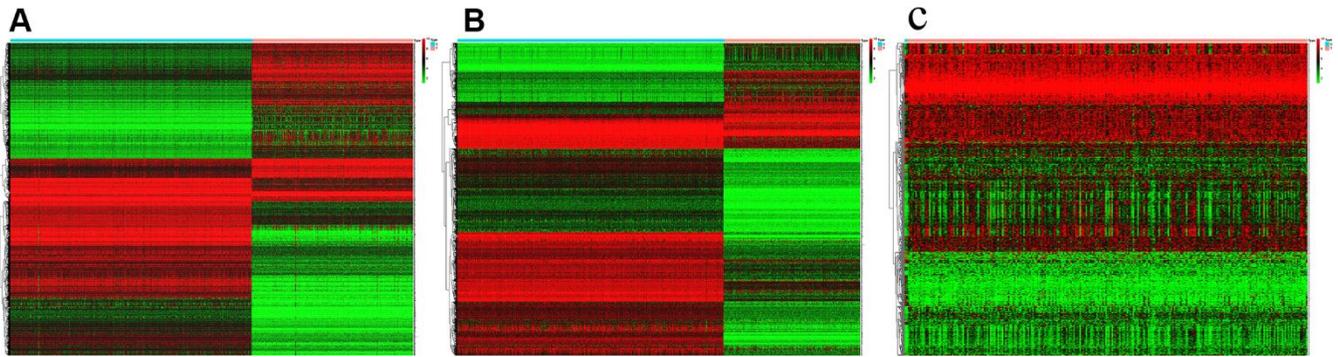
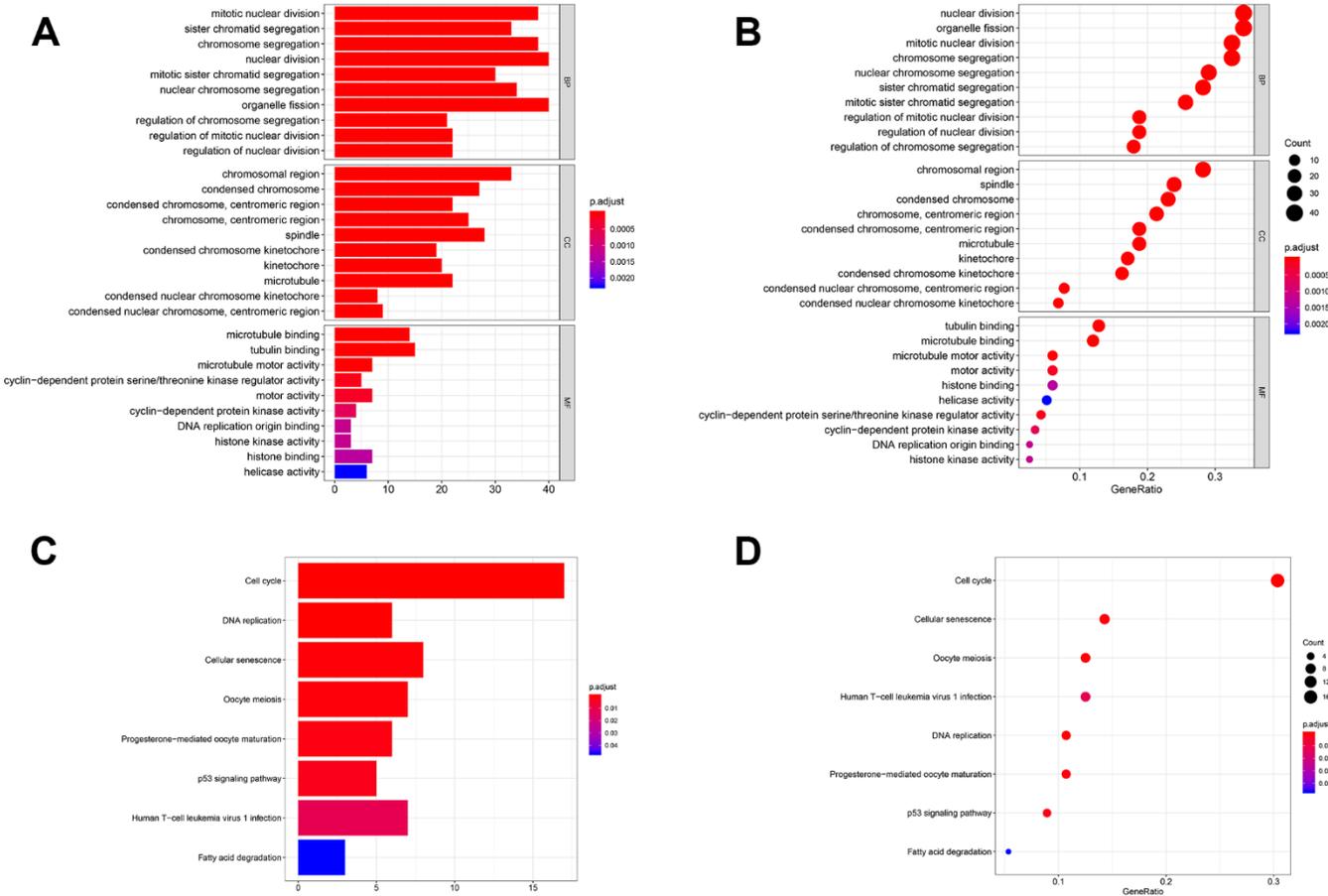


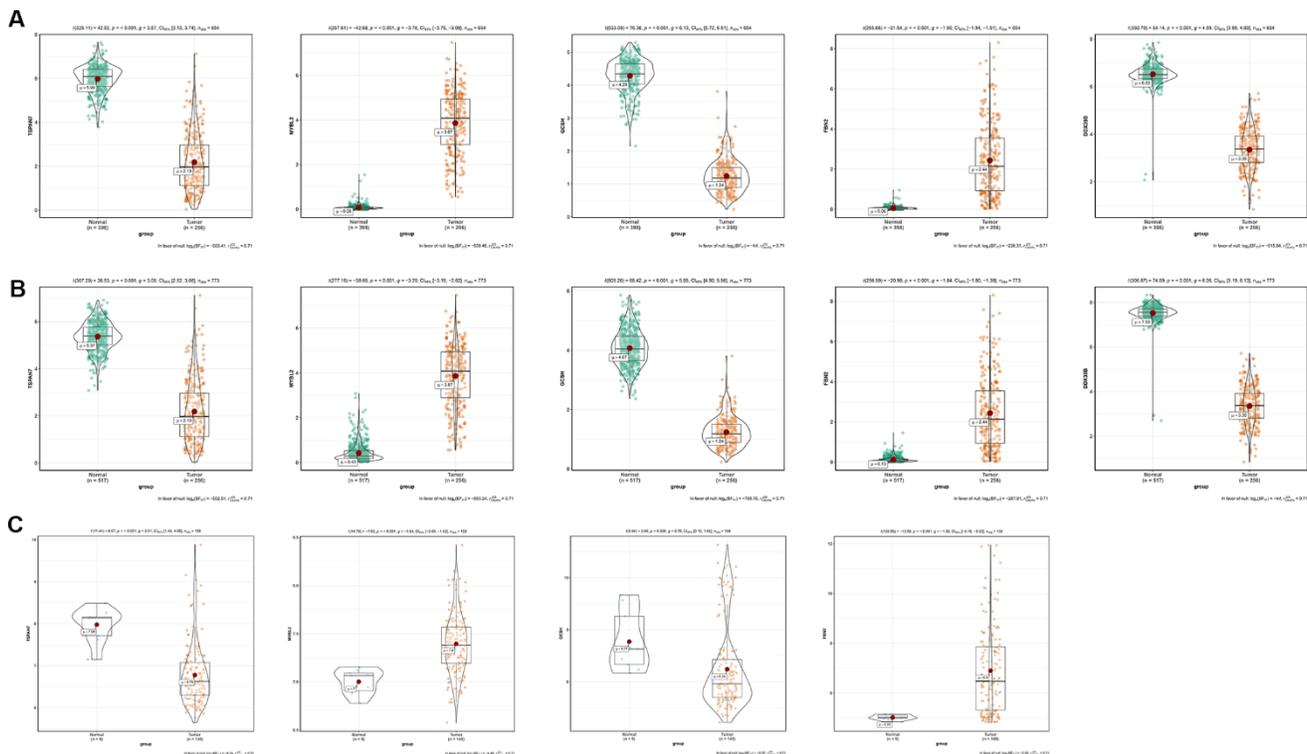
SUPPLEMENTARY FIGURES



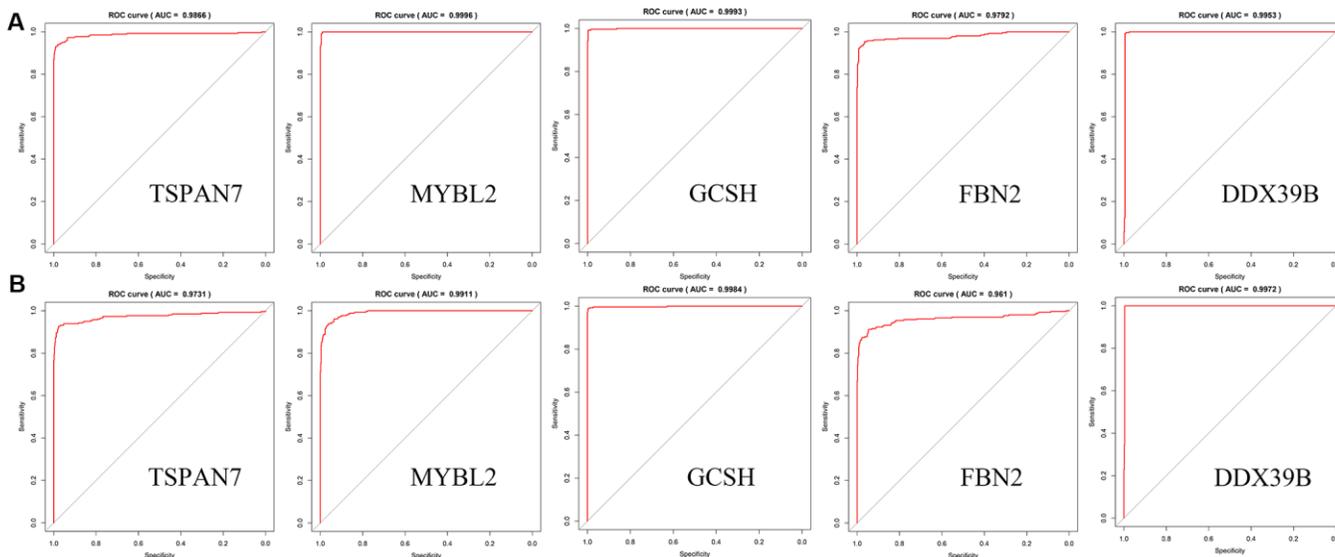
Supplementary Figure 1. Heatmaps of DEGs. Heatmaps of DEGs from “tumors” vs. “muscle controls” (A), “tumors” vs. “fat controls” (B), and “tumors” vs. “matched controls” (C).



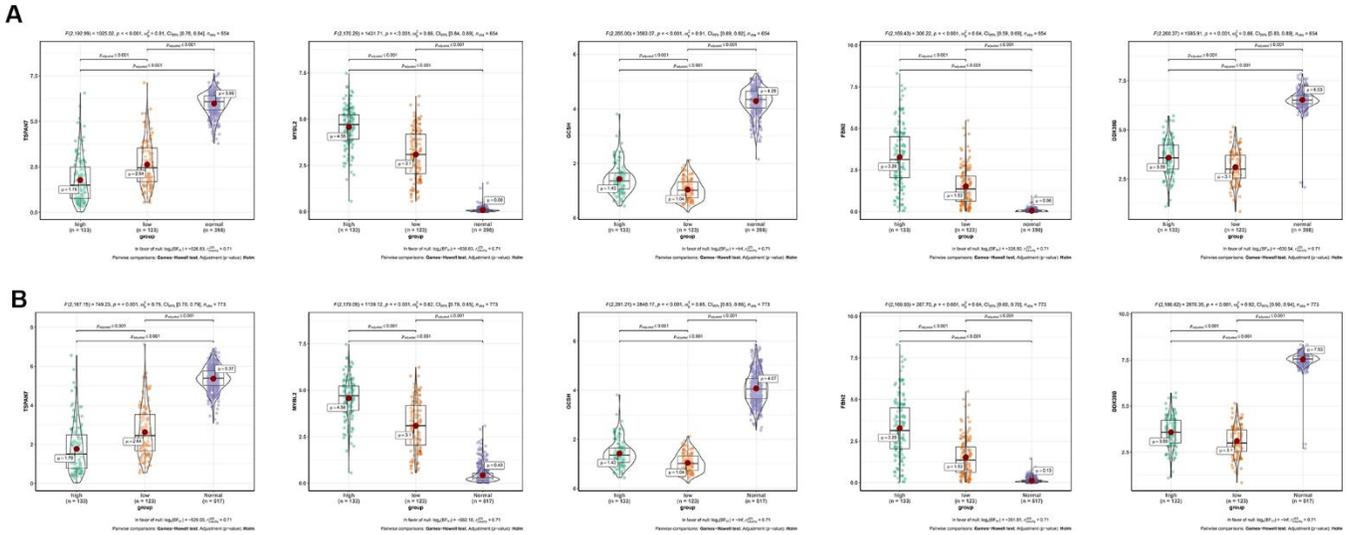
Supplementary Figure 2. Functional annotation of primary differentially expressed genes (DEGs). The Gene Ontology (GO) functional annotation (A and B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichments (C and D) of DEGs.



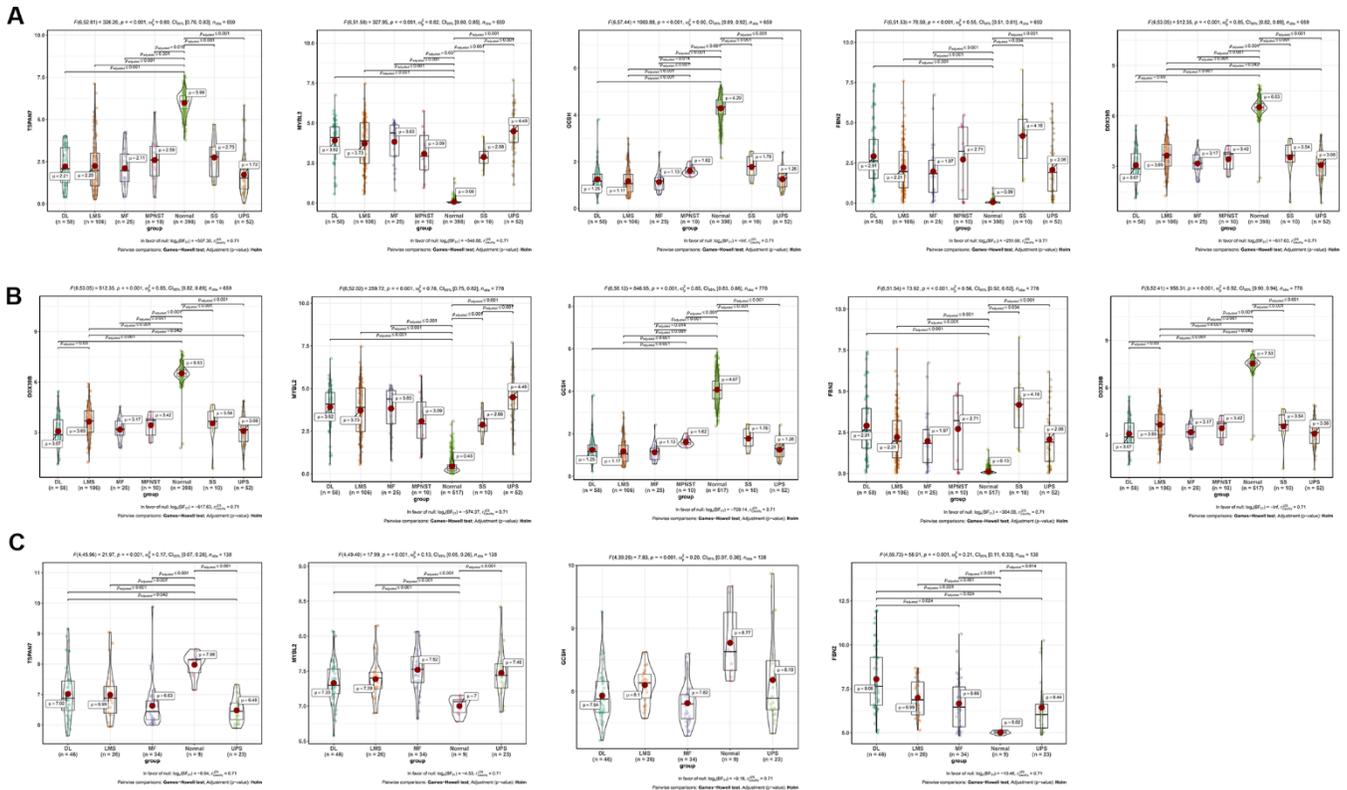
Supplementary Figure 3. Differences in the expression of key genes between soft tissue sarcoma (STS) and normal groups. (A) Differences in the expression of key genes between STS and muscle controls. (B) Differences in the expression of key genes between STS and fat controls. (C) Differences in the expression of five key genes between STS and normal groups in the GSE21122 datasets.



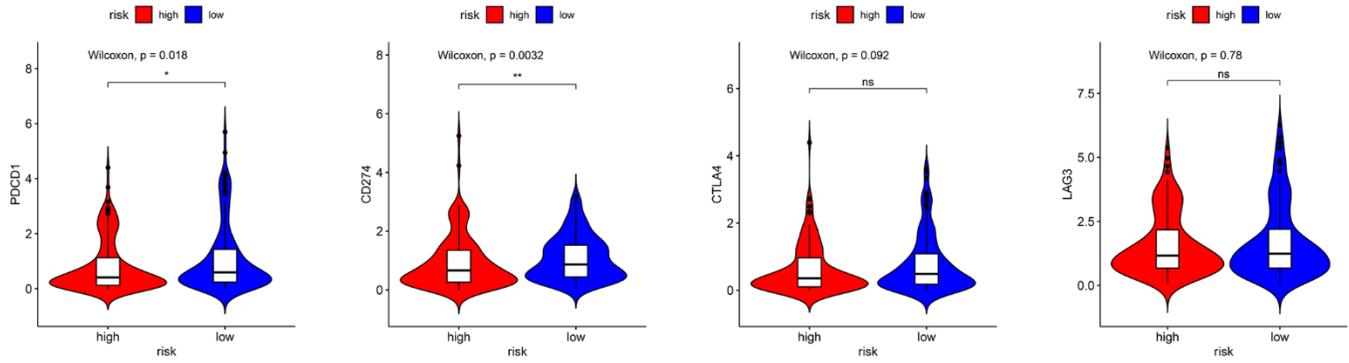
Supplementary Figure 4. Discrimination ability of key genes between STS and controls. (A) Discrimination ability of the five key genes between STS and muscle controls. (B) Discrimination ability of the five key genes between STS and fat controls.



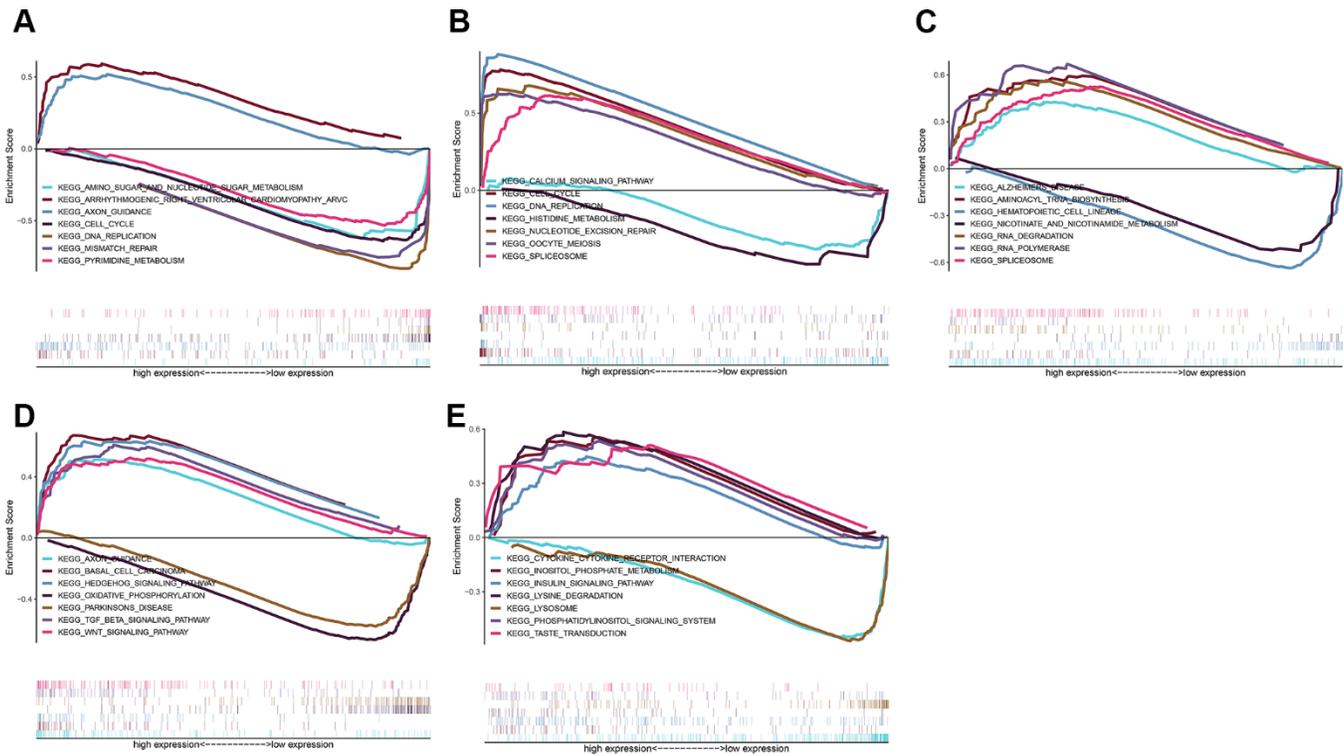
Supplementary Figure 5. Differences in the expression of key genes among high-risk and low-risk patients, and healthy (control) individuals. (A) Differences in the expression of key genes among high-risk and low-risk patients, and healthy (muscle controls) individuals. (B) Differences in the expression of key genes among high-risk and low-risk patients, and healthy (fat controls) individuals.



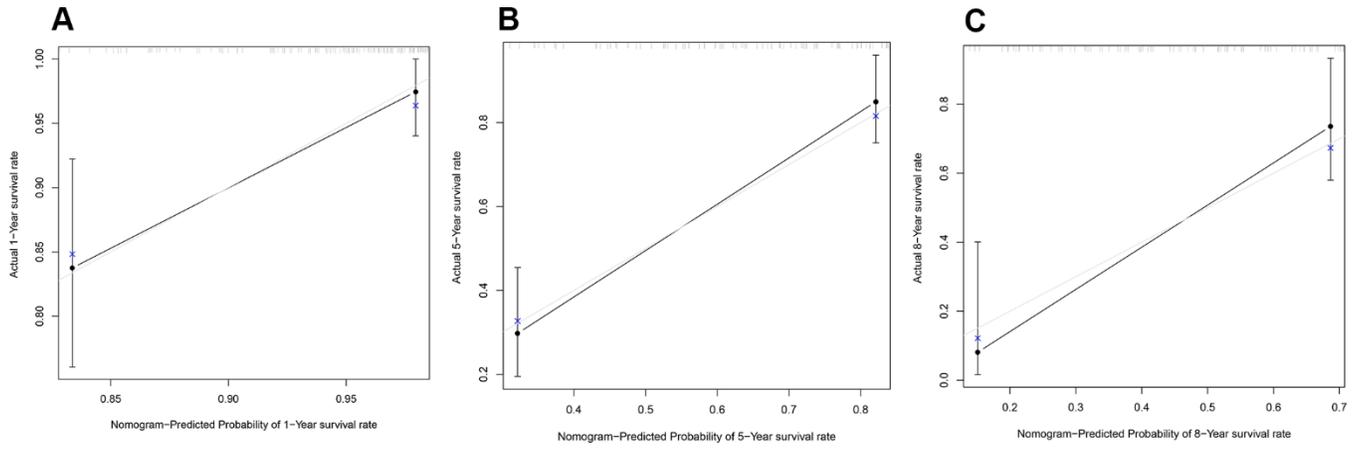
Supplementary Figure 6. Differences in the expression of key genes between all histological types and normal controls. (A) Differences in the expression of key genes between all histological types and muscle controls. (B) Differences in the expression of key genes between all histological types and fat controls. (C) Differences in the expression of key genes between all histological types and normal controls in the GSE21122 datasets.



Supplementary Figure 7. Differences in the common checkpoint molecules between high-risk and low-risk patients.



Supplementary Figure 8. Gene Set Enrichment Analysis (GSEA) of the five key genes. GSEA for TSPAN7 (A), MYBL2 (B), GCSH (C), FBN2 (D), and DDX39B (E).



Supplementary Figure 9. Accordance between actual survival rates and prediction of the nomogram.