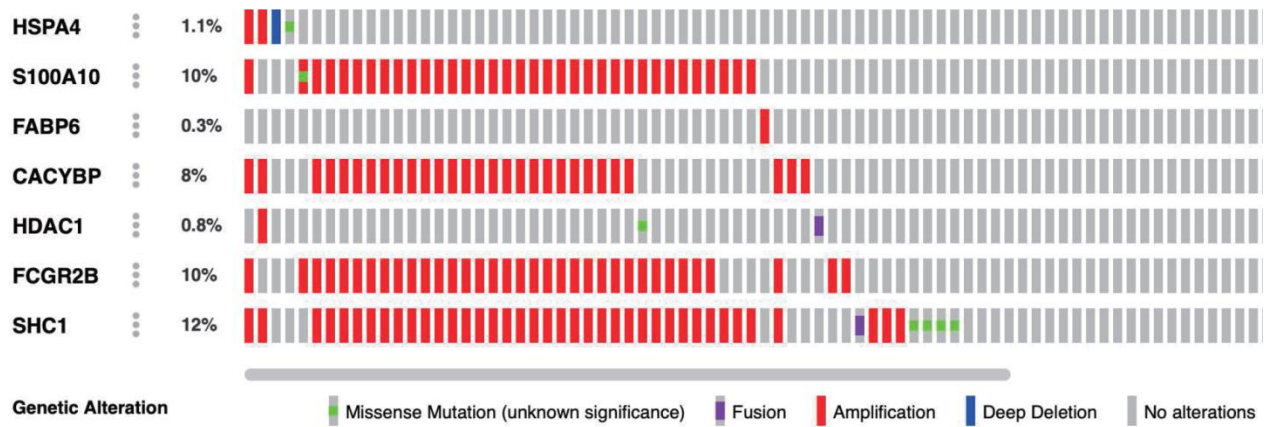
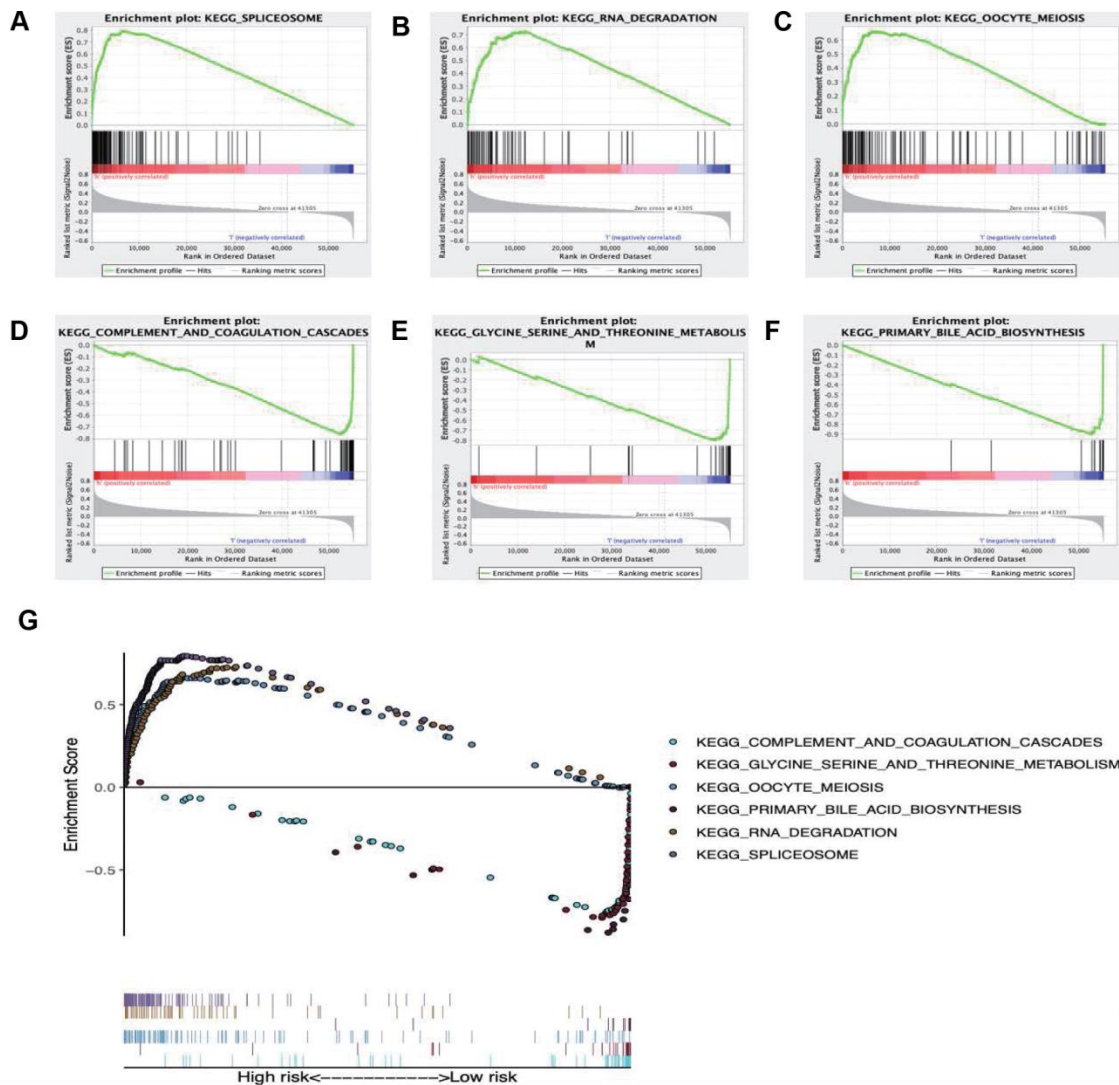


SUPPLEMENTARY FIGURES



Supplementary Figure 1. Genetic alternations of signature genes in TCGA-LIHC. *SHC1* is the gene with highest mutation frequency. There are 4 genes with a mutation rate $\geq 5\%$.



Supplementary Figure 2. Enrichment plots of Kyoto Encyclopedia of Genes and Genomes analysis from gene set enrichment analysis (GSEA). GSEA results showing (A) Spliceosome, (B) RNA degradation, (C) Oocyte meiosis were differentially enriched in high risk group, while (D) Complement and coagulation cascades, (E) Glycine serine and threonine metabolism, (F) Primary bile acid biosynthesis were primarily enriched in low risk group. (G) Summarizes the above six gene sets.