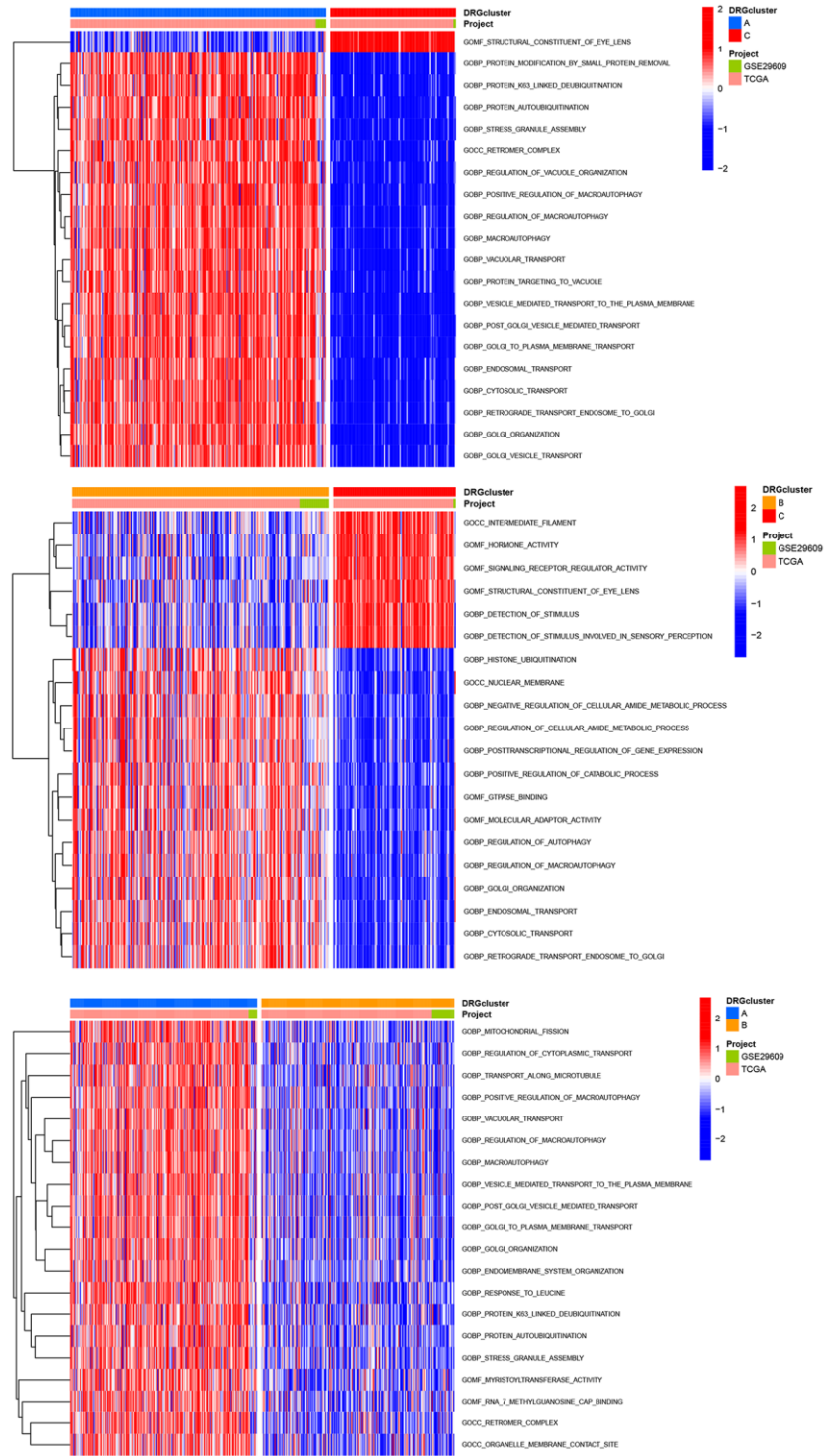
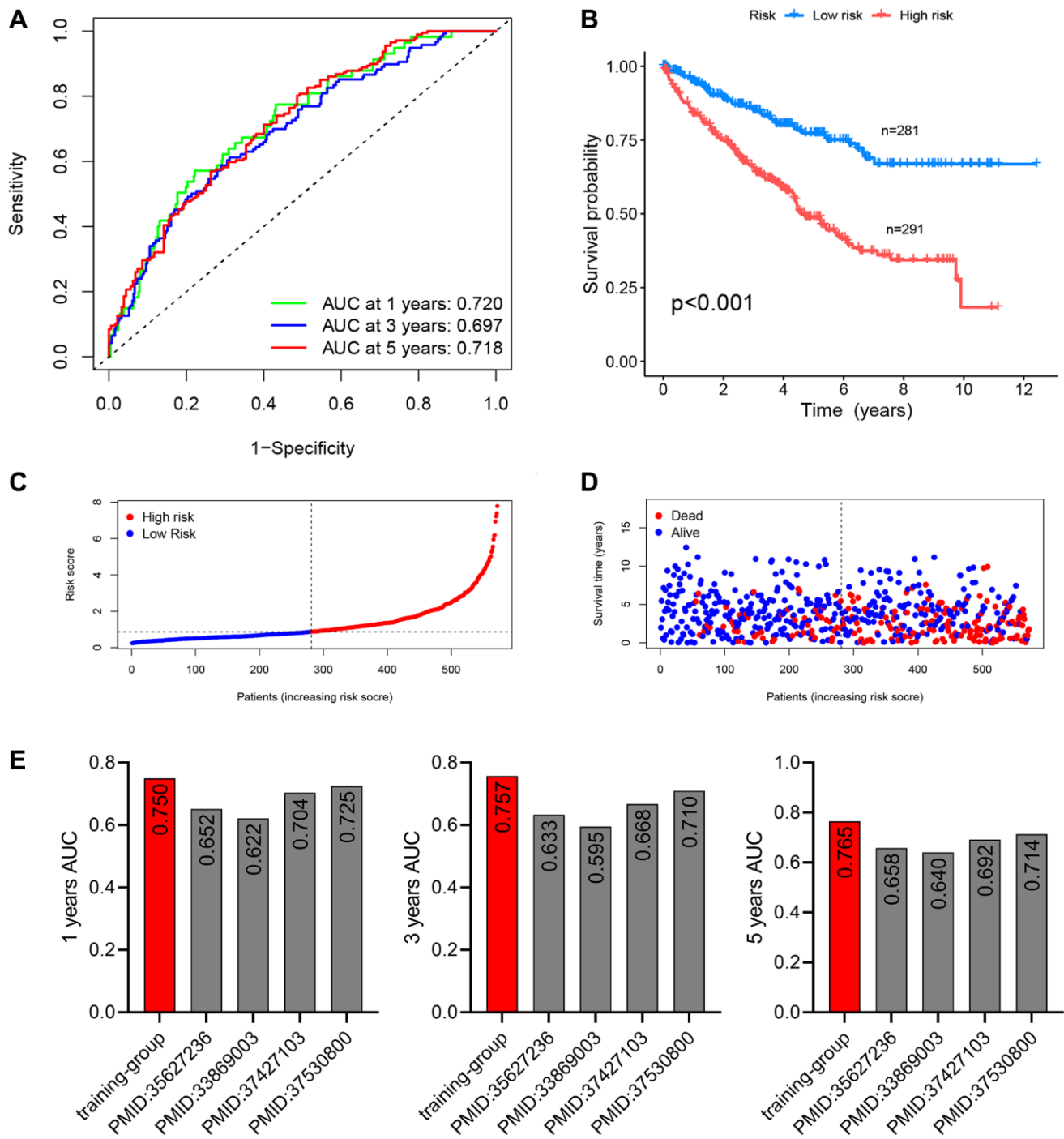


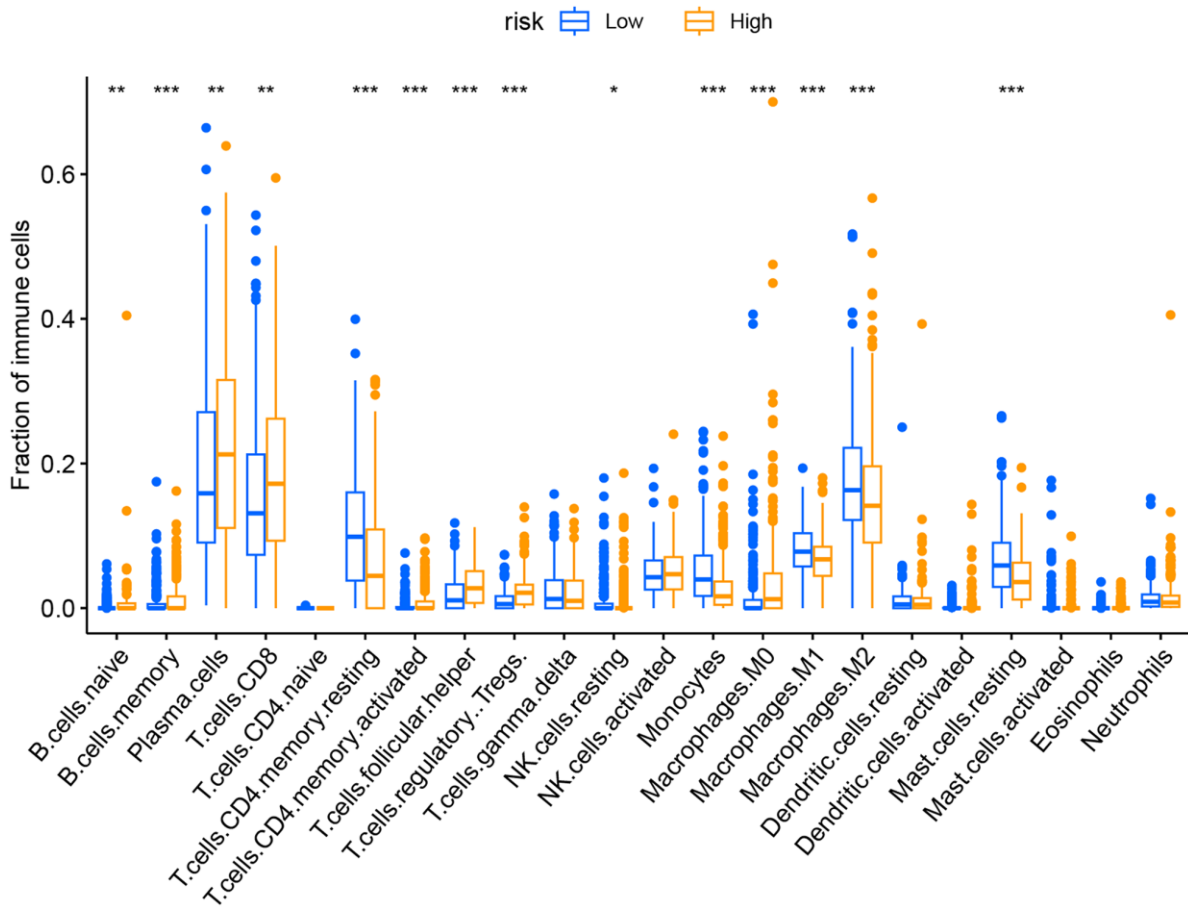
SUPPLEMENTARY FIGURES



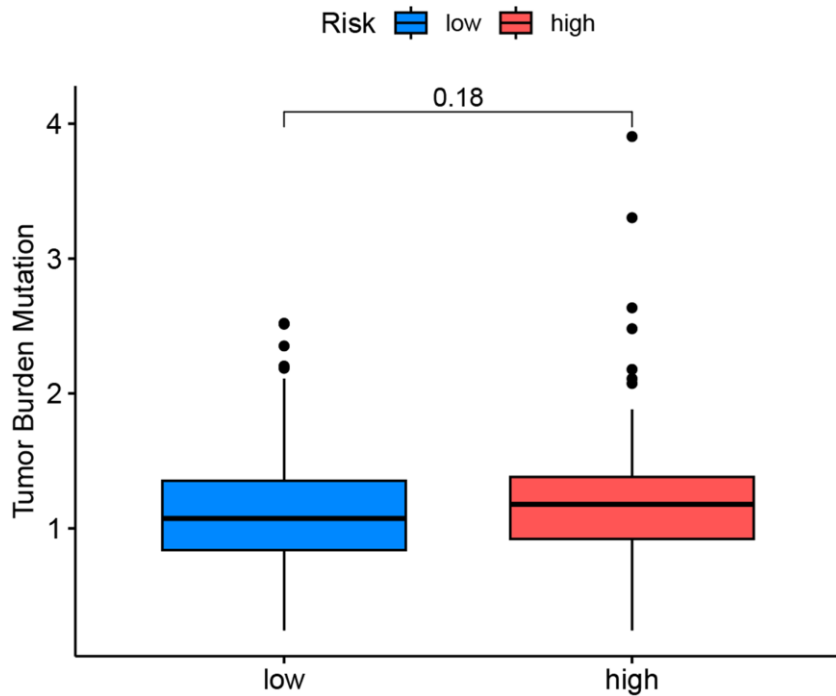
Supplementary Figure 1. GO GSVA analysis between DRG-related molecular subtypes.



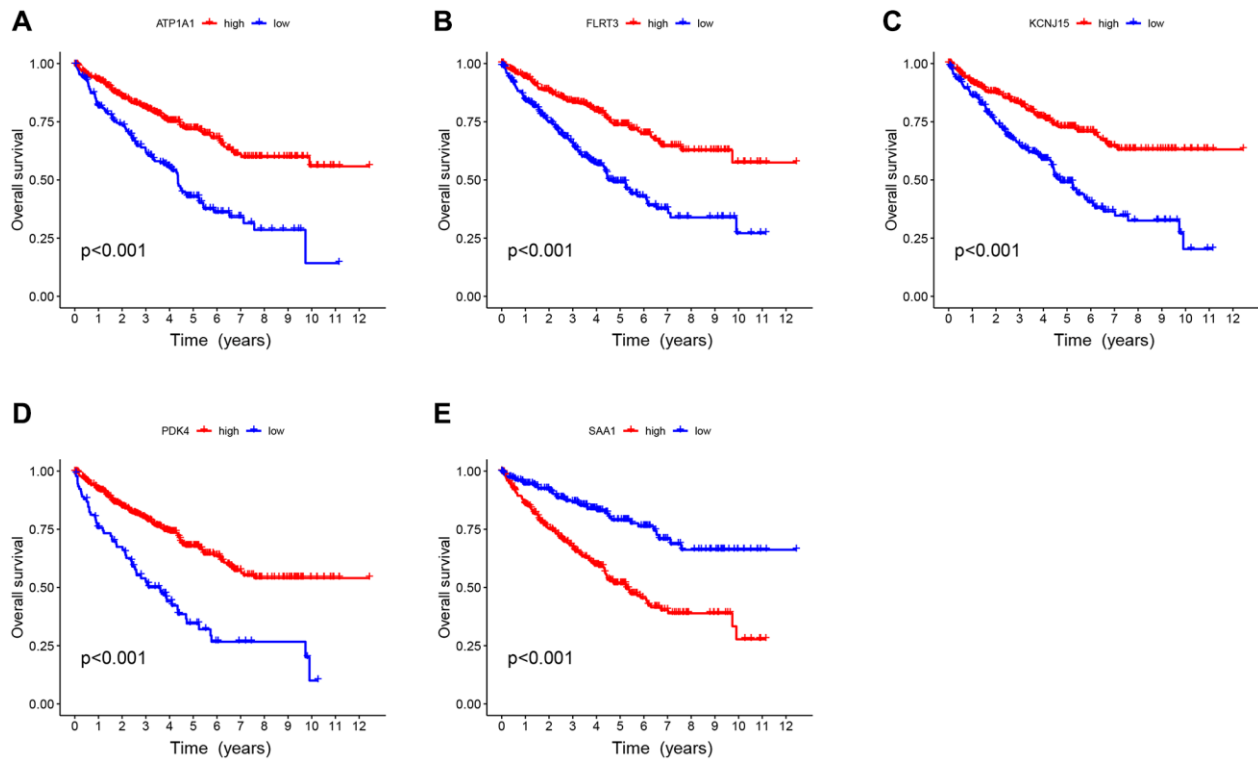
Supplementary Figure 2. (A–D) The ROC curves, KM curves, and point and scatter plots of risk score distribution and patient survival for the merged group. (E) Comparison of the DRG risk scoring model with other published ccRCC prognostic models.



Supplementary Figure 3. Analysis of the percentage of immune cells in high and low-risk groups.



Supplementary Figure 4. TMB analysis of high and low-risk groups.



Supplementary Figure 5. Overall survival analysis of risk scoring genes in ccRCC. Includes (A) ATP1A1, (B) FLRT3, (C) KCNJ15 (D) PDK4, and (E) SAA1.