# Analysing MaxQuant Output with R

### FGC Zurich

#### 30 September 2015

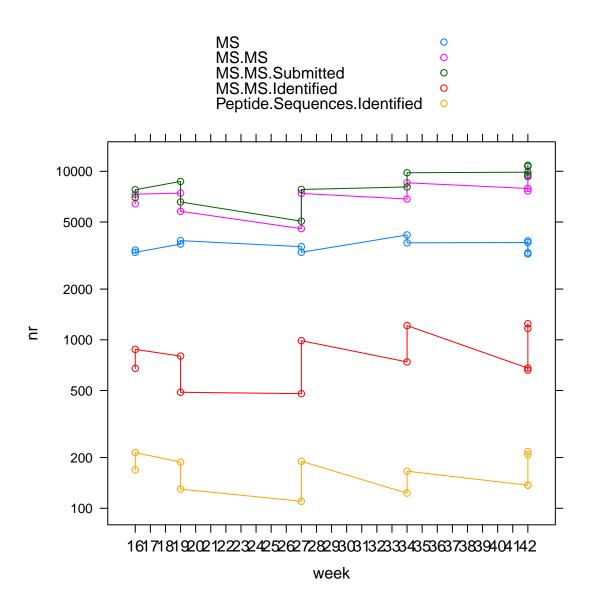
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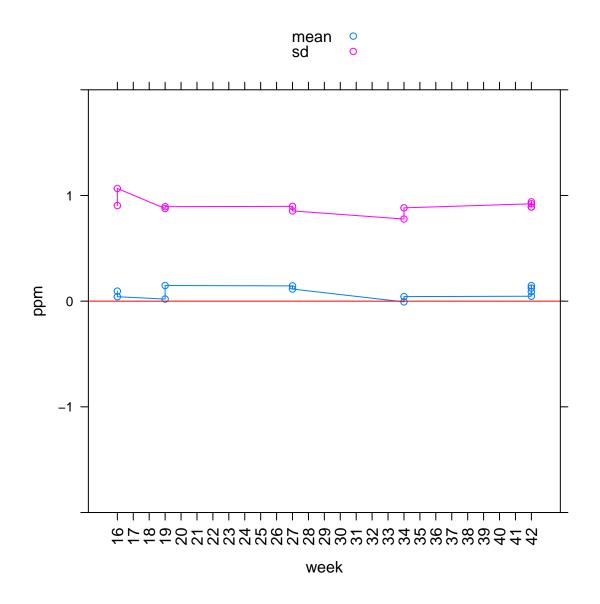
### Prepare mrm table

- 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 MPI\_VE



# Looking at measurement error



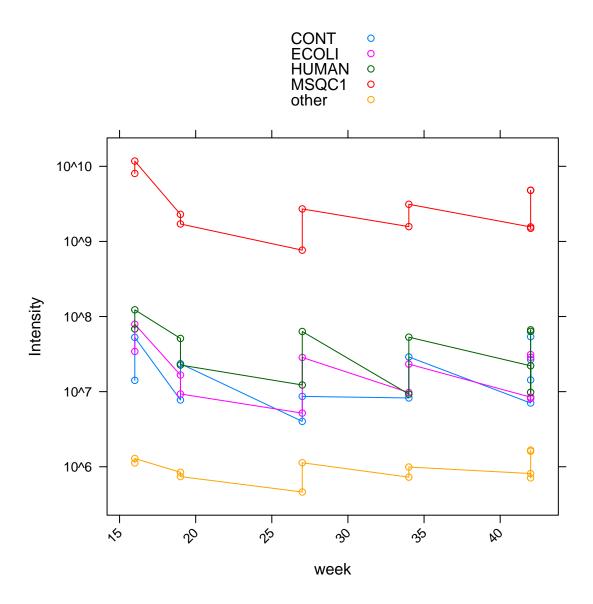
### Looking at MSQC 1 peptide counts

#### all peptide count . H+L H L **VLDALQAIK** SADFTNFDPR NLSVEDAAR **GYSIFSYATK GAGAFGYFEVTHDITK GGPFSDSYR** pepcount - 20 **FEDENFILK FSTVAGESGSADTVR** EGHLSPDIVAEQK ESDTSYVSLK AVQQPDGLAVLGIFLK ALIVLAHSER

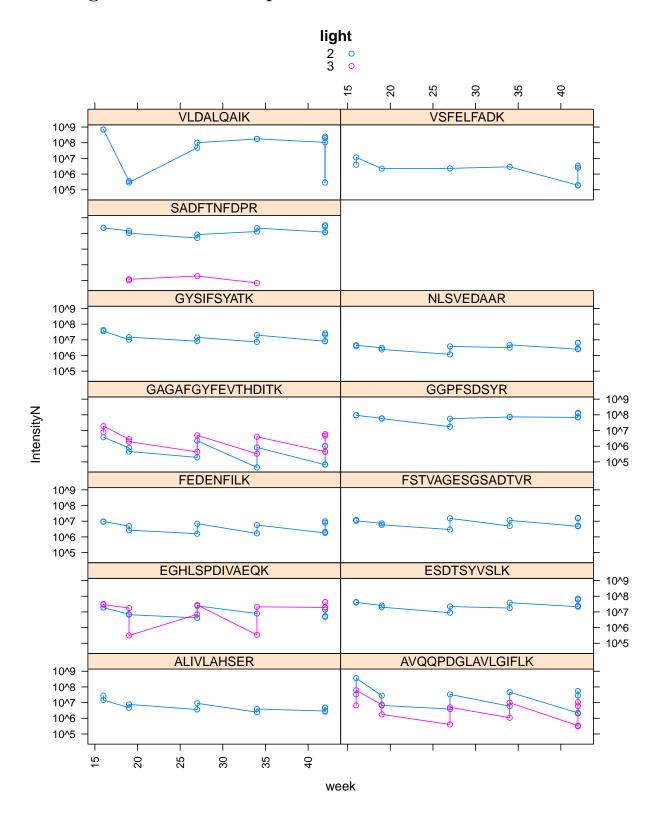
week

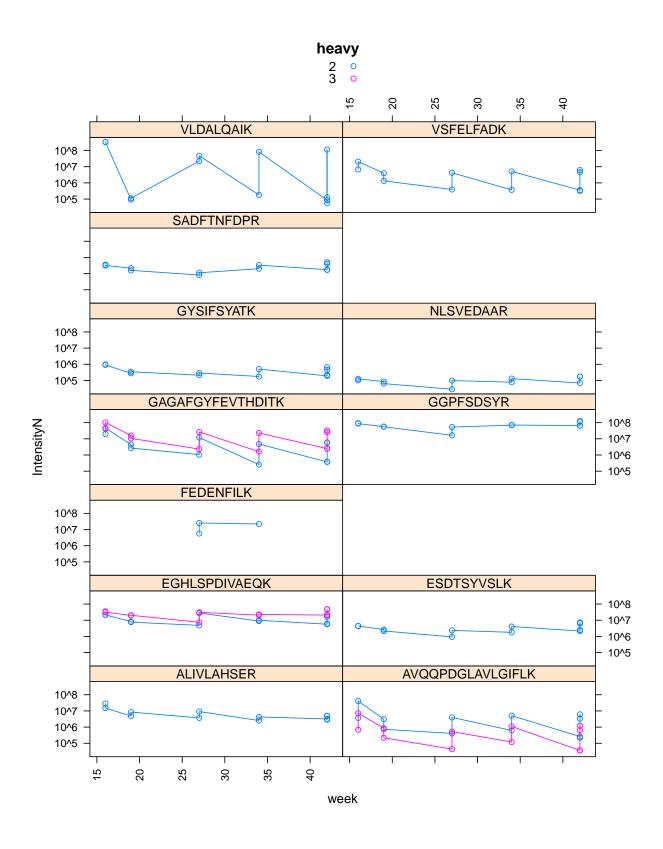
 $^{+++}$ 

# Look at Intensities (by species)

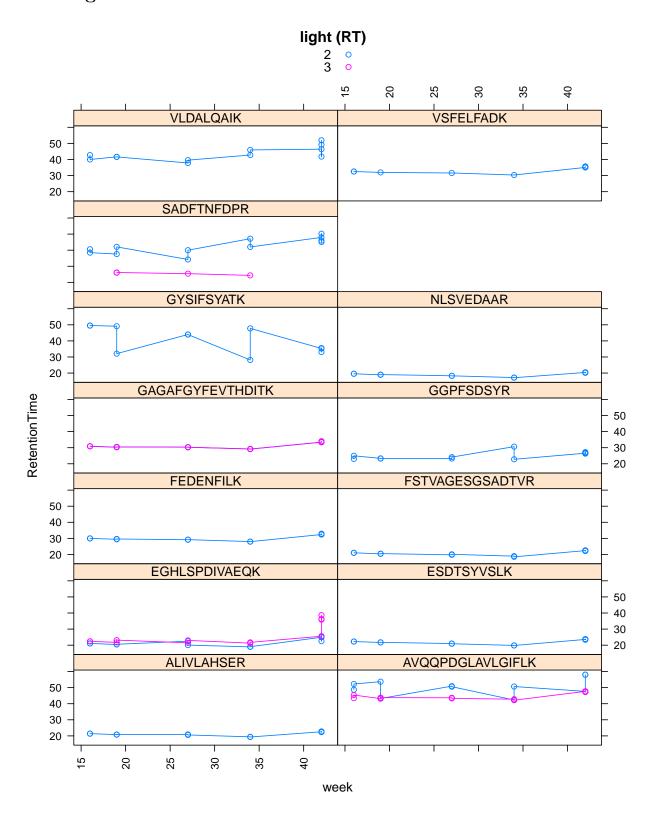


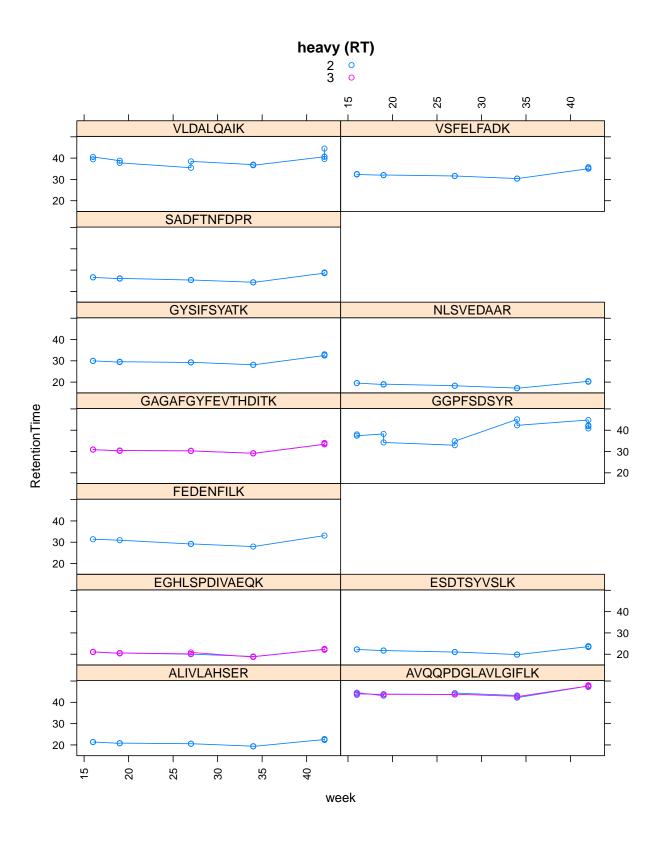
### Looking at intensities msqc1





### Looking at retention time





### Log fold change

## Warning in inner\_join\_impl(x, y, byx, byy): joining factors with ## different levels, coercing to character vector

