

Supplementary information:

Transcriptomic and functional network features of lung squamous cell carcinoma through integrative analysis of GEO and TCGA data

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Running title: Transcriptomic and functional network features of lung squamous cell carcinoma

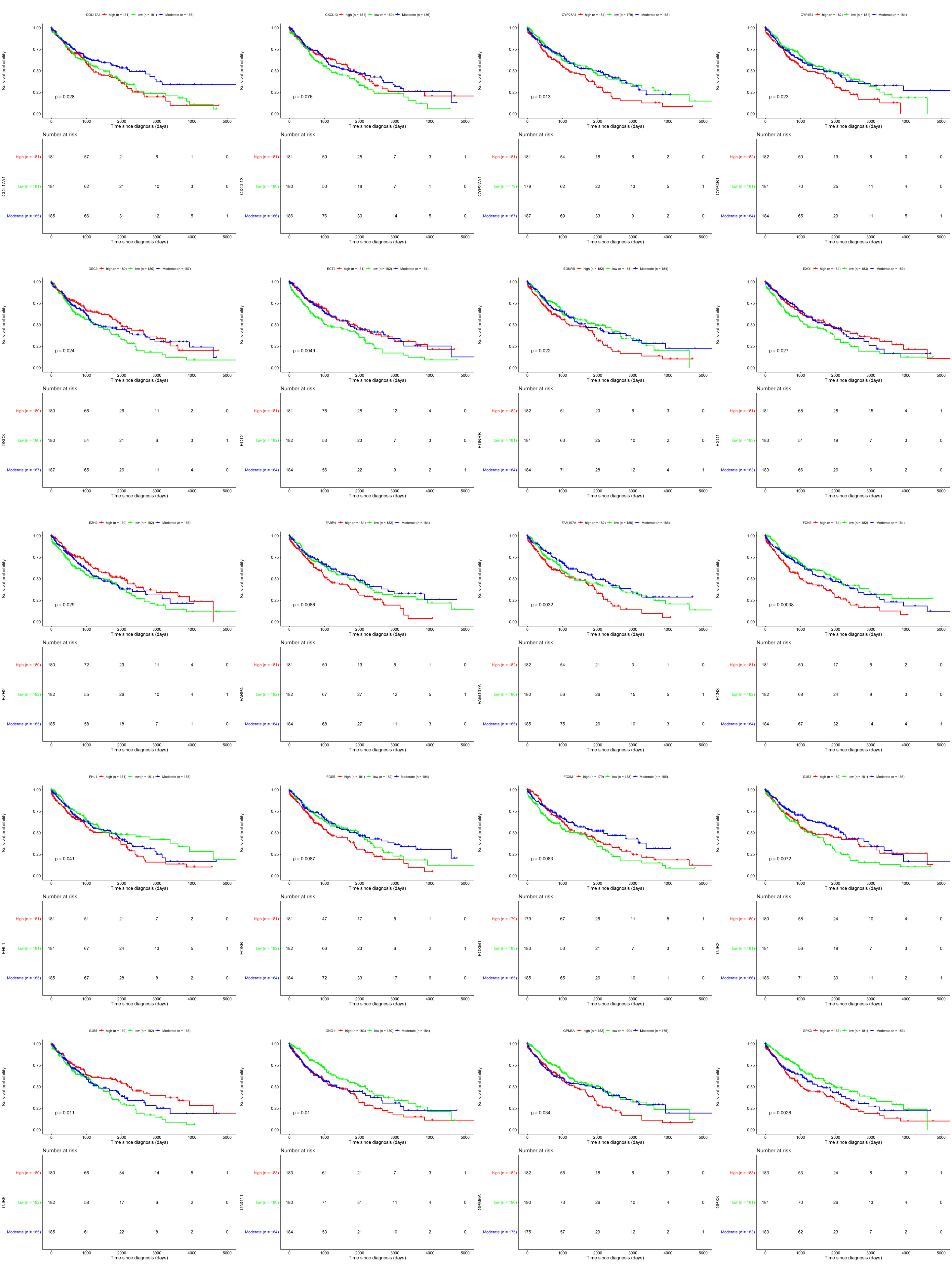
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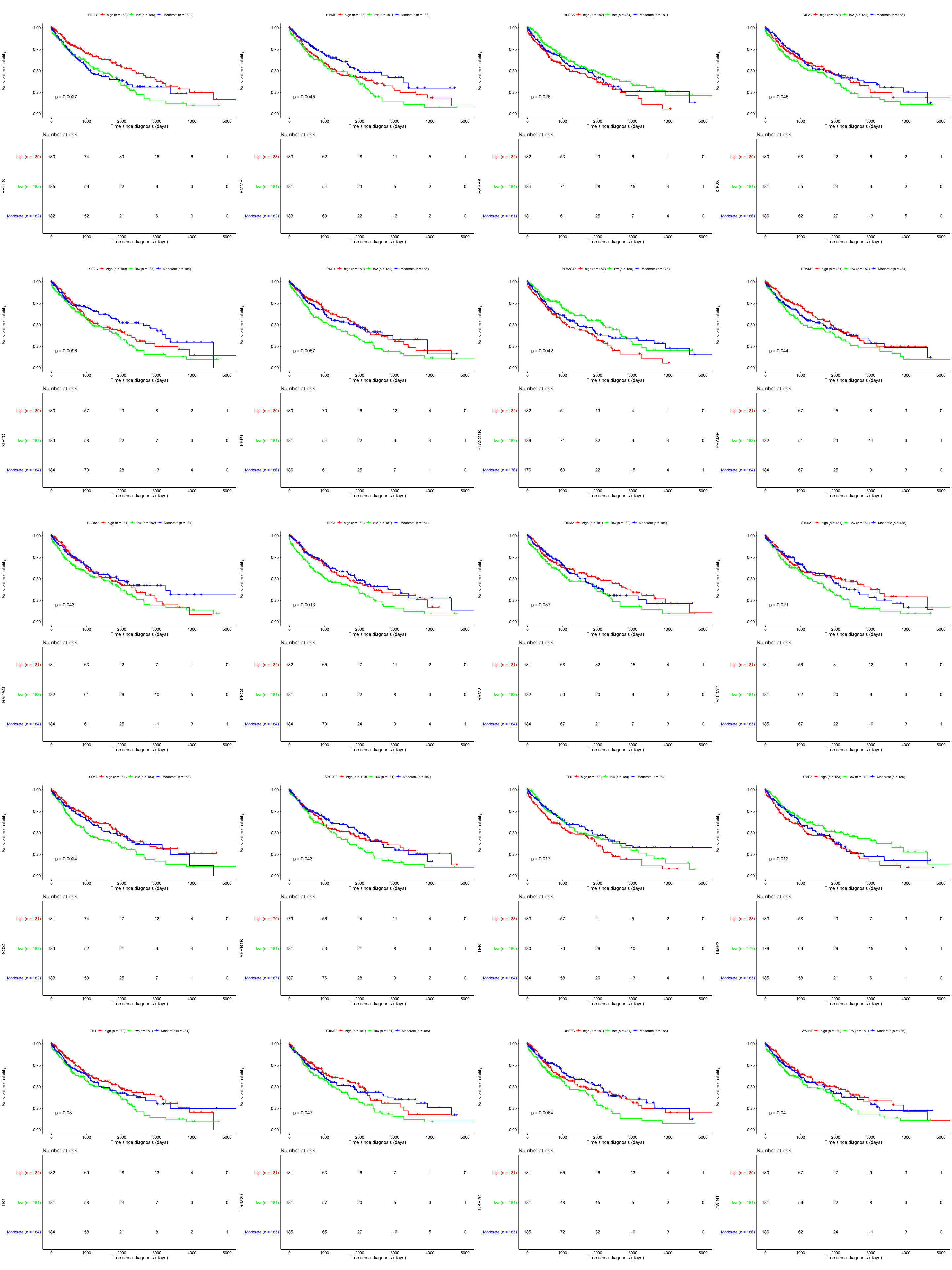
Supplementary figure 1. Survival analysis for differentially expressed genes in LUSC. Survival curves showing 20 genes which were related to overall patient survival rate. P-value set for this analysis is less than 0.05.

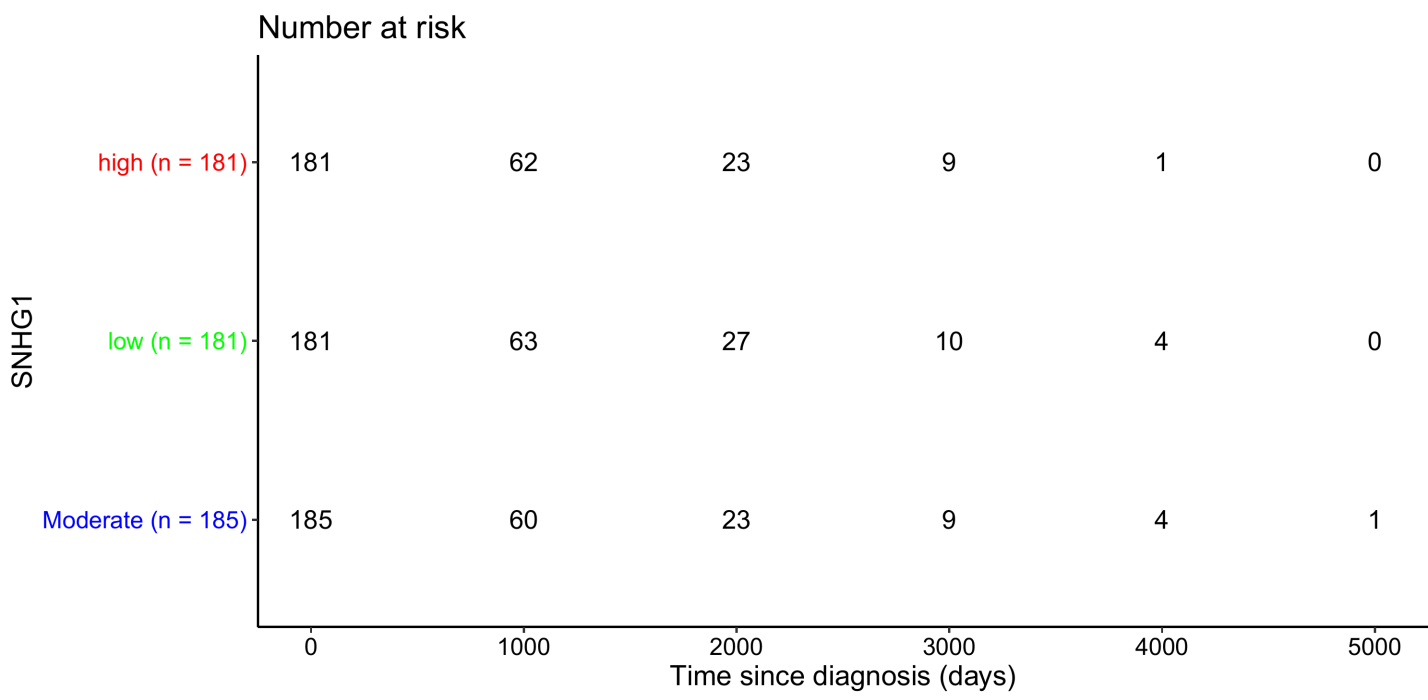
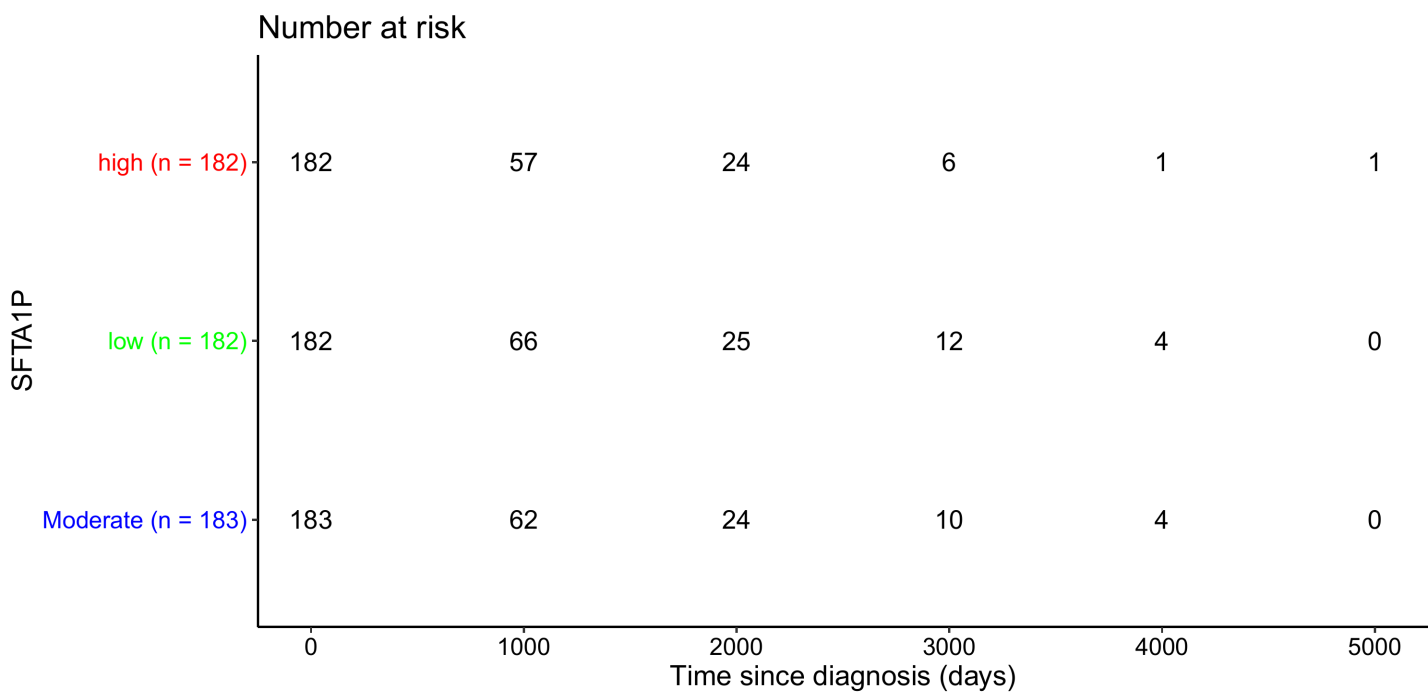
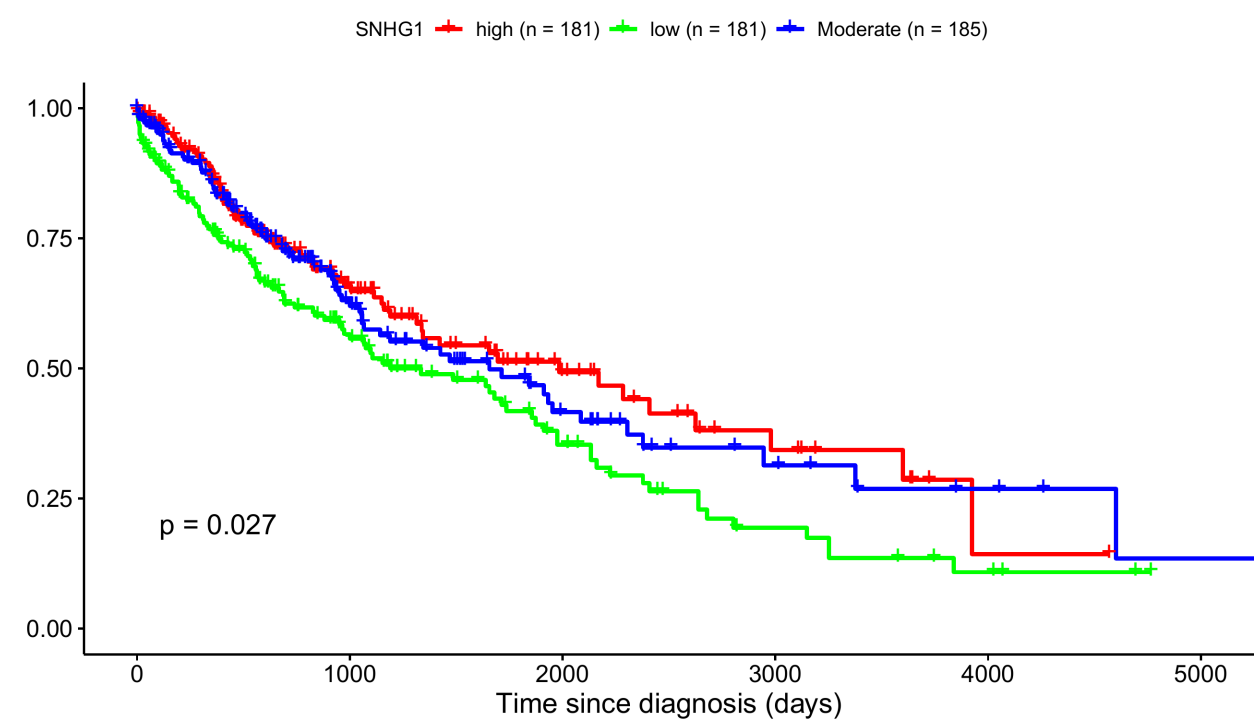
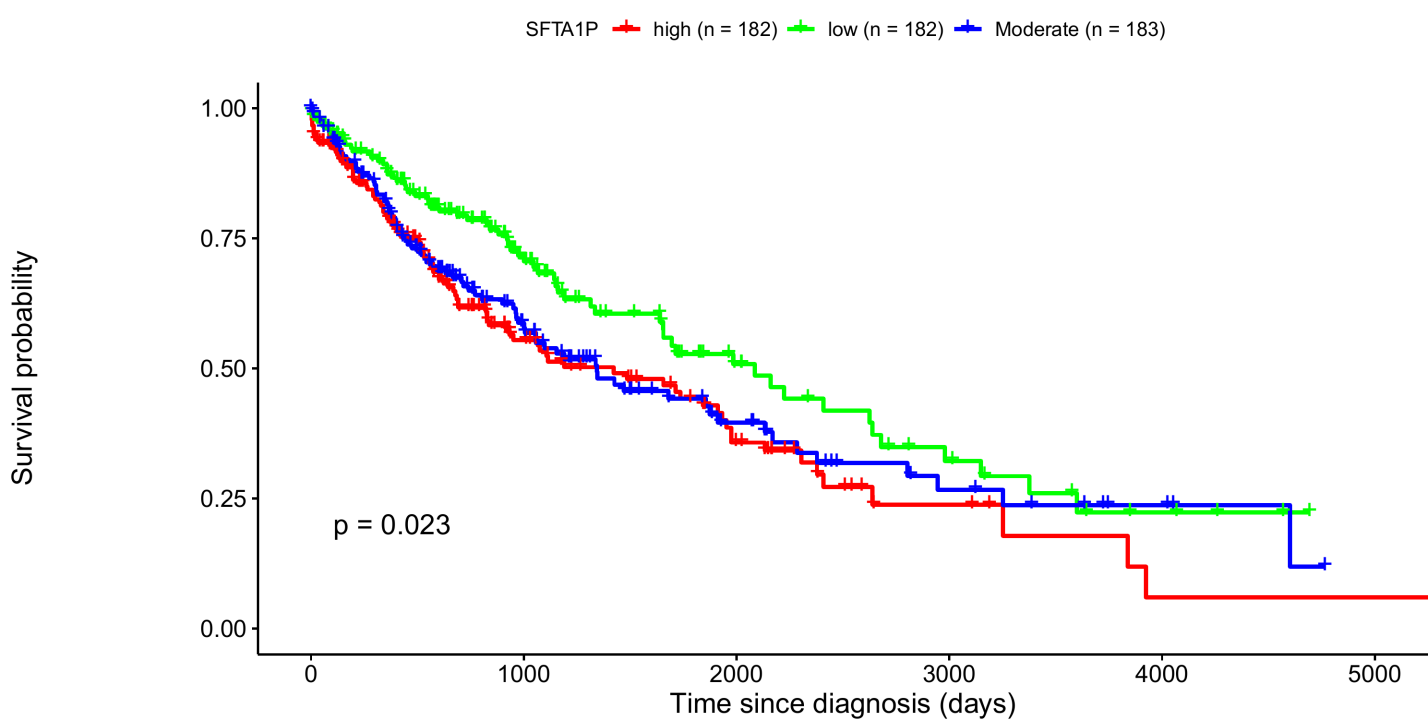
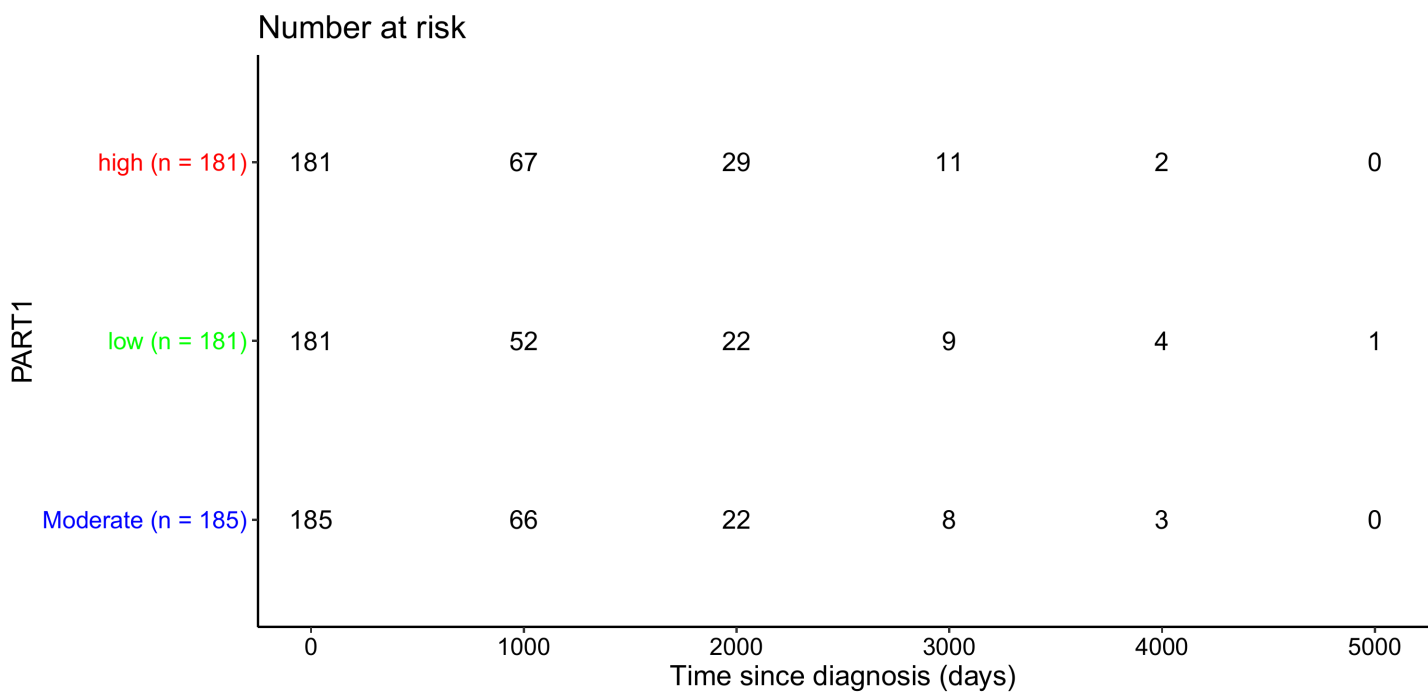
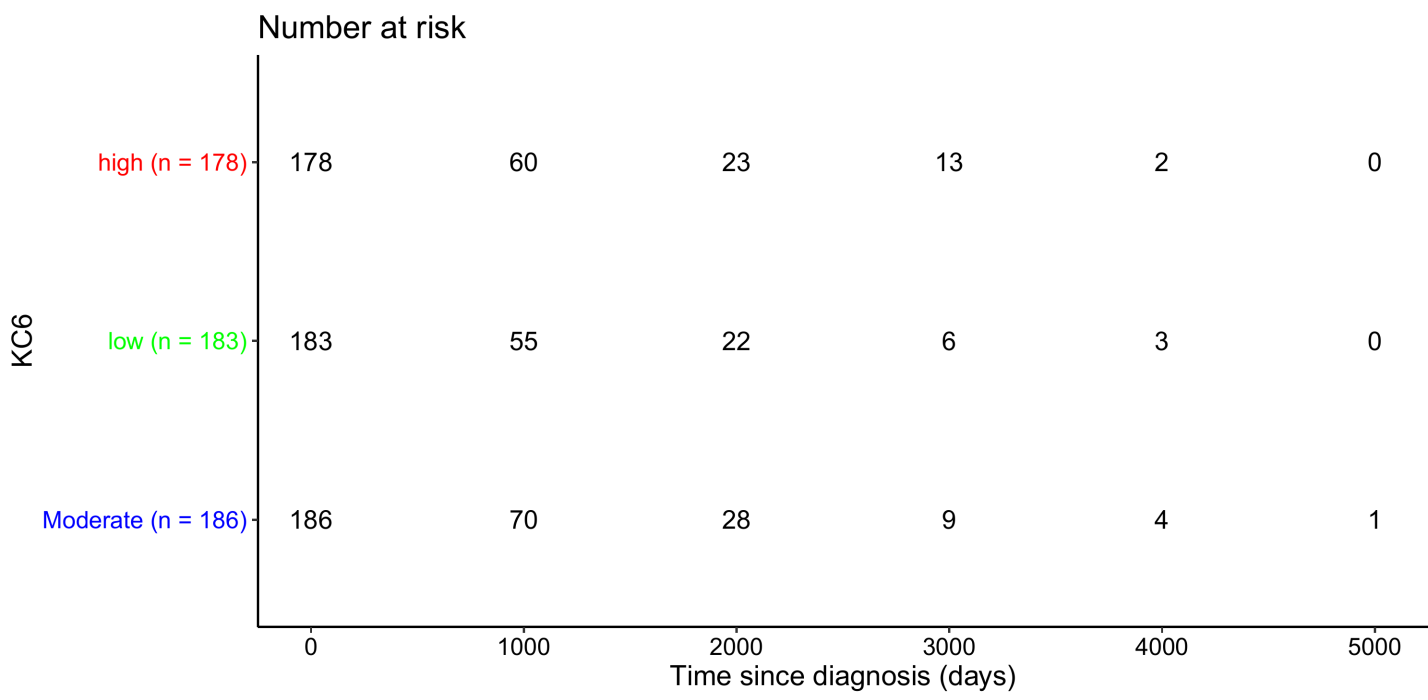
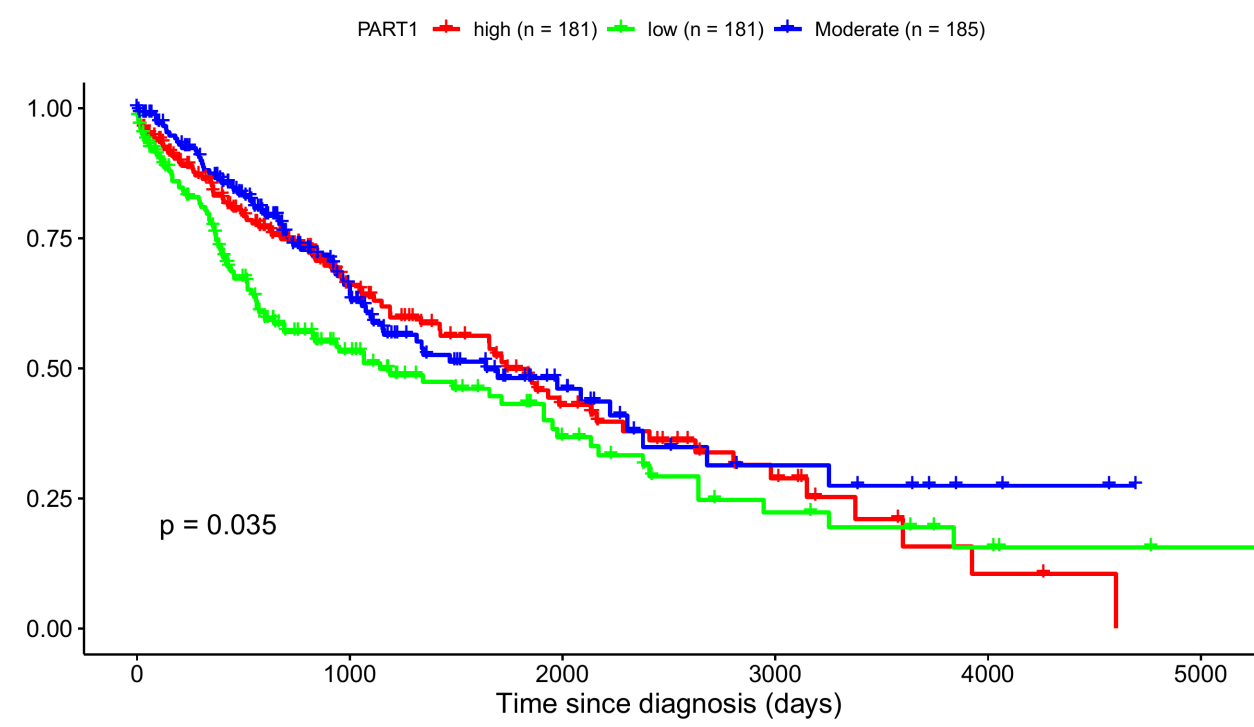
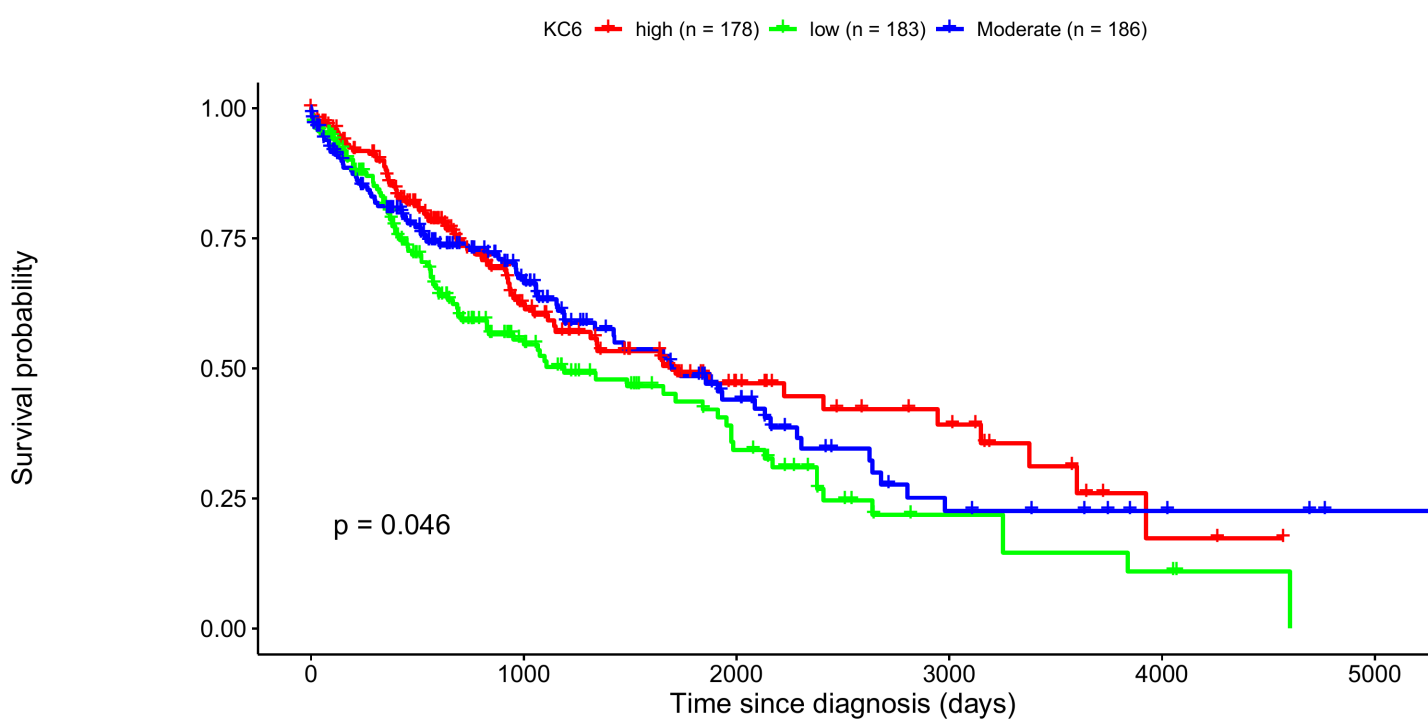
Supplementary figure 2. Survival analysis for differentially expressed genes in LUSC. Survival curves showing 20 genes which were related to overall patient survival rate. P-value set for this analysis is less than 0.05.

Supplementary figure 3. Survival analysis showing four lncRNAs were associated with patients overall survival ($p < 0.05$).

Supplementary figure 4. Functional enrichment analysis for the 60 survival-related genes.







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