An Orthogonal Extraction Workflow for High-Depth Plasma Proteomics with Metabolomic Compatibility from Low Microliter-Scale Samples

Chuanping Zhao[1], Huiting Hu[2], Xiaohong Qian[1], Wanjun Zhang*[1,2], and Weijie Qin[1,2,3]*

[1] State Key Laboratory of Medical Proteomics, National Center for Protein Sciences (Beijing), Academy of Military Medical Sciences, Beijing, 102206, China

[2] School of Basic Medical Science, Anhui Medical University, Hefei 230032, China

[3] Beijing Proteome Research Center, Beijing, 102206, China

* Corresponding author email: zwj2004zwj@126.com for Zhang W. J. and aunp_dna@126.com for Qin W. J.

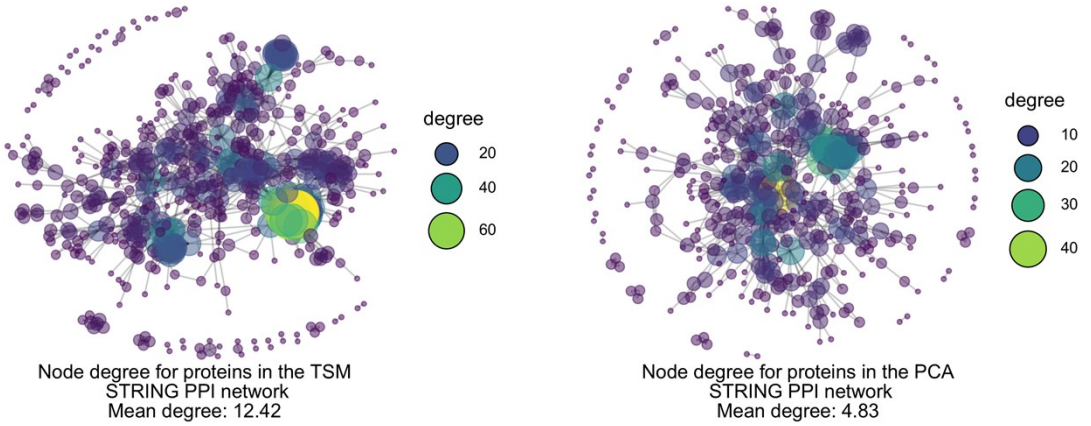

Figure S1. STRING PPI networks for proteins extracted by 60% TSM (left) and 5% PCA (right). Node size represents node degree (number of interaction partners), and the mean node degree is reported for each network (TSM: 12.42; PCA: 4.83).

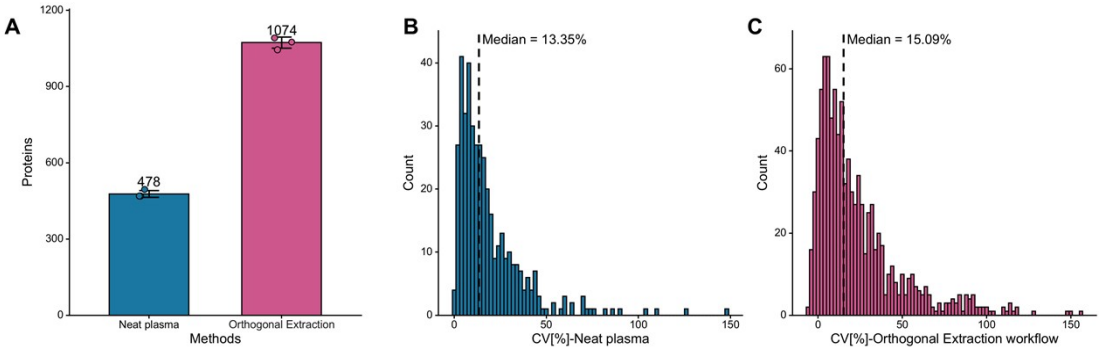

Figure S2. Proteome coverage and quantitative reproducibility of the neat plasma and orthogonal extraction workflows in three individual healthy donors. (A) Total numbers of proteins identified by the neat plasma workflow using neat plasma and the orthogonal extraction workflow across the three donor samples; (B) Distribution of protein-level coefficients of variation (CVs) for proteins quantified in the neat plasma workflow across three donors; (C) Distribution of protein-level CVs for proteins quantified in the orthogonal extraction workflow across three donors.