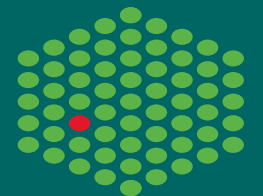


Updates Proteomics Core Facility Heidelberg

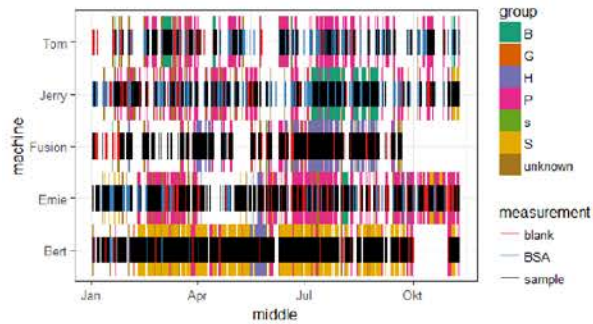
Frank Stein

EMBL



Pipeline

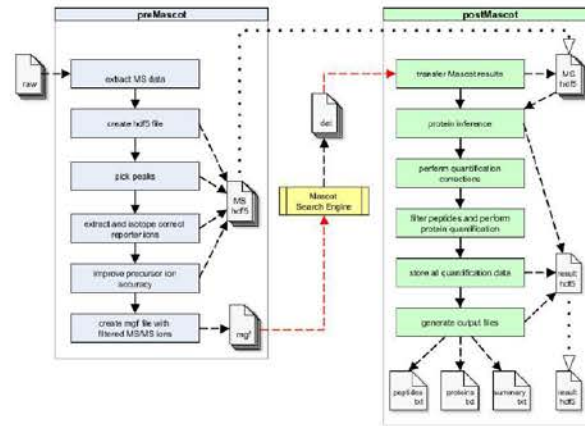
automatic monitoring of instrument usage



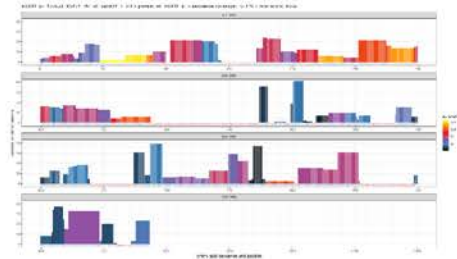
automatic file copying to server



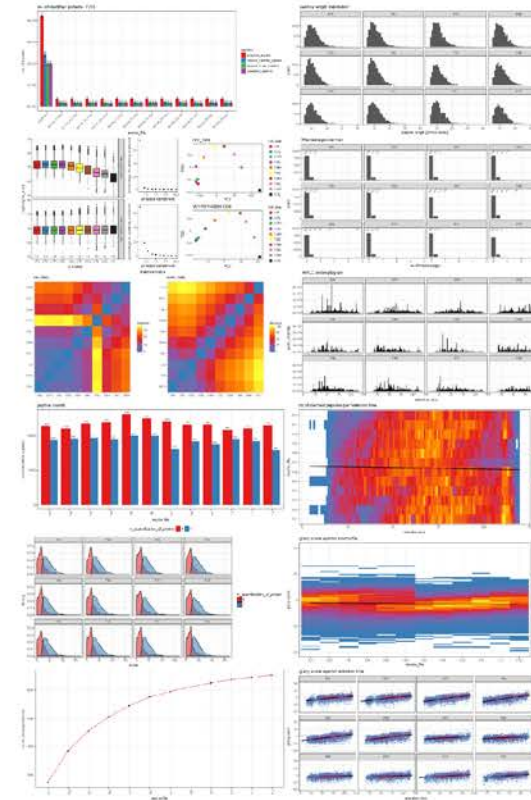
automatic start and progress report on raw data



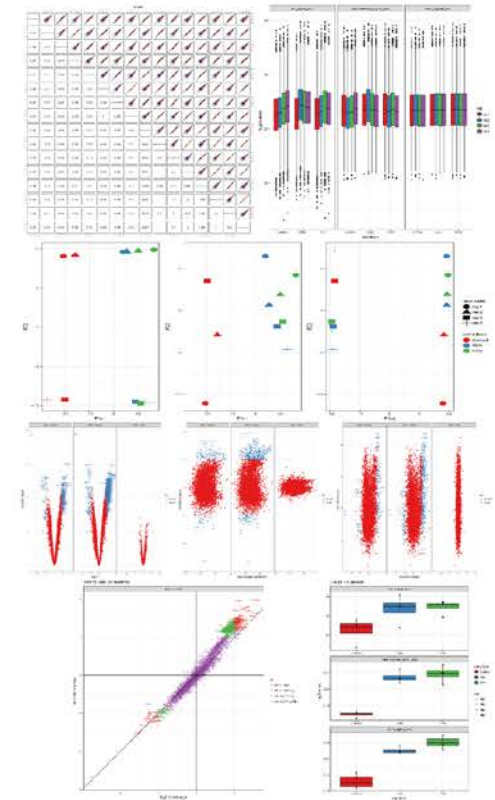
automatic protein coverage analysis



automatic generation of QC plots



customized statistical data analysis



LOOKING FOR AN ALTERNATIVE TO ISOBARQUANT

SpectroMine from Biognosys to replace IsobarQuant

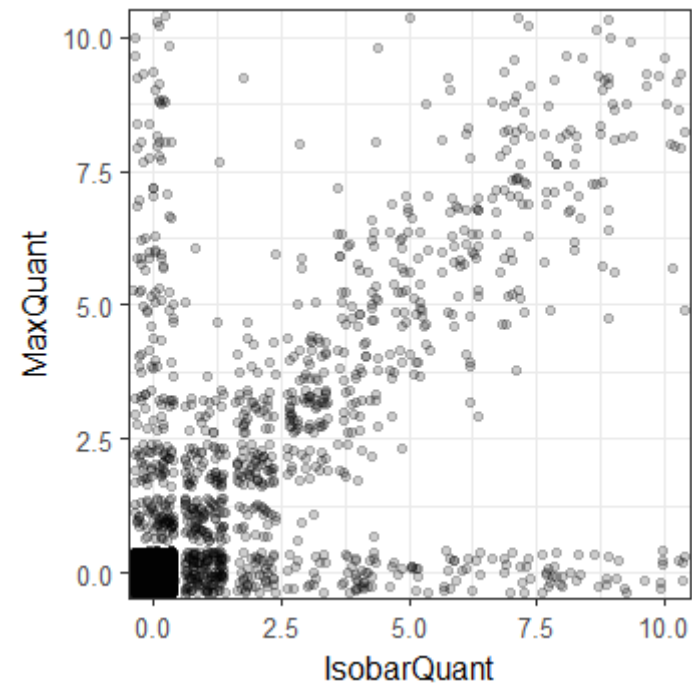
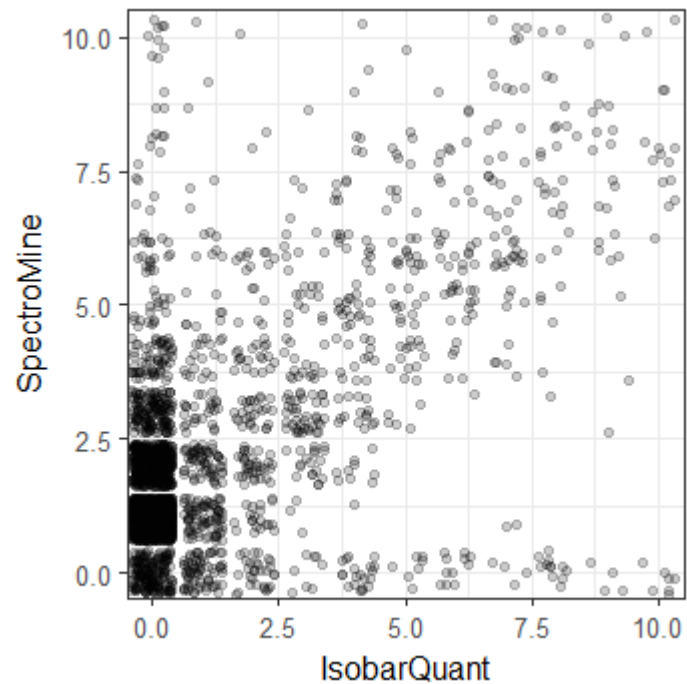
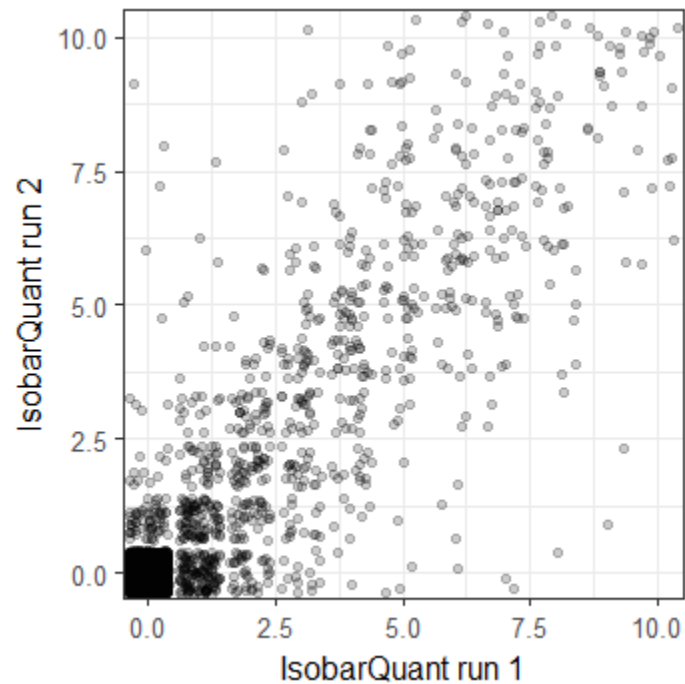
- Advantages:
 - Super fast
 - Intuitive User Interface
 - Command line interface
 - Customizable output sheets
 - Fast responding developer team
 - Versatile quantification
 - Commercial
- Disadvantages:
 - Commercial
 - Embed it again into the „system“



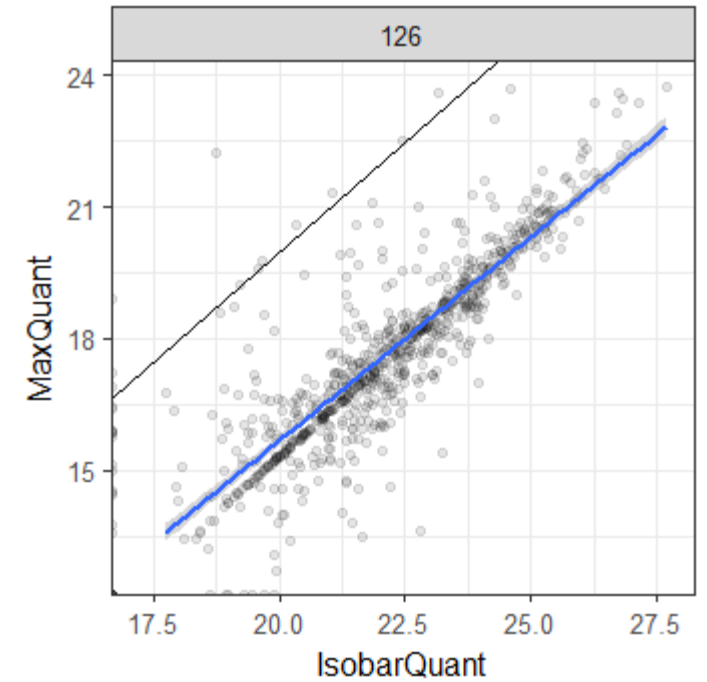
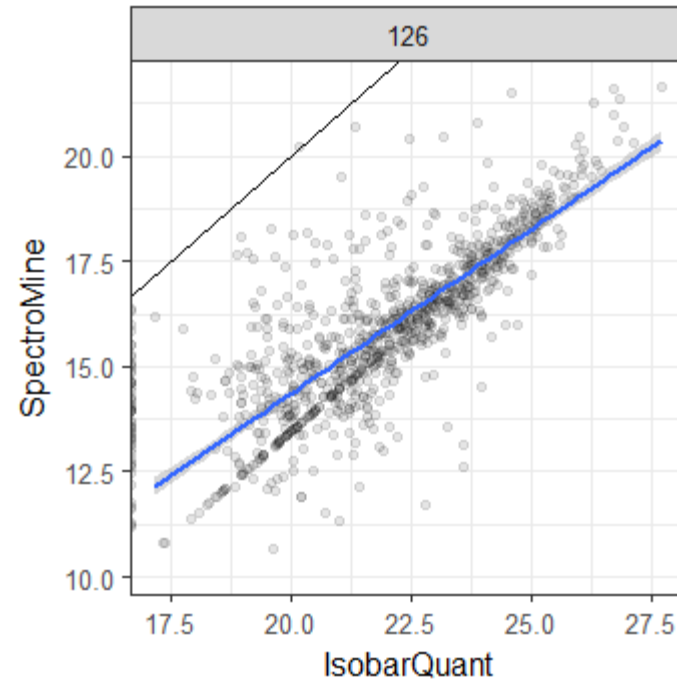
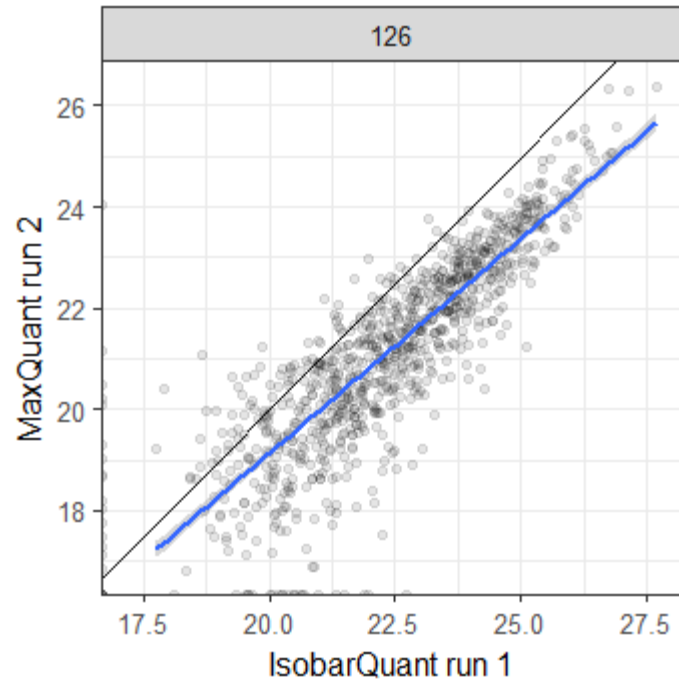
Comparitive analysis on QC sample (same raw file)

ISOBARQUANT VS SPECTROMINE

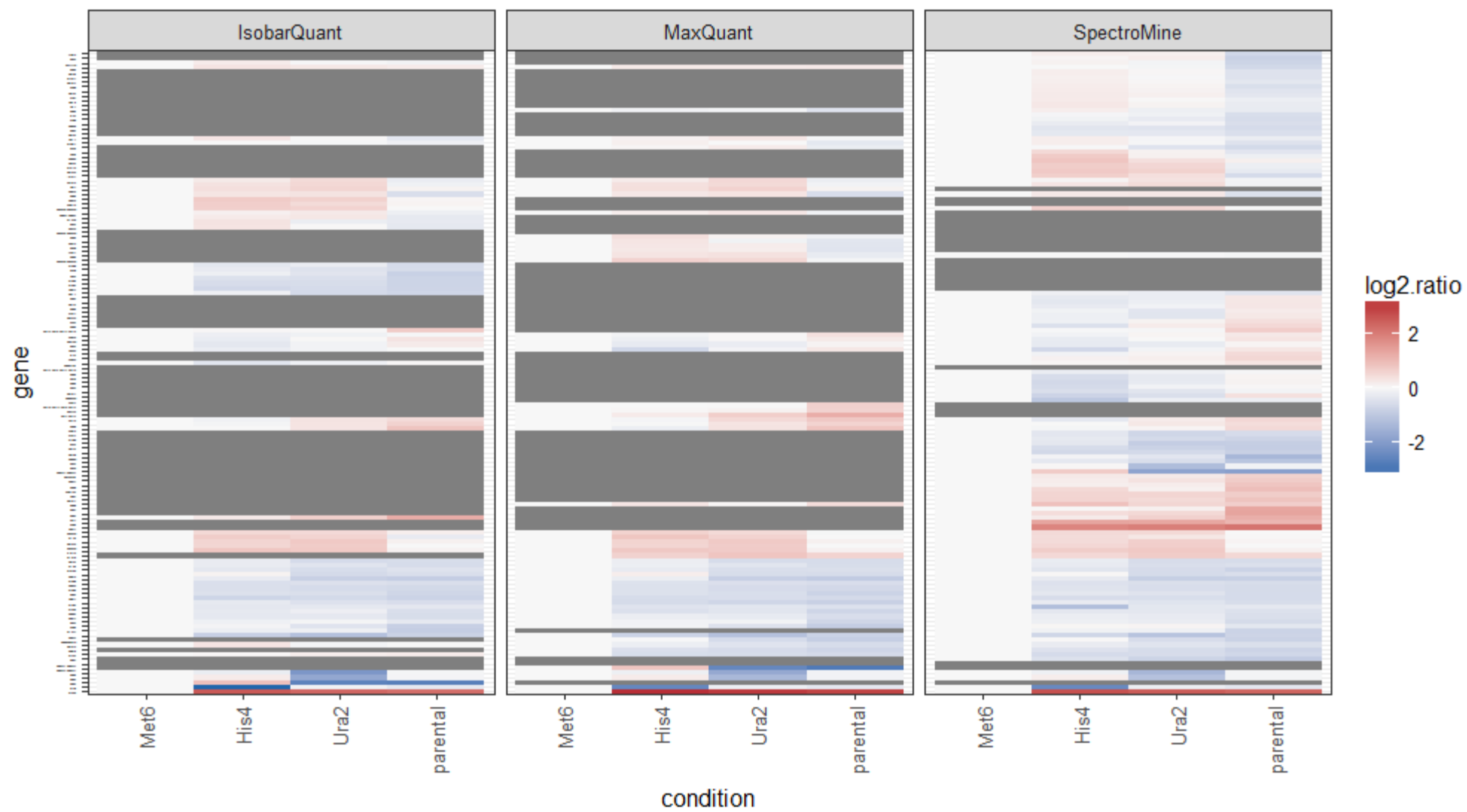
Correlation of number of unique peptides



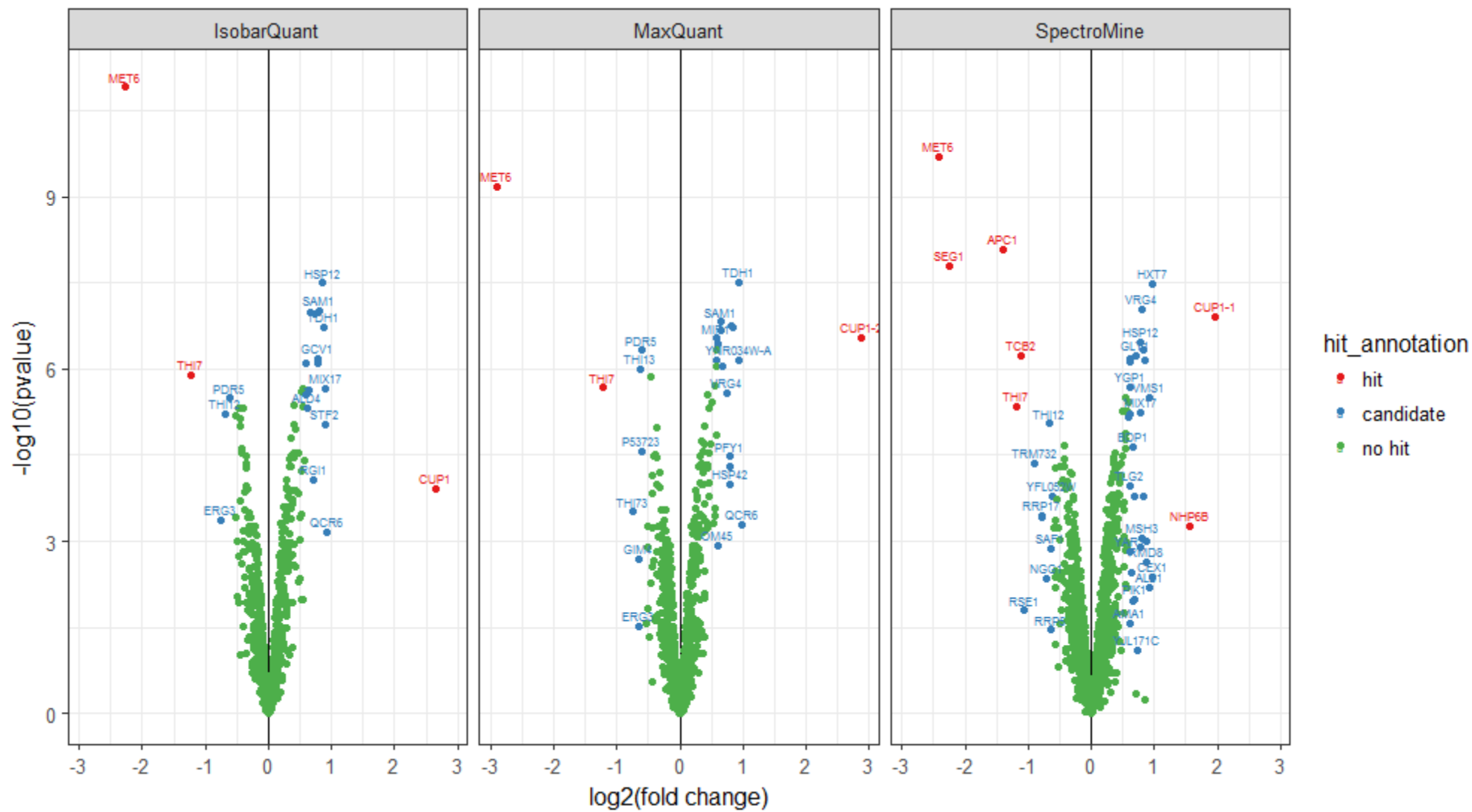
Correlation of TMT reporter ion intensity (sum)



Heatmap



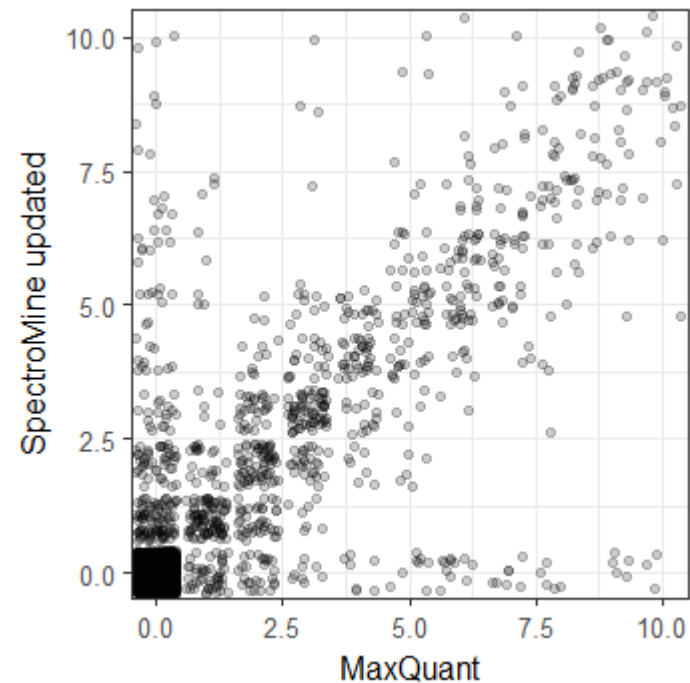
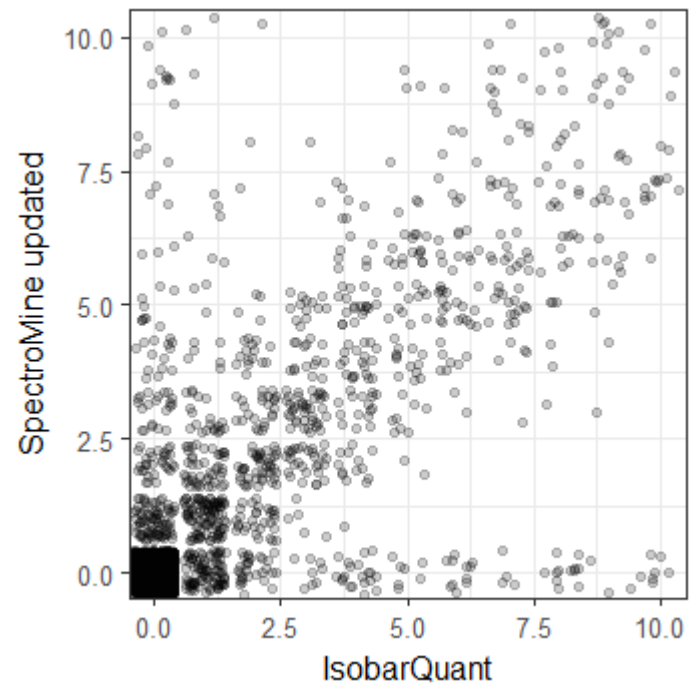
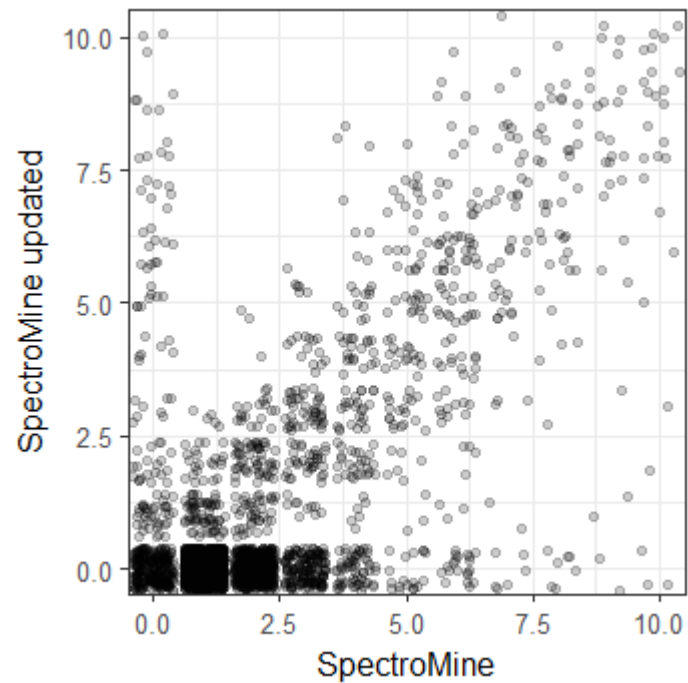
Statistical comparison Met6 KO against parental



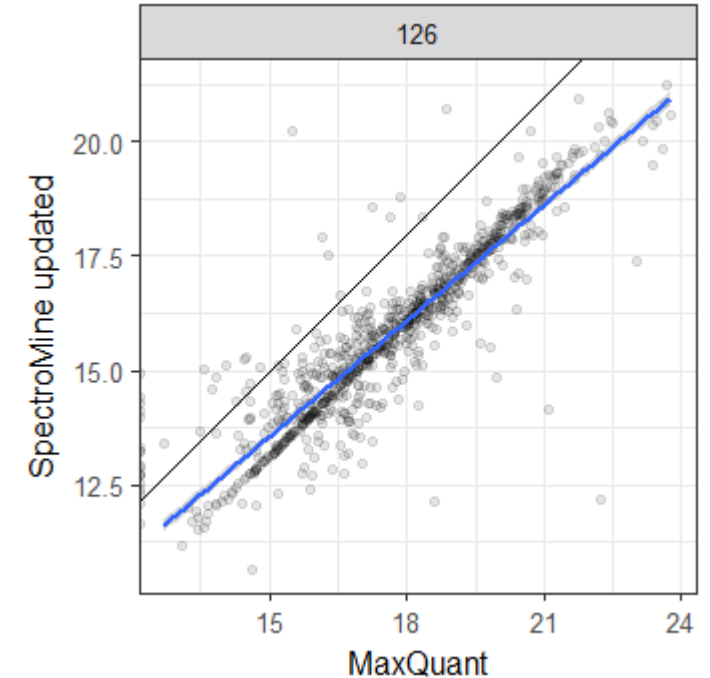
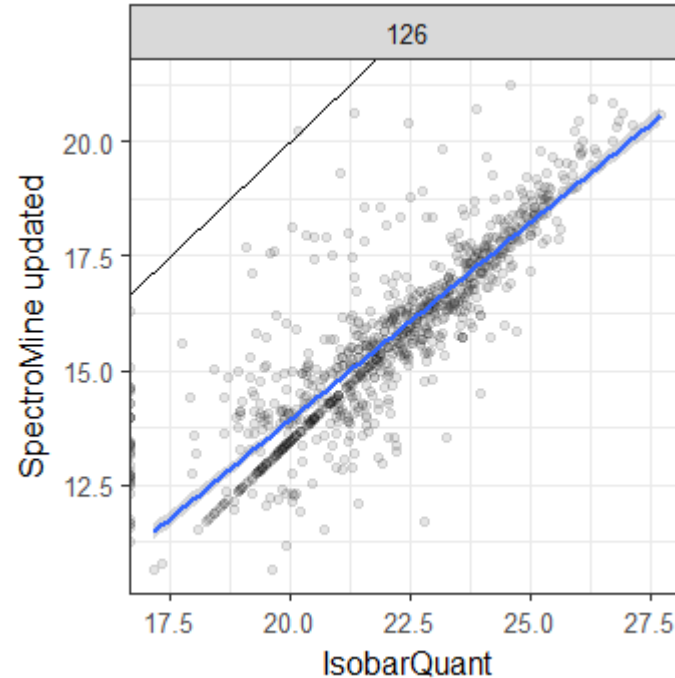
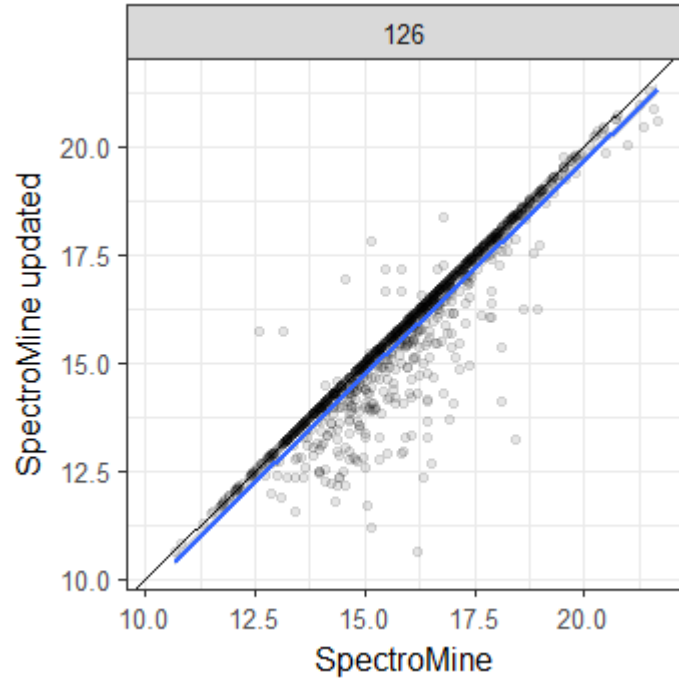
Comparitive analysis on QC sample (same raw file)

ISOBARQUANT VS SPECTROMINE AFTER UPDATE

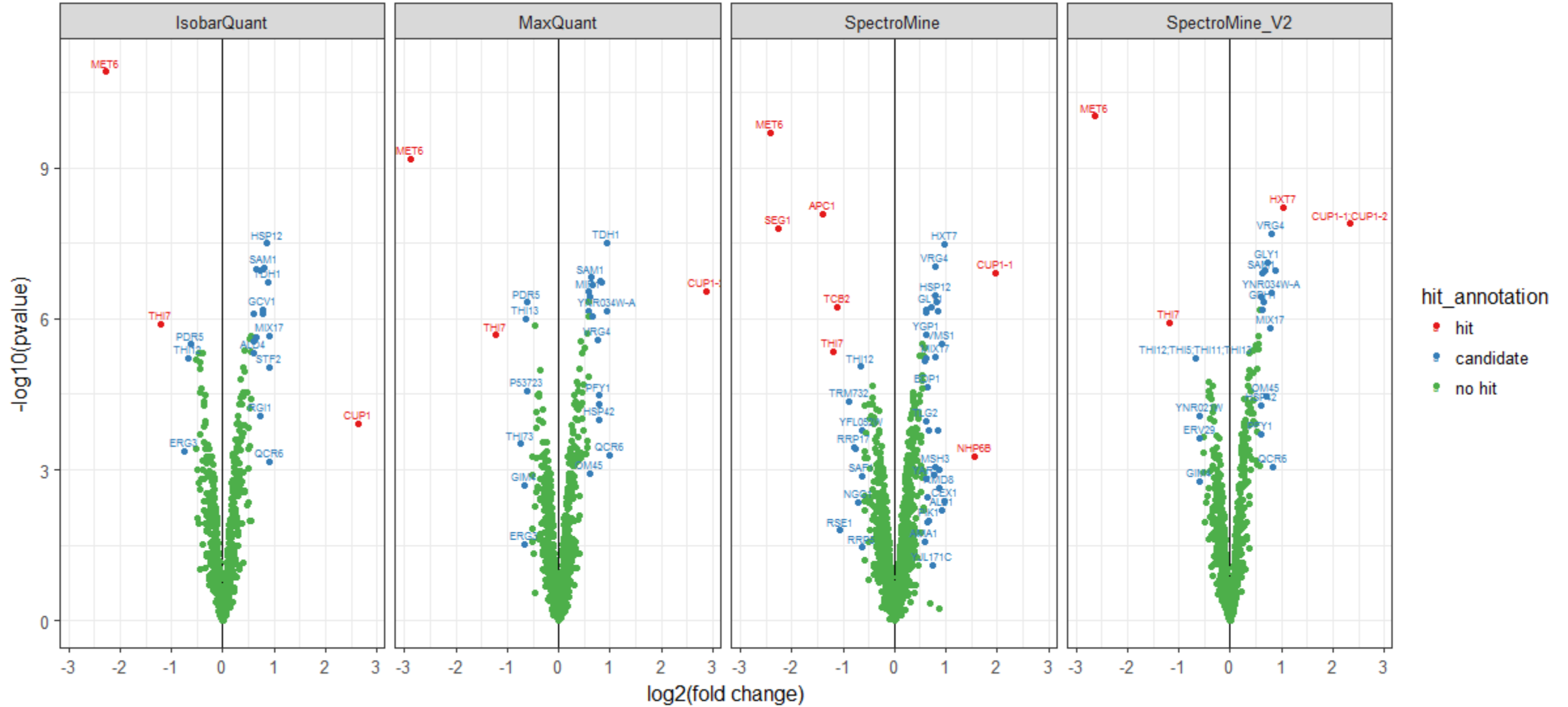
Correlation of number of unique peptides after SpectroMine update



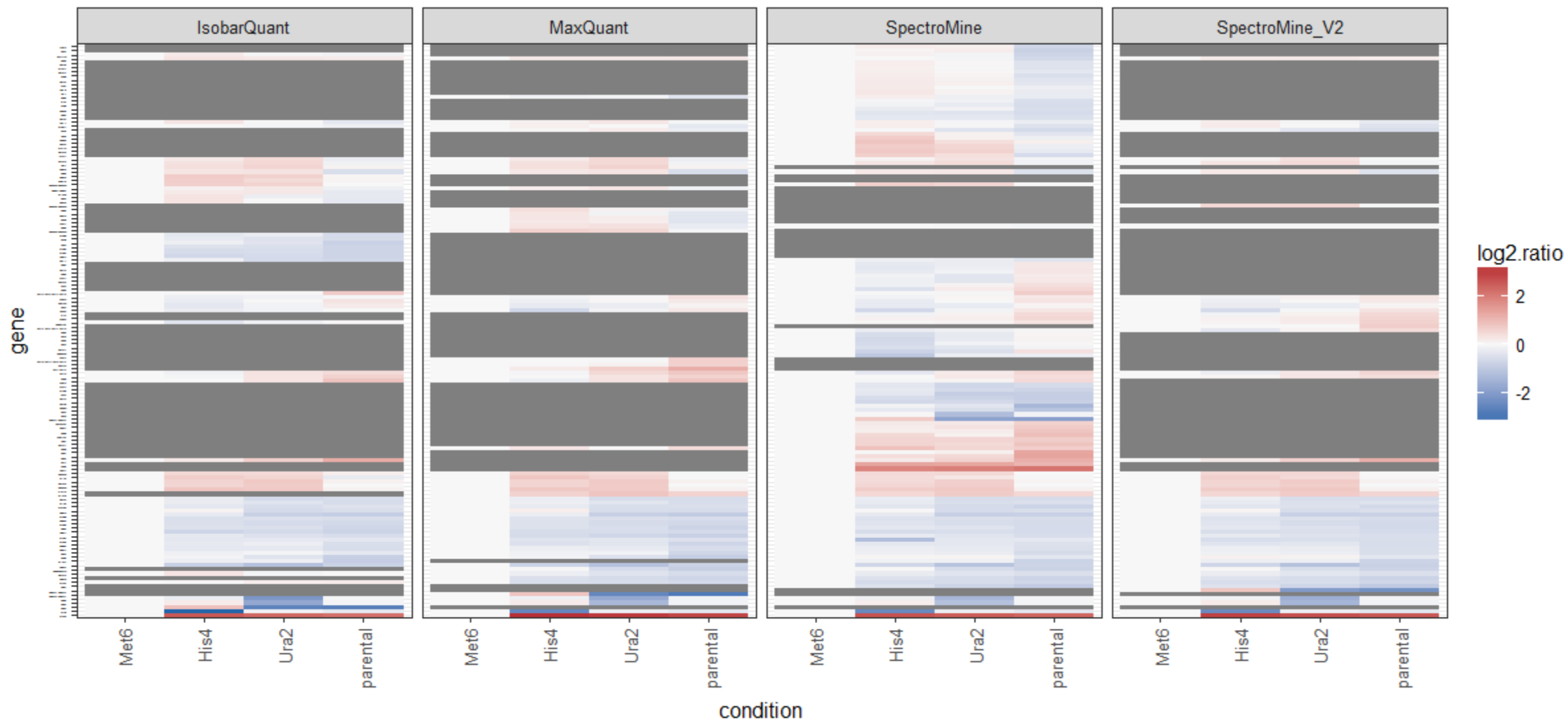
Correlation of TMT reporter ion intensity (sum) after SpectroMine update



Statistical comparison after update – Met6 KO against parental



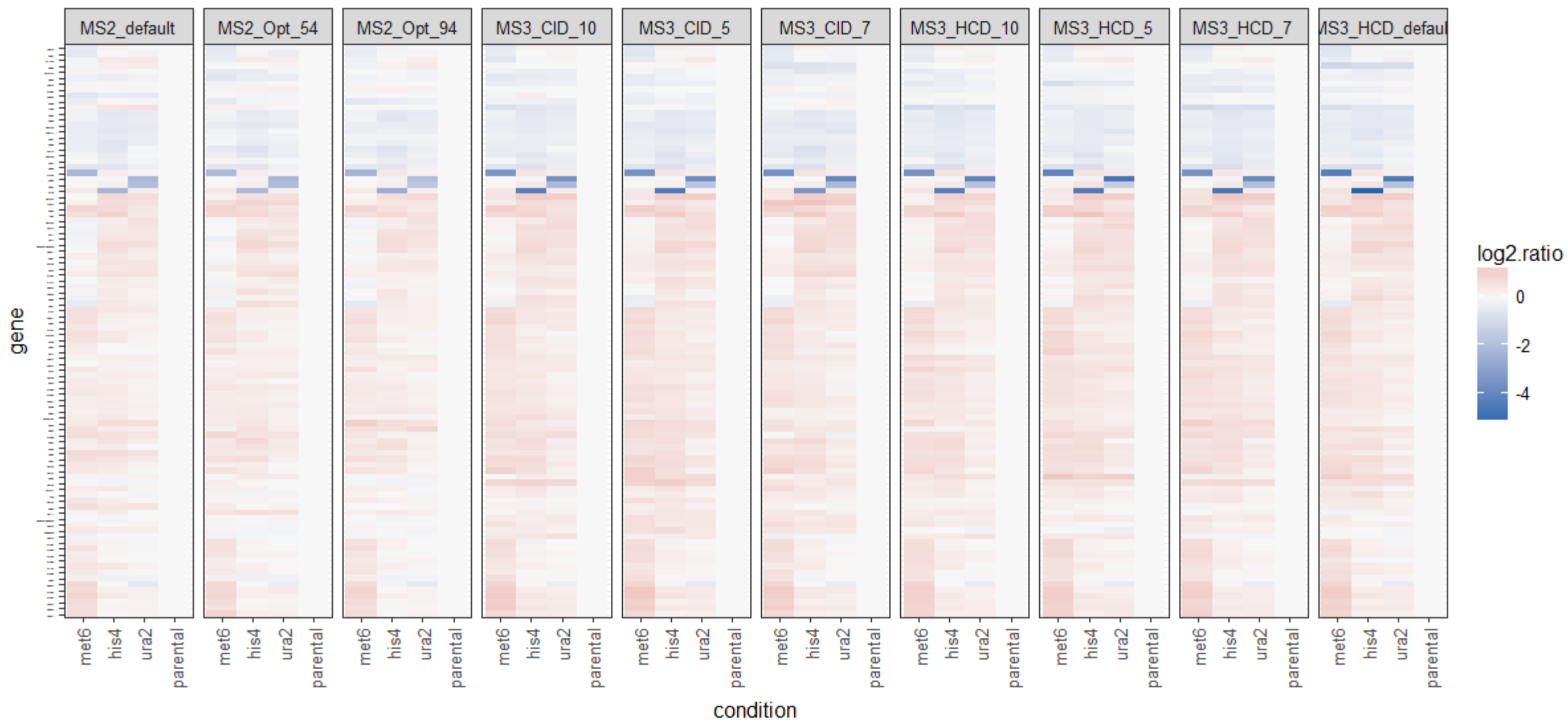
Heatmap



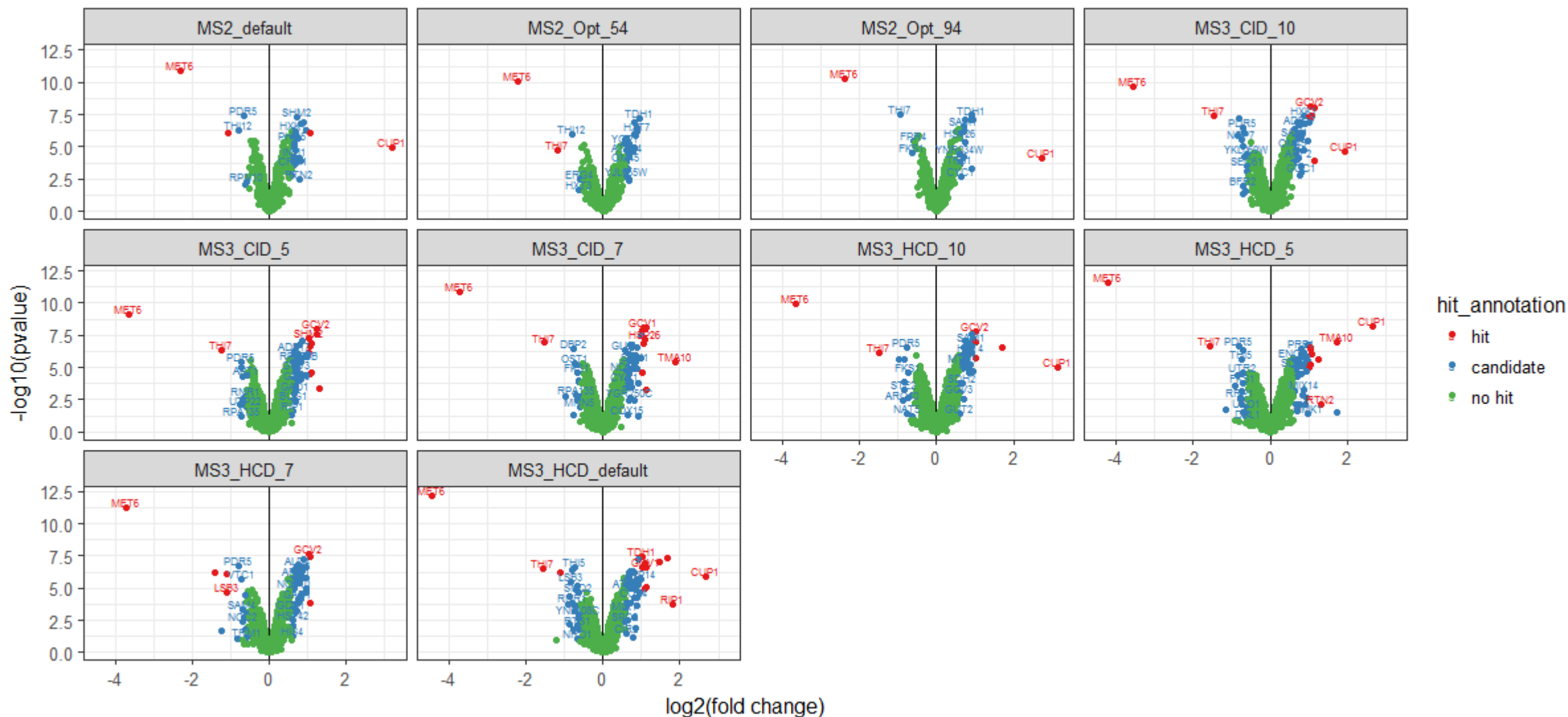
HOW MS METHODS INFLUENCE THE STATISTICS

- MS3 HCD 5/7/10 – number of fragment ions for ms3
- MS3 CID 5/7/10
- MS2 Opt 54/94

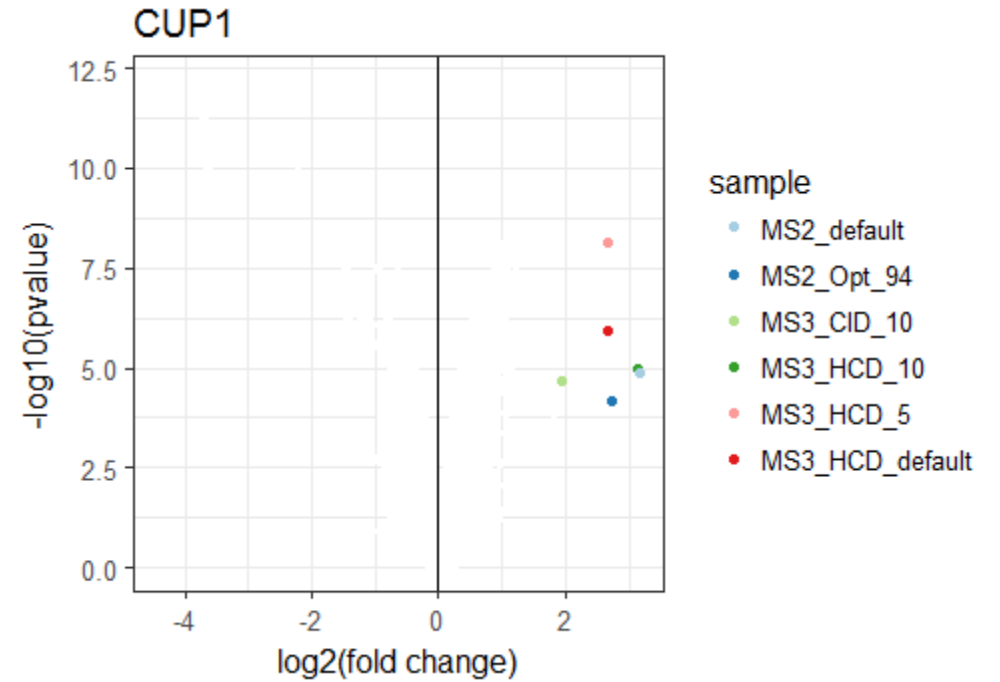
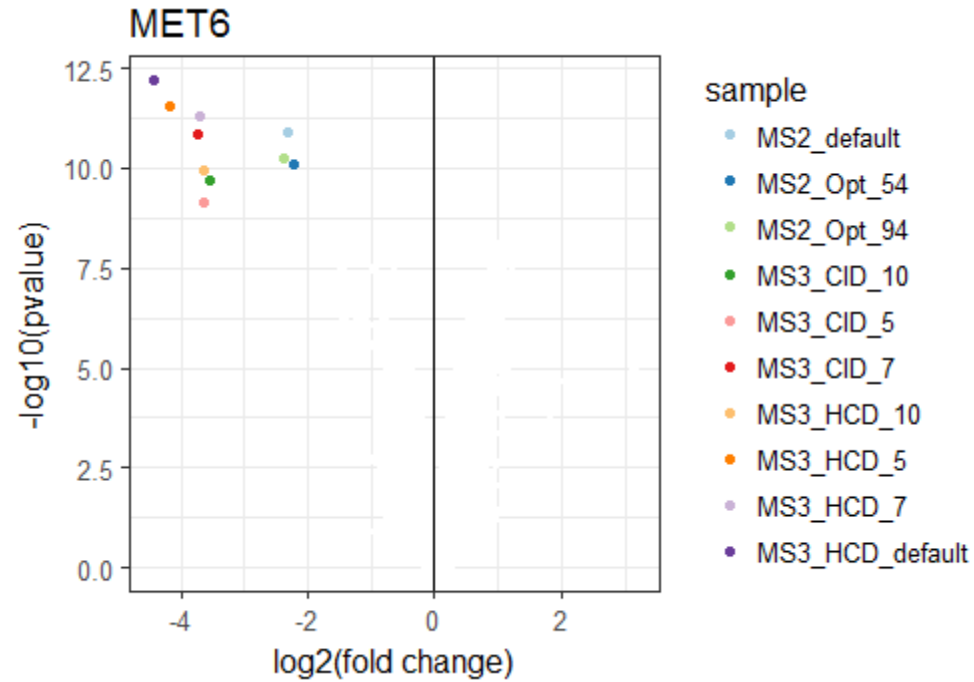
Heatmap



Volcano plots MET6 KO against parental



Volcano plots of individual proteins



URA2 - parental

