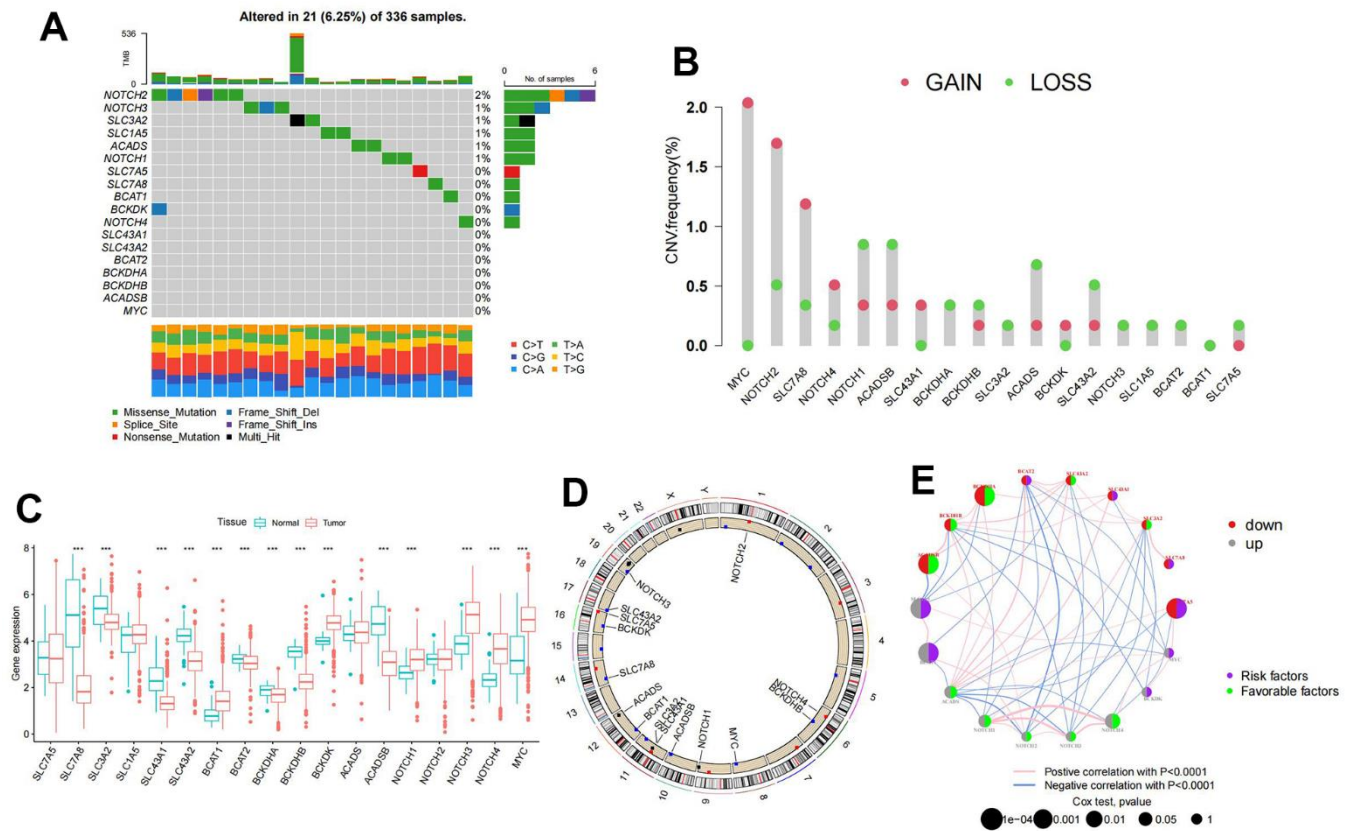
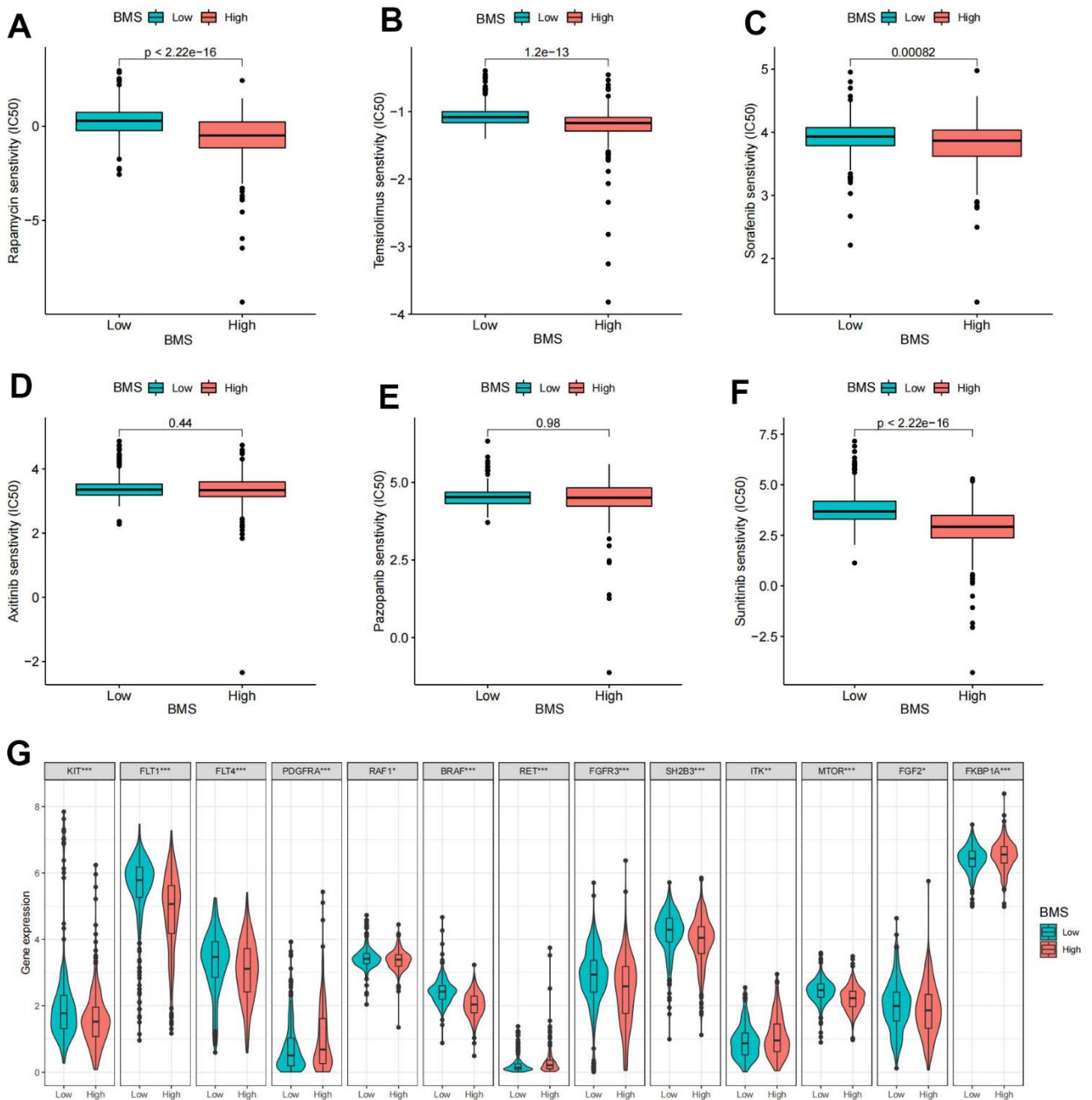


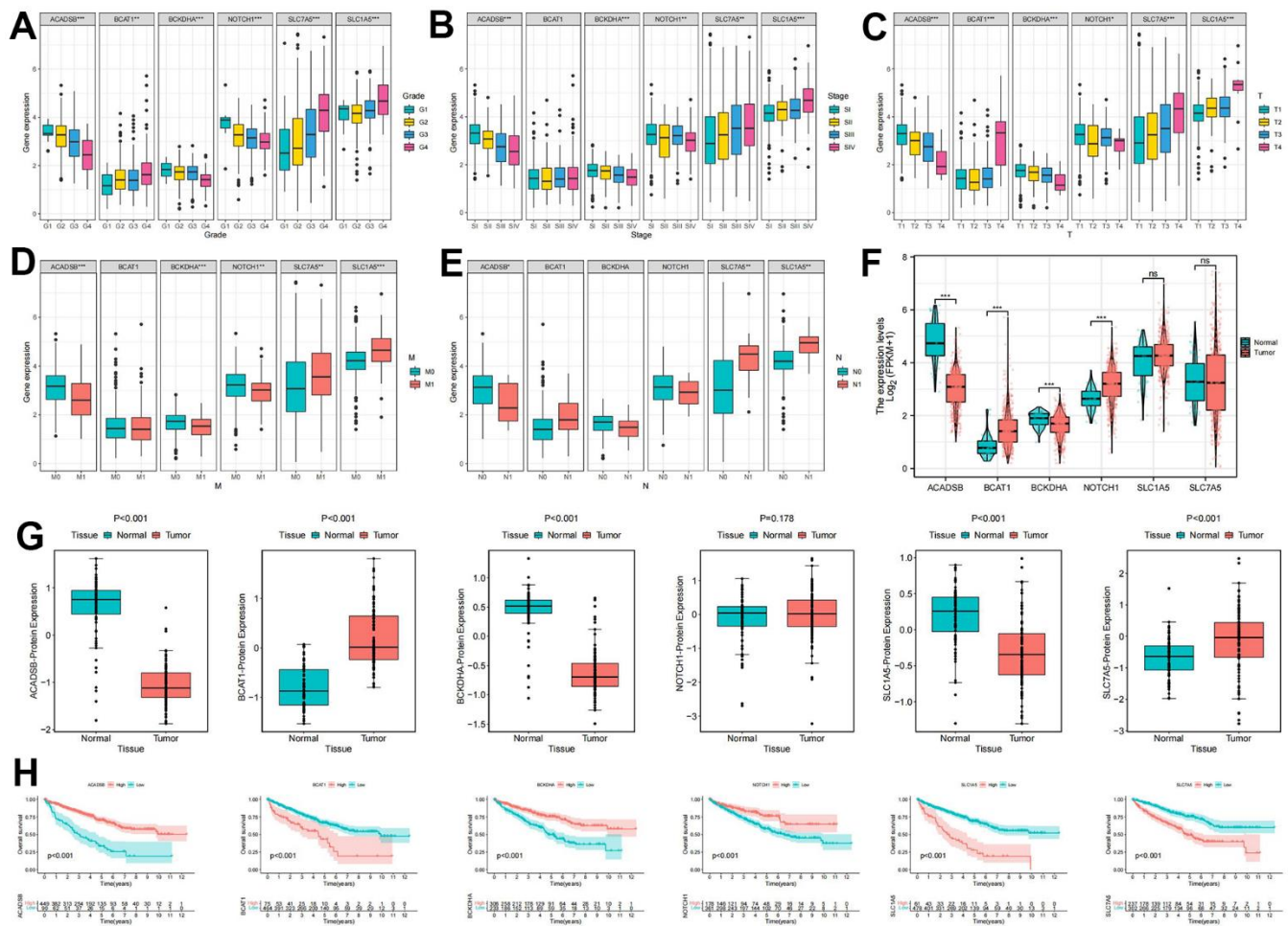
# SUPPLEMENTARY FIGURES



**Supplementary Figure 1. Multi-omics landscape of BMGs in ccRCC.** (A) Mutation frequency of 18 BMGs in 336 ccRCC patients. (B) Copy number variations (CNVs) of the 18 BMGs. (C) Differential expression of 18 BMGs in ccRCC and adjacent normal tissues. (D) Location of CNV alterations in the 23 chromosomes of 18 BMGs. (E) Association and prognostic characteristics of 18 BMGs in ccRCC. Wilcox test was used, and the asterisks represent the statistical  $P$ -value (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ).



**Supplementary Figure 2. Drug sensitivity analysis of BMS groups.** (A–F) Comparison of the sensitivity of patients in high- and low-BMS groups to (A) Rapamycin, (B) Temsirolimus, (C) Sorafenib, (D) Axitinib, (E) Pazopanib, and (F) Sunitinib. (G) Differential expression of target genes between high- and low-BMS groups after targeted drug treatment. Wilcoxon test was used, and the asterisks represent the statistical  $P$ -value ( $*p < 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ ).



**Supplementary Figure 3. Clinical, prognostic, and protein expression characteristics of model genes.** (A–E) Differential expression of model genes among different clinicopathological variables, including (A) histological grade, (B) pathological stage, (C) T stage, (D) M stage, and (E) N stage. (F) Differential mRNA expression of model genes between ccRCC and adjacent tissues. (G) Differential protein expression of model genes between ccRCC and adjacent tissues. (H) Survival analysis of model genes in ccRCC. Wilcox test was used, and the asterisks represent the statistical *P*-value (\**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001).