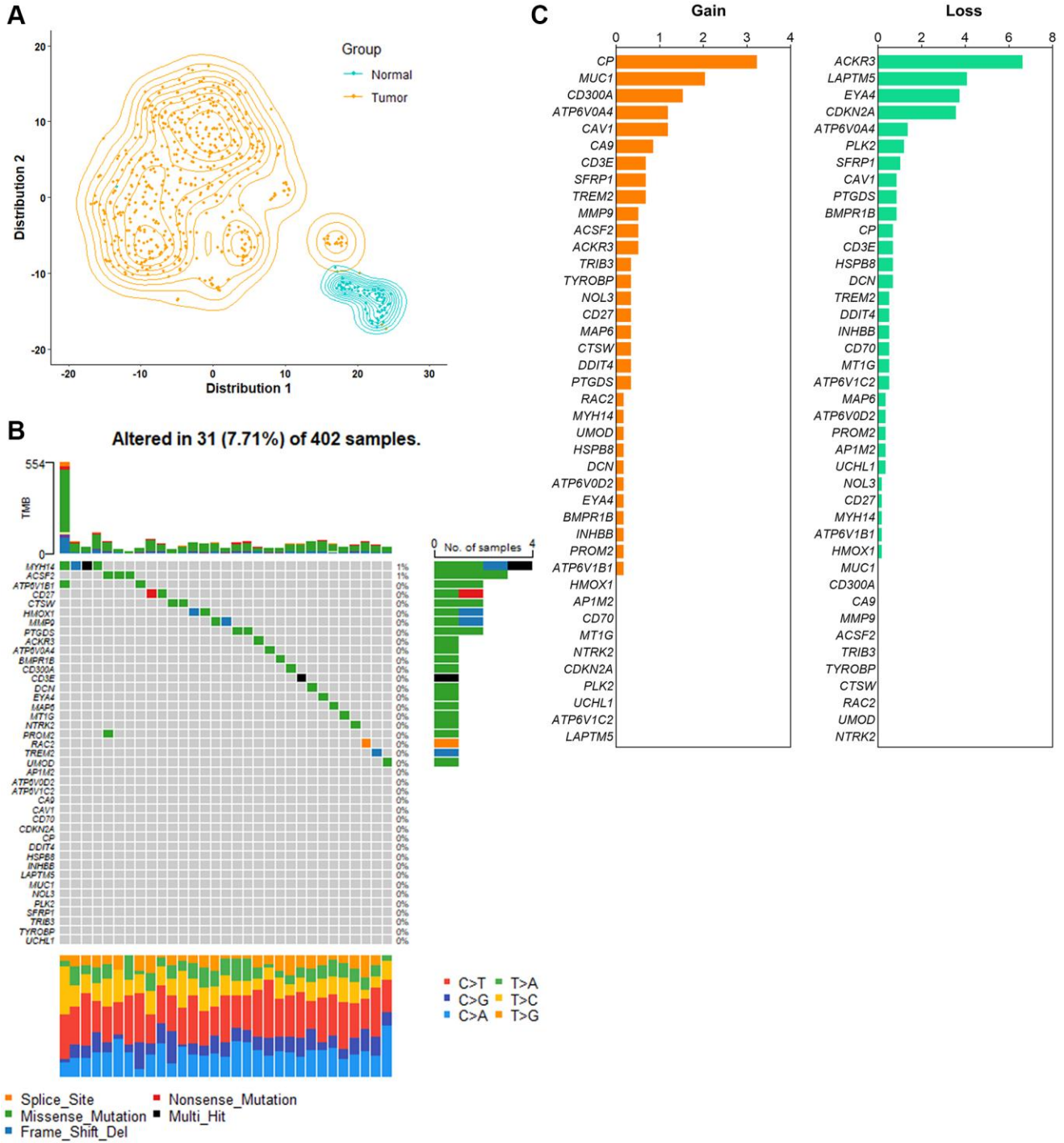
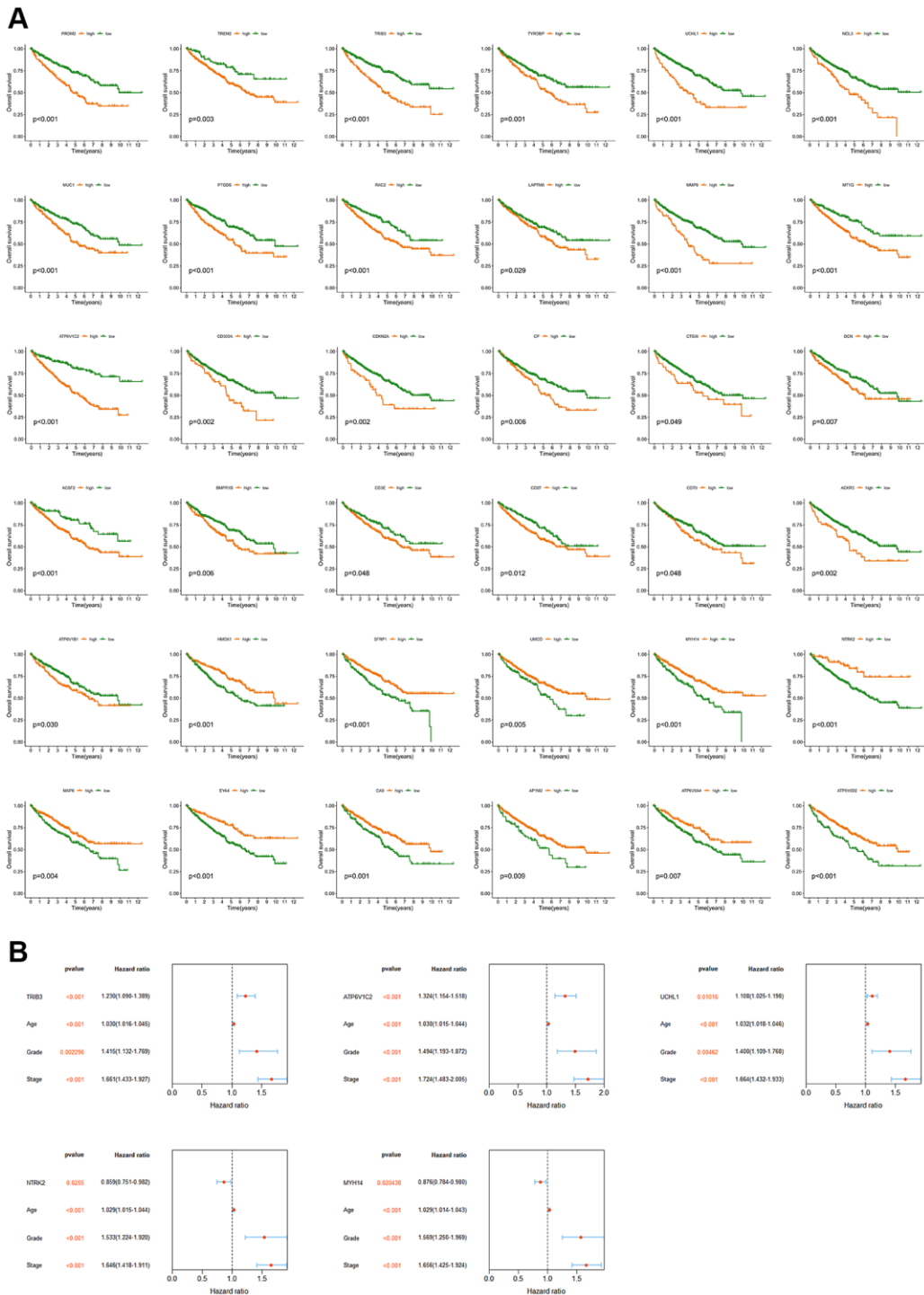


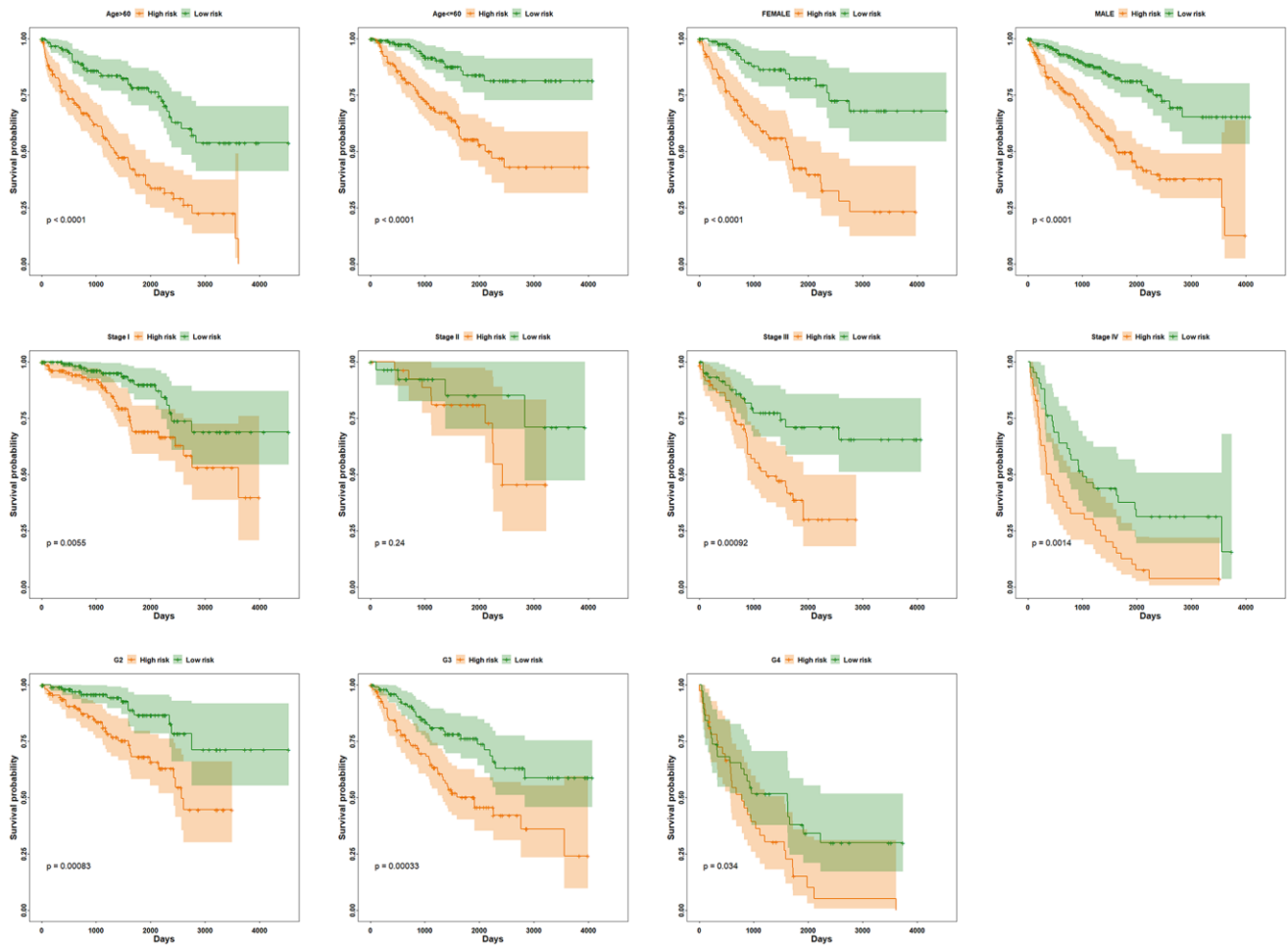
SUPPLEMENTARY FIGURES



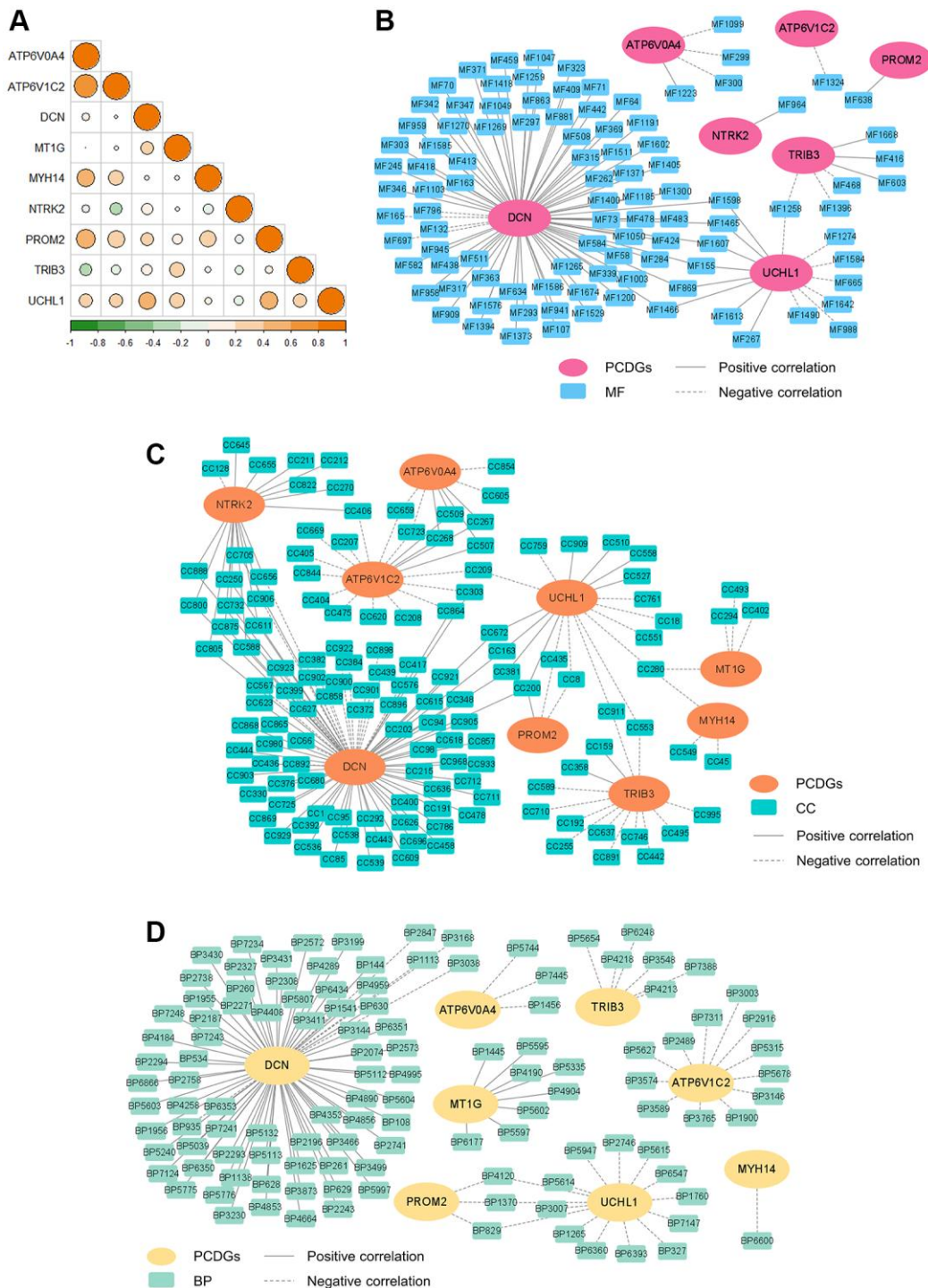
Supplementary Figure 1. (A) Distribution of tumor and normal groups calculated by t-SNE analysis in TCGA-KIRC database. Tumor mutation burden (TMB) (B) and copy number variations (CNVs) (C) analyses of these PCD-related DEGs in KIRC database.



Supplementary Figure 2. (A) Kaplan-Meier survival curves of these prognosis-related DEGs based on their expression in TCGA-KIRC database. **(B)** Forest plots of TRIB3, ATP6V1C2, UCHL1, NTRK2 and MYH14 depicted by multi-Cox regression analysis (adjusted by age, grade and stage).



Supplementary Figure 3. Validation of PRPCDGs risk signature's prognostic predictive performance on clinicopathologic features (age, gender, stage and grade) with Kaplan-Meier analysis in TCGA-KIRC cohort.



Supplementary Figure 4. (A) Correlation diagrams of the correlations among the 9-gene PRPCDGs risk signature expression in TCGA-KIRC database (positive correlations in orange dots, negative correlations in green and the size of the dots shows the significance level). (B–D) Network diagrams of the correlations between PRPCDGs’ expression and its highly correlated GO terms.