Supporting Information

A Cloud-Based Metabolite and Chemical

Prioritization System for the Biology/Disease-driven

Human Proteome Project

Kun-Hsing Yu^{1,2}, Tsung-Lu Michael Lee³, Yu-Ju Chen⁴, Christopher Ré⁵,
Samuel C. Kou², Jung-Hsien Chiang^{6,*}, Michael Snyder^{7,*,‡}, Isaac S. Kohane^{1,*,‡}

⁷ Department of Genetics, Stanford University

Table of Contents:

University, Taiwan

SupplementalInfomation.pdf Figures S-1, S-2, and S-3, Table S-1

SupplementalData1.xlsx Data S-1

SupplementalData2.xlsx Data S-2

¹ Department of Biomedical Informatics, Harvard Medical School

² Department of Statistics, Harvard University

³ Department of Information Engineering, Kun Shan University, Taiwan

⁴ Institute of Chemistry, Academia Sinica, Taiwan

⁵ Department of Computer Science, Stanford University

⁶ Department of Computer Science and Information Engineering, National Cheng Kung

Figure S-1. Metscape visualized the pathways involved with the prioritized metabolites. Metabolites associated with cancers, diabetes, glycoproteomics and the musculoskeletal system are shown.

Figure S-1

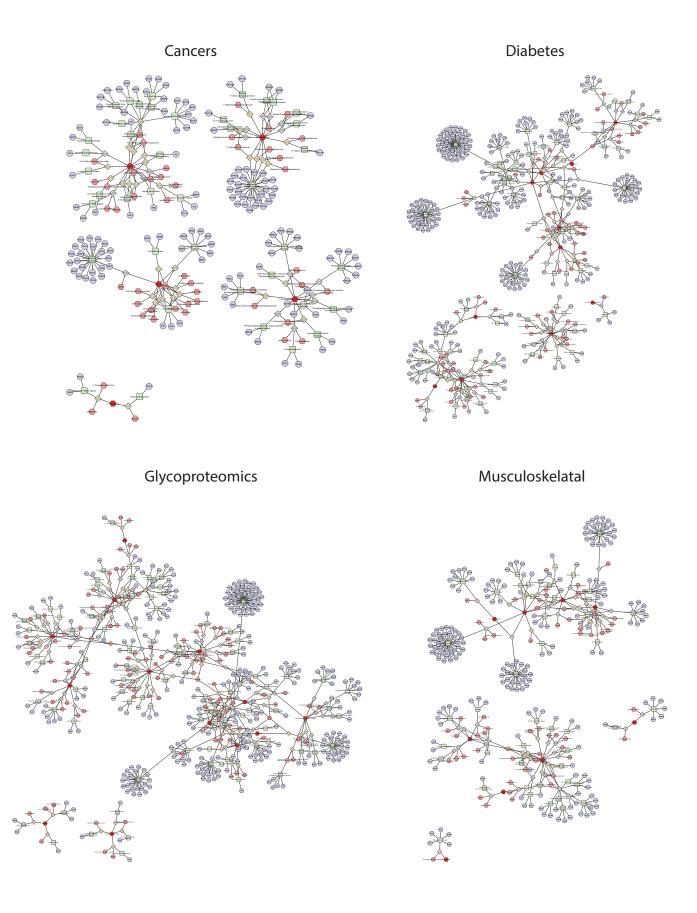
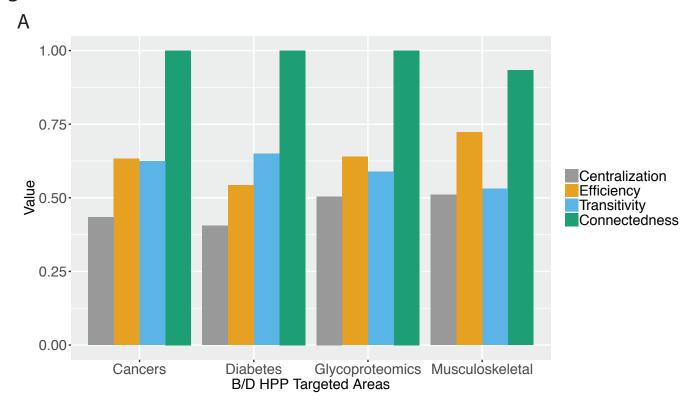


Figure S-2. The quantitative network statistics of the gene-metabolite interaction and gene-chemical interaction networks. (A) The centralization, efficiency, transitivity, and connectedness score of the gene-metabolite interaction networks. The gene-metabolite interaction networks of the four selected B/D-HPP targeted areas had high connectedness and moderate centralization, efficiency, and transitivity scores. (B) The centralization, efficiency, transitivity, and connectedness score of the gene-chemical interaction networks. Comparing with the gene-metabolite interaction networks, the gene-chemical interaction networks had slightly lower connectedness and centralization scores. The relative sparsity of the gene-chemical interaction networks contributed to the higher efficiency scores and varied transitivity scores.

Figure S-2



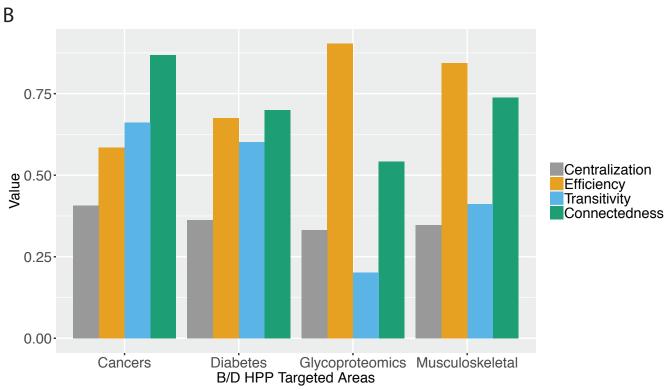


Figure S-3. Multidimensional scaling (MDS) visualization of the connections among B/D-HPP targeted fields and their associated chemicals. B/D-HPP fields with higher correlation in their associated chemicals' PURPOSE scores have shorter distances on the graph.



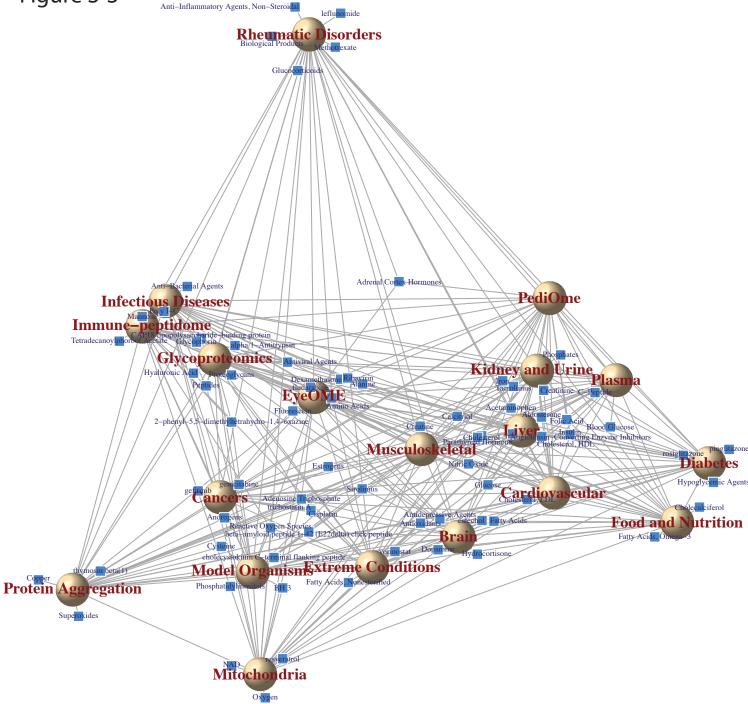


Table S-1. The PubMed search terms for the B/D-HPP targeted fields.	
B/D HPP Targeted Fields	PubMed Search Terms
Brain	brain
Cancers	cancer
Cardiovascular	cardiovascular
Diabetes	diabetes
EyeOME	eye OR ocular
Food and nutrition	food OR nutrition OR nutrients
Glycoproteomics	glycoproteins
Immune-peptidome	immune OR immune system
Infectious diseases	infectious OR infection
Kidney and urine	kidney OR urine
Liver	liver OR hepatic
Mitochondria	mitochondria
Model organisms	rat OR mouse
Musculoskeletal	muscle OR bone OR musculoskeletal
PediOme	pediatric OR newborn OR infant OR toddler OR child OR adolescent
Plasma	plasma OR serum
Protein aggregation	protein aggregation NOT platelet aggregation
Rheumatic disorders	rheumatic
Extreme conditions	hot OR cold OR alkaline condition OR acidic condition OR hypersaline OR radiation