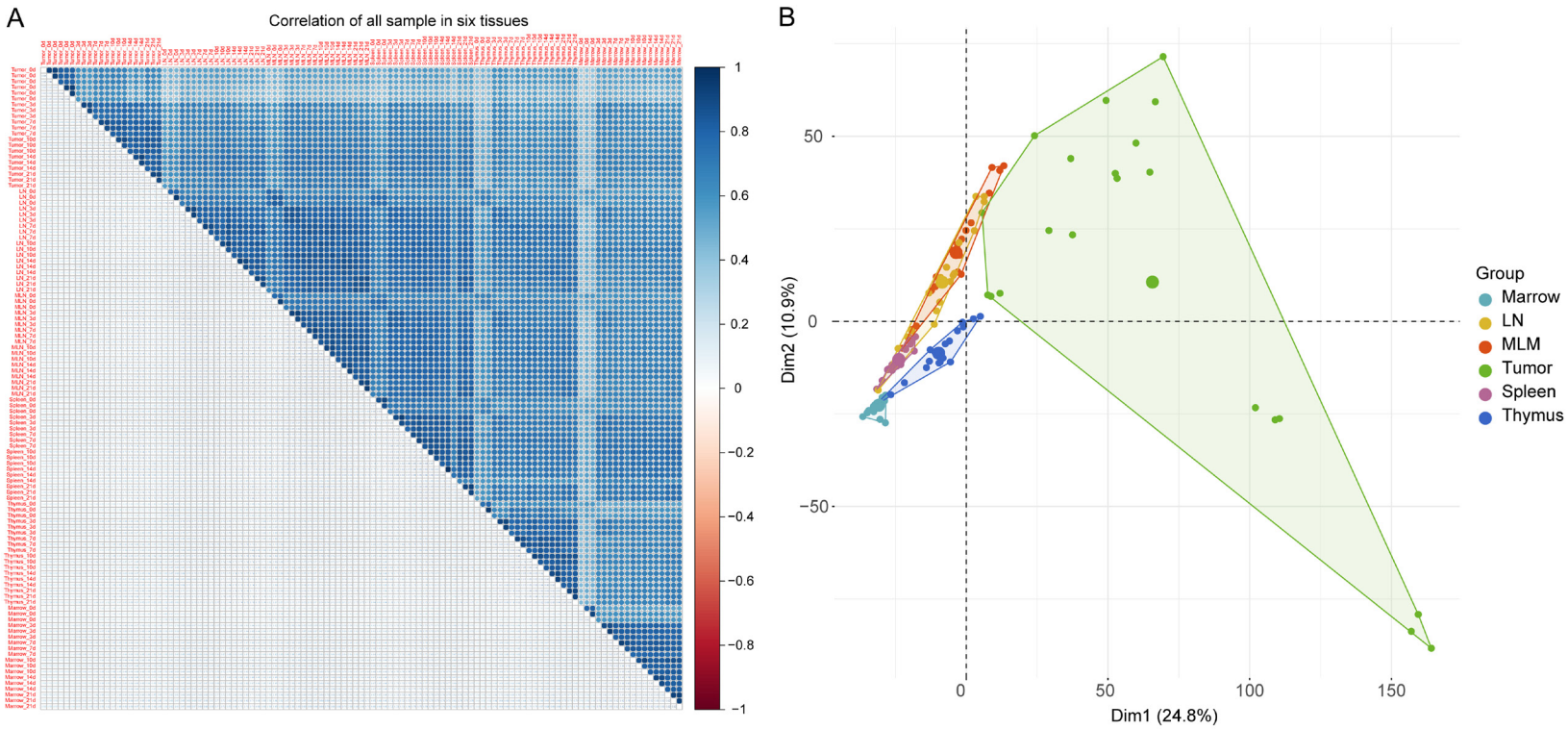


Figure S1. The distinctive boundaries of tumor and 5 immune organs. A. Correlation analysis of all tissues across 6 timepoints. B. The PCA of all tissues across 6 timepoints.

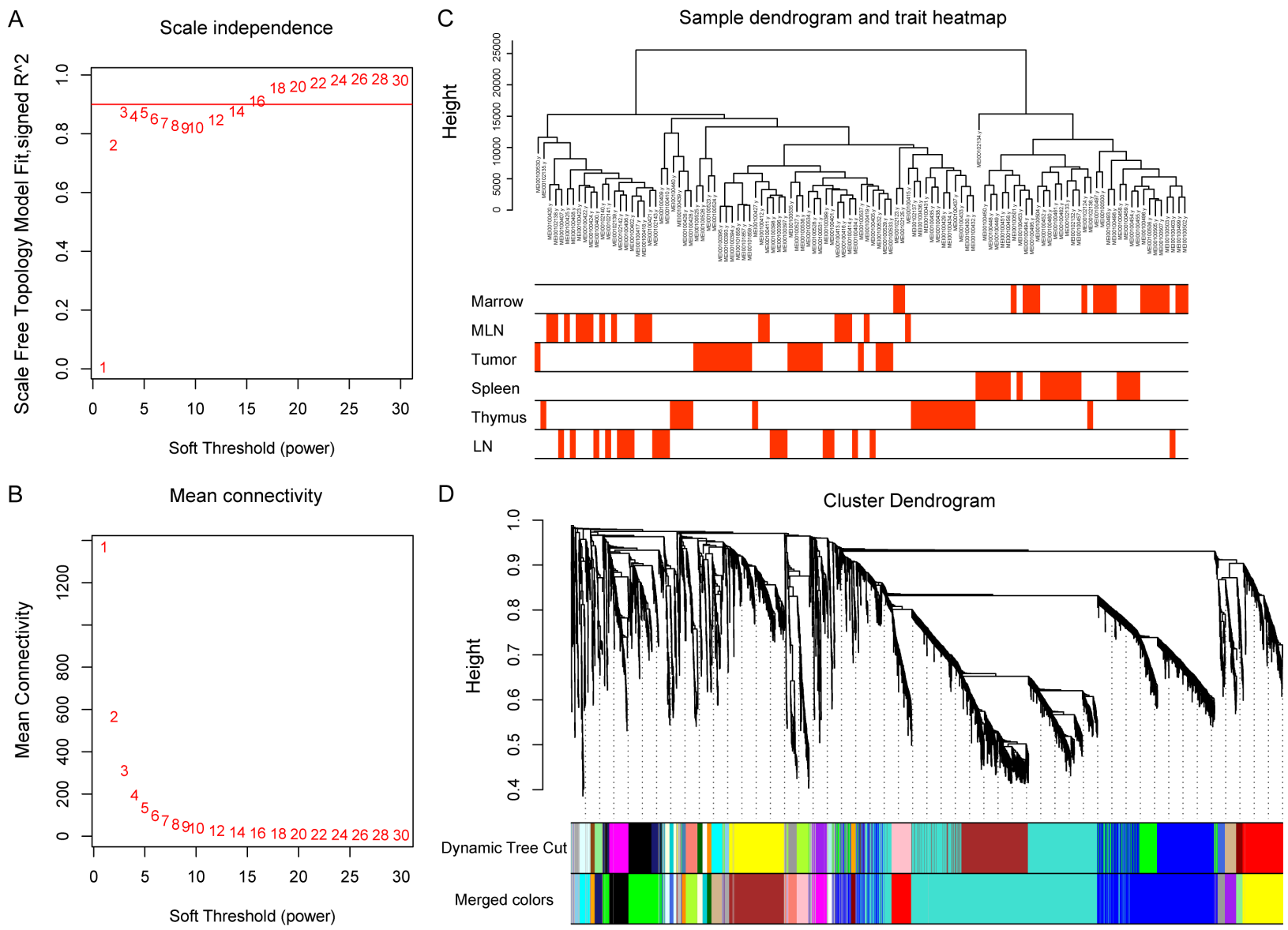


Figure S2. Determination of soft-threshold power and identification of modules in the WGCNA. A. Analysis of the scale-free index for various soft-threshold powers (β). B. Analysis of the mean connectivity for various soft-threshold powers. C. Clustering dendrogram of 111 samples. D. Dendrogram of all differentially expressed proteins clustered by the measurement of dissimilarity (1-TOM). The color band shows the results obtained from the automatic single-block analysis. TOM, topological overlap matrix.

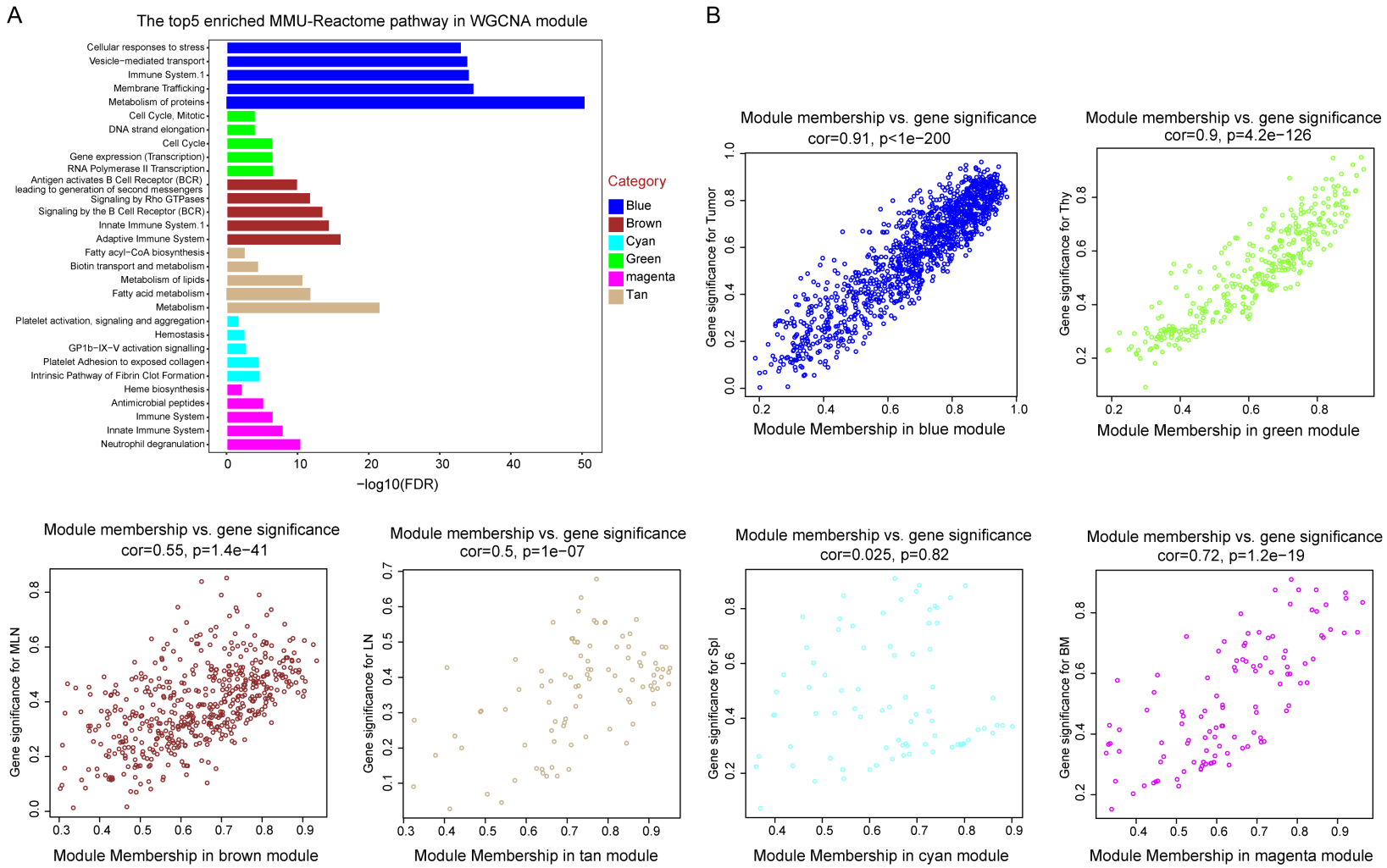
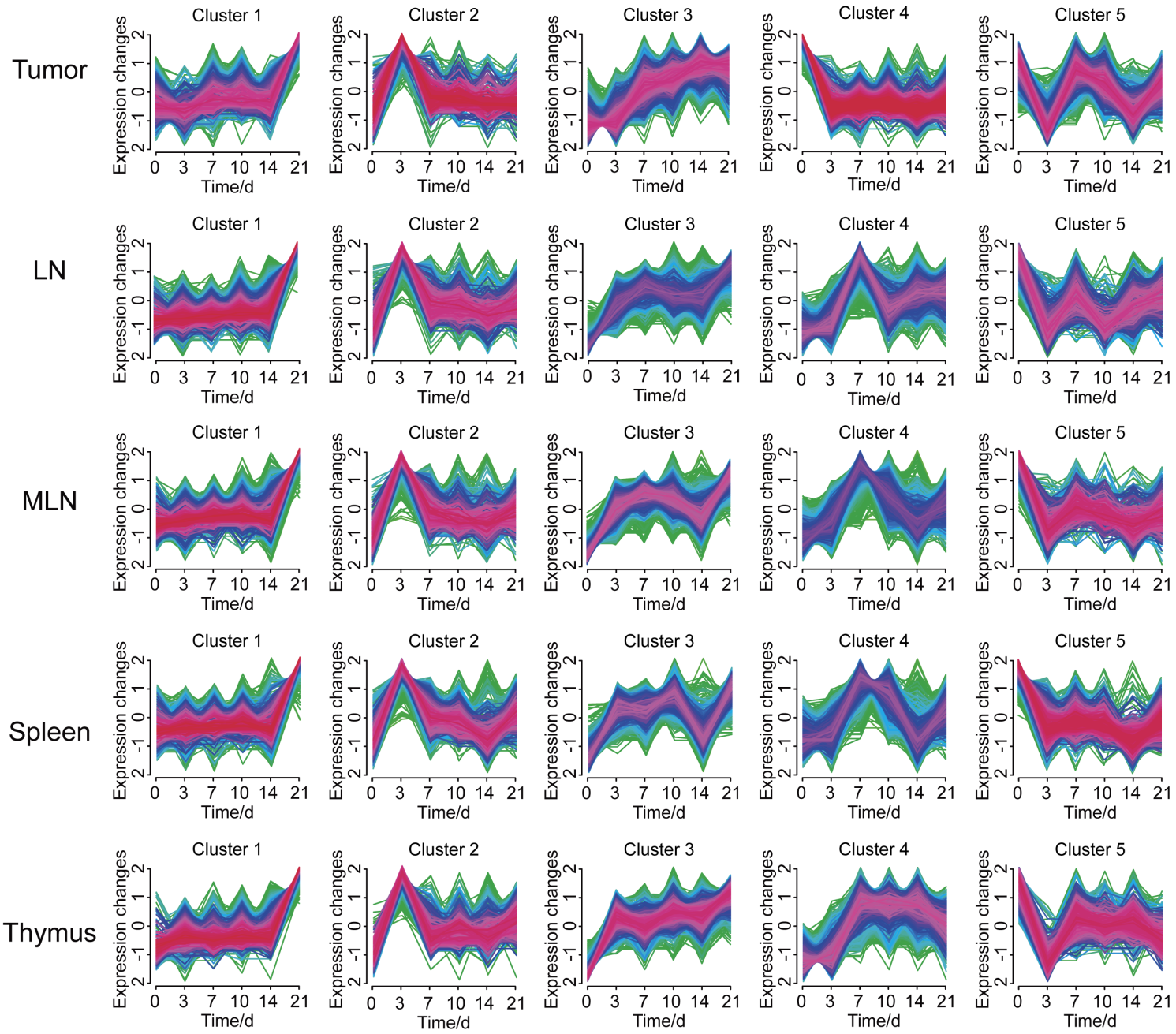


Figure S3. The top 5 enriched MMU-Reactome pathway and scatterplot of gene significance (y-axis) vs. module membership (x-axis) in high correlation of WGCNA module.

Dynamic proteomic changes of tumor and host immune organs



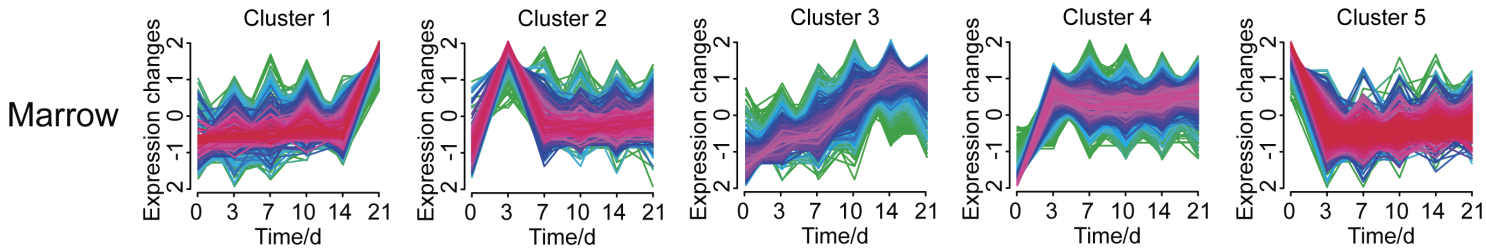


Figure S4. Proteins expression dynamics in all organs examined. For each of the 6 organs (rows), the average trajectory of proteins were grouped into five clusters according to the similar trajectory (expression).

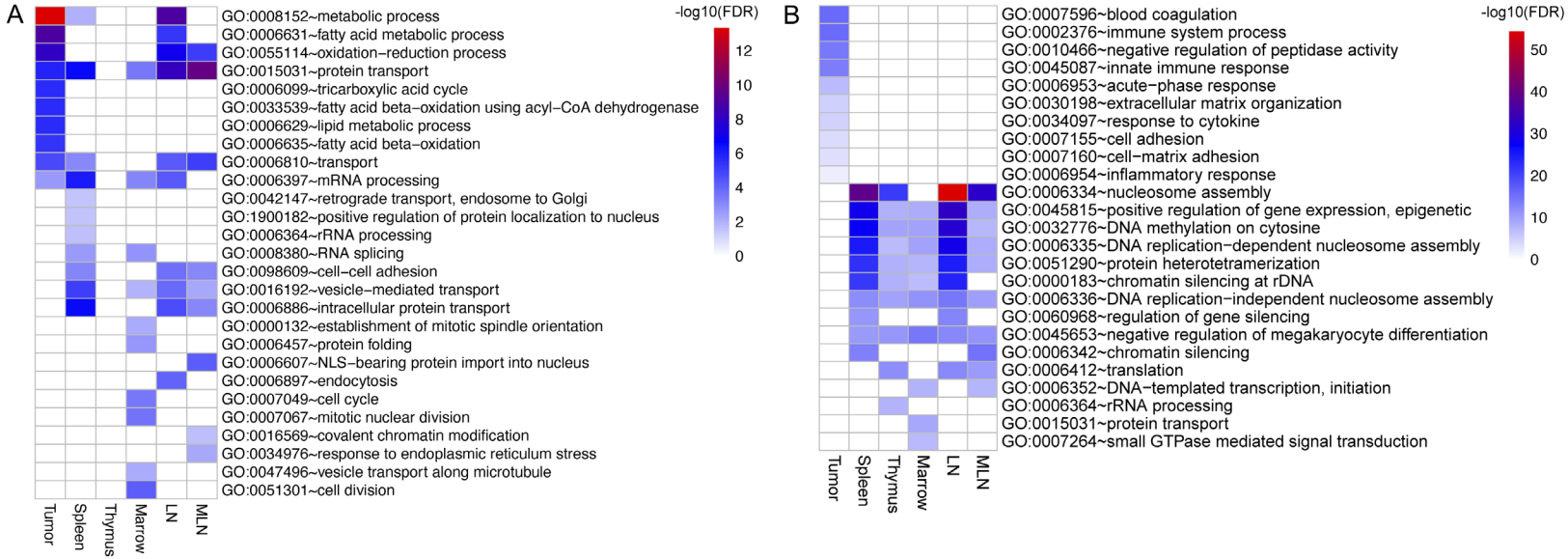


Figure S5. The GO term enrichments of similar trajectory across tissues. A. The top 10 GO terms for the 1st cluster in (Figure S4). B. The top 10 GO terms for the 2st cluster in (Figure S4).

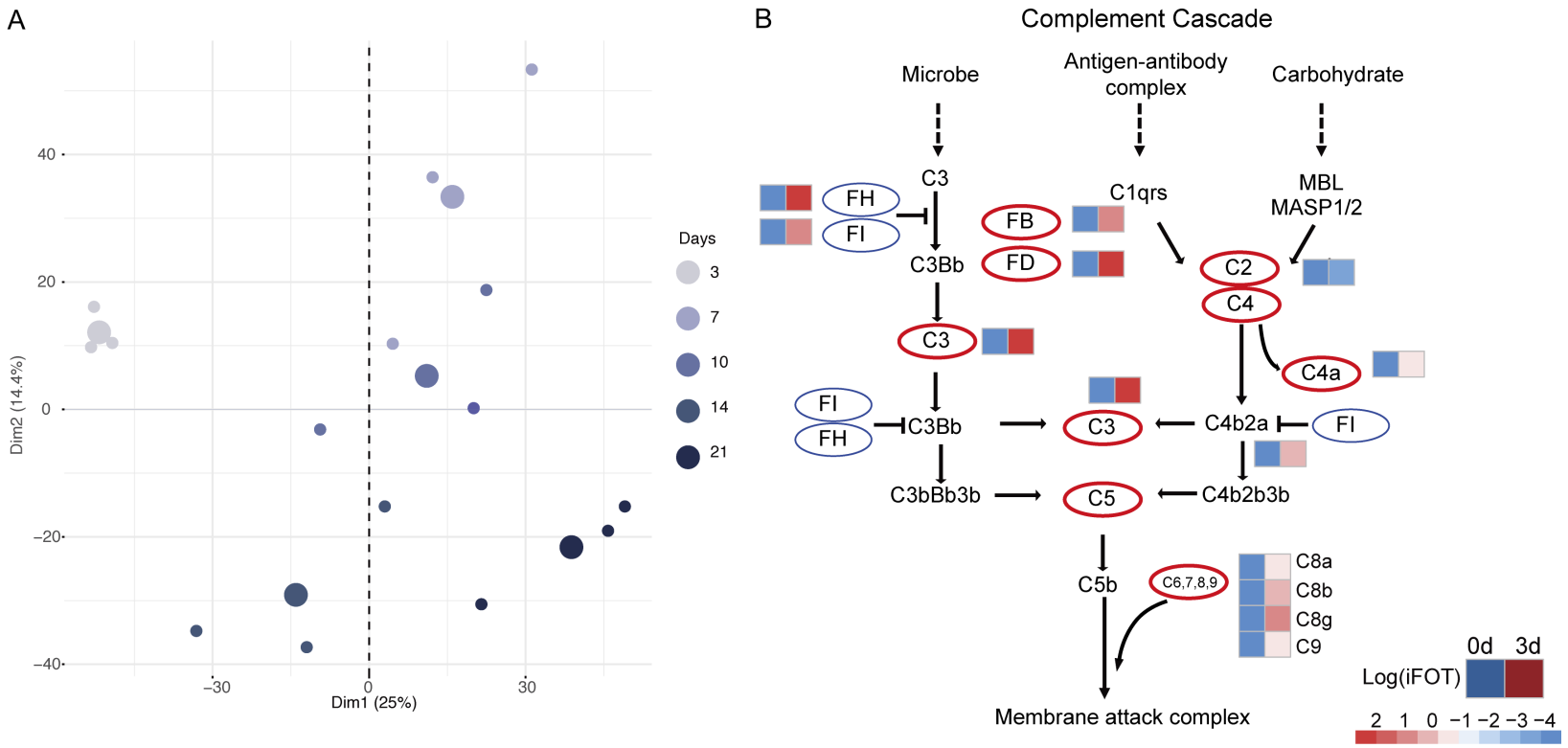


Figure S6. The PCA of tumor and iFOT of proteins in the complement cascade pathway.

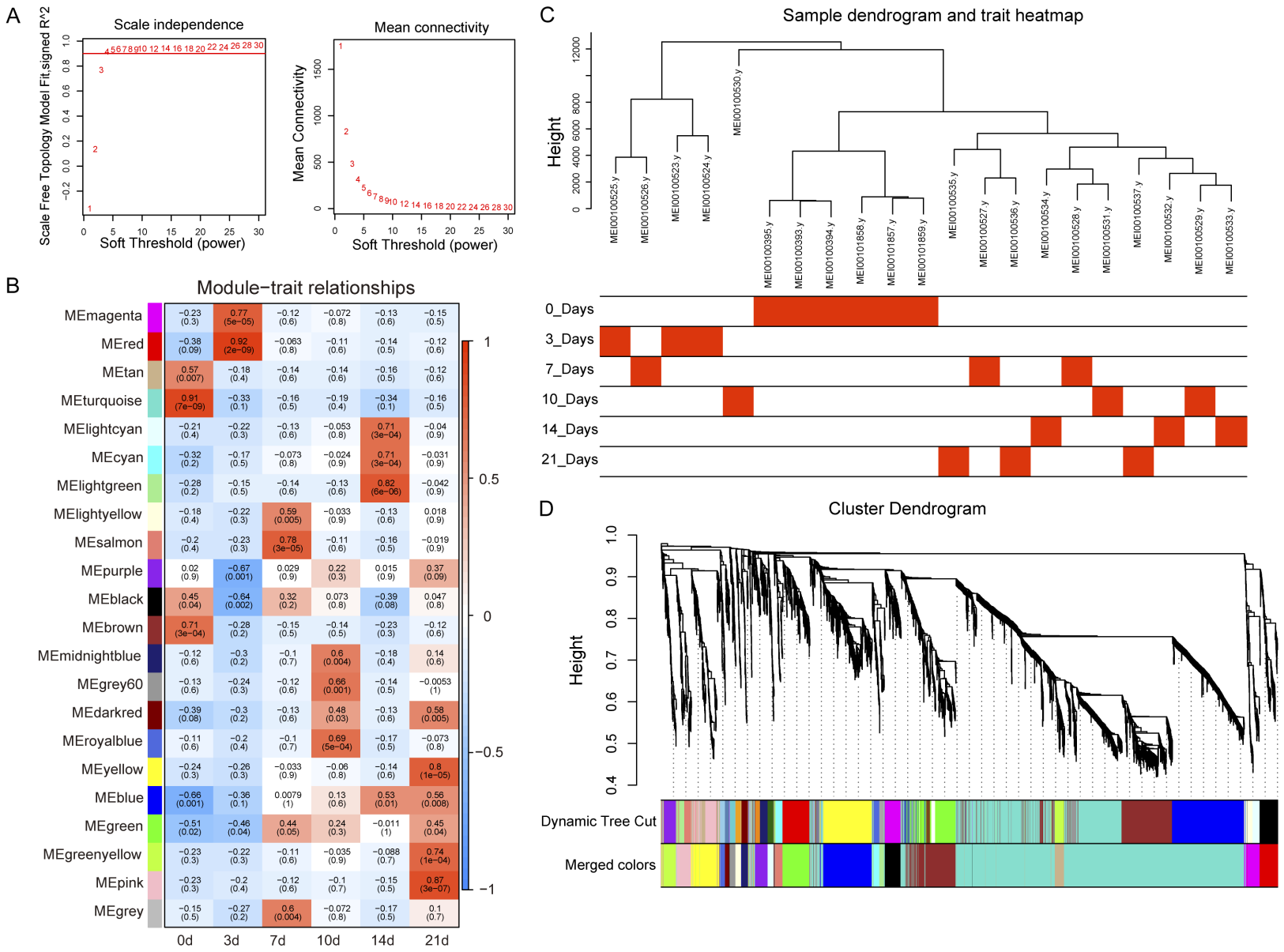


Figure S7. Determination of soft-threshold power and identification of modules in the WGCNA of tumor. A. Analysis of the scale-free index and mean connectivity for various soft-threshold powers. B. Clustering dendrogram of 21 samples. C. Heatmap of the correlation between the module eigengenes and traits of timepoint by WGCNA in tumor sample. D. Dendrogram of all differentially expressed genes clustered based on the measurement of dissimilarity (1-TOM).