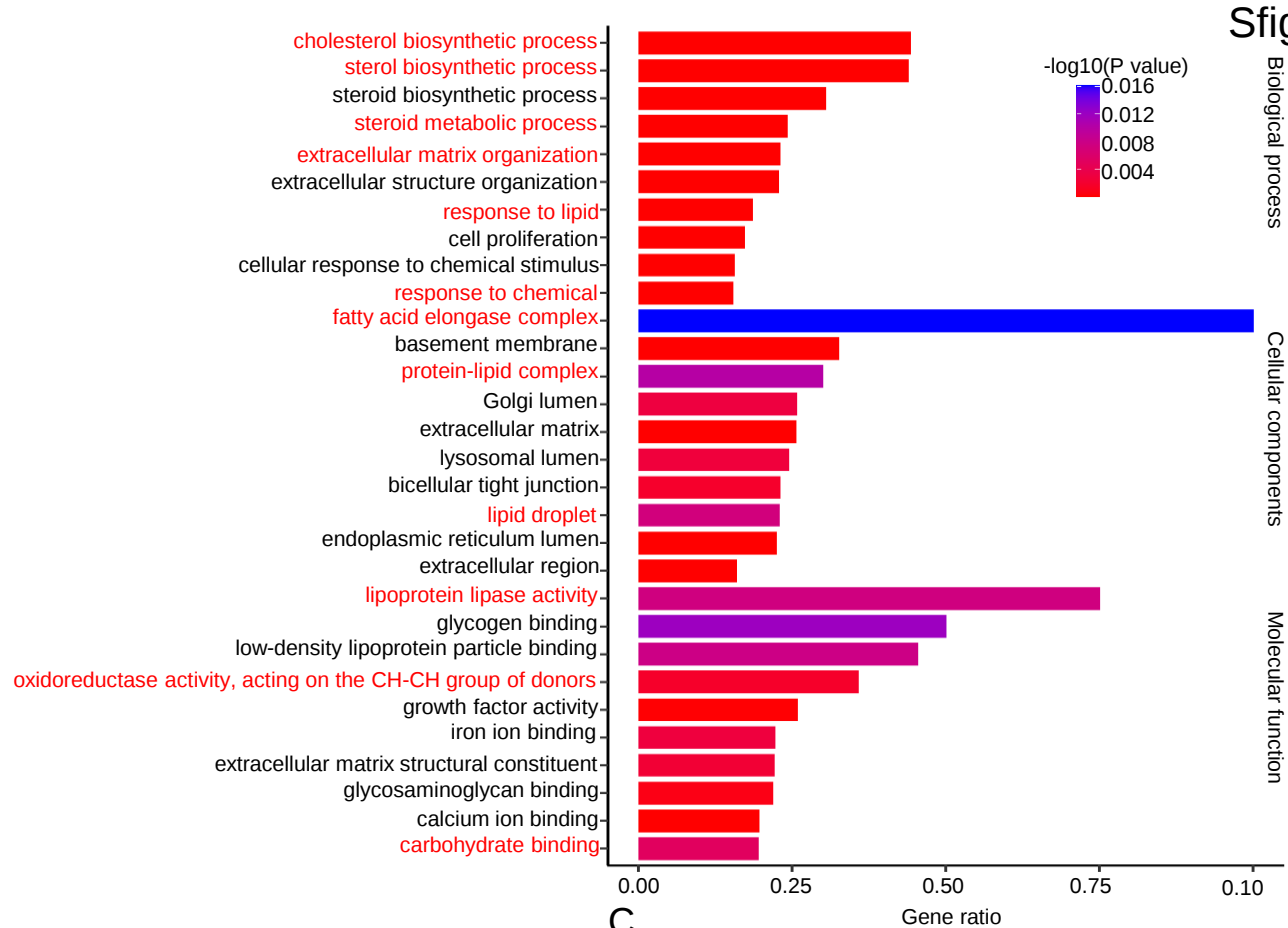
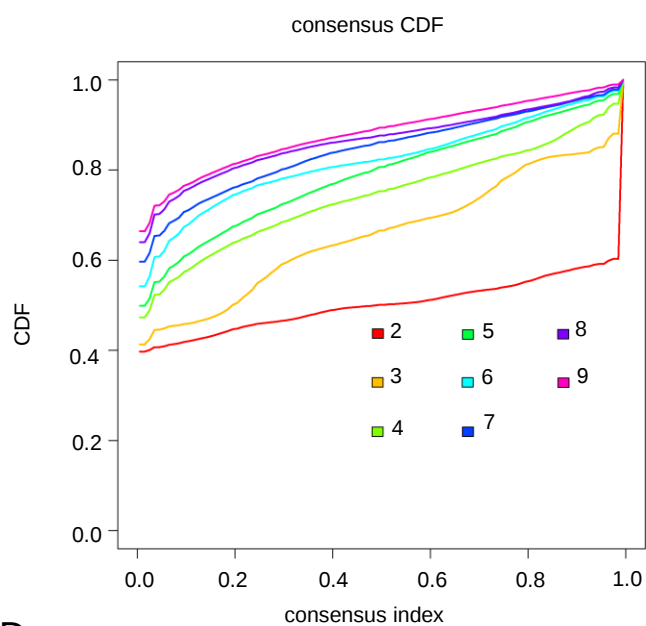


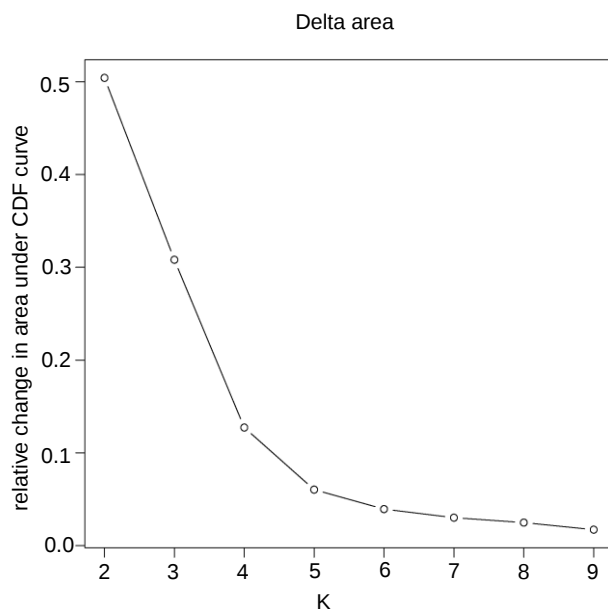
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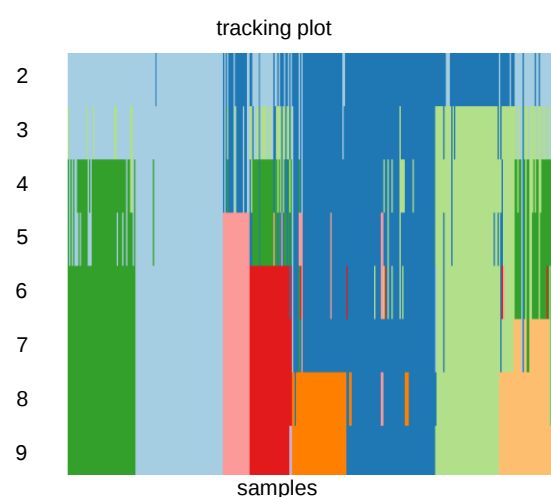
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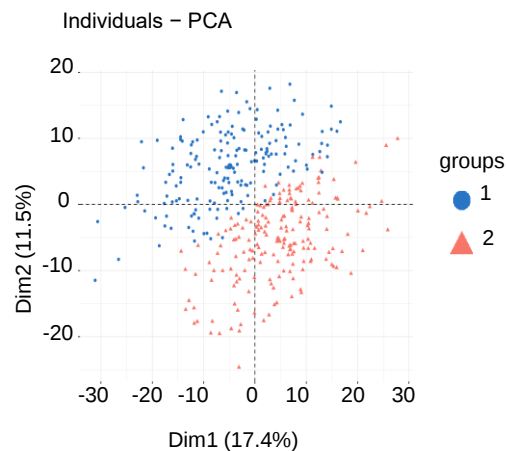
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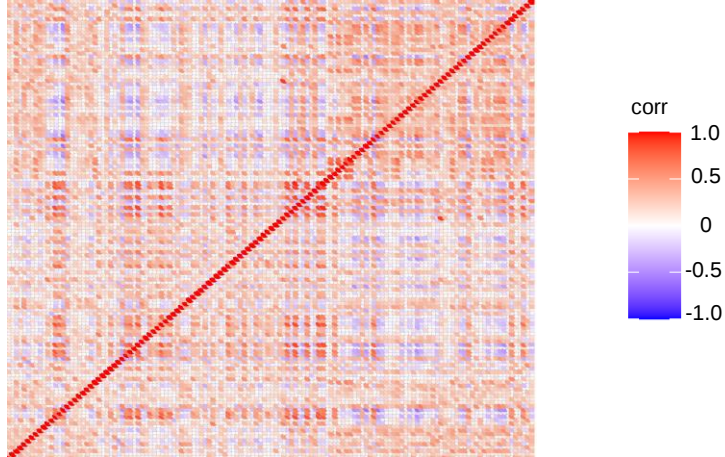
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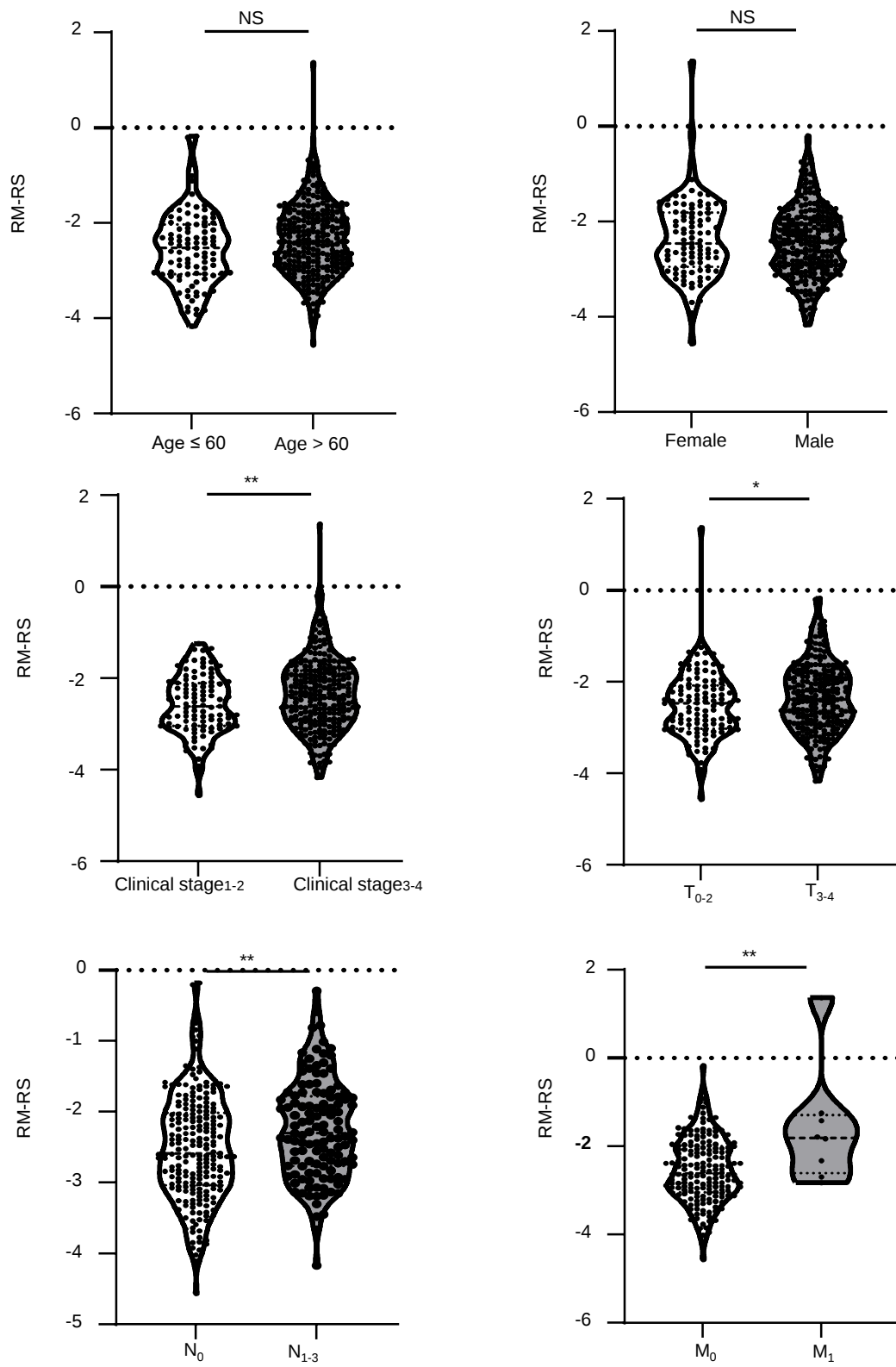
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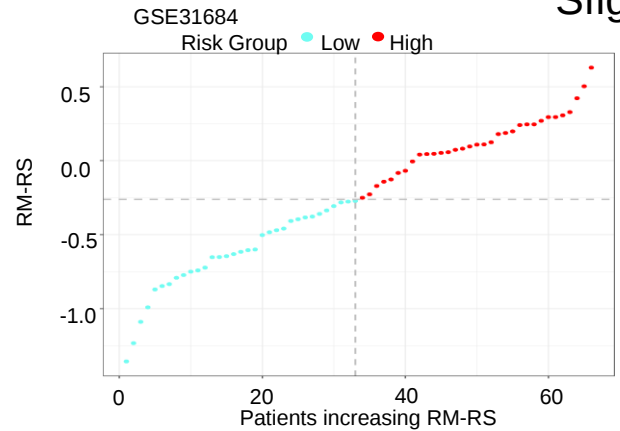
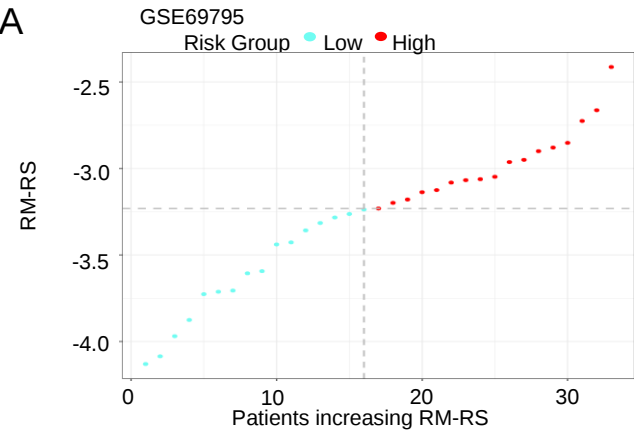
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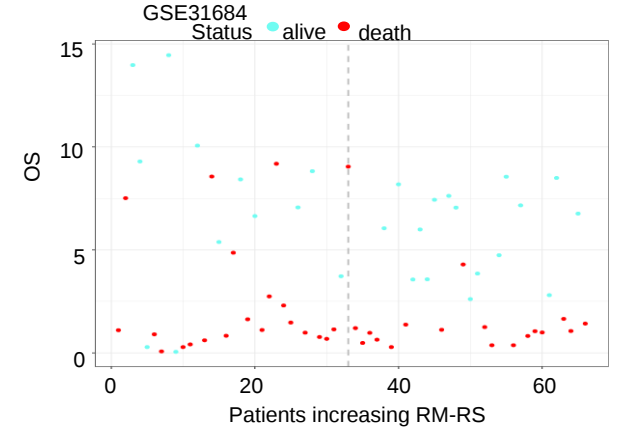
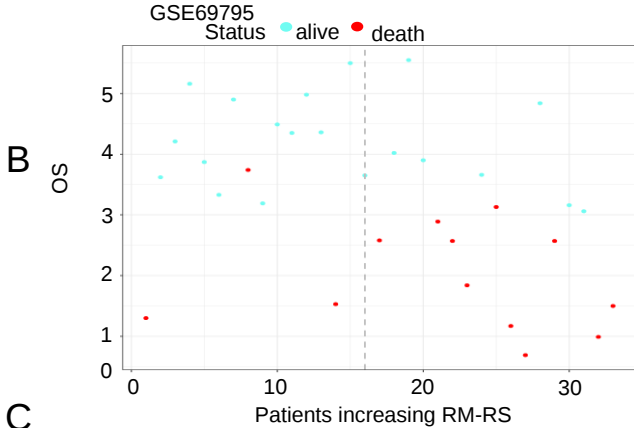
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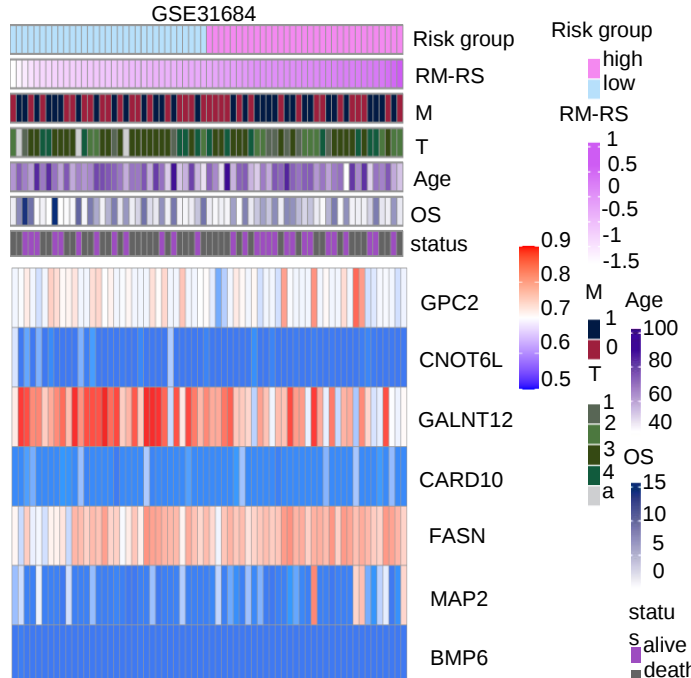
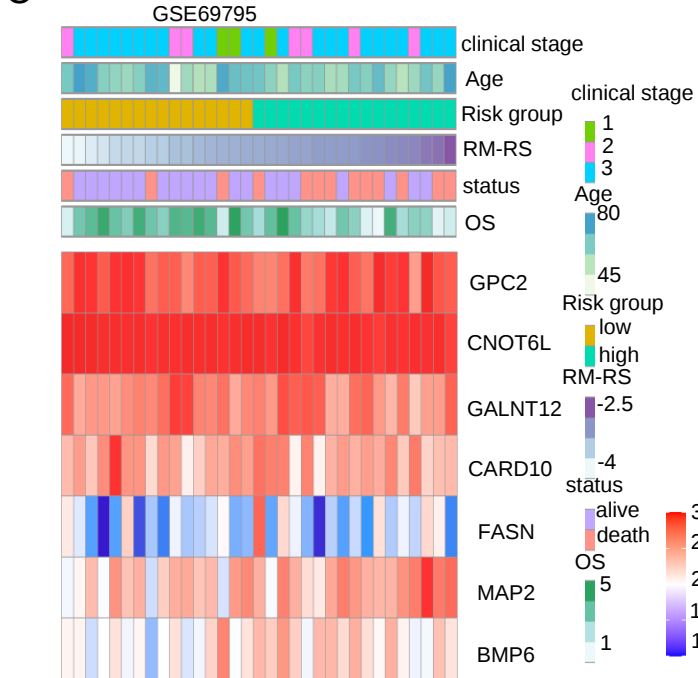
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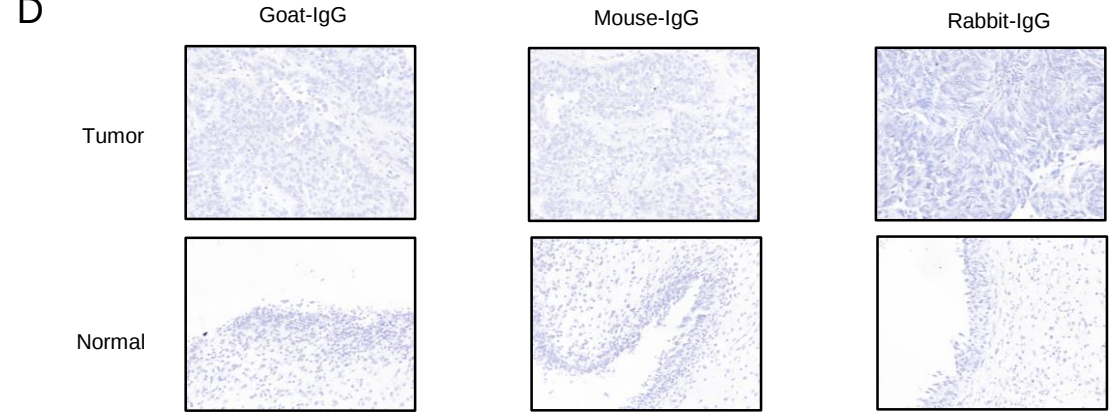
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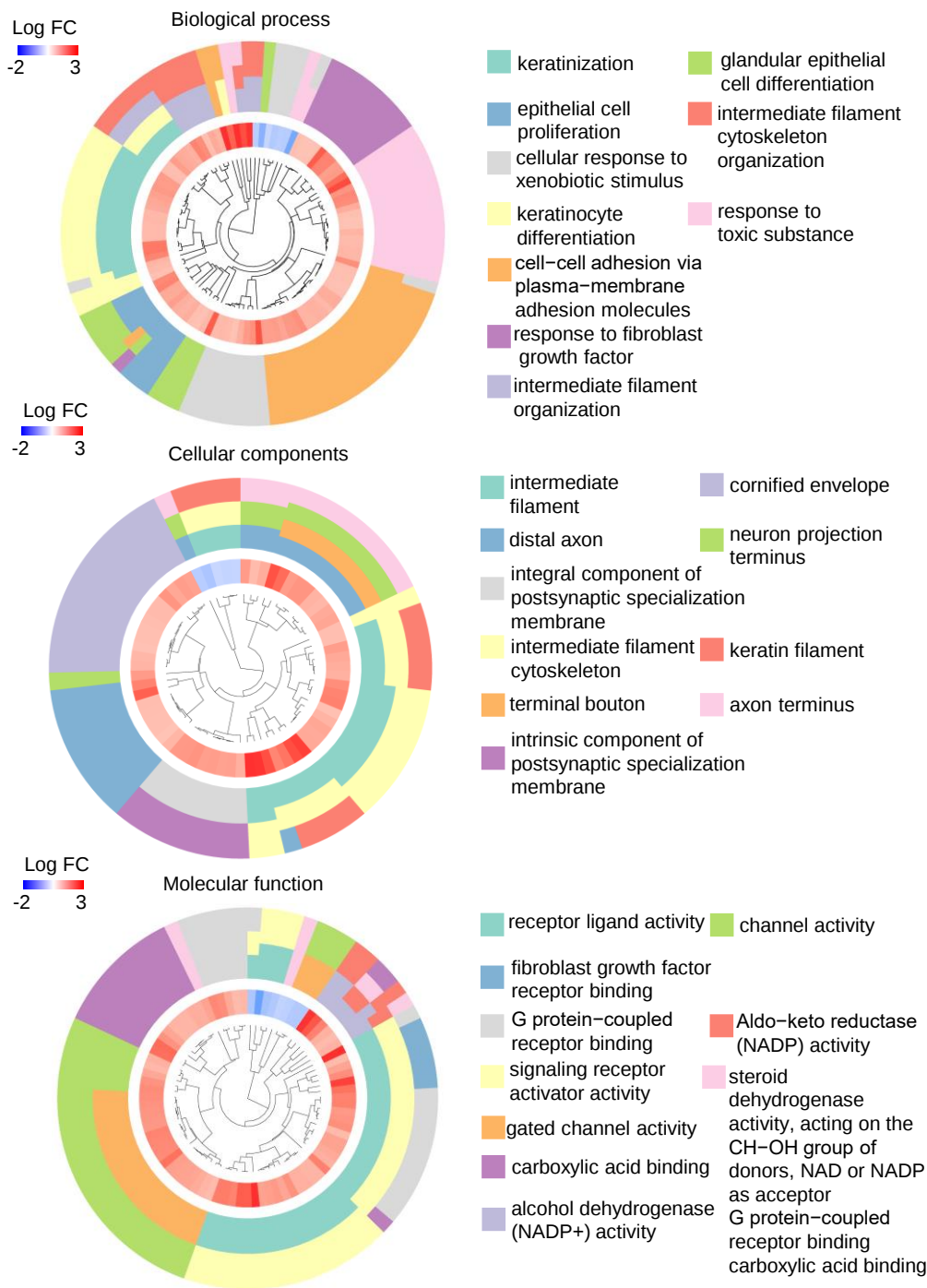
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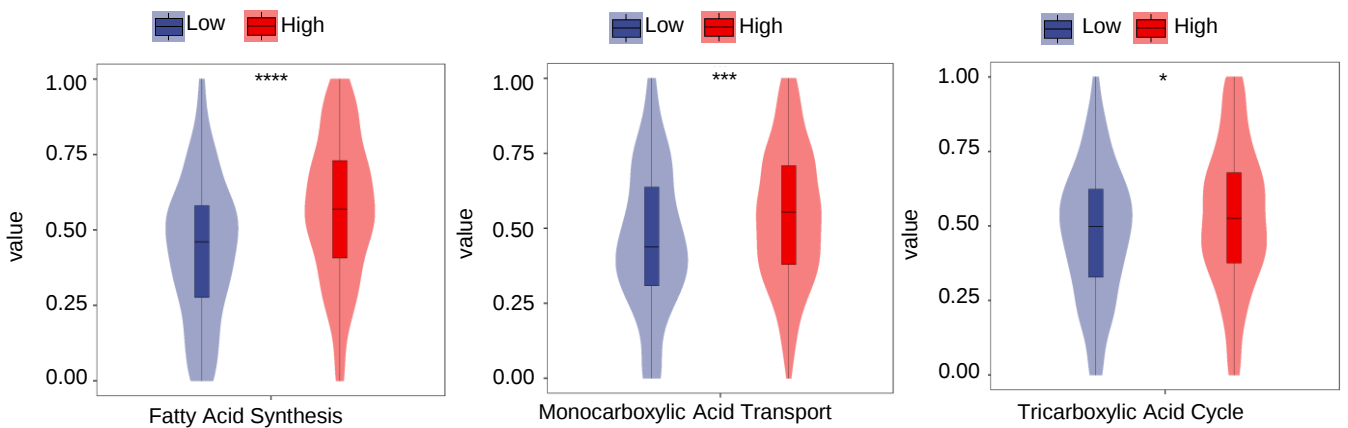
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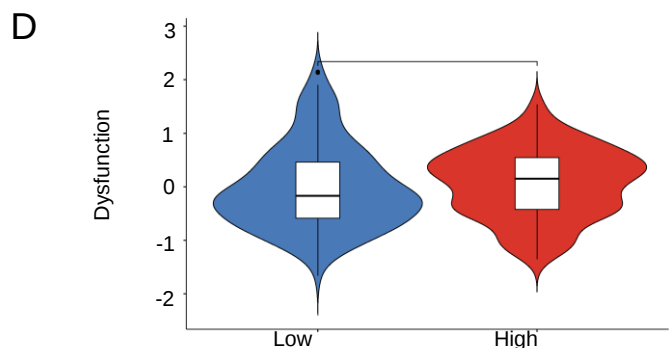
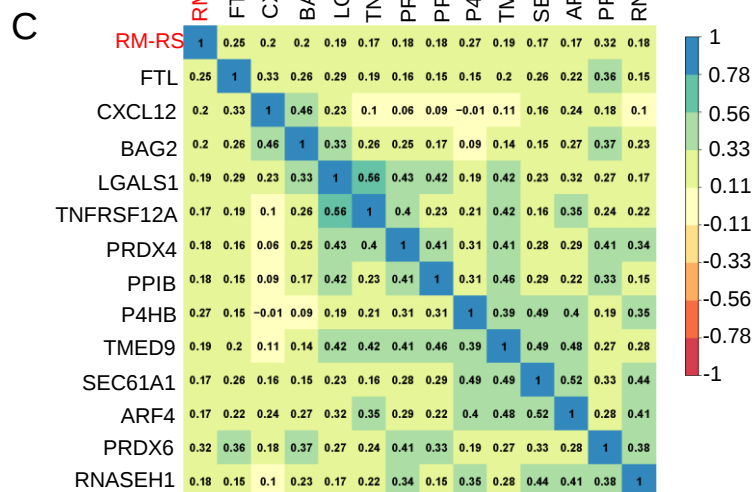
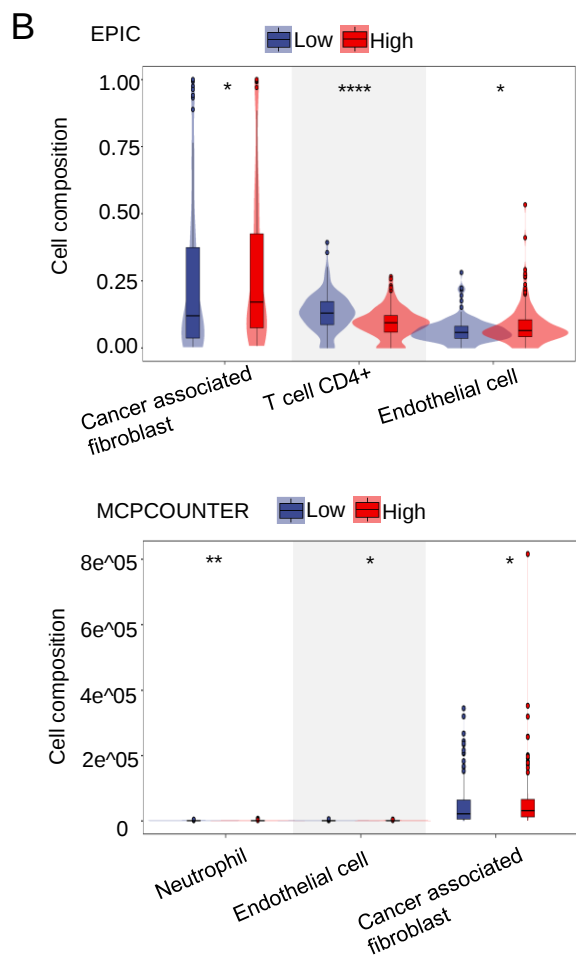
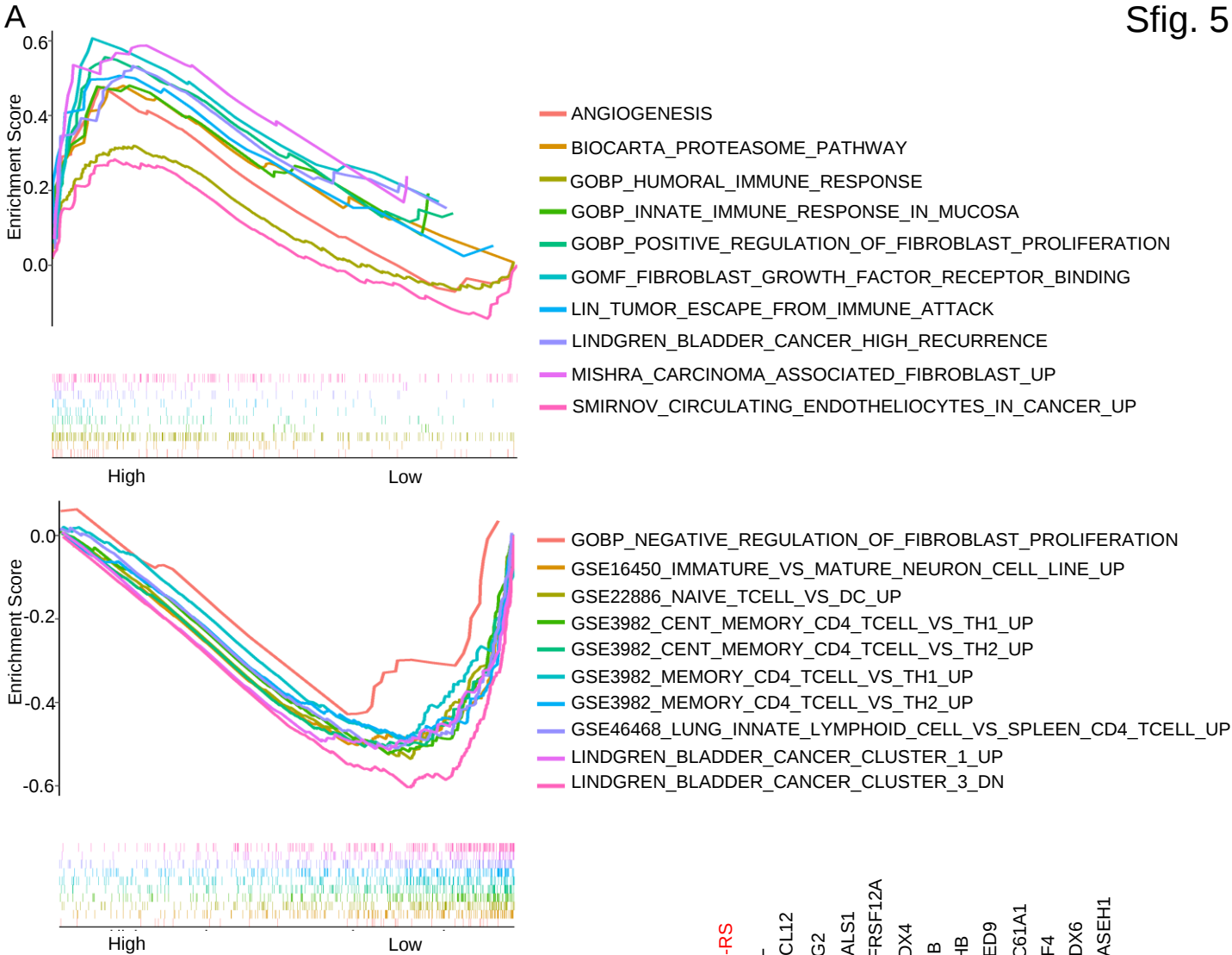


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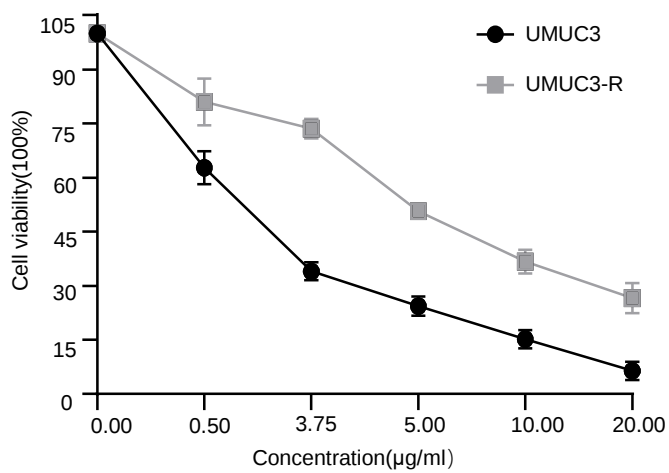
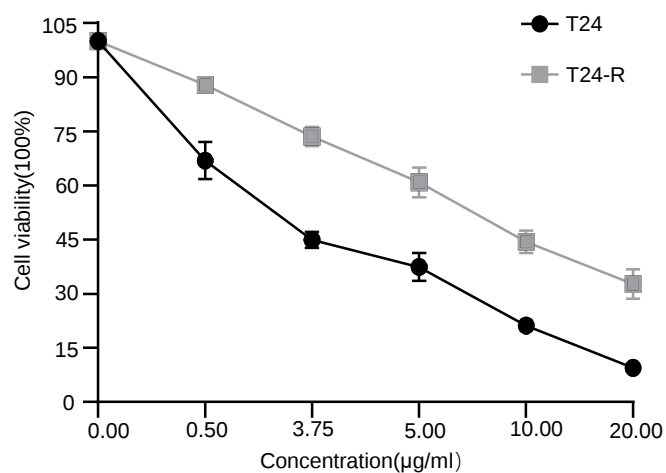


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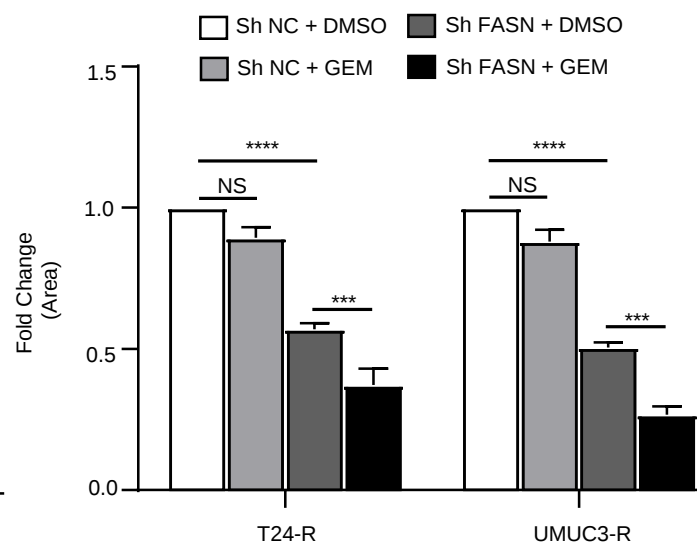
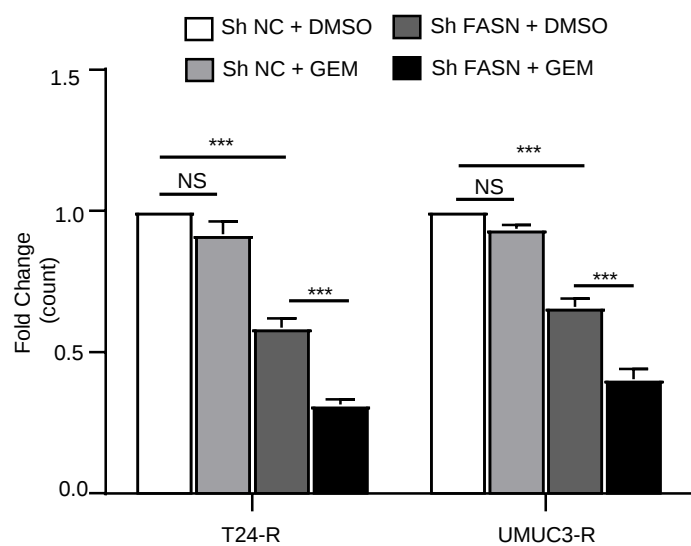




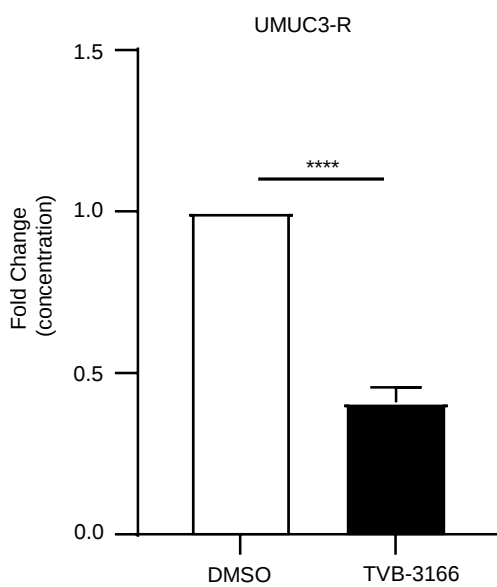
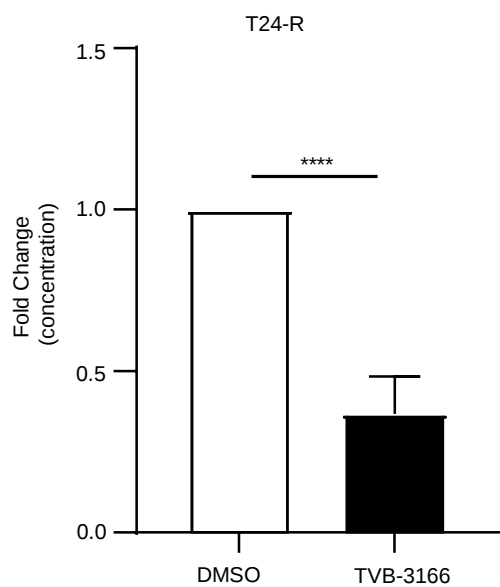
A



B



C



Supplementary Figure Legends

SFigure1. (A) Gene Ontology (GO) enrichment analysis for differentially expressed genes (DEGs). Adjusted $p < 0.01$ and $p < 0.05$ were considered significant. (B, C, and D) Consensus clustering distribution function (CDF), area under CDF curve increment, and tracking plot for $k = 2$ to 9. (E) Individuals of principal component analysis (PCA) with two groups.

SFigure2. (A) The correlation of the OS-related key RM-DEGs. (B) MRS was positively correlated with Clinical stage and TNM stage, but not with age and gender. Student's t test; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$.

SFigure3. (A) The distribution of risk scores in GSE69795 and GSE31684 database based on median of RM-RS. Blue represents low RM-RS subgroup, while red represents high RM-RS subgroup. (B) The Overall Survival (OS) distribution of patients (blue) or recurred (red) in subgroups. (C) The heatmap of RM-RM 7 component genes expression in GSE69795 and GSE31684 database, including RM-RS and clinical features. (D) Goat-IgG, Rabbit-IgG and Mouse-IgG as negative controls for immunohistochemistry with specific isoform-specific antibodies.

SFigure4. (A) Gene Ontology (GO) analysis for exploring molecular function and biological process involved in differentially expressed genes (DEGs) of two risk subgroups. (B) Metabolic pathways with significant differences between the two risk subgroups. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$.

SFigure5. (A) Tumor microenvironment (TME) related gene sets enriched in high and low risk subgroups ($p < 0.05$). (B) Tumor microenvironment (TME) cells with significant differences in different RM-RS subgroups based on EPIC and MCPCOUNTER algorithm. (C) Correlation heatmap of RM-RS and cancer-associated fibroblasts (CAFs) marker gene expression. (D) Comparison of Dysfunction score in

different risk subgroups.

SFigure6. (A) Establishment of gemcitabine-resistant cell lines. (B) The tumorigenic ability of single cells under all conditions were determined by Colony formation assay. The histogram showed the comparison of the count and area of tumors. (D) Enzyme-linked immunosorbent assay (ELISA) was used to determine the FASN content of T24-R cells and UMUC3-R cells treated with TVB-3166(1 μ mol).