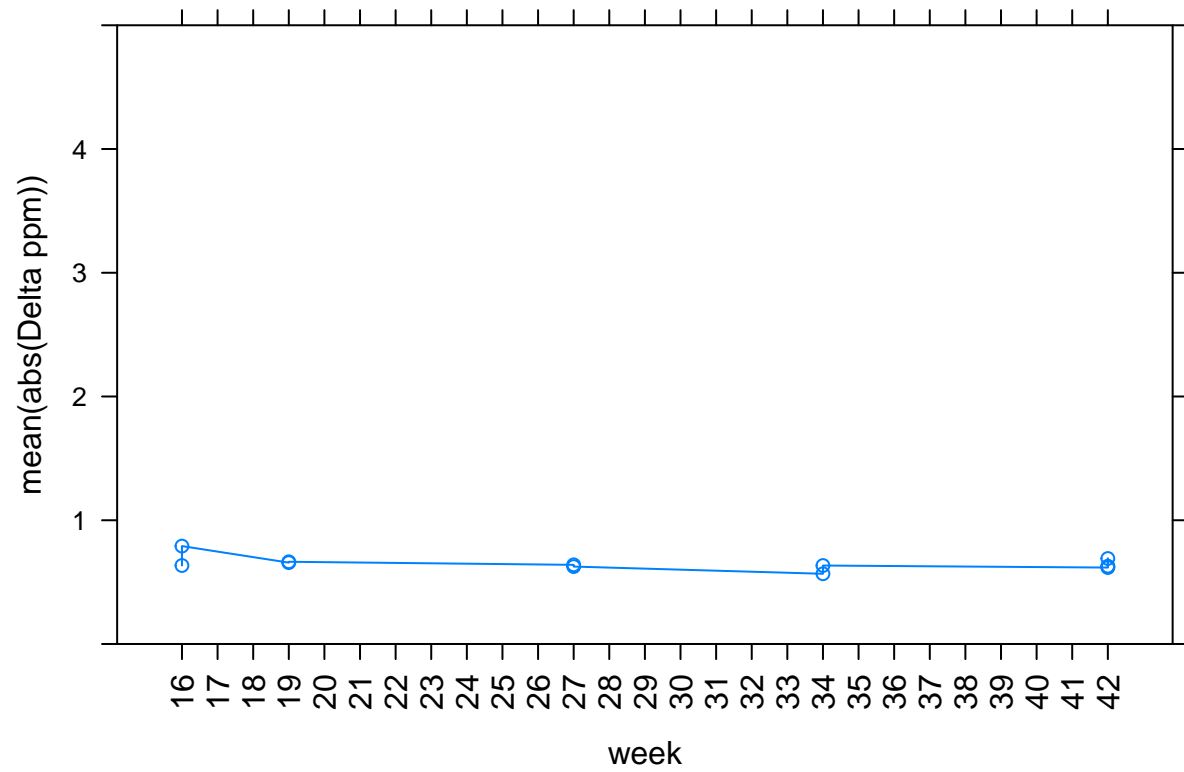
## Prepare mrm table

- 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

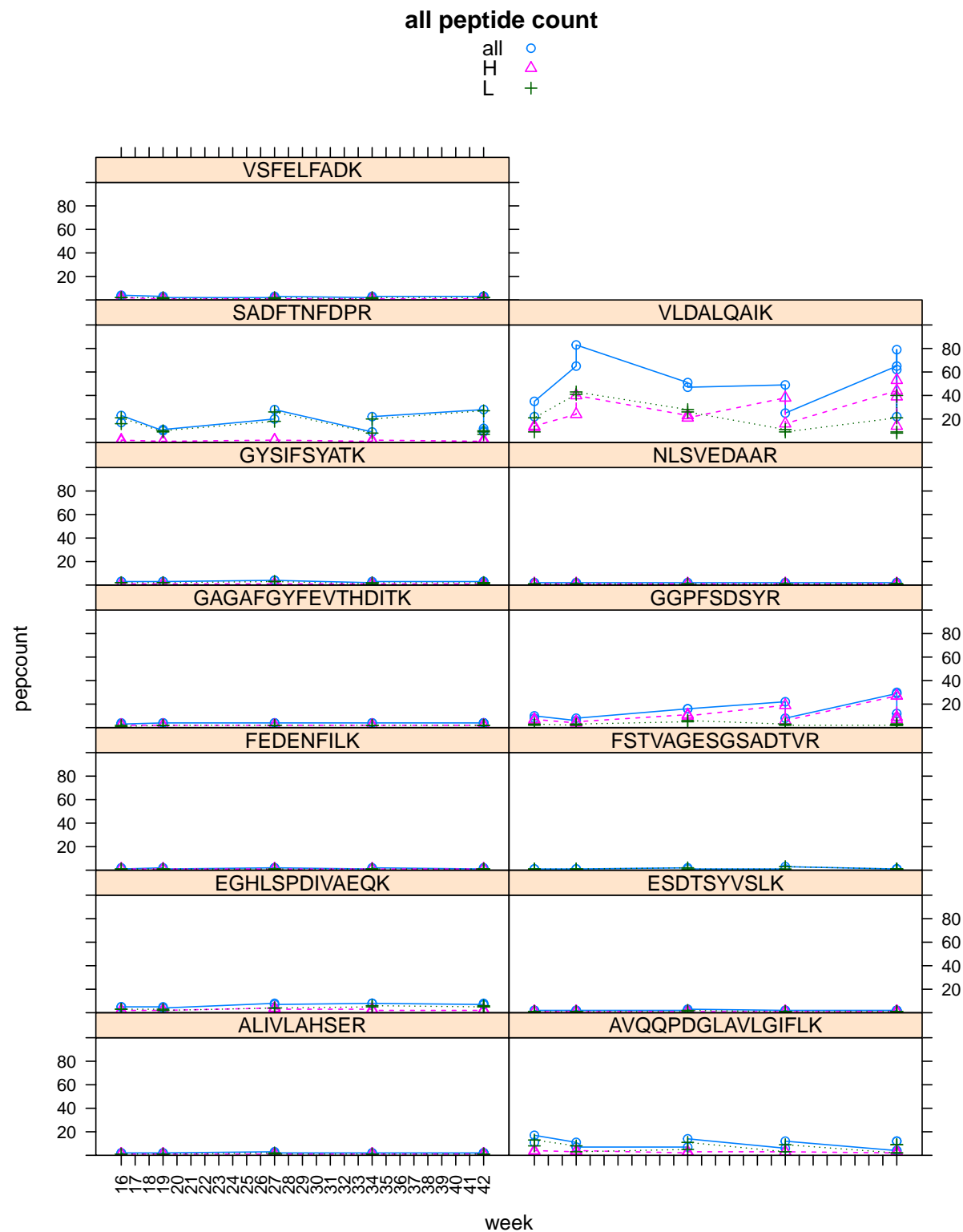
## Analysed Dataset is MPI\_VE



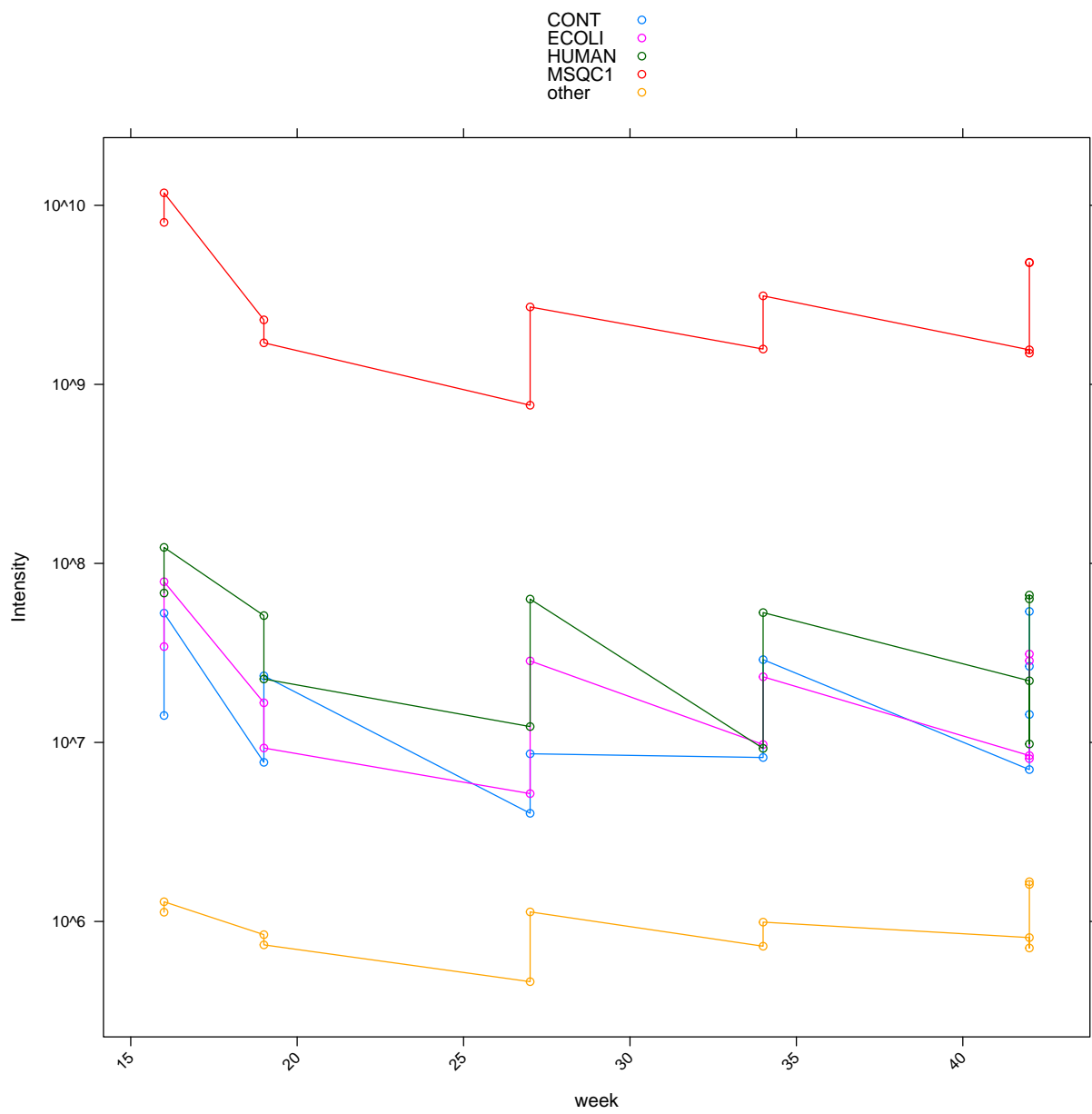
## Looking at measurement error



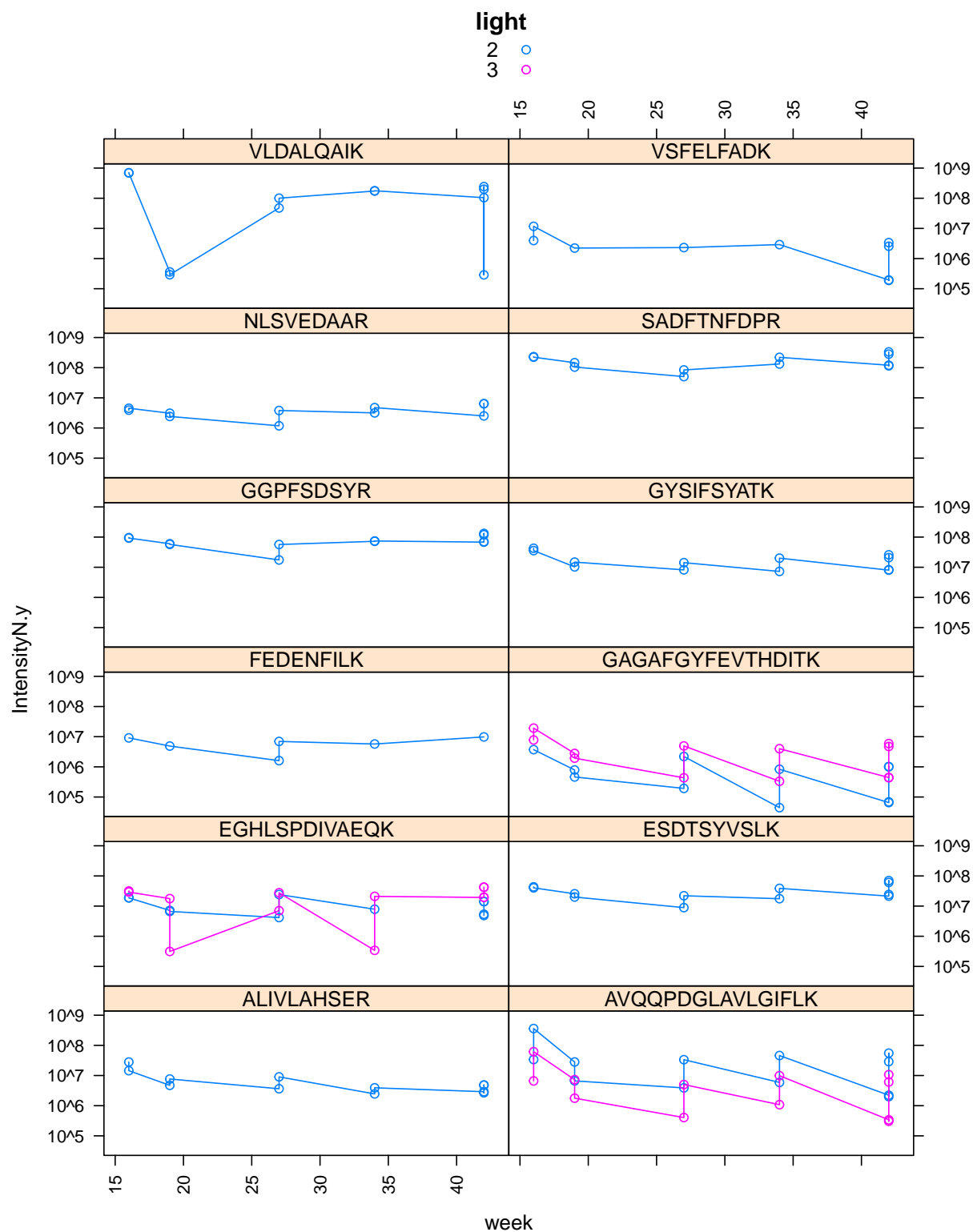
Looking at MSQC 1 peptide counts

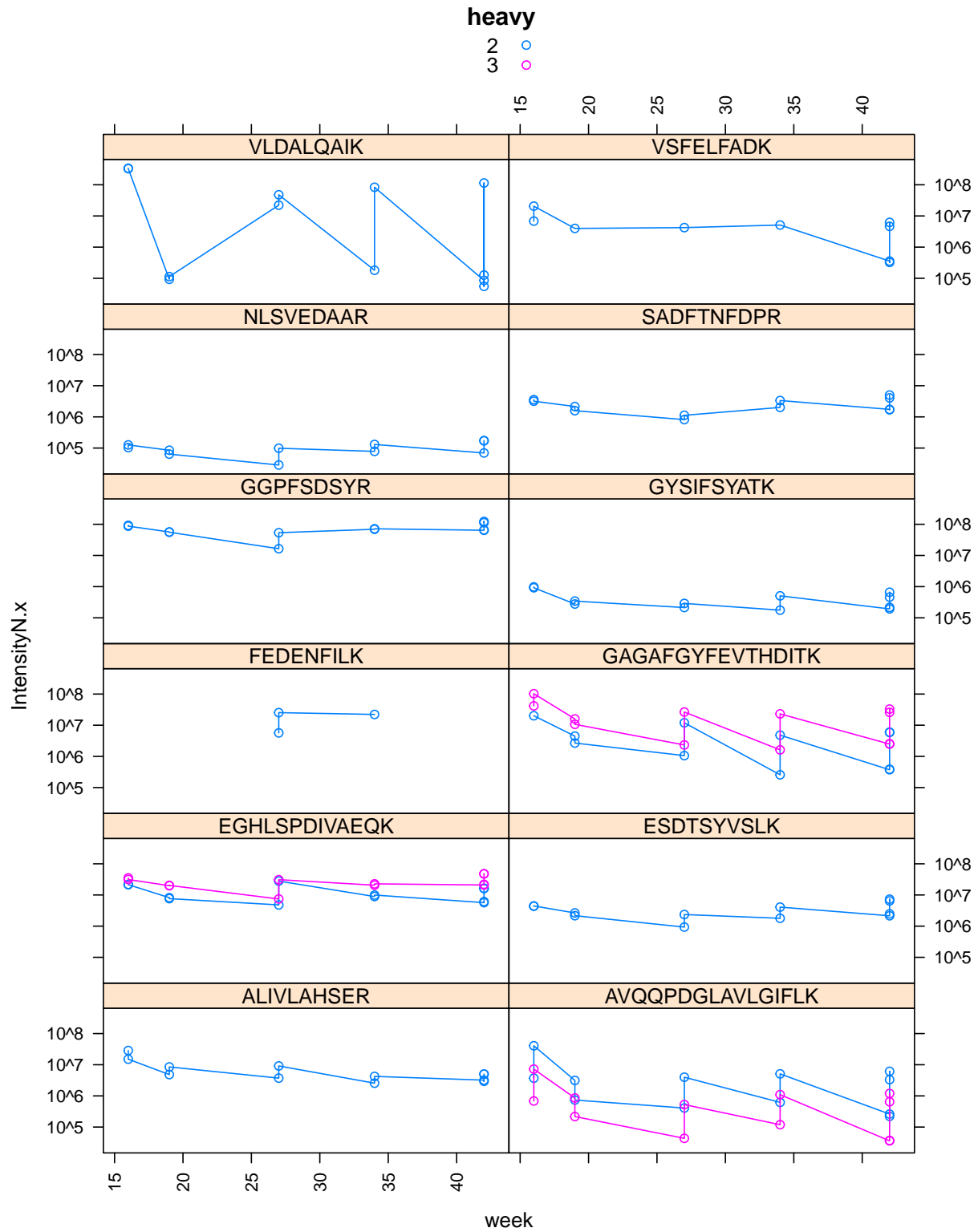


Look at Intensities (by species)



# Looking at intensities msqc1





Log fold change

