

Supplementary File 2:

Protein-centric omics integration analysis identifies candidate plasma proteins for multiple autoimmune diseases

Yingxuan Chen^{1,2†}, Shuai Liu^{1,2†}, Weiming Gong^{1,2}, Ping Guo^{1,2}, Fuzhong Xue^{1,2}, Xiang Zhou^{3,4}, Shukang Wang^{1,2*}, Zhongshang Yuan^{1,2*}

¹ Department of Biostatistics, School of Public Health, Cheeloo College of Medicine, Shandong University, 44, Wenhua West Road, Jinan, Shandong, 250012, China.

² Institute for Medical Dataology, Shandong University, 12550, Erhuan East Road, Jinan, Shandong, 250003, China.

³ Department of Biostatistics, University of Michigan, Ann Arbor, MI 48109, USA.

⁴ Center for Statistical Genetics, University of Michigan, Ann Arbor, MI 48109, USA.

† Y.C. and S.L. contributed equally to this work.

* Joint correspondence authors to:

Prof Shukang Wang

Department of Biostatistics, School of Public Health, Cheeloo College of Medicine, Shandong University, 44, Wenhua West Road, Jinan, Shandong, 250012, China.

Email: wsk2001@sdu.edu.cn

Prof Zhongshang Yuan

Department of Biostatistics, School of Public Health, Cheeloo College of Medicine, Shandong University, 44, Wenhua West Road, Jinan, Shandong, 250012, China.

Email: yuanzhongshang@sdu.edu.cn

Figure S1: The PPI network for PWAS significant proteins

The Network type is full STRING network (the edges indicate both functional and physical protein associations). The meaning of network edges is evidence (line color indicates the type of interaction evidence). The minimum required interaction score is medium confidence (0.400).

