Supporting Information for

Pseudo Isobaric Peptide Termini Labeling for Relative Proteome

Quantification by SWATH MS Acquisition

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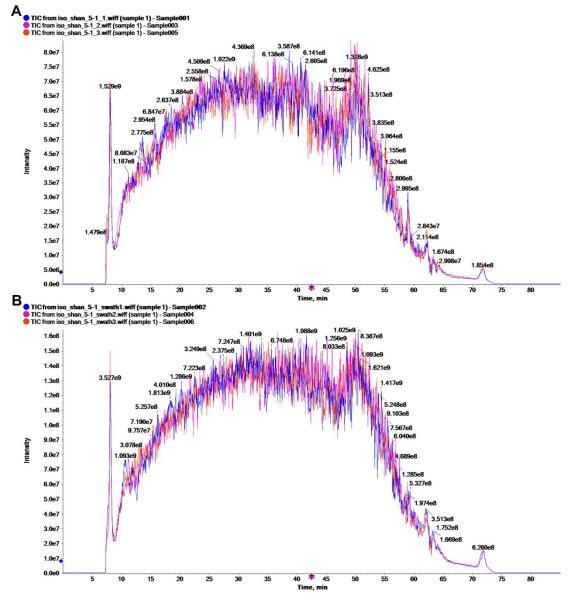


Figure S1. The TIC intensity graphs of three DDA-pseudo-IPTL replicates (A) and three SWATH-pseudo-IPTL replicates (B).

Expected value	Mean of DDA- pseudo- IPTL	Mean of SWATH- pseudo-IPTL	RE of DDA- pseudo-IPTL	RE of SWATH - pseudo- IPTL	RSD of DDA- pseudo -IPTL	RSD of SWATH- pseudo-IPTL
0.1	0.120	0.107	23.1%	9.3%	18.4%	6.4%
0.2	0.250	0.232	24.5%	9.8%	21.4%	6.3%
1	0.975	1.076	21.4%	12.5%	18.7%	11.5%
5	4.672	5.010	25.7%	16.9%	18.0%	12.0%
10	8.702	10.161	31.2%	18.2%	22.4%	10.8%

Table S1.The mean, average relative error (RE) and average relative standarddeviation (RSD) of DDA-pseudo-IPTL and SWATH-pseudo-IPTL.