

Supplementary Materials

Comprehensive Analysis of Genomic Alterations in Hepatoid Adenocarcinoma of the Stomach and Identification of Clinically Actionable Alterations

Rongjie Zhao, Hongshen Li, Weiting Ge, Xiuming Zhu, Liang Zhu, Xiangbo Wan, Guanglan Wang, Hongming Pan, Jie Lu and Weidong Han

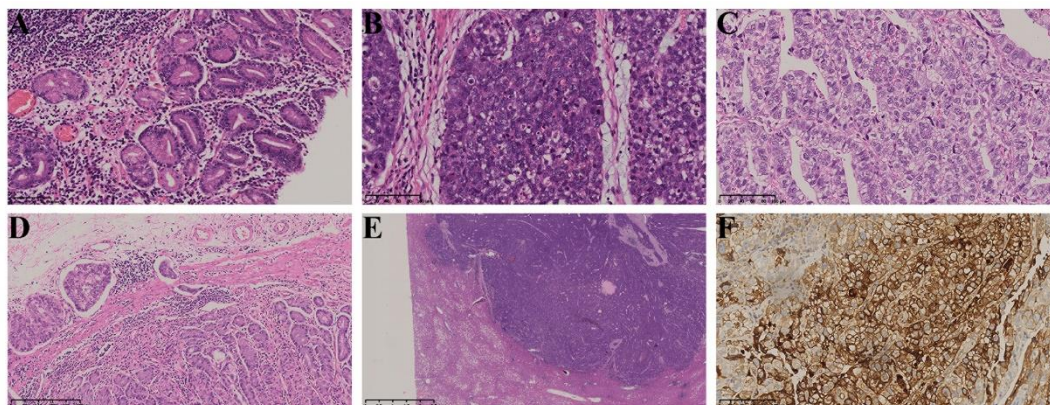


Figure S1. Representative pathological sections. (A) Normal gastric mucosa. (B) Hepatoid-differentiated cells are irregular in shape and arranged in nest, (C) trabeculae, and glandular tubules. (D) Cancer thrombus. (E) Liver metastasis. (F) Positive expression of AFP.

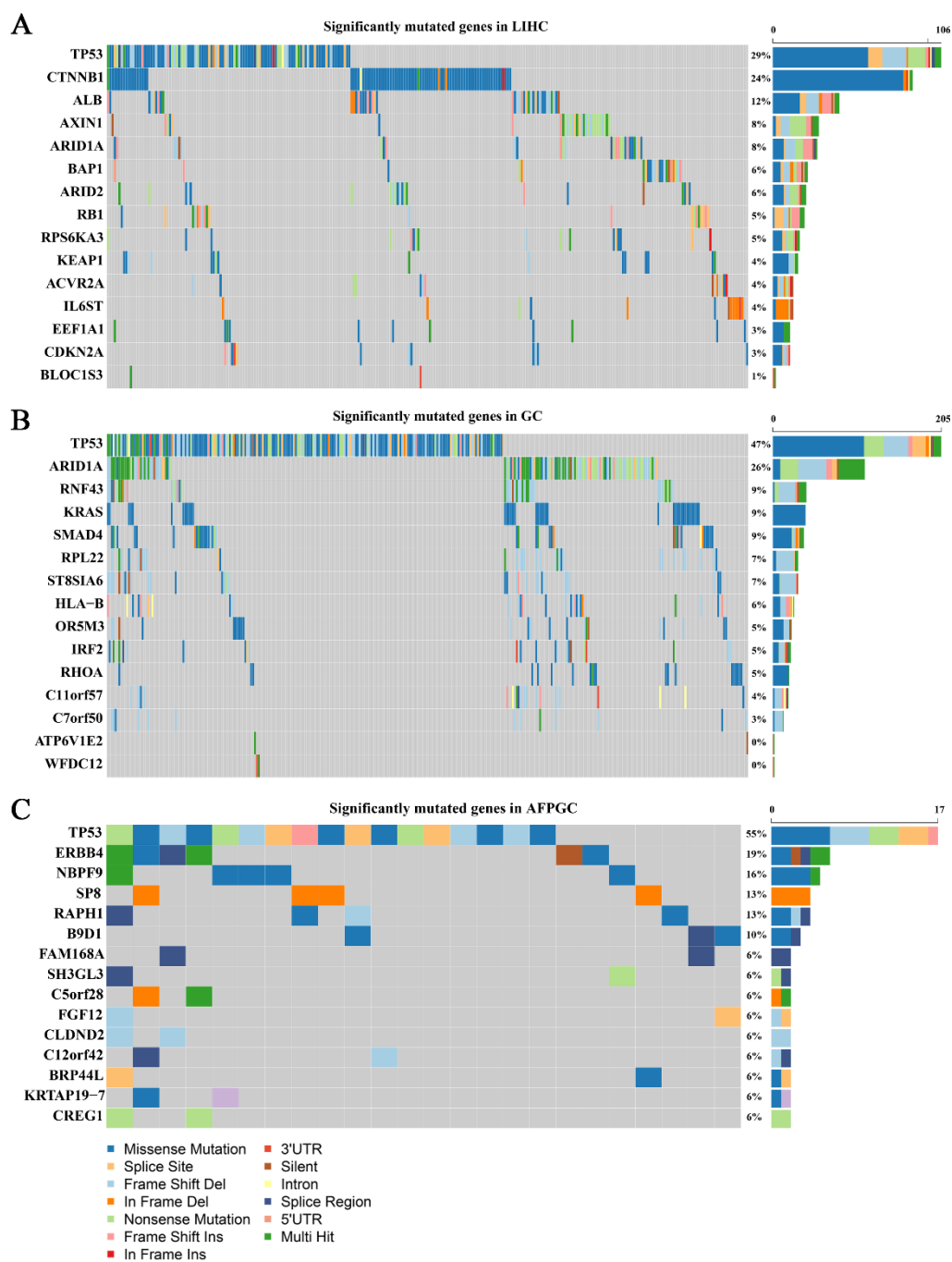


Figure S2. Mutational landscapes of LIHC, GC and AFPGC. The top 15 significantly mutated genes (SMGs) in (A) LIHC, (B) GC and (C) AFPGC. Different variant types are highlighted in different colors. $P < 0.001$ is statistically significant.

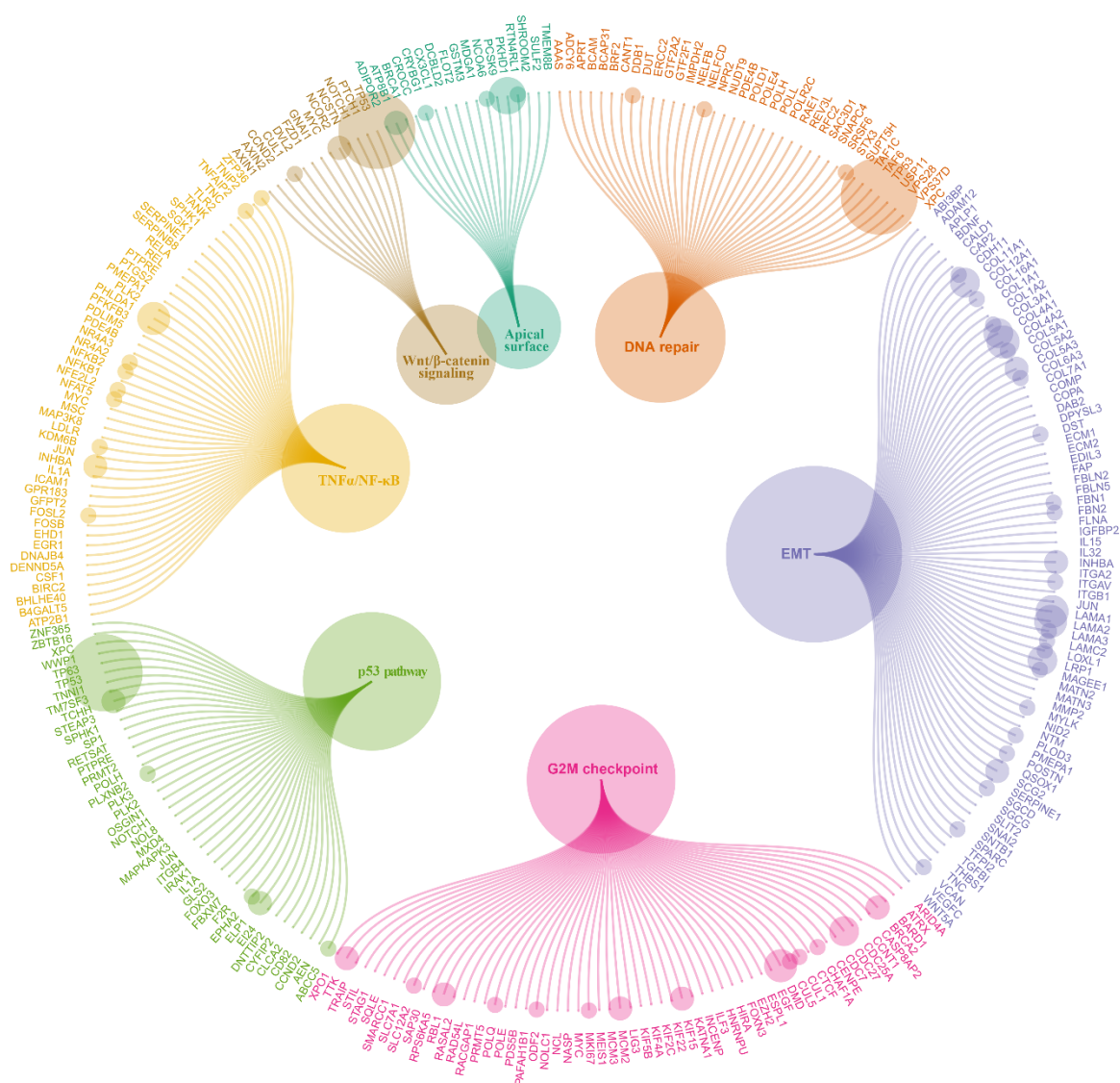


Figure S3. Representative mutated pathways in HAS. The size of node near each gene represents the mutation frequency.

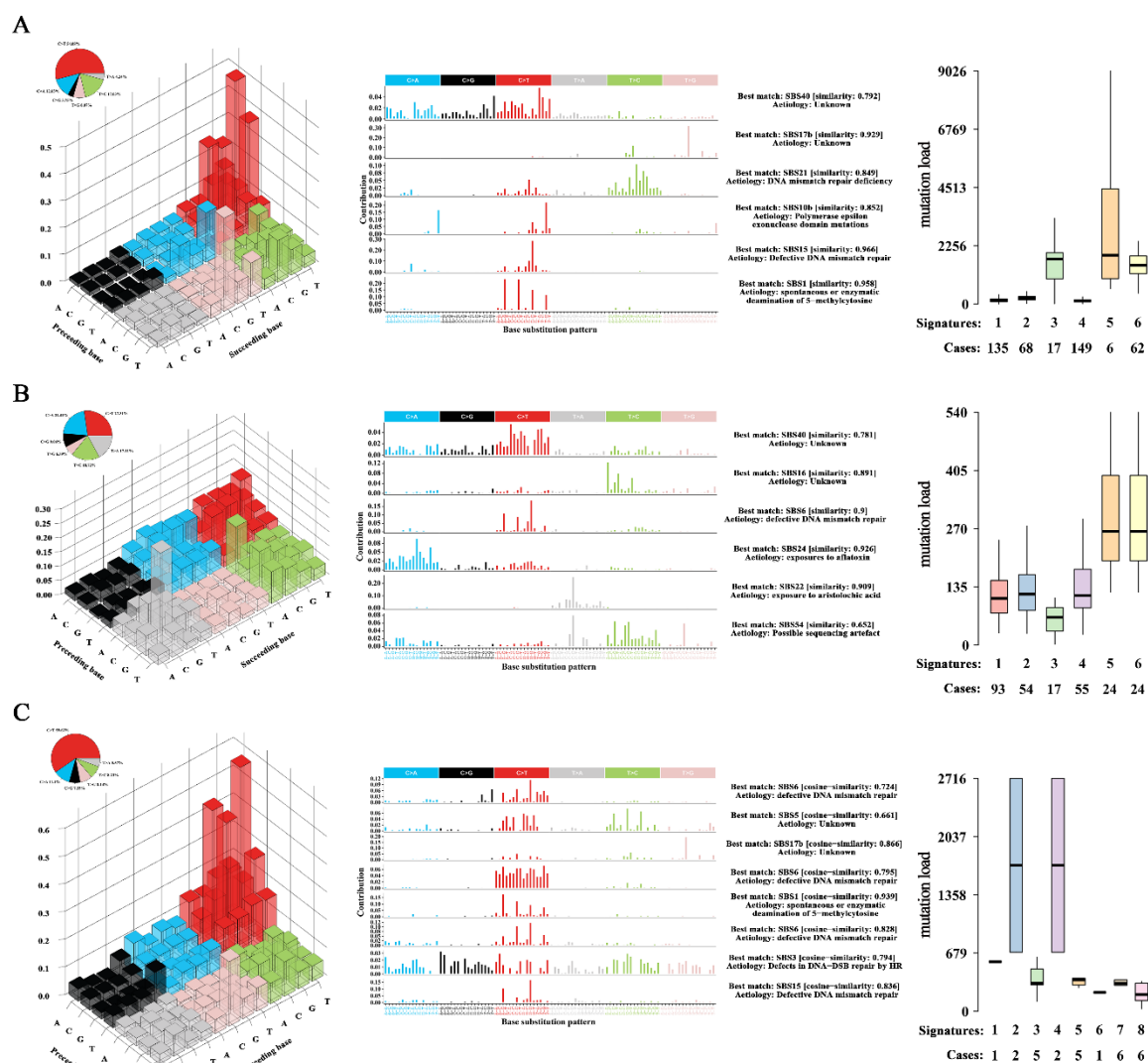


Figure S4. Base substitution patterns and mutation signatures. 96 types of base substitution patterns, signatures inferred from these patterns, and the distribution of patients and mutation load in each signature in (A) GC, (B) LIHC, and (C) AFPGC.

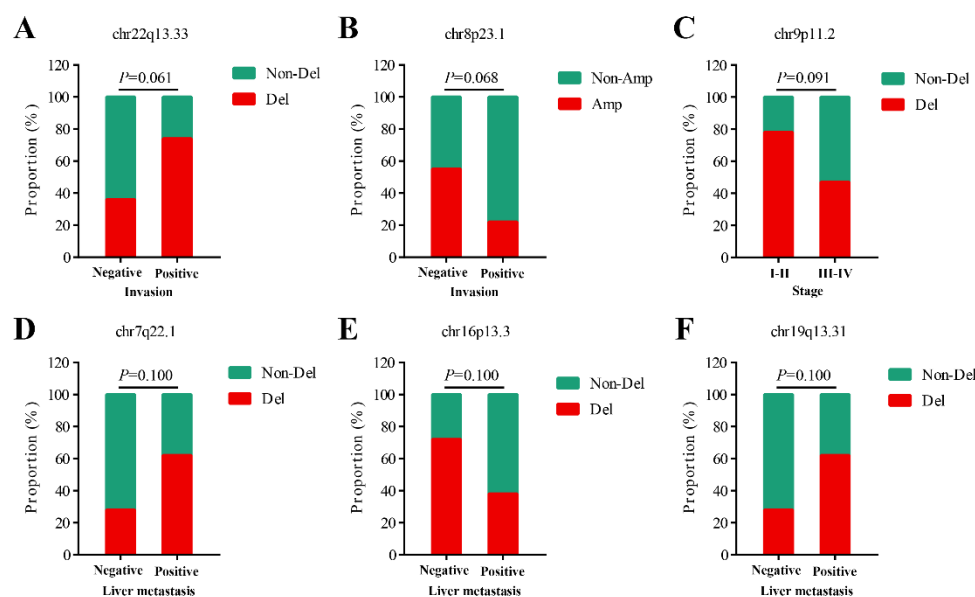


Figure S5. Potentially aggressive behavior-related regions.

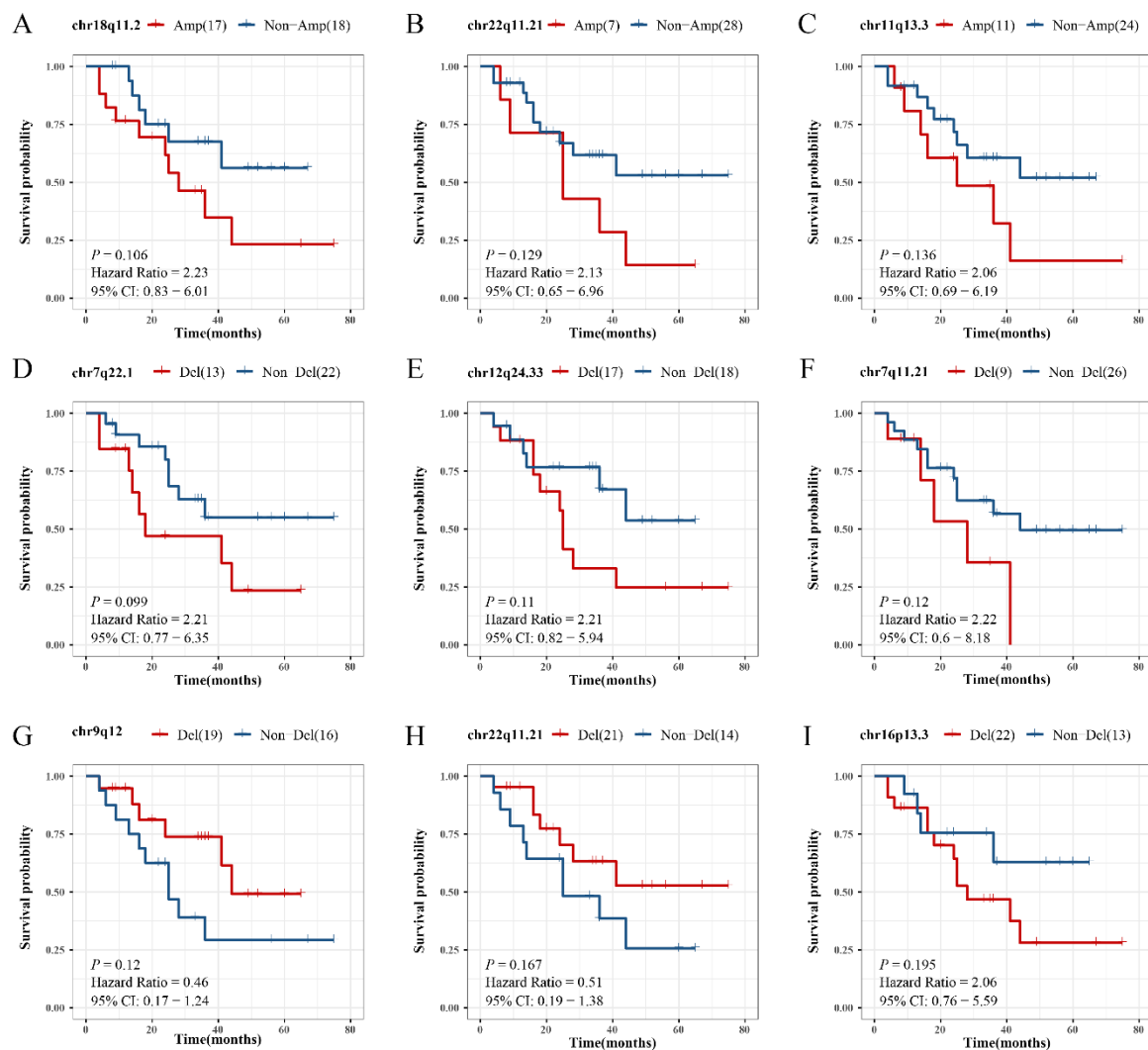


Figure S6. Potentially overall survival-related regions.

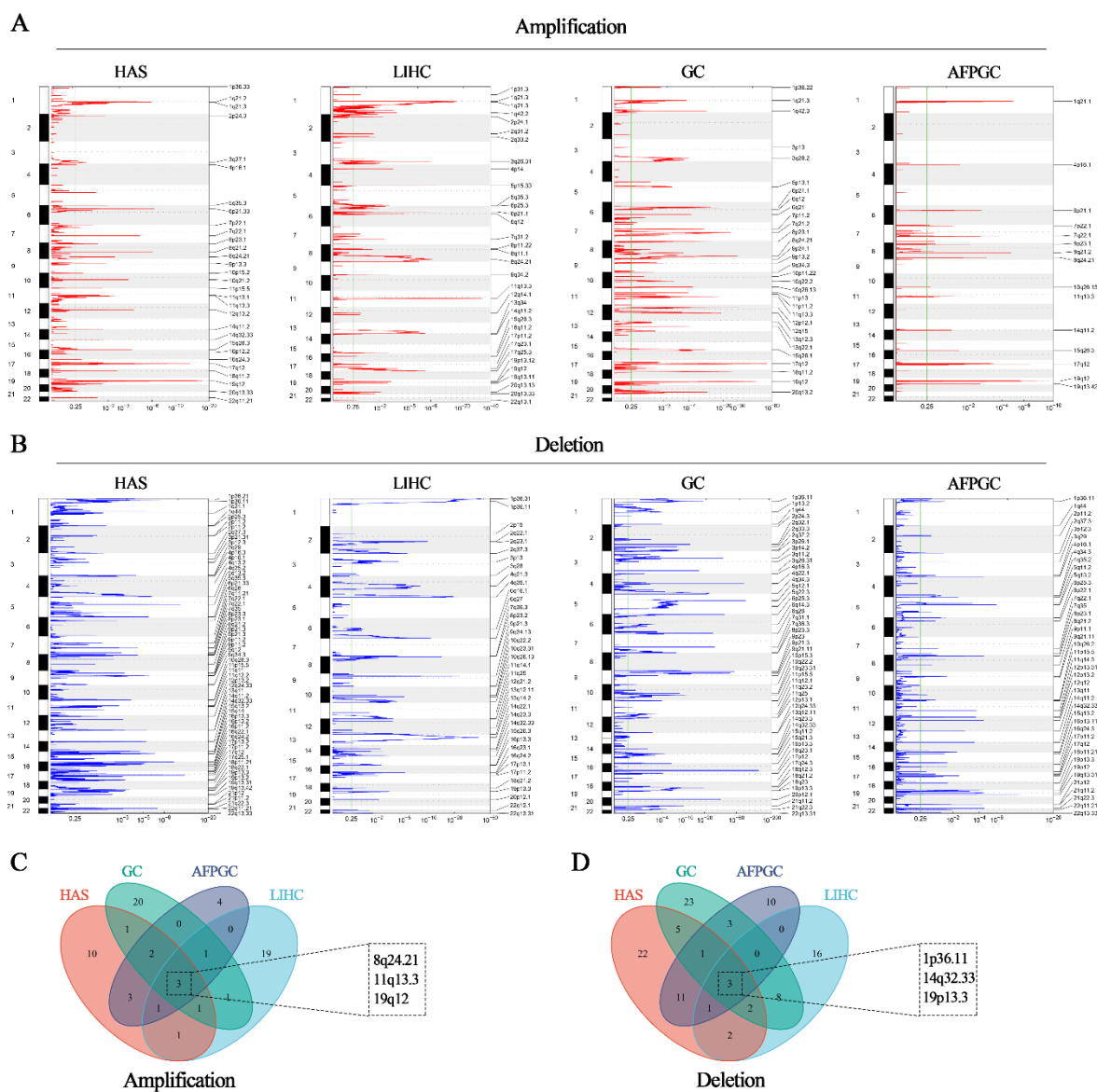


Figure S7. The landscape of significantly altered regions. The distribution of (A) amplified or (B) deleted regions in HAS, LIHC, GC and AFIGC. Red: amplification; Blue: deletion. The overlap in (C) amplified regions and (D) deleted regions.

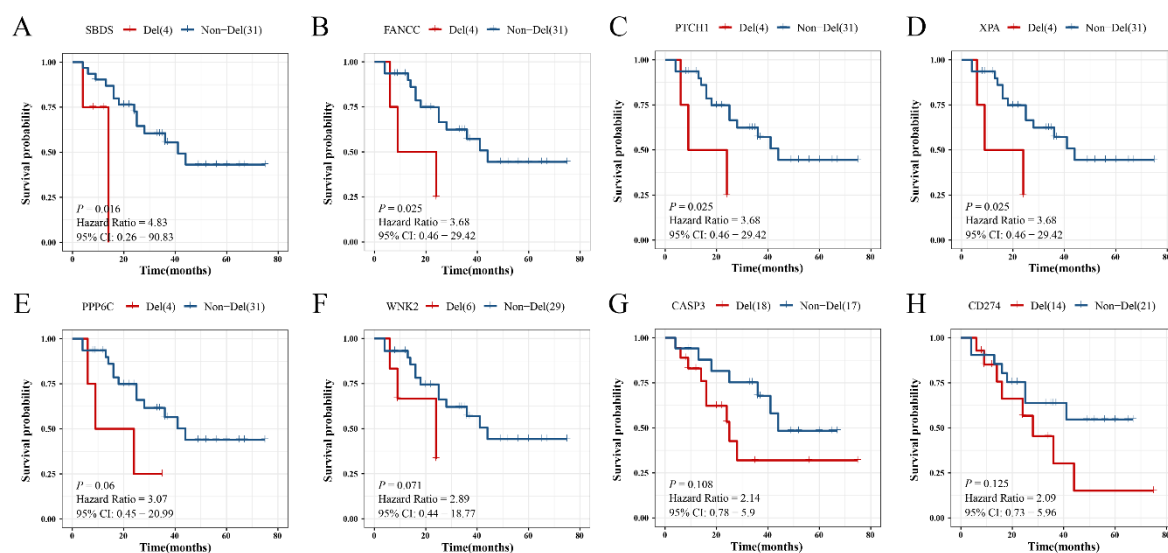


Figure S8. The role of tumor suppressor genes (TSGs) in HAS overall survival.

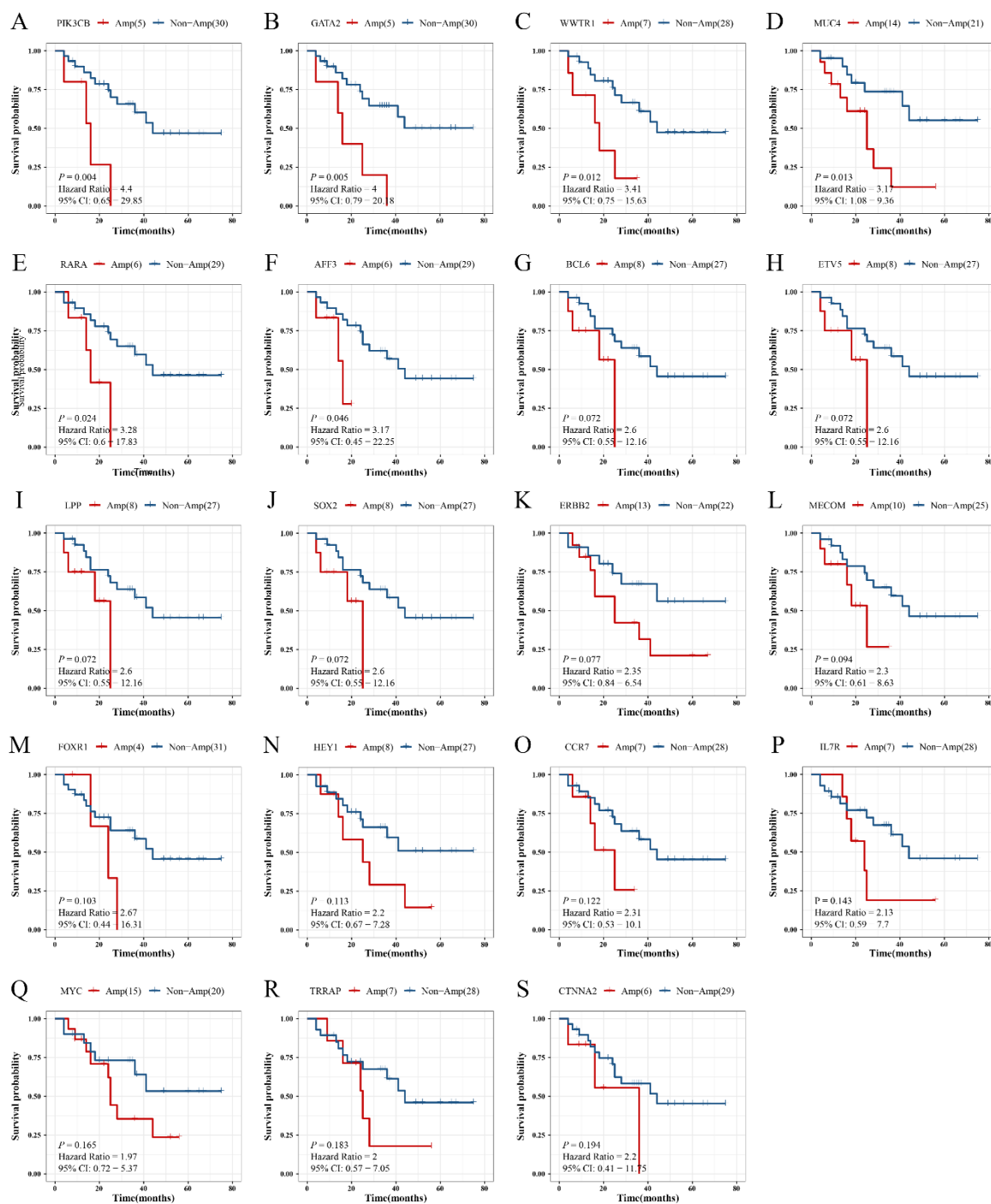


Figure S9. The role of oncogenes in HAS overall survival.

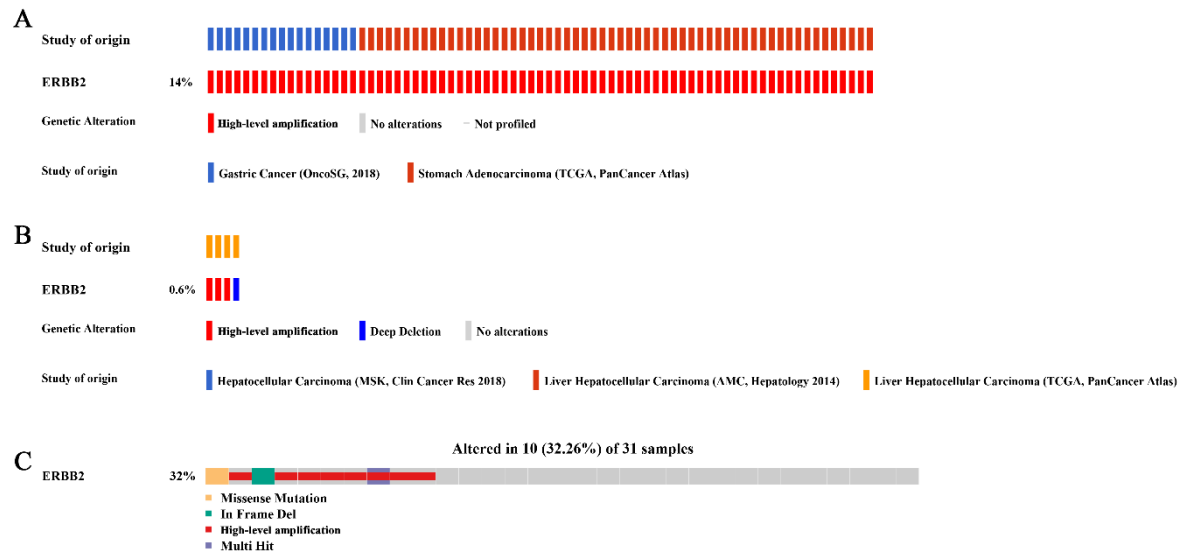


Figure S10. The amplification of ERBB2 in GC, LIHC and AFPGC. The proportion of high-level *ERBB2* amplification in (A) GC and (B) LIHC from cBioPortal. Unaltered samples (grey) are not shown. Red: amplification; Blue: deletion. The proportion of high-level *ERBB2* amplification in (C) AFPGC.

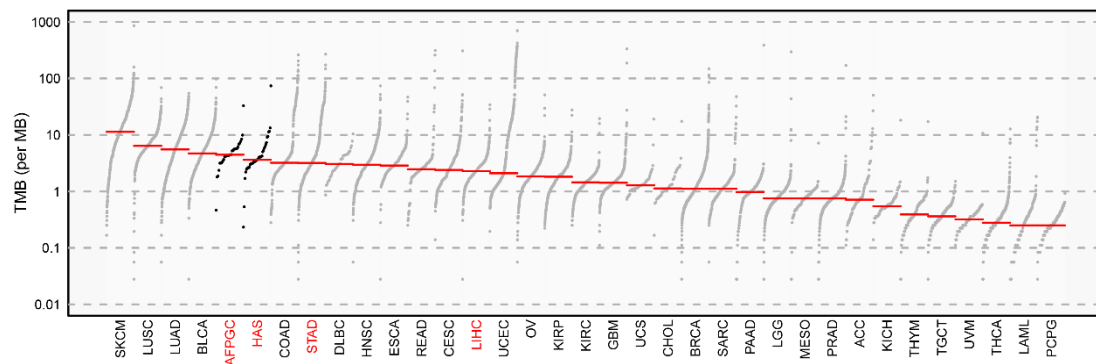


Figure S11. Distribution of Tumor Mutational Burden (TMB).