SUPPLEMENTAL DATA

Wang et al: ICD risk signature for CRC prognosis

Immunogenic cell death-related risk signature for tumor microenvironment profiling and prognostic prediction in colorectal cancer

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DOI: https://doi.org/10.17305/bb.2025.12028

Full article is available at the following link:

https://www.bjbms.org/ojs/index.php/bjbms/article/view/12028

Figure S1. Differential expression analysis of ICD-related genes in regard to clinical features.

Distribution of the expression levels of ICD-related genes in the groups separated by lymphatic invasion (A), perineural invasion presence (B), age (C), and sex (D).
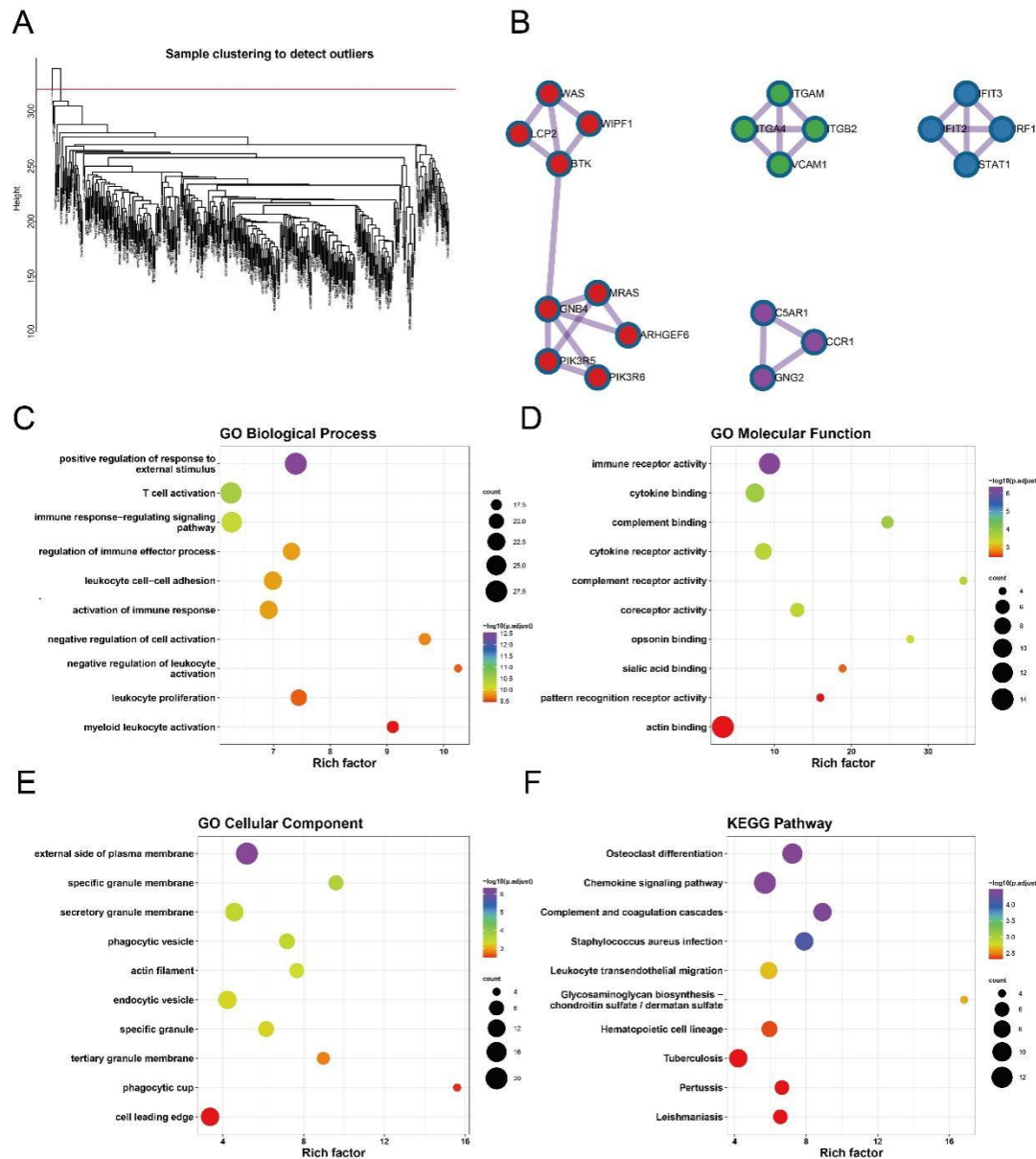

Figure S2. PPI and function enrichment analysis of ICD-related gene clusters revealed using WGCNA. Clustering of samples using WGCNA. (B) PPI networks of ICD-related genes. (C-E) GO enrichment analysis. (F) KEGG enrichment analysis.