## **Supplementary Information for**

## Integrated Platform with Combination of Online Digestion and <sup>18</sup>O Labeling for

## Proteome Quantification via Immobilized Trypsin Microreactor

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**Figure S1.** Evaluation of the back-exchange of <sup>18</sup>O labeling. After labeling using IMER, samples were analyzed immediately (A) and again after 1 week at room temperature (B) by MALDI-TOF-MS. The amino acid sequences of peptide A, B depicted in all figure are YLYEIAR and LGEYGFQNALIVR.

Figure S2. The LC-MS/MS spectrum of the platform.

- (A) The TIC MS spectrum of three LC-MS/MS analysis of the yeast sample analyzed by the platform
- (B) A typical MS spectrum of yeast sample

**Figure S3.** Evaluation of the quantitative accuracy and reproducibility of the integrated platform by 100 ng <sup>18</sup>O and <sup>16</sup>O online labeled yeast sample at a mixing ratio of 1:1

- (C) The observed log<sub>2</sub> (H/L) ratios of proteins quantified in all of three technical replicates.
- (D) The RSD distribution of the ratios of proteins quantified in all three technical replicates.

**Figure S4.** Box plots showing the ratios measured at mixing ratios of 1:1, 1:5 and 1:10.

**Figure S5.** The  $\log_2$  (H/L) ratios distribution of peptides with or without misscleavage sites from the first run of 1:1 mixed yeast sample.



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Figure S2. The LC-MS/MS spectrum of the platform.

(E) The TIC MS spectrum of three LC-MS/MS analysis of the yeast sample analyzed

by the platform

(F) A typical MS spectrum of yeast sample



**Figure S3.** Evaluation of the quantitative accuracy and reproducibility of the integrated platform by 100 ng <sup>18</sup>O and <sup>16</sup>O online labeled yeast sample at a mixing ratio of 1:1

- (A)The observed log<sub>2</sub> (H/L) ratios of proteins quantified in all of three technical replicates.
- (B) The RSD distribution of the ratios of proteins quantified in all three technical replicates.



Figure S4.Box plots showing the ratios measured (box and whiskers) at mixingratiosof1:1,1:5and1:10.



Figure S5. The  $\log_2$  (H/L) ratios distribution of peptides with or without misscleavage sites from the first run of 1:1 mixed yeast sample.

IPI	Protein Name	Ratio (Hca-F/Hca- P)
IPI00124700	Transferrin receptor protein 1	$2.47 \pm 0.13$
IPI00123639	Calreticulin	$2.44\pm0.04$
IPI00123281	Leucine-rich repeat-containing protein 59	$2.27\pm0.02$
IPI00129519	Brain acid soluble protein 1	$2.18\pm0.06$
IPI00126072	Synaptic vesicle membrane protein VAT-1 homolog	$2.16 \pm 0.03$
IPI00279079	Fibrinogen beta chain	$0.41 \pm 0.02$
IPI00553798	Ahnak protein	$0.39\pm0.01$
IPI00469114	Hemoglobin subunit alpha	$0.33\pm0.03$
IPI00885793	Fibrinogen A-alpha-chain	$0.27\pm0.01$
IPI00122312	Fibrinogen gamma chain	$0.21 \pm 0.02$

**Table S1.** Differentially expressed proteins in Hca-F and Hca-P cell lines.