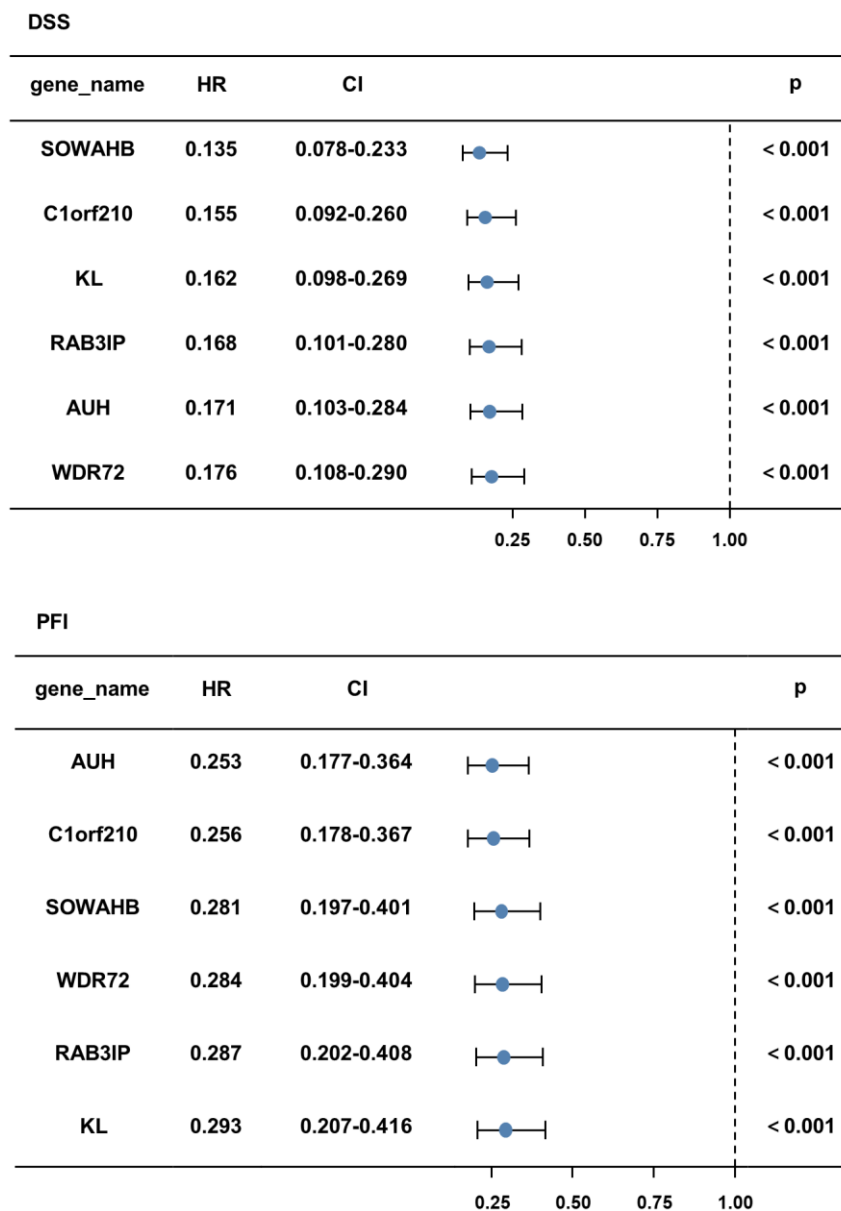
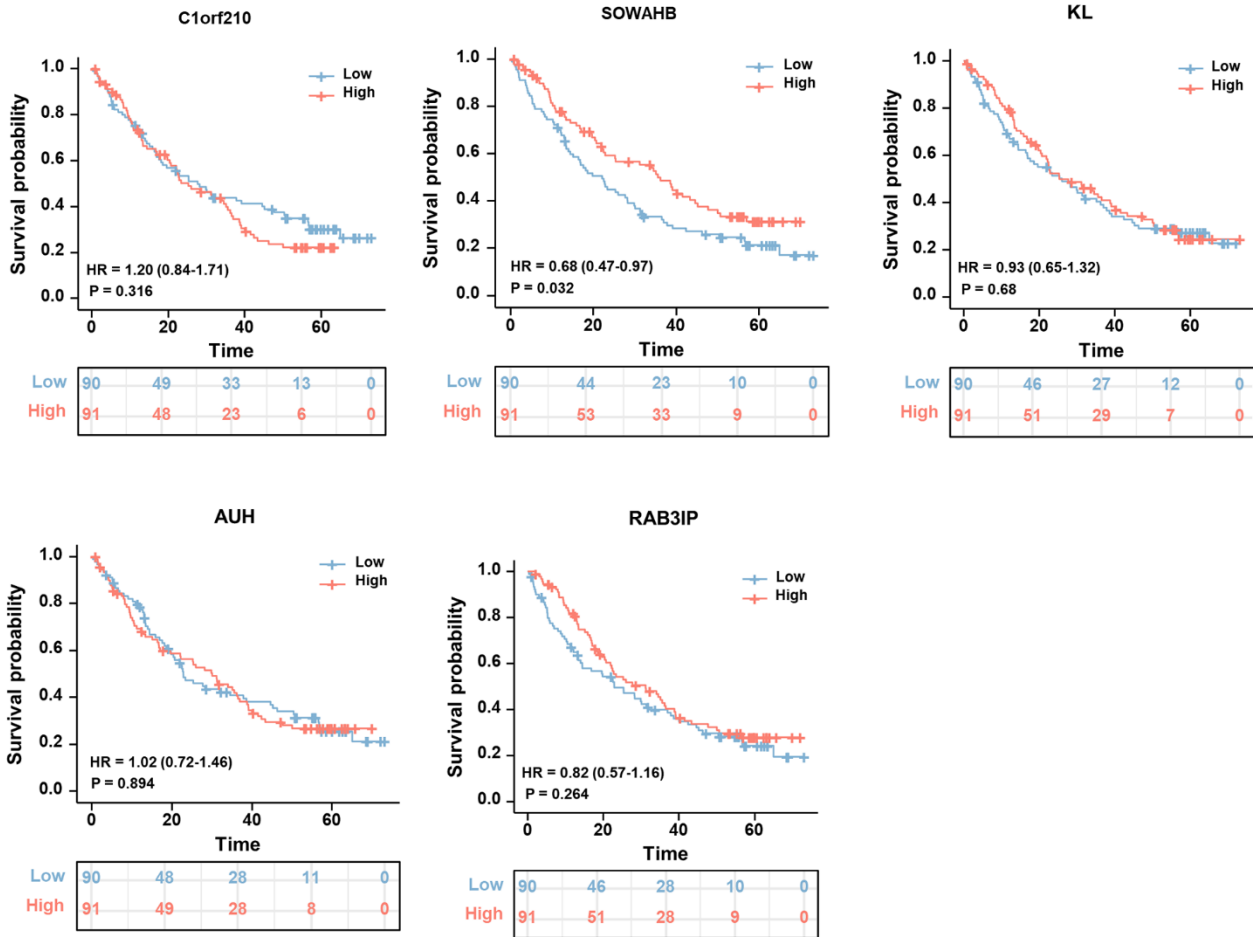


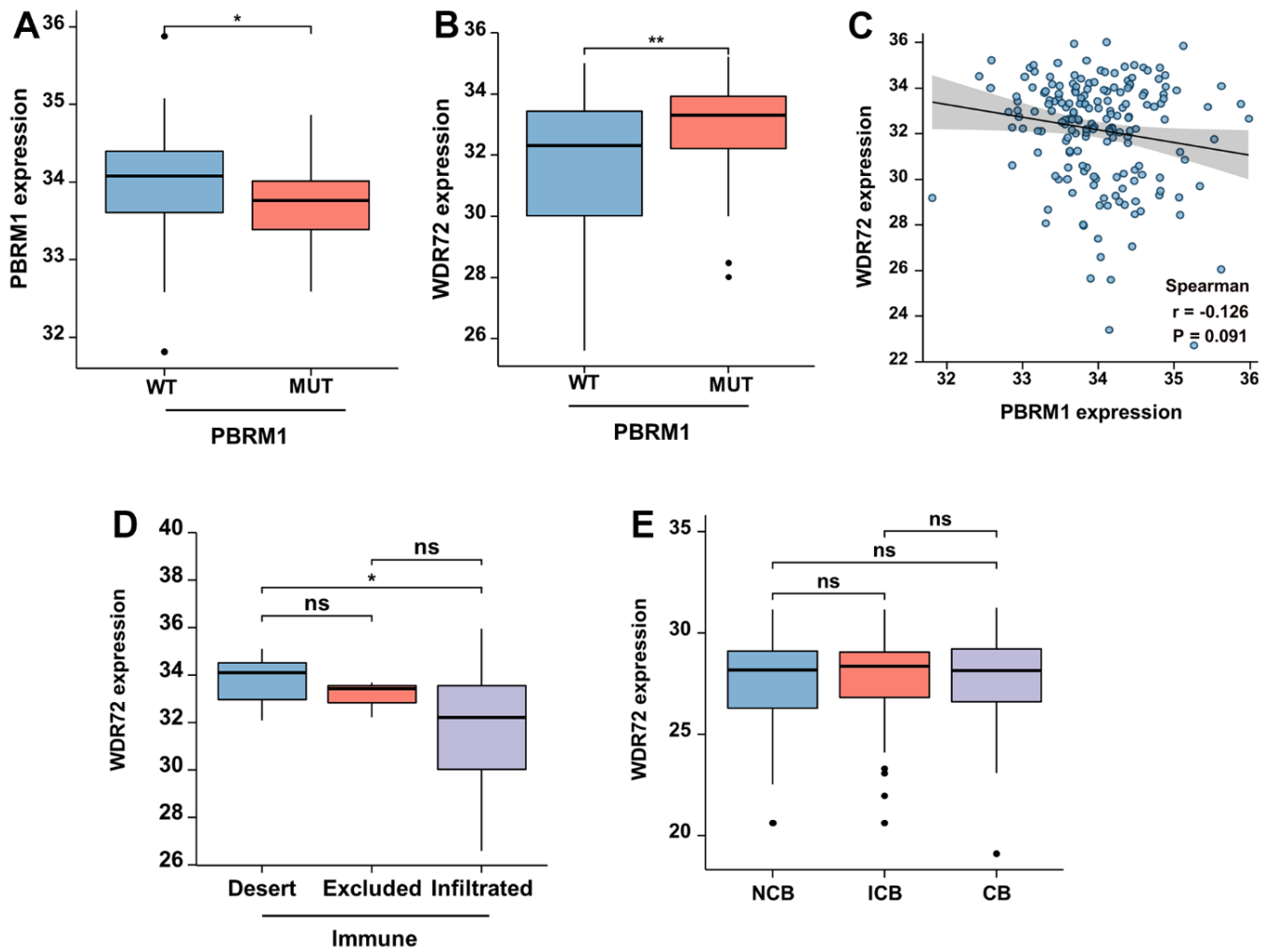
SUPPLEMENTARY FIGURES



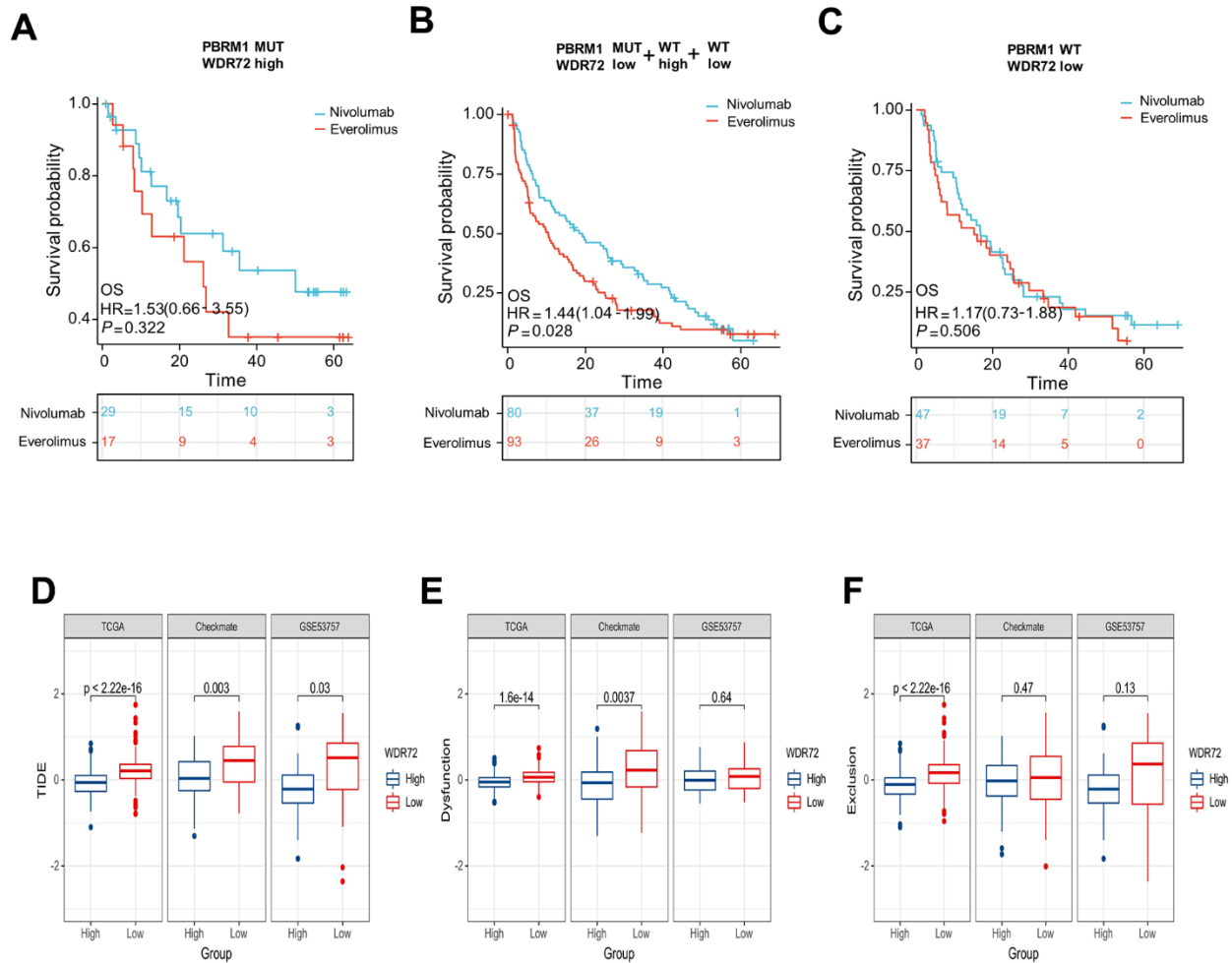
Supplementary Figure 1. DSS and PFI analysis of 6 overlapping genes in ccRCC based on TCGA databases. DSS, disease specific survival; PFI, progress free interval; HR, hazard ratio; CI, confidence interval.



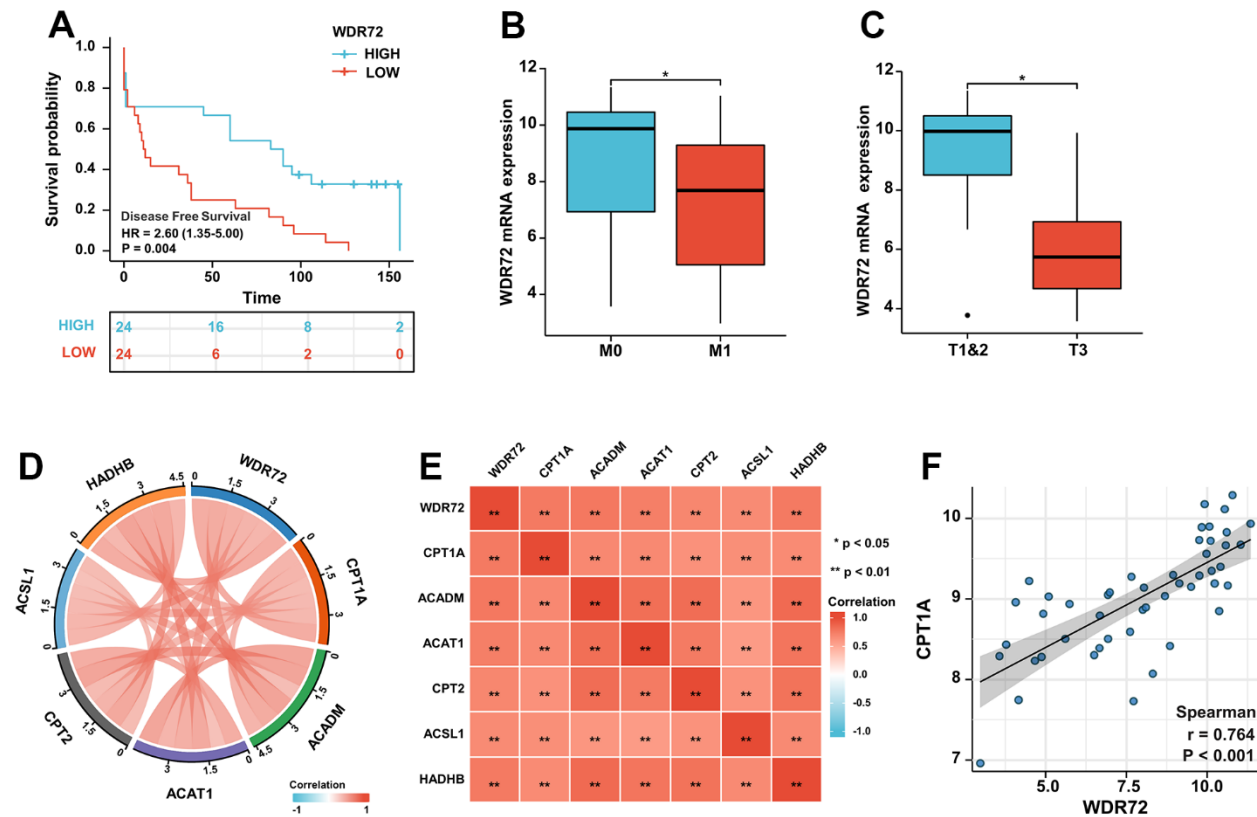
Supplementary Figure 2. Overall survival analysis for patients with advanced ccRCC treated with Nivolumab and stratified by overlapping gene expression except for WDR72.



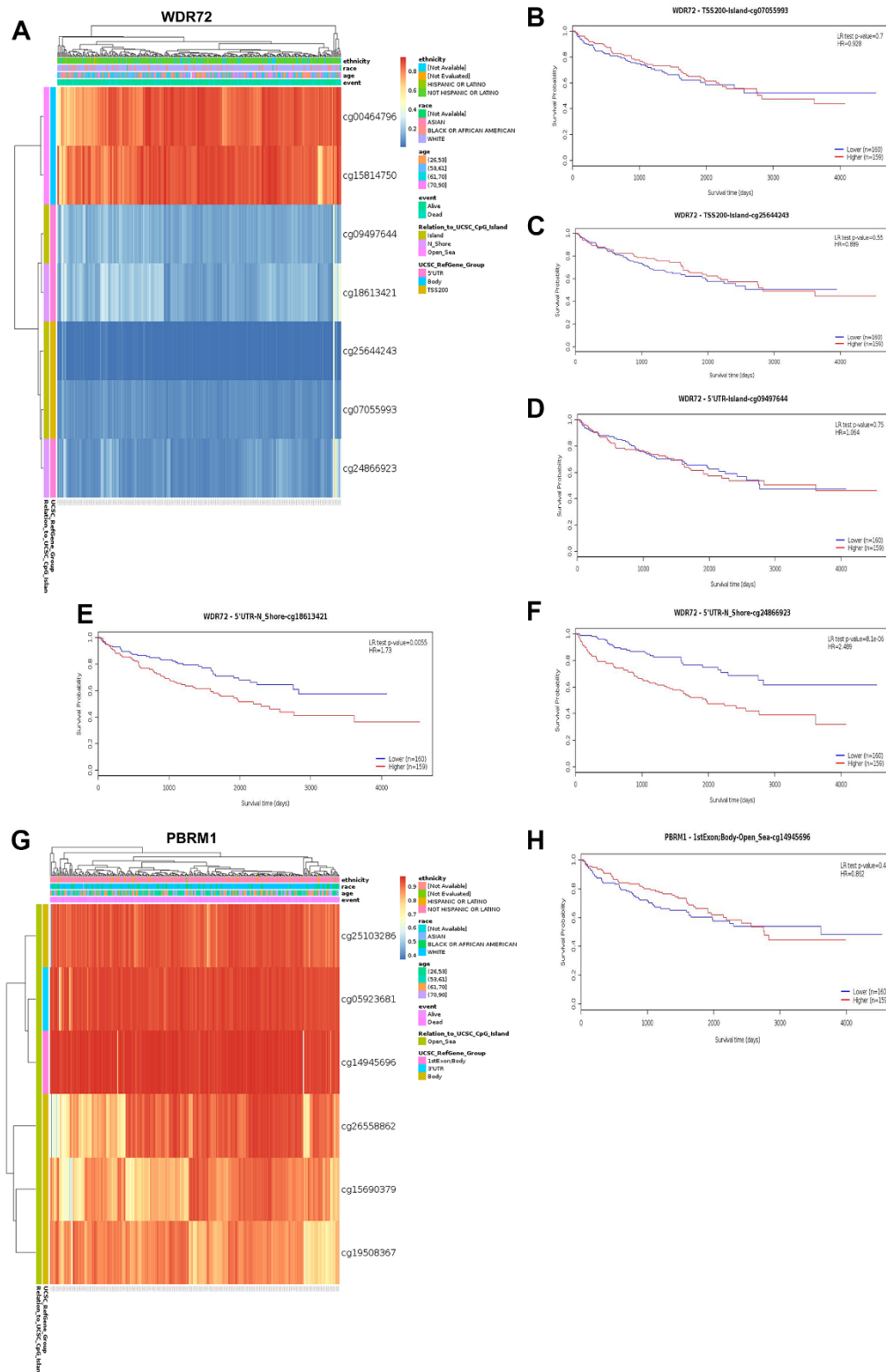
Supplementary Figure 3. The expression of PBRM1 and WDR72 in patients treated with Nivolumab in all checkmate cohorts. (A) PBRM1 expression in samples from PBRM1-WT and PBRM1-MUT patients. (B) WDR72 expression in samples from PBRM1-WT and PBRM1-MUT patients. (C) The scatterplot showing Spearman correlation between WDR72 and PBRM1 expression. (D) WDR72 expression in samples from immune desert, immune excluded and immune infiltrated patients. (E) WDR72 expression in samples from NCB, ICB and CB patients. Abbreviations: MUT, mutated; WT, wild type; NCB, no clinical benefit; ICB, intermediate clinical benefit; CB, clinical benefit. * $P < 0.05$; ** $P < 0.01$, ns, no significance.



Supplementary Figure 4. Survival analysis for patients with advanced ccRCC treated with Nivolumab or Everolimus and TIDE analysis for WDR72 in ccRCC. (A) Kaplan-Meier curves showing OS in patients treated with Nivolumab or Everolimus in PBRM1-MUT plus WDR72-High group. **(B)** Kaplan-Meier curves showing OS in patients treated with Nivolumab or Everolimus in PBRM1-MUT plus WDR72-Low, PBRM1-WT plus WDR72 High group and PBRM1-WT plus WDR72-Low group. **(C)** Kaplan-Meier curves showing OS in patients treated with Nivolumab or Everolimus in PBRM1-WT plus WDR72-Low group. **(D–F)** TIDE score analyses showing differences between the WDR72 high- and low-expression group in TCGA ccRCC cohort, CheckMate 009, 025, 010 trials and GSE53757 dataset. Abbreviation: TIDE, Tumor immune dysfunction and exclusion.



Supplementary Figure 5. Expression and function analysis of WDR72 gene in ccRCC dataset GSE22541. (A) Analysis of the prognostic significance of WDR72 expression in ccRCC patients (DFS). (B) WDR72 expression between M0 and M1 stage. (C) WDR72 expression in low and high T stage (T1 and T2 vs. T3). (D, E) Correlation analyses between WDR72 and overlapping genes in Fatty acid degradation and Fatty acid beta oxidation pathway in ccRCC. (F) Correlation analyses between WDR72 and CPT1A. Abbreviation: DFS, disease free survival.



Supplementary Figure 6. The methylation of WDR72 and PBRM1 genes in ccRCC. (A) Heat map depicting clustering of the CpG methylation levels within WDR72 gene. **(B–F)** Kaplan-Meier curves showing OS stratified by methylation level of WDR72 in CpG sites of promoter region. **(G)** Heat map depicting clustering of the CpG methylation levels within PBRM1 gene. **(H)** Kaplan-Meier curve showing OS stratified by methylation level of PBRM1 in CpG sites of promoter region. Abbreviations: TSS, transcription start site; 5'UTR, 5'untranslated region; 1stExon, the first exon; HR, hazard ratio; LR, Log-likelihood ratio.