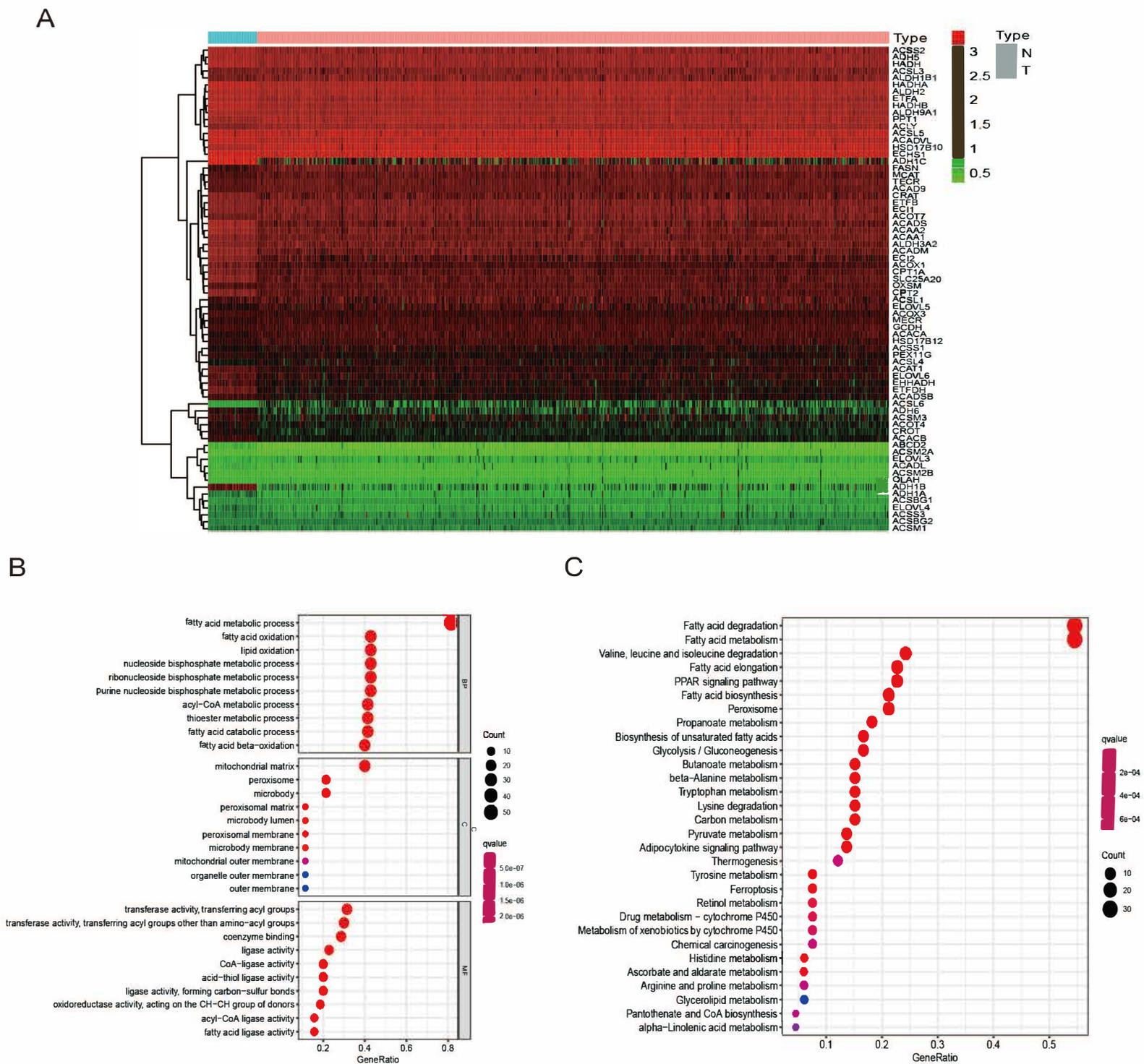


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## **Supplemental information**

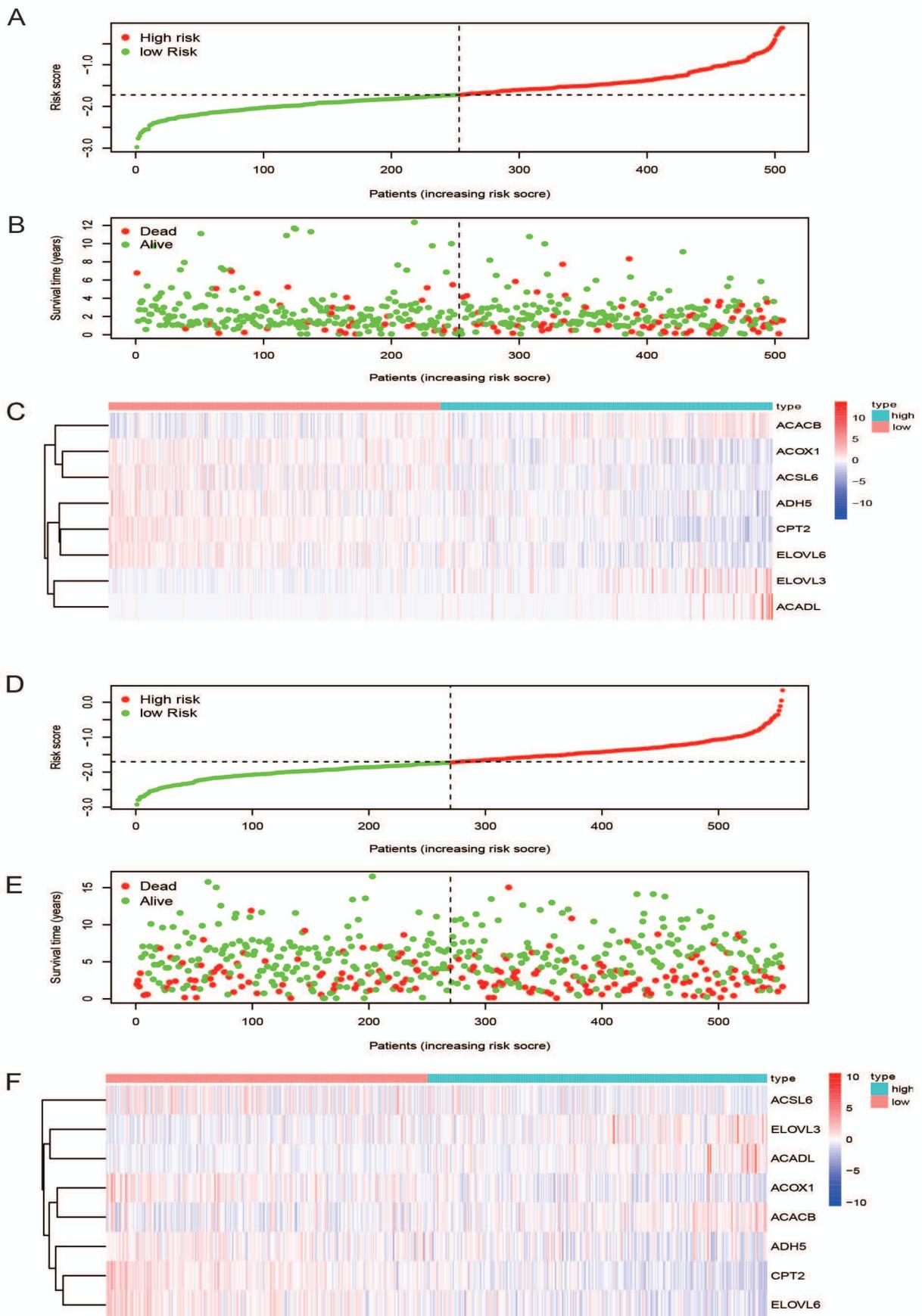
### **Characterization of the fatty acid metabolism in colorectal cancer to guide clinical therapy**

**Chengsheng Ding, Zezhi Shan, Mengcheng Li, Hongqi Chen, Xinxiang Li, and Zhiming Jin**



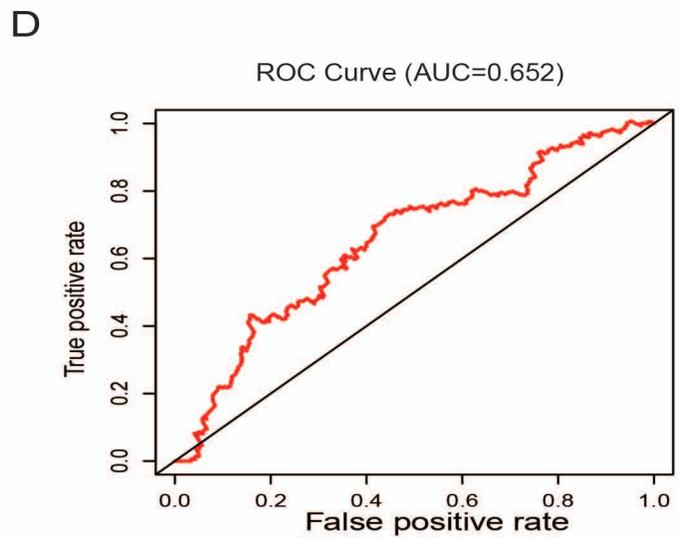
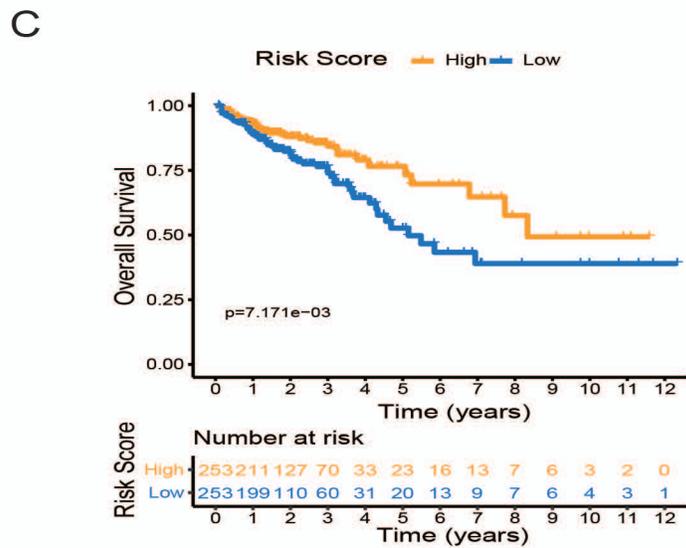
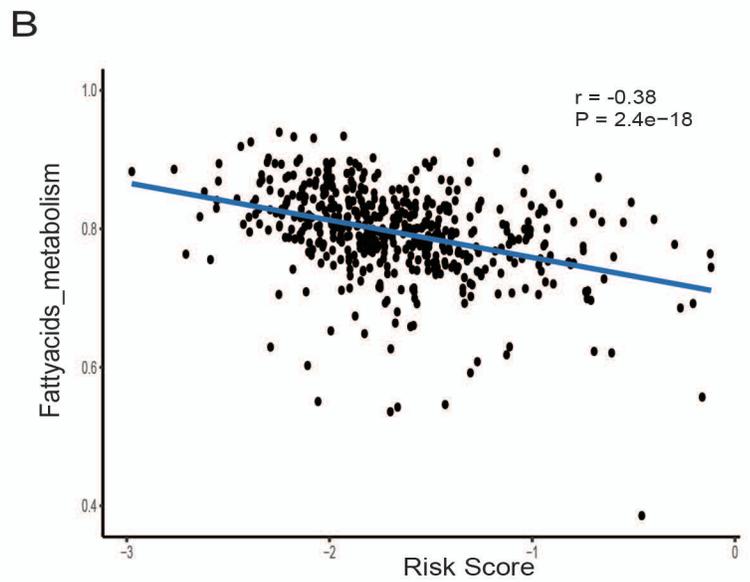
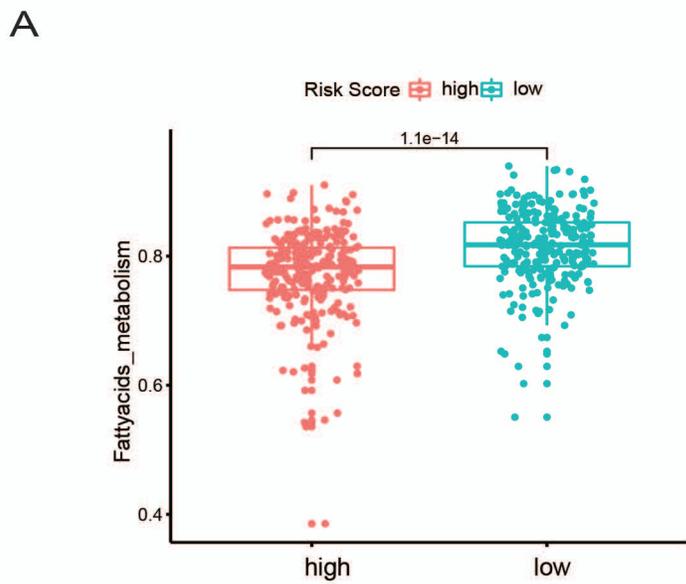
**Figure S1. Comparison between colorectal cancer tissue and normal tissue samples in the TCGA cohort.**

**A.** The heat map of 70 differentially expressed fatty acid metabolism-related genes. **B.** The result of GO enrichment analysis of differentially expressed fatty acid metabolism-related genes. **C.** The result of KEGG enrichment analysis of differentially expressed fatty acid metabolism-related genes.



**Figure S2. The relationship between risk scores and survival status of samples in the training set and validation set.**

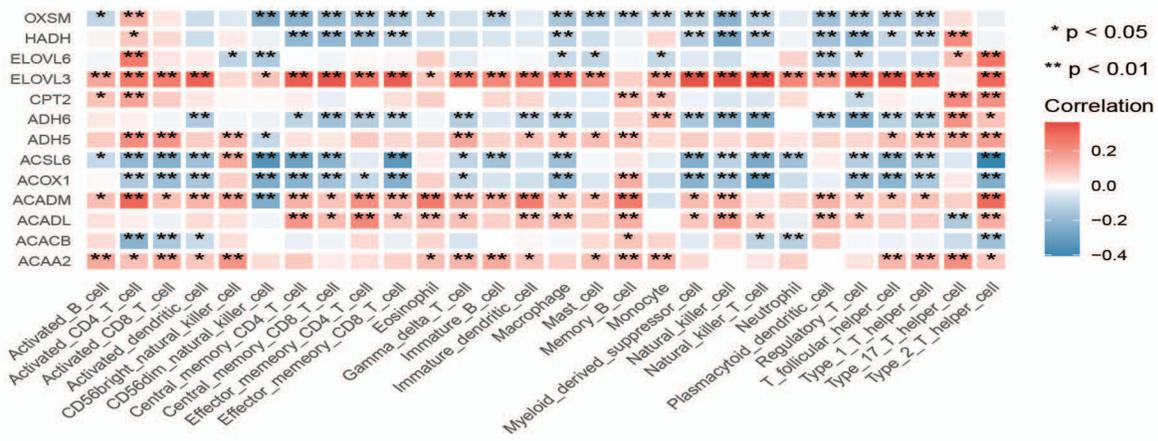
**A-C.** In the training set. **D-F.** In the validation set. **A and D.** Distribution of risk scores ranked from low to high. **B and E.** Comparison of survival status between low- and high- risk score groups. **C and F.** Heat map of 8 genes selected by LASSO Cox regression analysis.



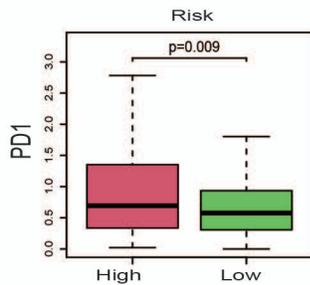
**Figure S3. Construction of fatty acid metabolism score model.**

**A.** The fatty acid metabolism score difference between high risk score and low risk score groups. **B.** The relationship between risk score model and fatty acid metabolism score. **C.** Survival analysis for subgroup patients stratified by fatty acid metabolism score. **D.** The predictive value of fatty acid metabolism score in CRC patients. AUC, 0.652.

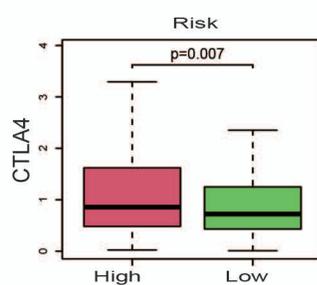
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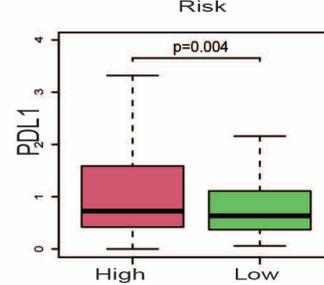
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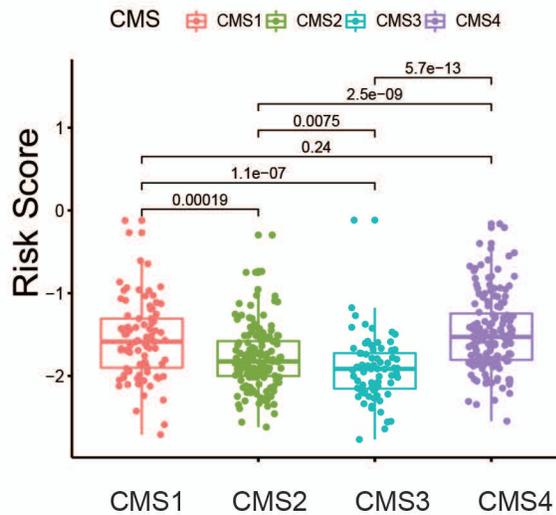
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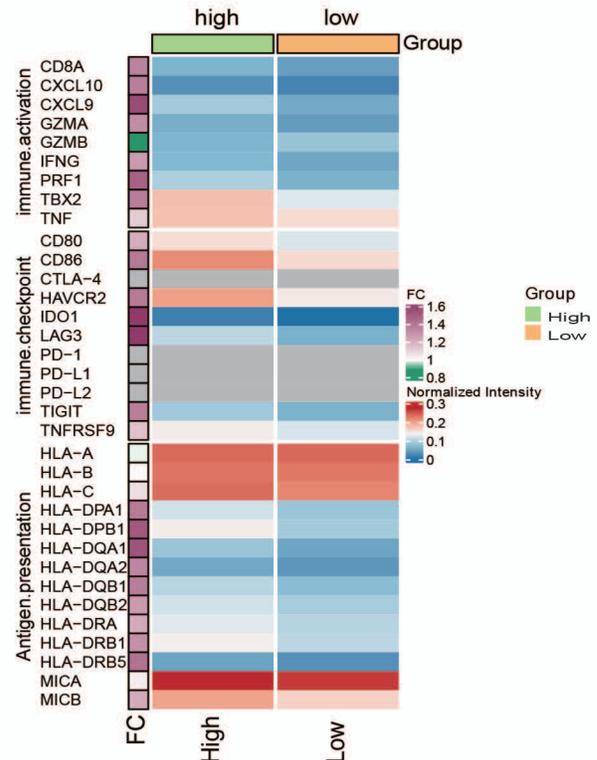
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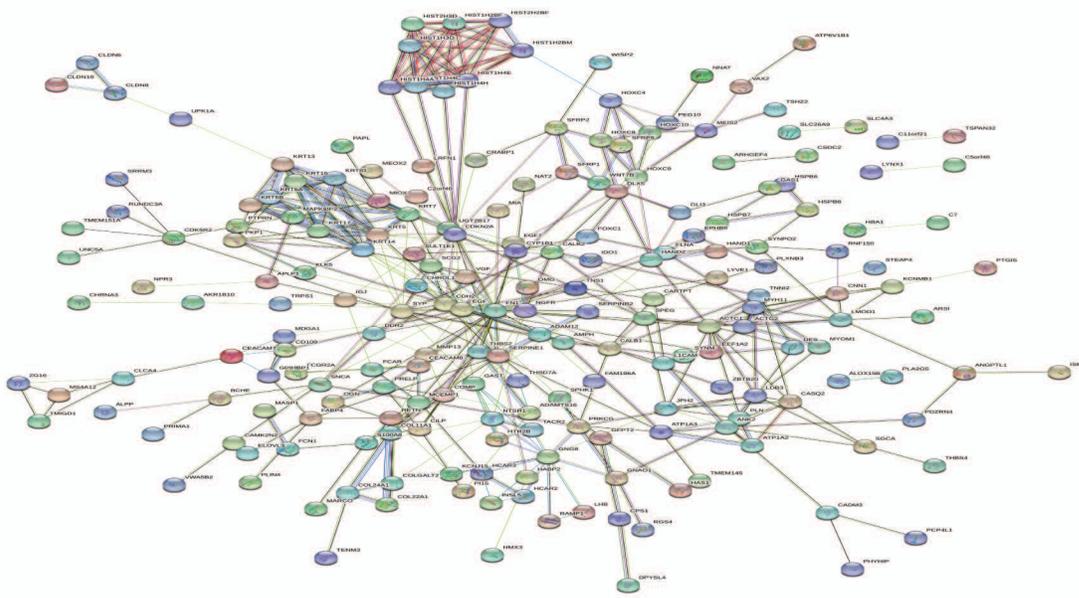
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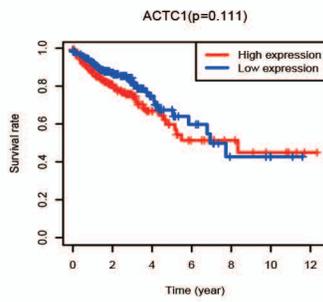
**Figure S4. Characteristics of immune-checkpoint related gene and known signatures in patients with high risk score and low risk score.**

**A.** Correlation between TME infiltration cells and fatty acid metabolism genes associated with prognosis. **B-D.** The immunity- checkpoint related gene expression difference in high score group and low score group. **E.** The risk score difference in CMS subtypes. **F.** Heat map showed known signatures genes expression in risk score model.

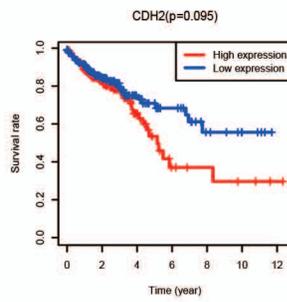
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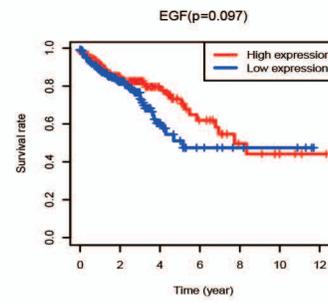
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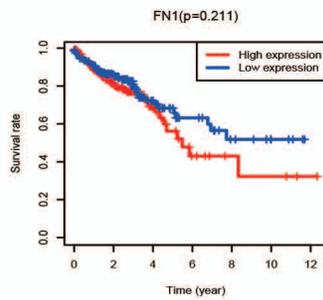
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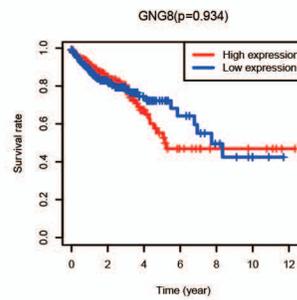
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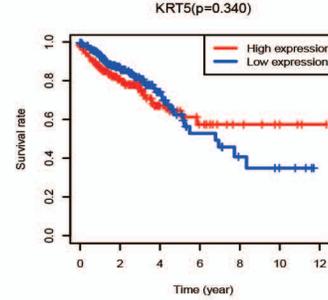
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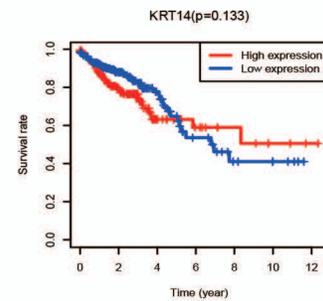
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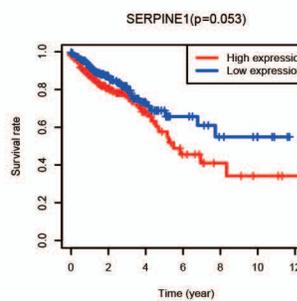
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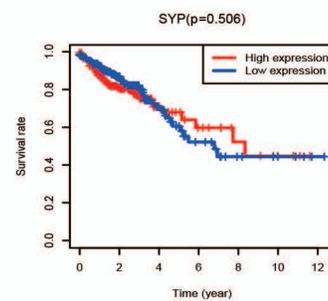
H



I



J



**Figure S5. Construction of Protein-protein interaction (PPI) network and prognostic value of top 10 hub genes.**

**A.** PPI network of DEGs between low- and high- risk score groups. **B-J.** Survival analysis for patients with high or low ACTC1 (B), CDH2 (C), EGF (D), FN1(D), GNG8 (E), KRT5 (F), KRT14 (G), CDKN2A (H), SERPINE1 (I) as well as SYP (J).