## New Quantitative Proteomics Technology Improves Data Quality and Reduces Cost

## **Background/objective**

Quantitative proteomics is a promising technique that allows the quantification of thousands of proteins among multiple conditions, e.g. perturbations, time points, or organelles. Nevertheless, current technology lacks the sensitivity required to measure low-abundance proteins and suffers from poor measurement accuracy or precision.

#### **Approach**

We have developed a new quantification strategy called TMTc+, that makes use of so-called "complement reporter ions".

#### **Results**

- TMTc+ permits the simultaneous measurement of thousands of proteins among multiple conditions with unprecedented sensitivity and quality.
- TMTc+ is compatible with comparatively simple instrumentation, thereby reducing cost and increasing access for researchers.

# A Label Free TMTc+ 1:1:1:1:1 HeLa 1:1:1:1:1 HeLa 842 proteins 3,941 proteins В 0.6 n = 59,218, Mdn = .04 0.5 0.4 = 34,683, Mdn = .26 Fraction of 0.2

### **Significance**

TMTc+ advances quantitative proteomics and will enable us to more accurately measure protein-abundances in yeast strains. This information will help us to better understand metabolic regulation and inform engineering strategies.



0.4 CV

0.3

0.1

0.2

0.5

0.6