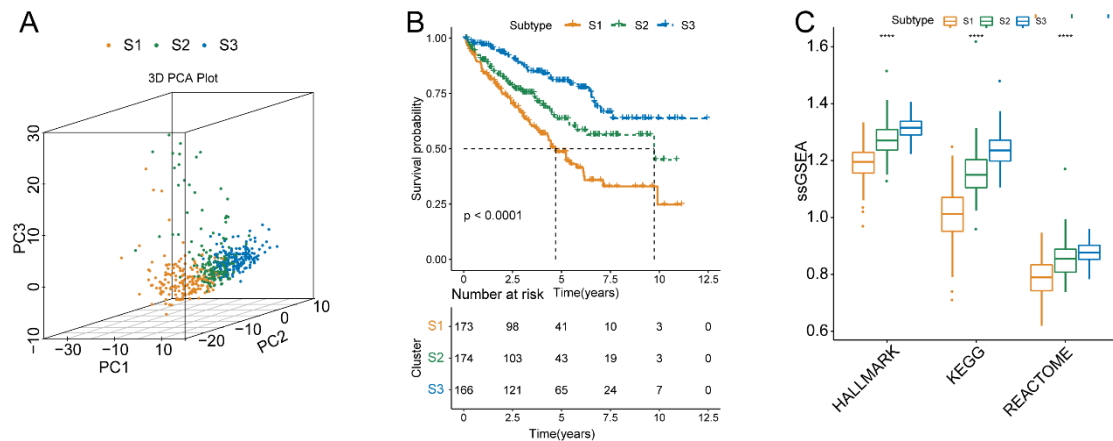**SUPPLEMENTARY FIGURE S1 FAM characteristics of ccRCC in the TCGA cohort.**
(A) Differences in FAM enrichment scores between cancer and para-cancer samples. (B) Differences in FAM enrichment scores among diverse clinicopathological features of patients.
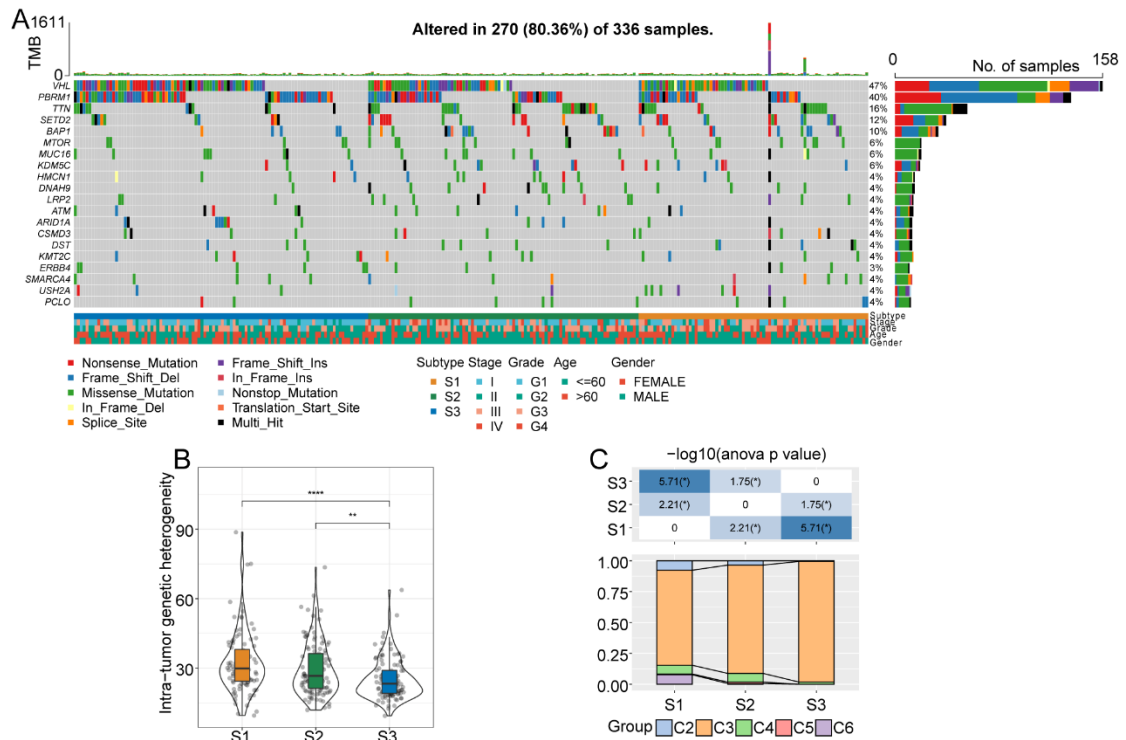

SUPPLEMENTARY FIGURE S2 Consensus clustering of FAMGs of ccRCC in TCGA cohort.
(A) CDF curves for k = 2–10. (B) CDF Delta area curves for k = 2–10. (C) Heatmap for the consensus matrix at k = 3.
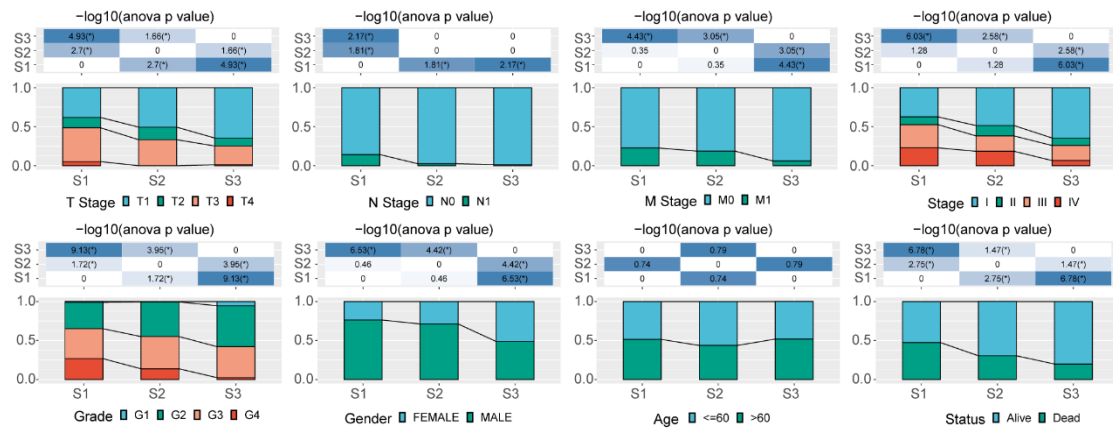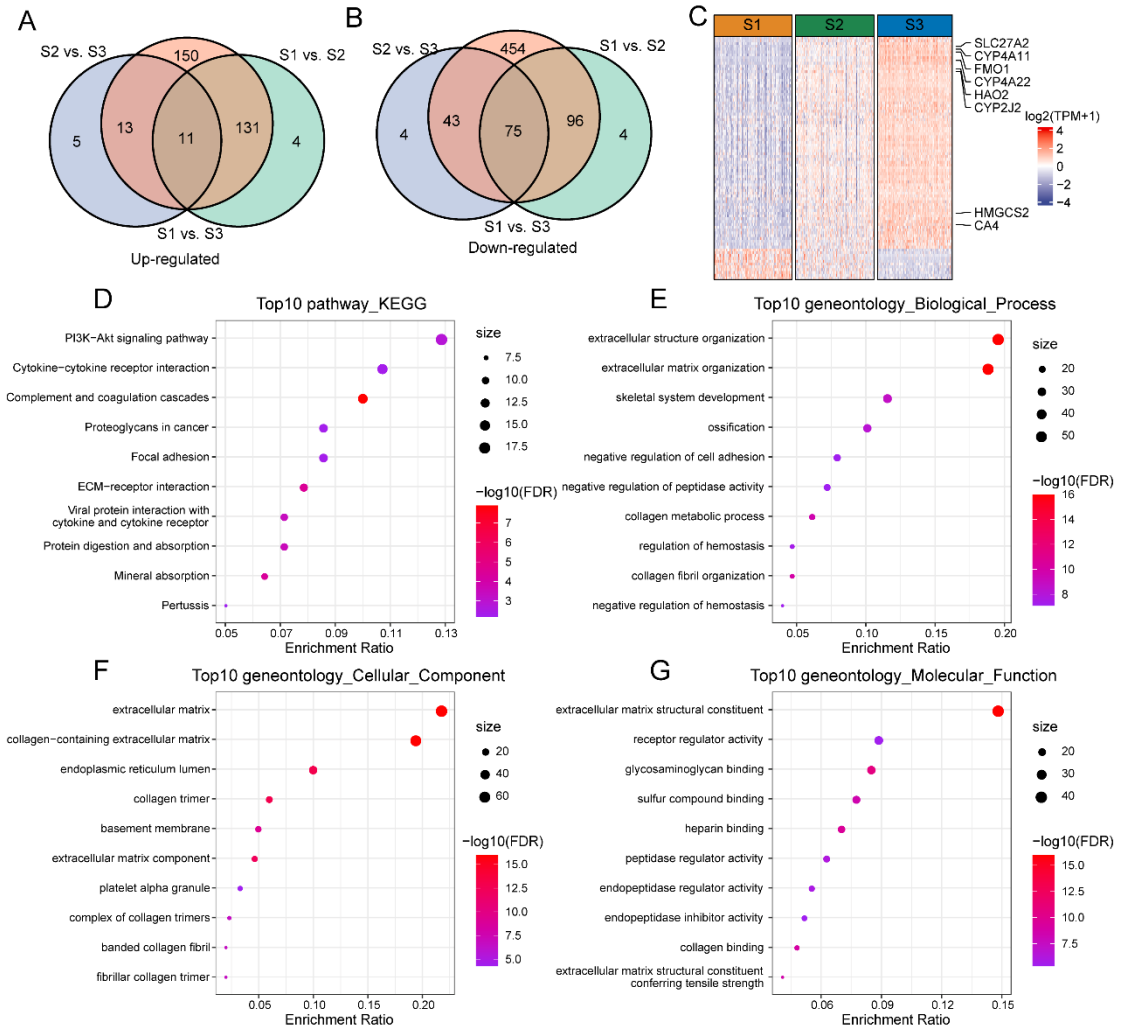
SUPPLEMENTARY FIGURE S3 Differences in clinical features among the three subtypes in the TCGA cohort.


SUPPLEMENTARY FIGURE S4 Mutation signatures among the three subtypes of ccRCC in the TCGA cohort.
(A) Oncoplot of the somatic landscape of top 20 ccRCC mutated genes. (B) MATH differences among the three subtypes. (C) Comparison of the three subtypes with previously published subtypes.

SUPPLEMENTARY FIGURE S5 DEGs among the FAM-related subtypes in the TCGA cohort.
(A) Distribution of upregulated genes among the three subtypes. (B) Distribution of downregulated genes among the three subtypes. (C) Heatmap of common DEGs among the three subtypes. (D-G) KEGG and GO analysis of the common DEGs between S1 and S3.
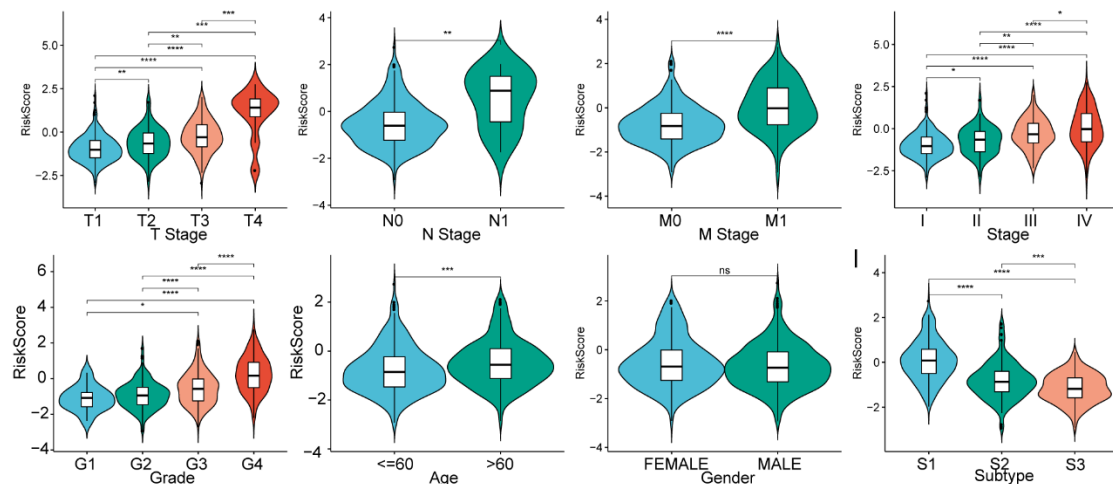
SUPPLEMENTARY FIGURE S6 Association of the risk score with patients' clinical characteristics.