

Coexpression Analysis to Identify Key Modules and Hub Genes Associated with COVID19 in Platelets

Supplementary Information

Ahmed B. Alarabi^{1,+}, Attayeb Mohsen^{2,+}, Kenji Mizuguchi^{2,3}, Fatima Z. Alshbool¹, and Fadi T. Khasawneh^{4,*}

¹Department of Pharmacy Practice, Irma Lerma Rangel College of Pharmacy. Texas A&M University, Kingsville, Texas, USA;

²Laboratory of Bioinformatics, Artificial Intelligence Center for Health and Biomedical Research (ArCHER), National Institutes of Biomedical Innovation, Health and Nutrition, 7-6-8 Saito-Asagi, 567-0085, Ibaraki, Osaka, Japan;

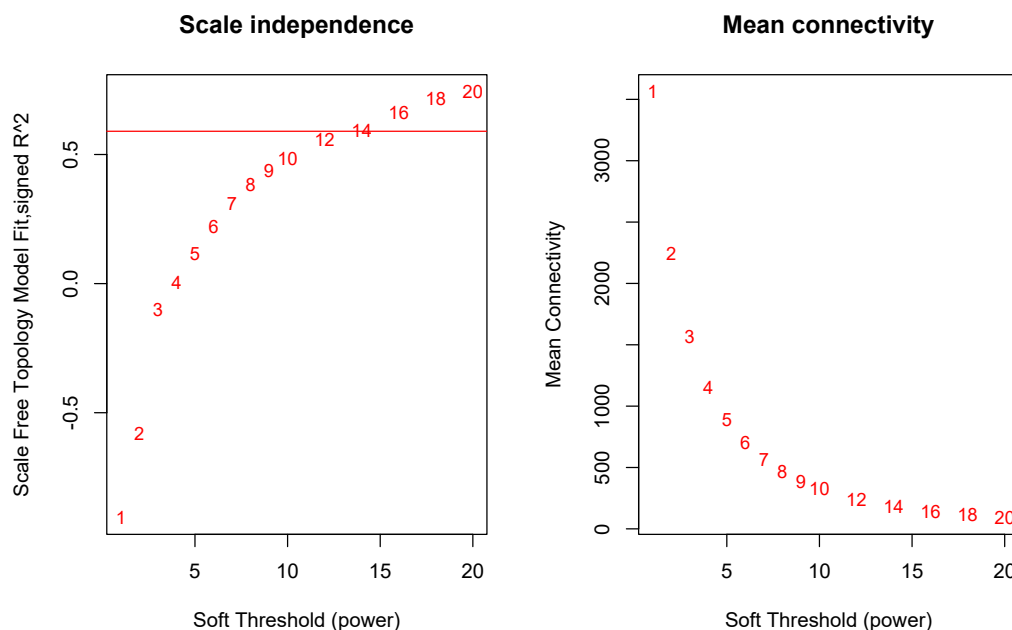
³Institute for Protein Research, Osaka University, 3-2 Yamadaoka, 567-0085, Suita, Osaka, Japan;

⁴Department of Pharmaceutical Sciences, Irma Lerma Rangel College of Pharmacy, Texas A&M University, Kingsville, Texas, USA.

*Correspondence to- Fadi T. Khasawneh, f khasawneh@tamu.edu

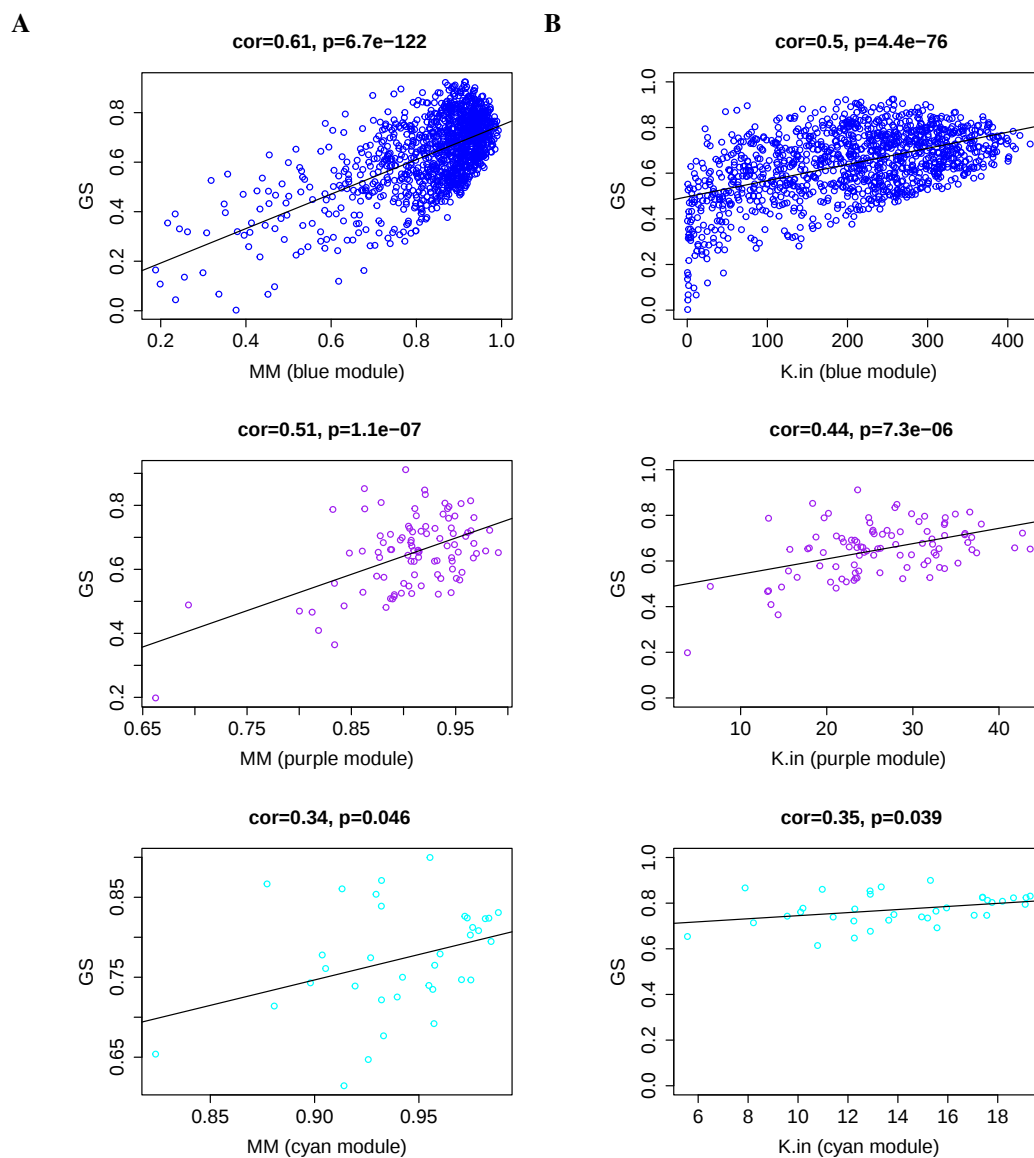
⁺These two authors contributed equally to this work

Supplementary Figure 1



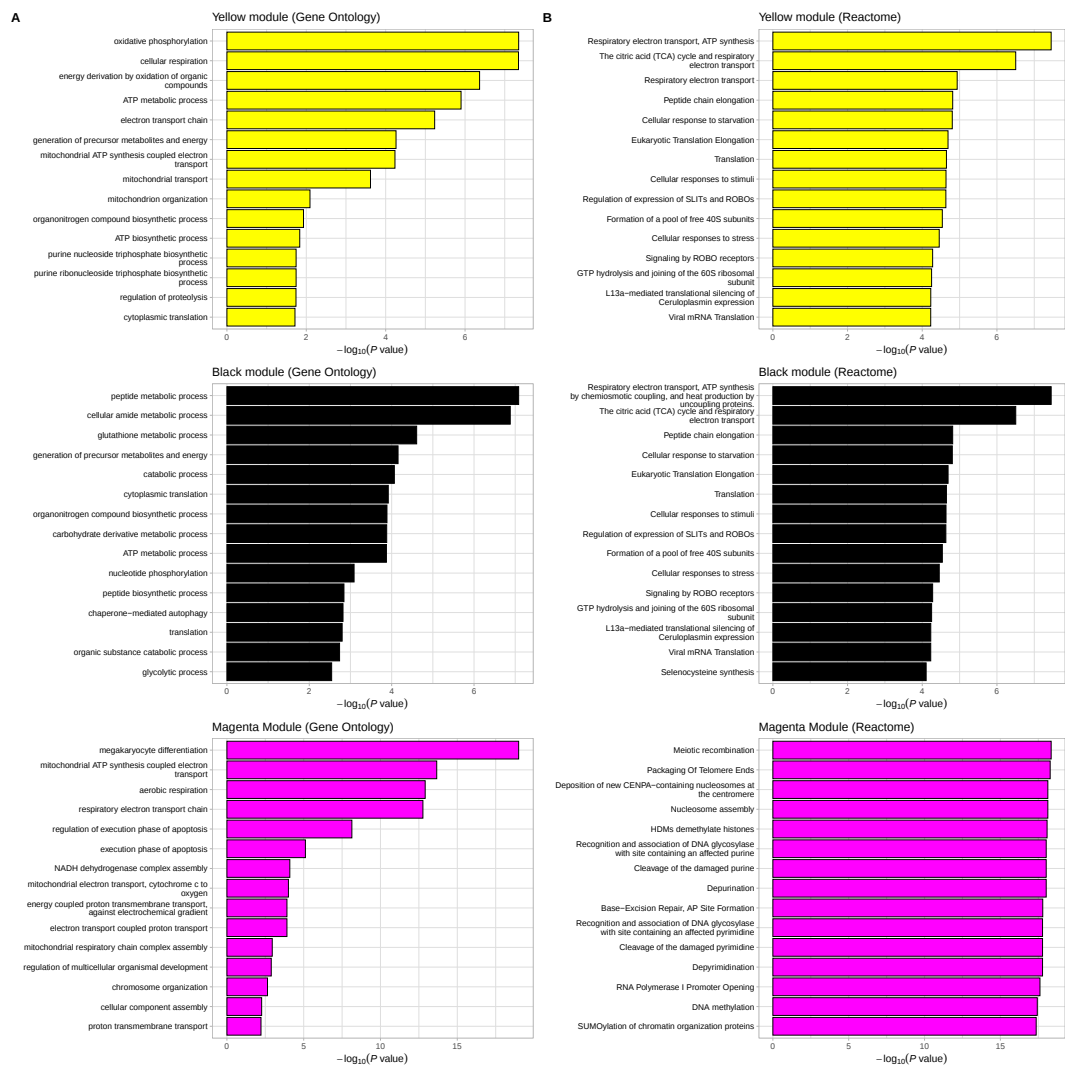
Supplementary Figure 1: Network Soft threshold

Supplementary Figure 2



Supplementary Figure 2: Module Membership and gene significance in other modules.

Supplementary Figure 3



Supplementary Figure 3: Detailed enrichment analysis. A; Gene Ontology of biological function. B; Reactome pathways enrichment.

Supplementary Tables

Supplementary Table S1: Color Modules: Lists the genes and their corresponding modules (in colors) assigned by WGCNA.

Supplementary Table S2: Eignegenes: The Eignegenes of all WGCNA modules.

Supplementary Table S3: Gene significance: lists gene significance in COVID-19 computed in WGCNA (correlation of gene expression to COVID-19 phenotype).

Supplementary Table S4: Intra-modular connectivity: lists the genes network parameters; kTotal: total connectivity, kWithin: intramodular connectivity; KOut: extra-modular connectivity; kDiff: the difference of the intra- and extra-modular connectivities.