MTXQCvX - Experimental Setup - PROJECT TITLE *

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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

Project-related experimental setup

Sample extraction and derivatisation have been performed by Jenny. According to her notes documented in OneNote section: Collaborations/Landthaler/ODC1 experiment

Sample extraction

Extraction protocol:

- 1. 5 ml MeOH (50%)
- 2. 1 ml Chlorform
- 3. dried 3.5 ml of polar phase
- 4. 2nd extraction: yes (in two replicates)

Polar phases have been split into two equal fractions of 280 ul (added 600 ul 20% MeOH).

Quant-Mix extraction protocol

Quant-Mixes batch: Quant v4

- 1. 1 ml MCW for extraction
- 2. 0.5 ml H2O for phase separation
- 3. dried 0.5 ml of polar phase (twice)

^{*}Kempa Lab - MTXQCvX ExperimentalSetup, provided by Ch. Zasada, processed 'September 26, 2018'

Derivatisation protocol

Applied the following protocol for derivatisation protocol

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1. MEOX/Pyridine (final conc: 40 mg MEOX/ 1 ml Pyridine)
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- Volume: 20 ul

- Incubation time: 90 min

- Temp: 30 C

2. Alkan-mix/MSTFA (10 ul mix/1 ml MSTFA)

- Volume: 80 ul

- Incubation time: 60 min

- Temp: 37 C

Prepared aliquots: three-times 28 ul, big glas vials, crimped.

GC-MS measurement

Samples have been measured using the following methods

Injector-method: hamilton_1ul
 GC-method: 5/7/12 1.2ml/min

3. Split: 1:5

4. MS-method: Lizzy-like

General MTXQC parameter

MTXQC_params.csv written.

Proceed with MTXQC_metmax in order to generate required input files.

Table 1: Experimental parameters of the project.

Value	Parameter
annotation.csv	ann
Sample_extracts.csv	sample_ext
qMTX	data
TRUE	instd
Quant1_v3	quant
none	substr
500	quant_vol
no	addQ_Int
no	addQ
metmax	inputformat
2	backups
cell extracts	samples
test2	subf