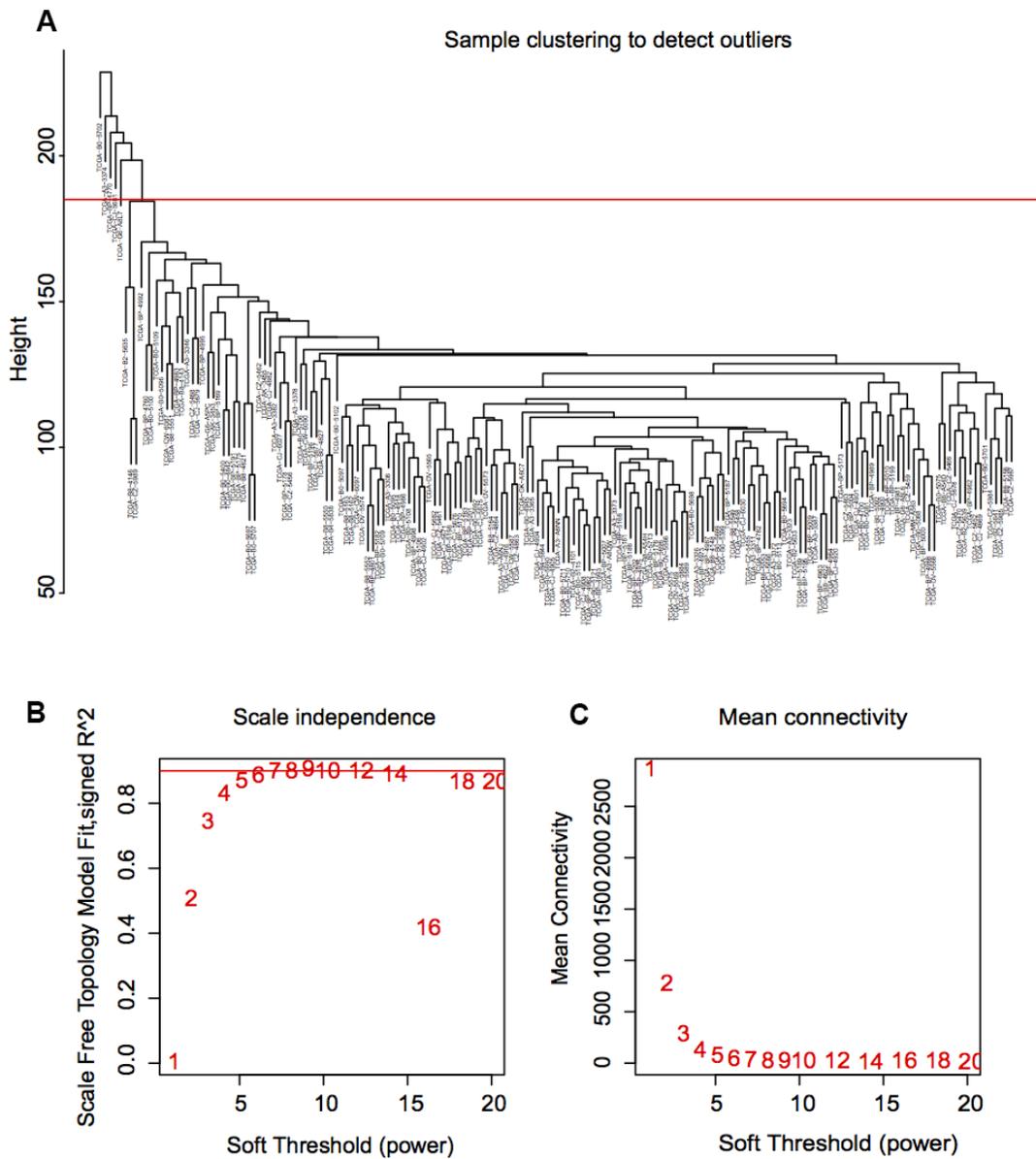
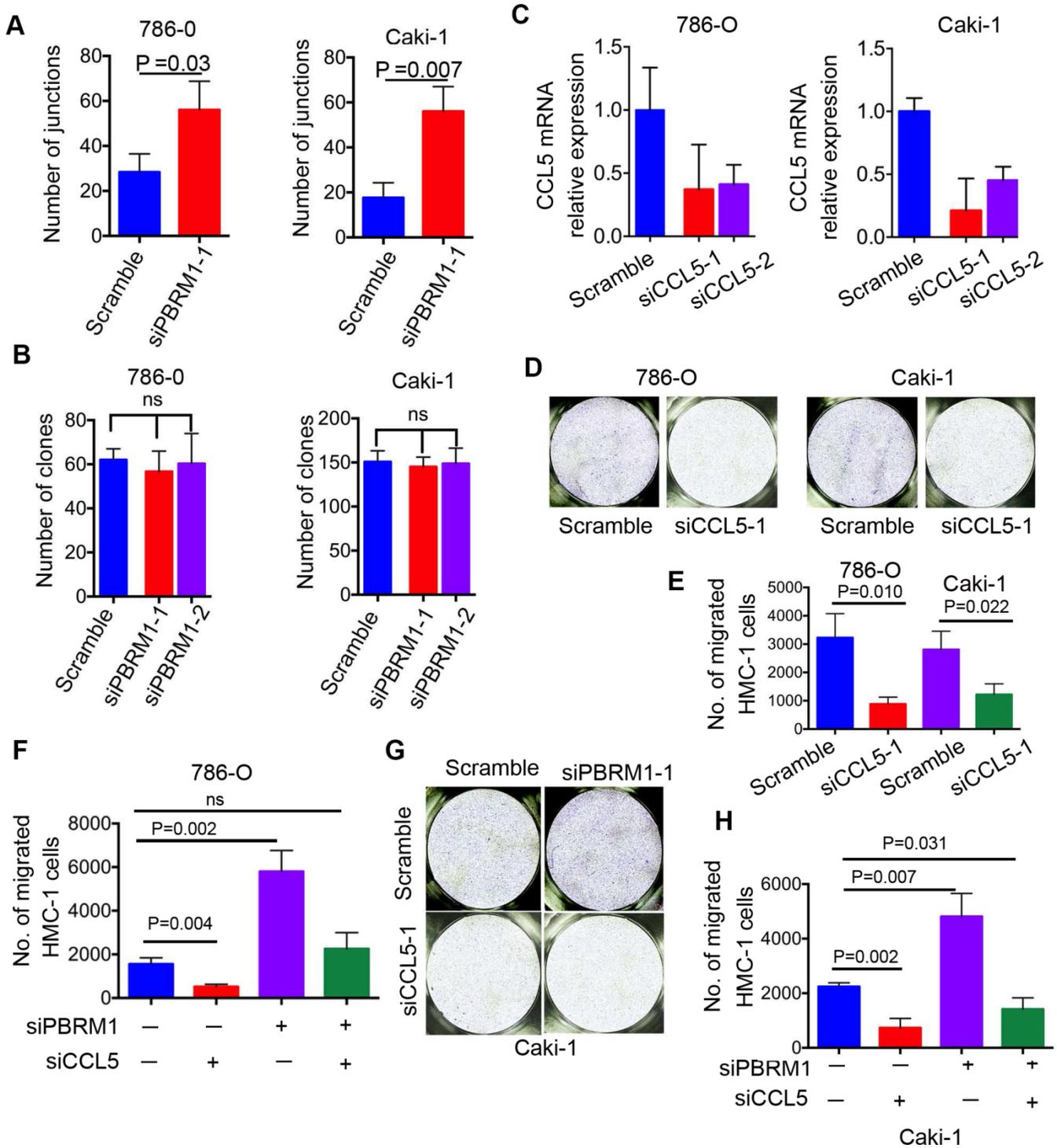


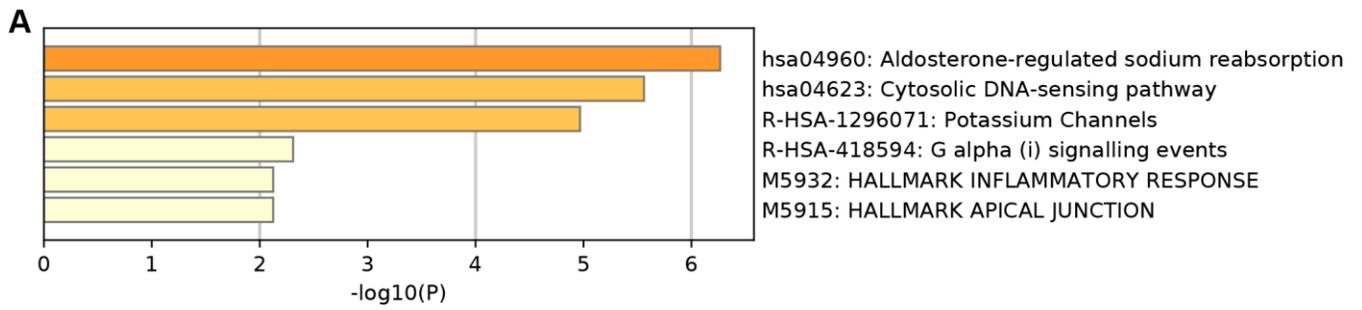
Supplementary Figure 2. Sample heterogeneity screening. (A, B) Dendrogram shows differentially expressed genes in VHL^{MUT} (177), VHL^{WT} (155), PBRM1^{MUT} (197) and PBRM1^{WT} (135) ccRCC samples. The red lines in the dendrograms represent cutoffs and samples outside these lines are considered outliers.



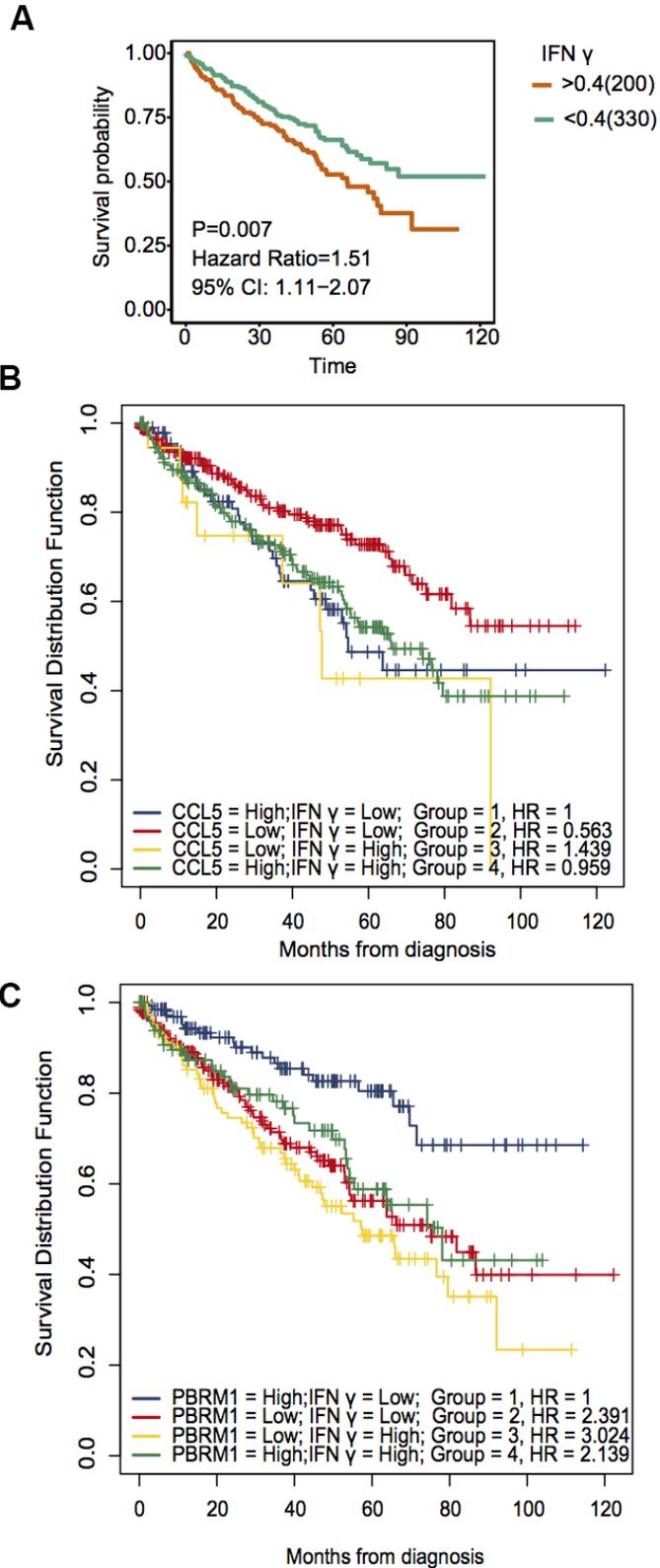
Supplementary Figure 3. Sample quality control. (A) Clustering dendrogram of ccRCC samples based on their Euclidean distance. (B, C) Analysis of the network topology for various soft-thresholding powers. The left panel shows the scale-free fit index (y-axis) as a function of the soft-thresholding power (x-axis). The right panel displays the mean connectivity (degree, y-axis) as a function of the soft-thresholding power (x-axis).



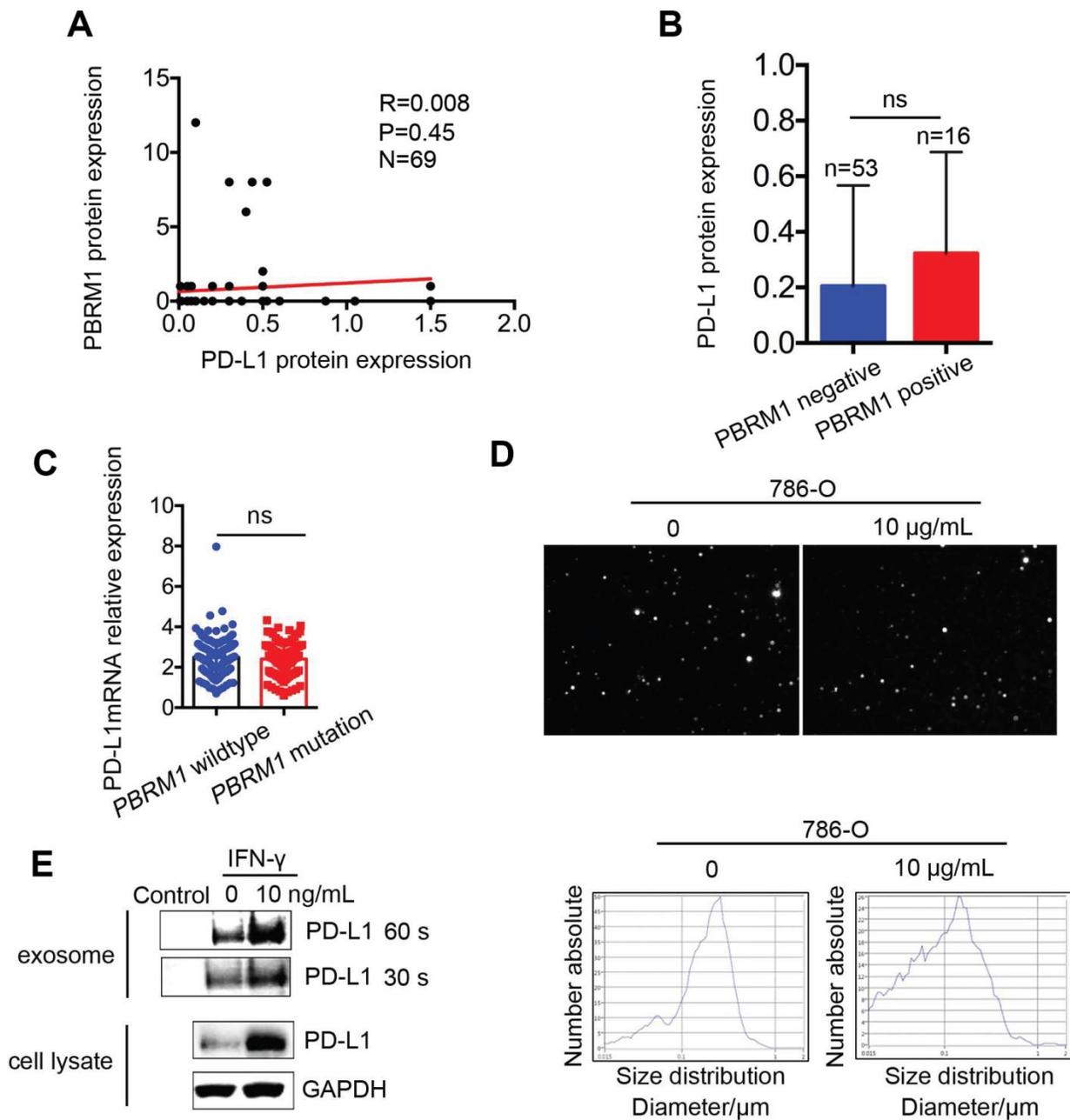
Supplementary Figure 4. The bio-function of PBRM1 protein in ccRCC cells. (A) The tube formation ability of control and PBRM1-silenced 786-O- and Caki-1 cells is shown. (B) Colony formation assay shows the number of colonies formed by control and PBRM1-silenced 786-O and Caki-1 cells. (C) qRT-PCR analysis shows CCL5 mRNA expression in control and siCCL5-transfected 786-O and Caki-1 cells, respectively. (D, E) Transwell migration assay shows migration ability of HMC-1 cells when co-cultured with CCL5-silenced in 786-O and Caki-1 cells, respectively. Note: All experiments were performed in triplicate; data was analyzed by Student's t-test and expressed as means \pm SD; ns denotes not statistically significant. (F–H) Transwell migration assay shows migration ability of HMC-1 cells when co-cultured with PBRM1-silenced and PBRM1-silenced plus CCL5-silenced in 786-O and Caki-1 cells, respectively. Note: All experiments were performed in triplicate; data was analyzed by Student's t-test and expressed as means \pm SD; ns denotes not statistically significant.



Supplementary Figure 5. The inflammatory response signaling pathway is suppressed in PBRM1-overexpressing ccRCC cells.
 (A) Pathway enrichment analysis of differentially expressed genes (DEGs) between control and PBRM1-overexpressing Caki-2 cells in the GSE76199 dataset.



Supplementary Figure 6. High IFN- γ expression predicts worse overall survival in ccRCC patients from the TCGA KIRC database. (A) Survival analysis using survival and survminer packages shows overall survival of ccRCC patients with high (200) and low IFN- γ (330) expression. P<0.05 was considered statistically significant. (B) Survival analysis shows overall survival rates and HR values of ccRCC patients in the TCGA KIRC database, classified based on high and low CCL5 and IFN- γ expression. (C) Survival analysis shows overall survival rates and HR values of ccRCC patients in the TCGA KIRC database, classified based on high and low PBRM1 and IFN- γ expression.



Supplementary Figure 7. PBRM1 expression does not correlate with PD-L1 expression in ccRCC. (A) The correlation analysis of PD-L1 IHC staining score and PBRM1 IHC staining score in ccRCC tissues. (B) PD-L1 mRNA expression in PBRM1-negative and PBRM1-positive ccRCC patients. (C) PD-L1 expression in PBRM1^{WT} and PBRM1^{MUT} ccRCC patients in the TCGA KIRC dataset. “ns” denotes ‘not statistically significant’. (D) Characterization of exosomes purified from conditioned media of 786-O cells. Exosomes were identified by Zeta View, and the video data is included in the supplementary data. (E) Western blot analysis shows exosomal and total cellular PD-L1 protein levels in control and 10 ng/ μL IFN- γ -treated 786-O cells and their corresponding. The loading buffer is loaded as “Control”. ‘30 s’ and ‘60 s’ denote exposure time of 30 and 60 seconds, respectively.