**Code:** ZH\_01

**internal code:** ZH\_MEF\_DKO\_ULK

**organism/cell type:** mouse, MEF cells

**experimental design:**

triple SILAC (label swap)

groups: dko\_hbss, ulk\_dmem, ulk\_hbss

5 replicates (phospho and whole proteome, each 12 fractions)

|  |  |  |  |
| --- | --- | --- | --- |
| **replicate** | **light** | **medium (Arg6, Lys4)** | **heavy (Arg10, Lys8)** |
| 1 | dko\_hbss | ulk\_dmem | ulk\_hbss |
| 2 | ulk\_hbss | dko\_hbss | ulk\_dmem |
| 3 | ulk\_dmem | ulk\_hbss | dko\_hbss |
| 4 | dko\_hbss | ulk\_dmem | ulk\_hbss |
| 5 | ulk\_hbss | dko\_hbss | ulk\_dmem |

**raw datafiles:**

phospho: 20191216\_ZH\_MEFs\_phosphoproteome\_TiO2 (HFX)

ft: 20191231\_ZH\_MEFS\_phosphoproteome\_FT (QE and HFX -4/5)

**MaxQuant version:** 2.0.1.0

**parameters:**

experimental design:

- phospho peptide enriched sample and whole proteome in the same search

- fraction settings according to file name

- phospho peptide enriched samples in separate parameter group and PTM set to TRUE

parameter group setting:

- Type according to experimental design – SILAC, max labelled set to 4

- include Phospho(STY) as additional variable modification for phospho samples

- max missed cleavages set to 3

- tick re-quantify in misc. tab

global parameter:

- fasta file according to experimental design (Human\_2016, yeast\_2016)

- identification tab: set min unique peptides to 1, allow match between runs

increase number of processors, e.g. 100