# MTXQCvX - Part1: pSIRM \*

#### test test

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This document provides an evaluation of GC-MS derived metabolomics data. It assesses GC-MS performance, the absolute quantification and the stable isotope incorporation. ADD HERE FURTHER PROJECT RELEVANT FACTS.

Keywords: MTXQCvX, GC-MS, metabolomics, data analysis and processing

## MTXQCvX part1

Summary

\*\* Summarise your major findings and important details. DO NOT skip this part.\*\*

General project settings

```
##
## Attaching package: 'gplots'
## The following object is masked from 'package:stats':
##
## lowess

Data import
## MTXQCparams.csv imported!
## Metmax_params.csv imported.
```

<sup>\*</sup>Kempa Lab - Template MTXQCvX part1 - processed 'September 27, 2018'

```
## Experimental setup does not include additional quantification standards!
```

- ## File imported! annotation.csv
- ## File imported! Sample\_extracts.csv
- ## WARNING: No file detected: InternalStandard.csv
- ## File imported! Alcane\_intensities.csv
- ## No file with m/z 73 values defined for this input format!
- ## No file defined for this input format!
- ## File imported! quantMassAreasMatrix.csv
- ## It's not a pSIRM experiment!
- ## Correct column names in file sample\_extracts.csv
- ## Correct column names in sample annotation
- ## Input files checked!
- ## Annotation and Sample\_extract.csv correctly imported!

### MTXQC - GC-MS perfomance

Alkane standards

## QC-metric successfully exported: alkanes

Data normalization

Internal standard cinnamic acid

## Empty data frame OR no peak areas for internal standard detectable!

Sum of Area of annotated metabolites per file

## No SumOfArea file generated in Metmax parser!

Derivatization check

## No input files detected. Either MassSum-73.csv or PeakDensities-Chroma.csv

HeatMap - GC-MS performance

Table 1: Summary of parameter evaluating GC-Performance

| Batch_Id | qc_metric | title   |
|----------|-----------|---------|
| e18627jg | 0.9663448 | alkanes |

## Export of GC-Performance values done!

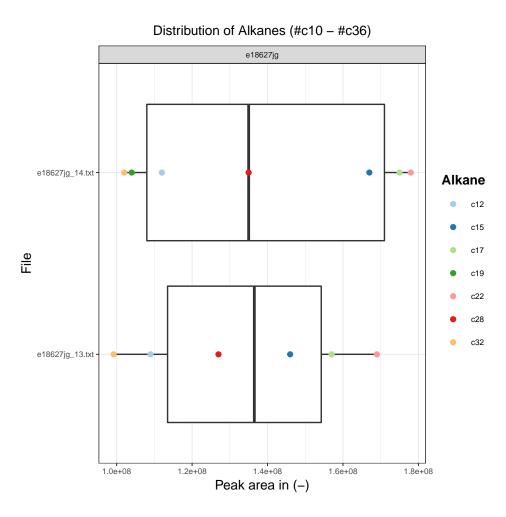


Figure 1: Alkane intensities summarised per each file. Drop of intensities shows questionable files.

#### MTXQC - Quantitative metabolomics

Generation of ManualQuantTable: Quant-Standards (Qstd)

```
## File imported! quant1_values.csv
## ManualQuantTable imported!
Generation of ManualQuantTable: Additional calibration curves (Qadd)
Determination of calibration curves
## top5_QMQcurveInfo.csv generated!
if (nrow(qc_calcurve != 0)) {
  ggplot(qc_calcurve, aes(Lettercode, Par_value, color = Parameter)) +
        geom_point(aes(shape = Parameter), size = 3) +
    coord_flip() +
    ggtitle('Calibration curve: adj. R square and nb of data points') +
    ylim(0,1) +
    geom_hline(aes(yintercept = 0.75), linetype = 'dashed', color = 'grey30') +
    scale_color_manual(values = c('tomato3', 'black')) +
    scale_shape_manual(values = c(17,20)) +
    facet_grid(Origin ~ Batch_Id, scales = "free_y") +
        xlab('Derivate') +
        ylab('Parameter value in (-)') +
    theme(legend.position = "bottom")
Evaluation of experimental data
```

Determination extraction factor

```
## The quantification factor for that experimental setup: 0.3333333333333333
```

## The sample factor for that experimental setup: 1

## The extraction factor for that experimental setup: 0.33333333333333333

Quantification range and limits

## Position of data points regarding calibration curves evaluated.

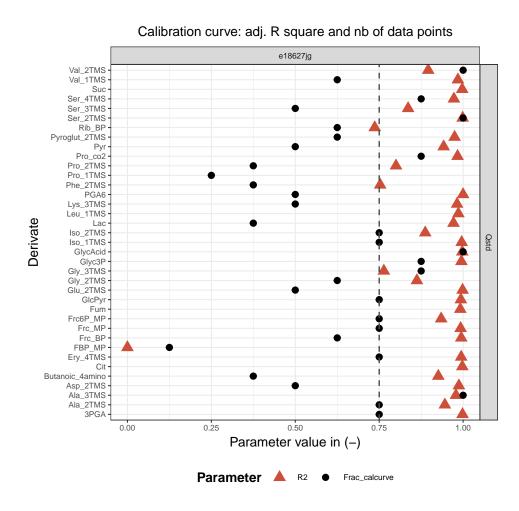


Figure 2: Calibration curves: Nb. of data points.

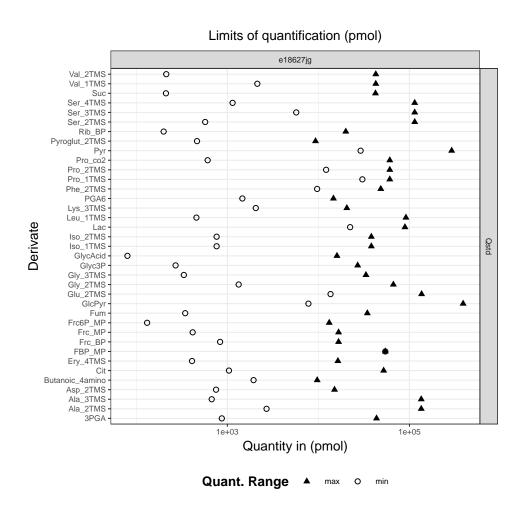


Figure 3: Limits of quantifiable range per metabolite

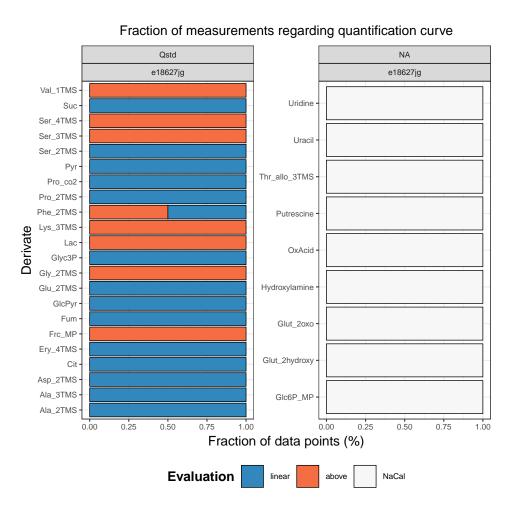
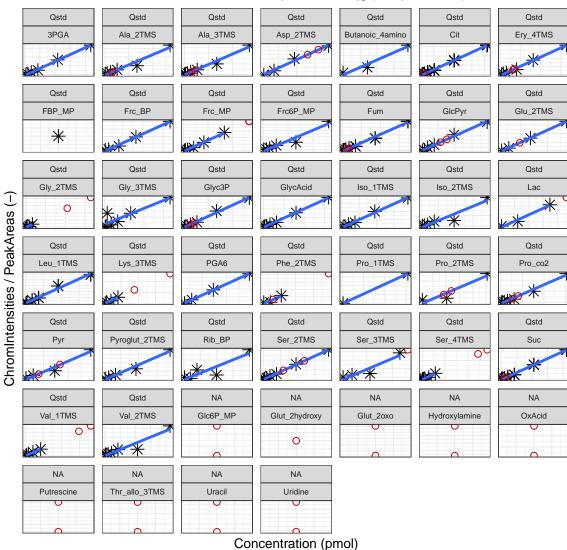


Figure 4: Distribution of data points regarding linear range of the calibration curve

## Absolute quantification samples



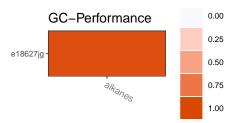
## Calibration curve and samples: e18627jg (samples in red)

Normalisation of absolute quantities

- ## WARNING: Sum of area normalisation factor set to value = 1 due to missing input.
- ## WARNING: Internal Standard normalisation factor set to value = 1 due to missing input.
- ## Absolute quantification and normalisation have been performed: CalculationFileData.csv

# HeatMap - Quantification

- ## WARNING: Correlation between internal standard and sum of area normalisation not possible!
- ## No evaluation of isotope data included.



# HeatMap - Metabolite - Pathway

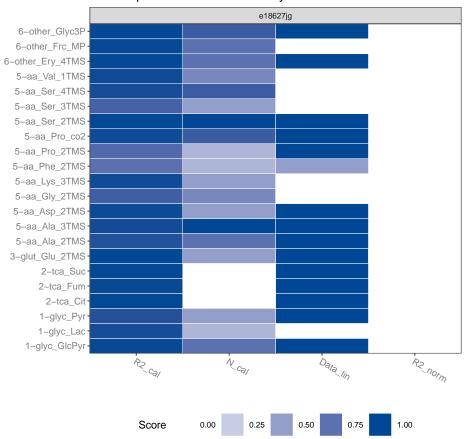


Figure 5: MTXQCvX - Heatmap overview