

Figure S1. Analysis of DEGs and WGCNA of the data obtained from the GEO. (A) Volcano plot of the data obtained from the GEO. (B) WGCNA power selection. (C) Dendrogram of the WGCNA modules. (D) Relationship between the co-expression modules and external traits. (E) Scatter plot of module membership and gene significance for cancer in the red module. DEG, differentially expressed gene; WGCNA, weighted gene co-expression network analysis; GEO, Gene Expression Omnibus.

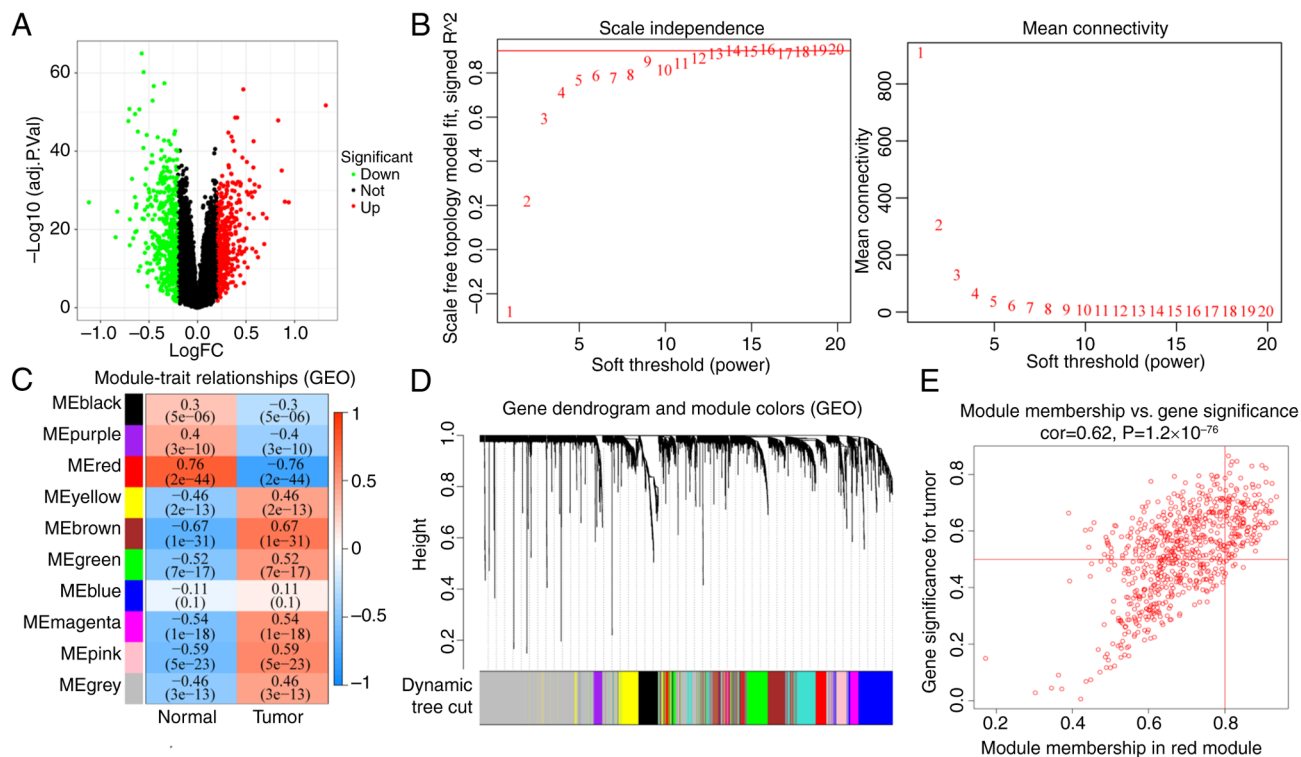


Figure S2. Protein-protein interaction networks. (A and B) Networks of overlapping genes. (C) Hub genes from the networks.

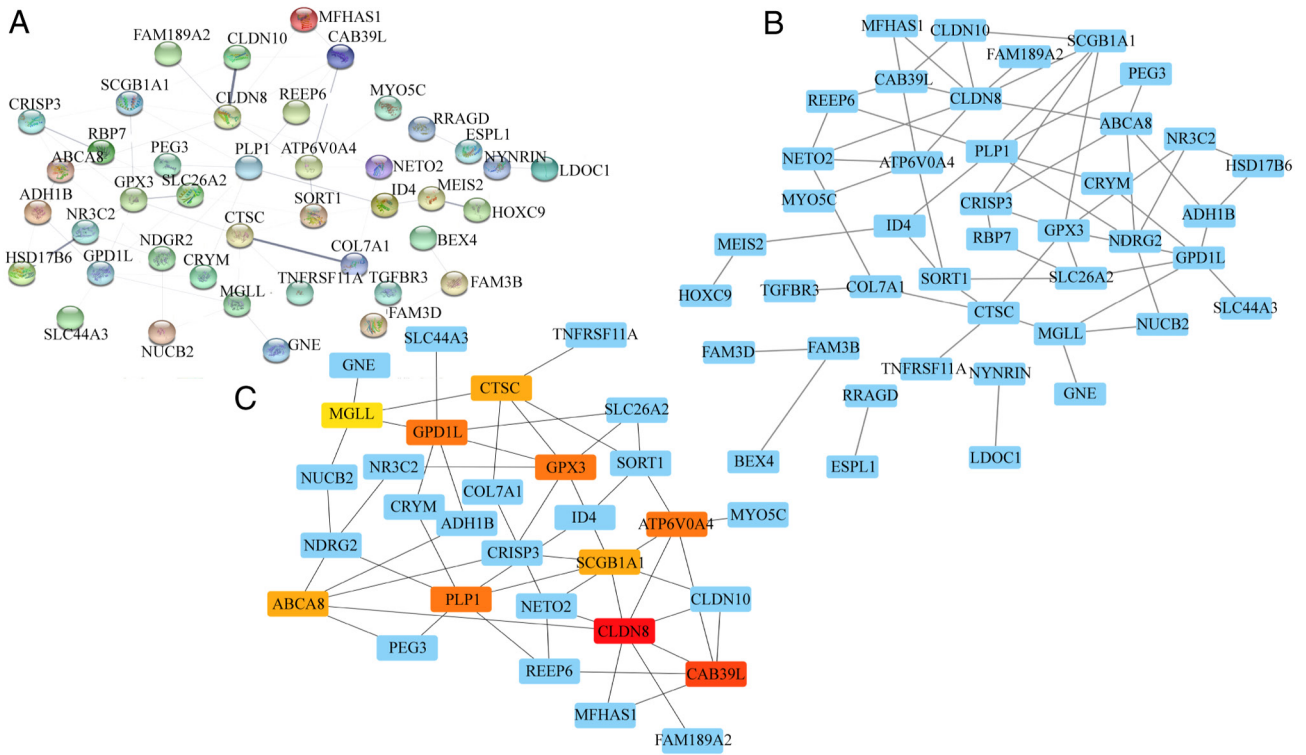




Figure S4. Disease-free survival analysis. (A-H) Disease-free survival analysis of each hub gene. ABCA8, ATP binding cassette subfamily A member 8; CLDN8, claudin 8; CAB39L, calcium binding protein 369-like; PLP1, proteolipid protein 1; GPX3, glutathione peroxidase 3; ATP6V0A4, ATPase H<sup>+</sup> transporting V0 subunit a4; GPD1L, glycerol-3-phosphate dehydrogenase 1-like; SCGB1A1, secretoglobulin family 1A member 1.

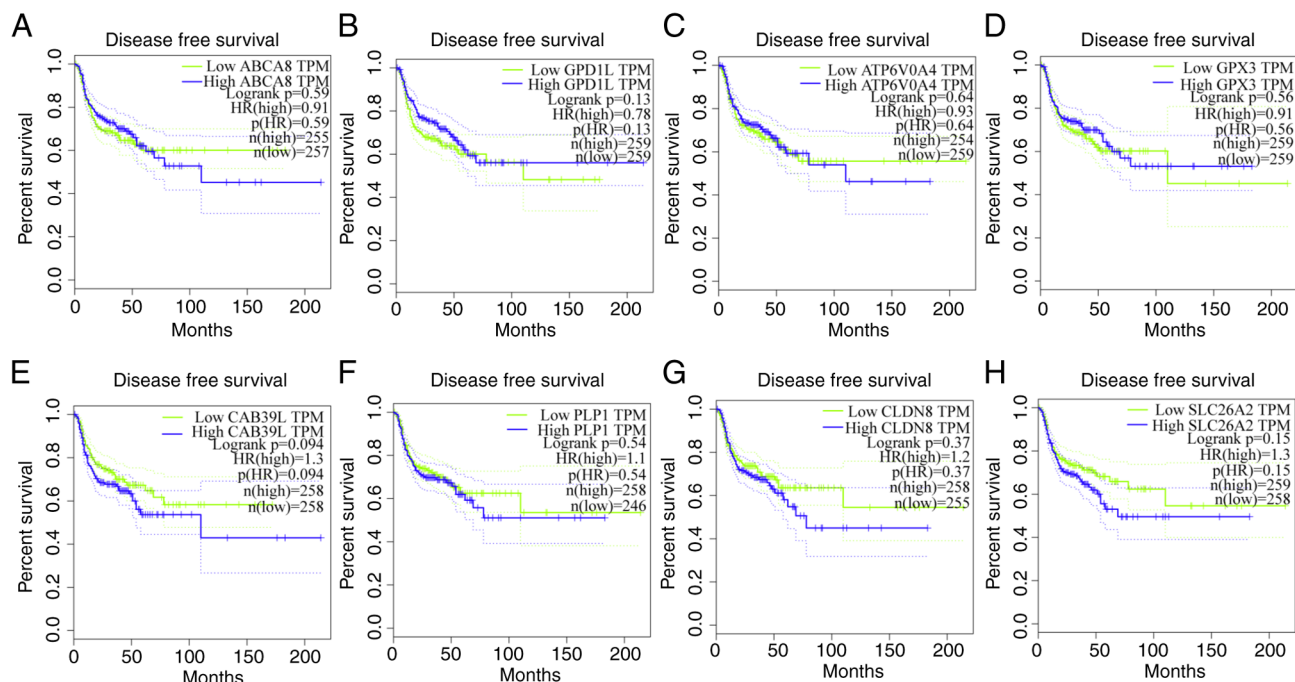


Figure S5. Sankey diagram of *SCGB1A1*. (A) Sankey diagram of *SCGB1A1* expression and pTNM stage. (B) Sankey diagram of *SCGB1A1* and tumor grade. pTNM, pathological TNM; *SCGB1A1*, secretoglobin family 1A member 1.

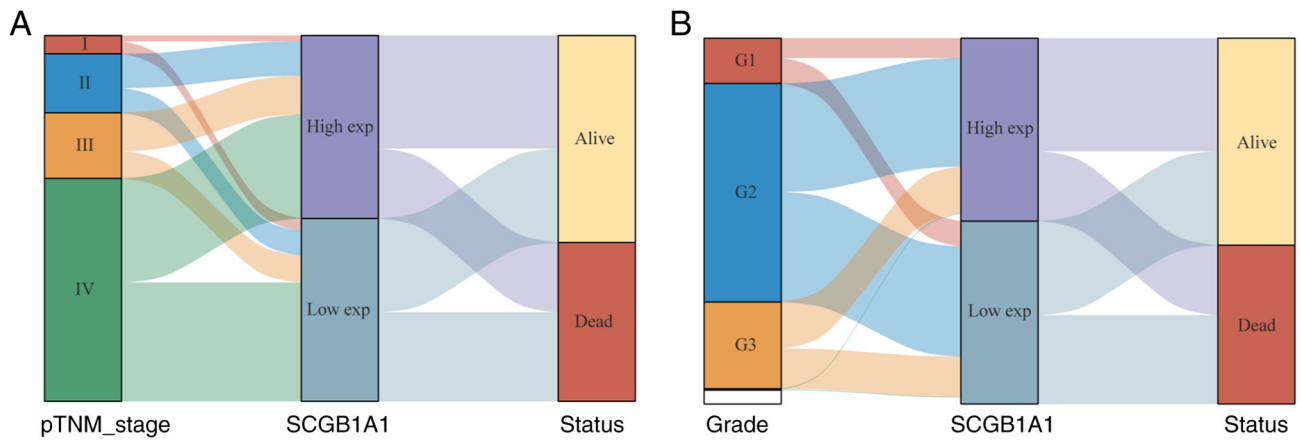


Figure S6. Drug sensitivity analysis of *SCGB1A1*. Drug sensitivity analysis based on (A) TL-1-85, (B) SB52334, (C) NG-25, (D) MS-275, (E) Pyrimethamine, (F) CAY10603, (G) BMS-754807, (H) Linifanib, (I) JW-7-24-1 and (J) GSK429286A. SCGB1A1, secretoglobulin family 1A member 1.

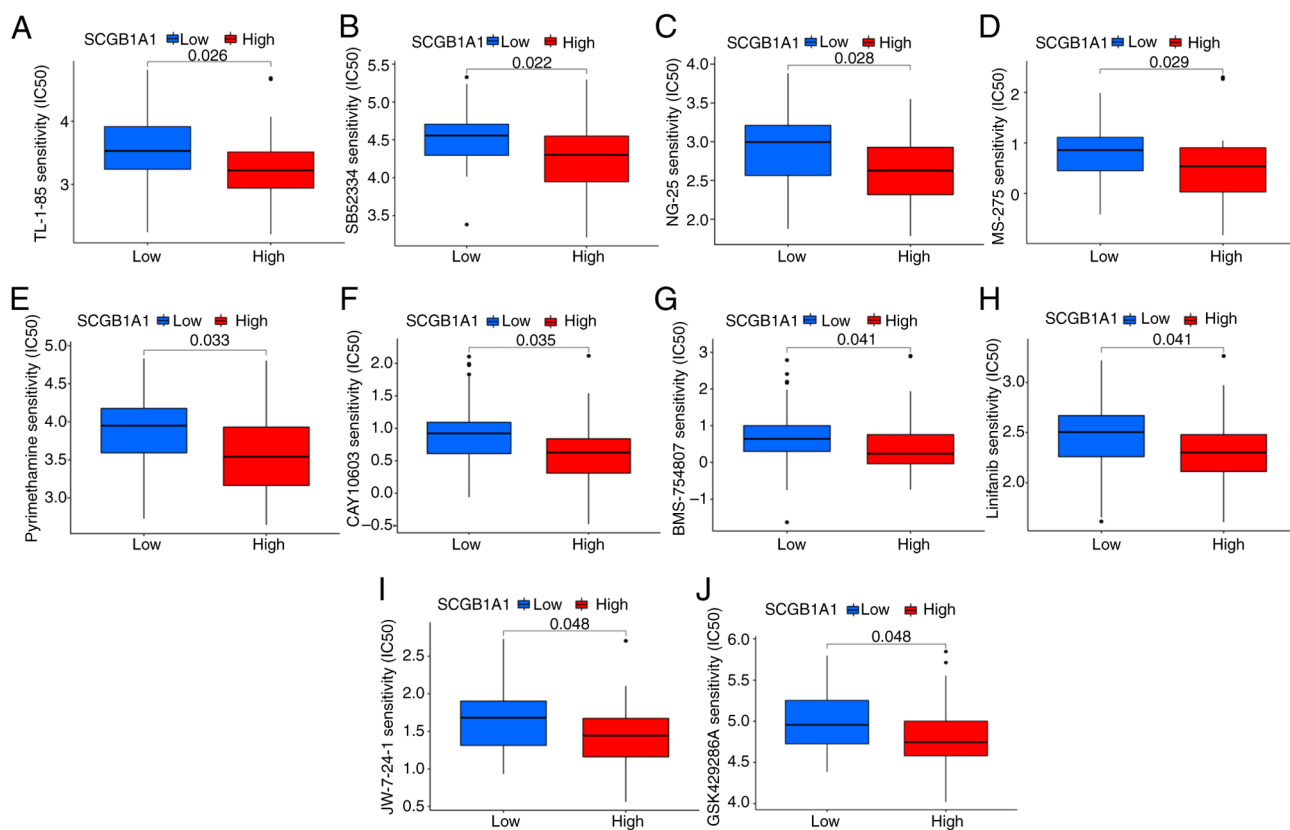


Figure S7. GSEA of secretoglobin family 1A member 1. GSEA based on (A) ASCORBATE AND ALDARATE METABOLISM, (B) DRUG METABOLISM CYTOCHROME P450, (C) STARCH AND SUCROSE METABOLISM, (D) METABOLISM OF XENOBIOTICS BY CYTOCHROME P450, (E) TYROSINE METABOLISM, (F) PORPHYRIN AND GHOROPHYLL METABOLISM, (G) TYROSINE METABOLISM, (H) RETINOL METABOLISM and (I) ARACHIDONIC ACID METABOLISM. GSEA, Gene Set Enrichment Analysis KEGG, Kyoto Encyclopedia of Genes and Genomes.

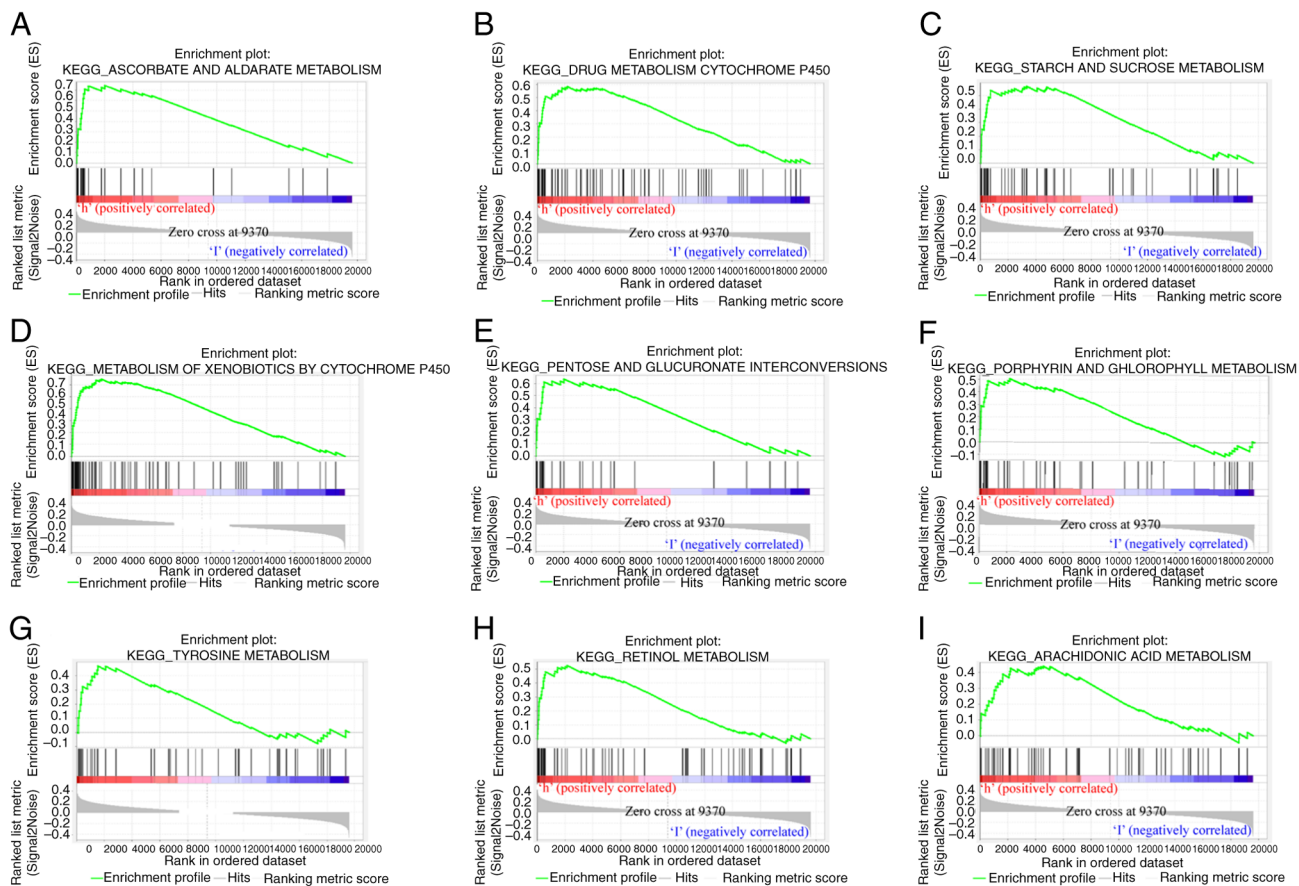


Figure S8. Overall Survival analysis based on the expression levels of glycolytic genes. Overall Survival analysis based on (A) *NT5E*, (B) *BIK*, (C) *CYB5A*, (D) *MERTK*, (E) *CLDN3* and (F) *IDUA* expression. *NT5E*, 5'-nucleotidase ecto; *BIK*, BCL2 interacting killer; *CYB5A*, cytochrome b5 type A; *MERTK*, MER proto-oncogene, tyrosine kinase; *CLDN3*, claudin 3; *IDUA*,  $\alpha$ -L-iduronidase.

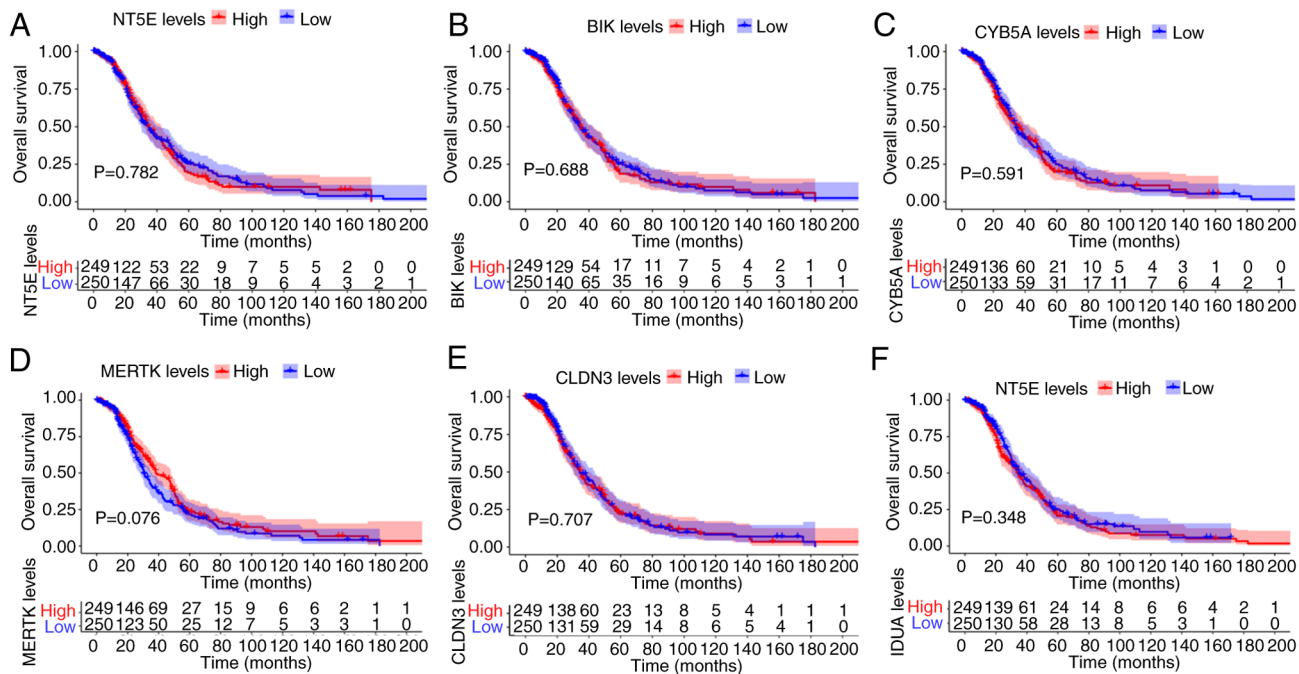


Figure S9. Correlation analysis of glycolytic genes and immune cells. (A-H) Correlation analysis between the glycolytic gene, *COL5A1*, and immune cells. (I-N) Correlation analysis between the glycolytic gene, *NASP*, and immune cells. *COL5A1*, collagen type V  $\alpha 1$  chain; *NASP*, nuclear autoantigenic sperm protein.

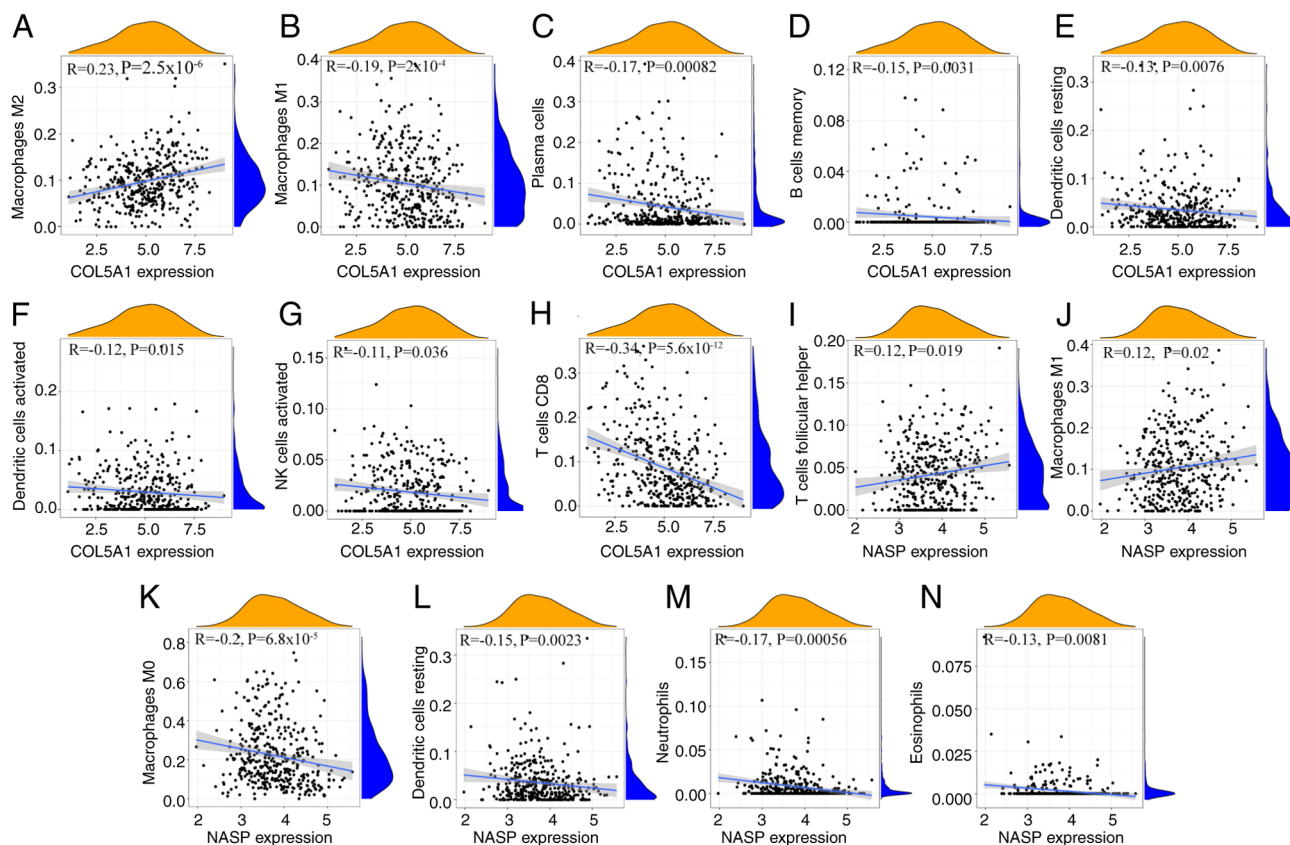


Figure S10. *SCGB1A1* correlation analysis. (A-F) Correlation analysis between *SCGB1A1* and glycolysis-related genes. *SCGB1A1*, secretoglobulin family 1A member 1; *NT5E*, 5'-nucleotidase ecto; *BIK*, BCL2 interacting killer; *CYB5A*, cytochrome b5 type A; *MERTK*, MER proto-oncogene, tyrosine kinase; *CLDN3*, claudin 3; *IDUA*,  $\alpha$ -L-iduronidase; TPM, transcripts per million.

