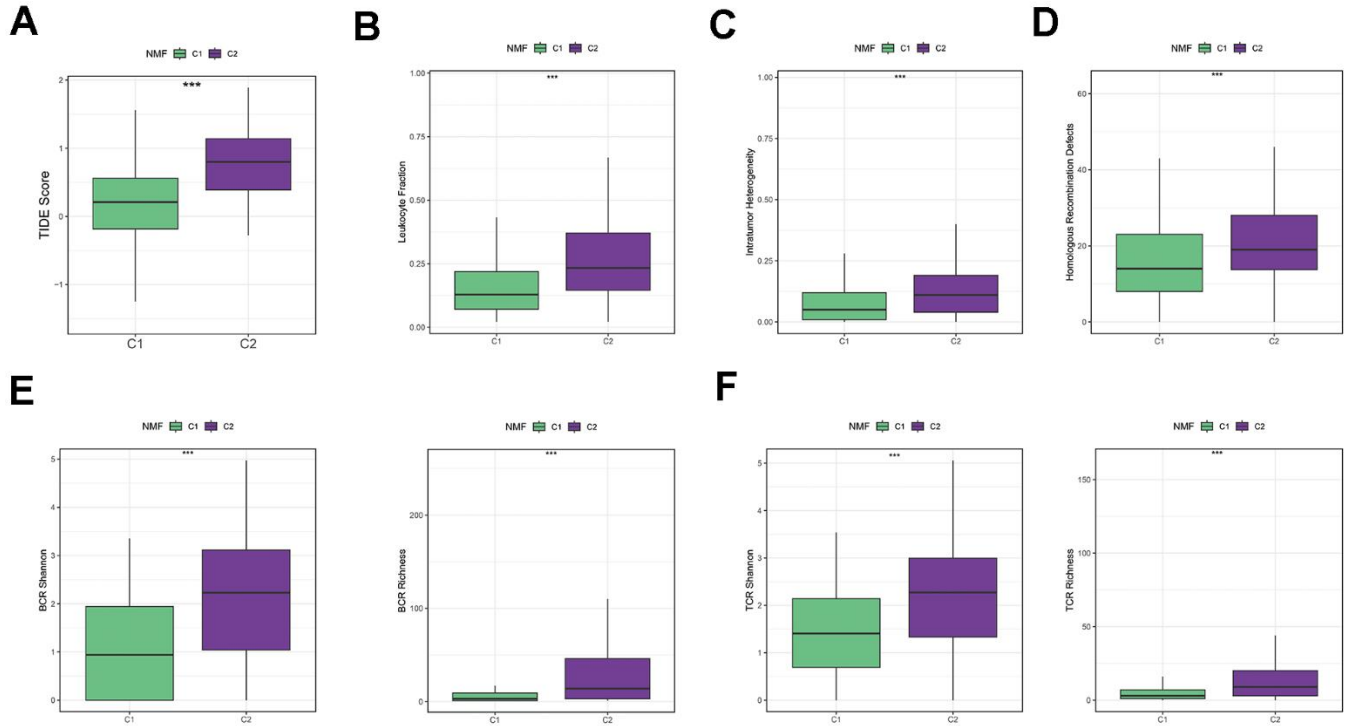
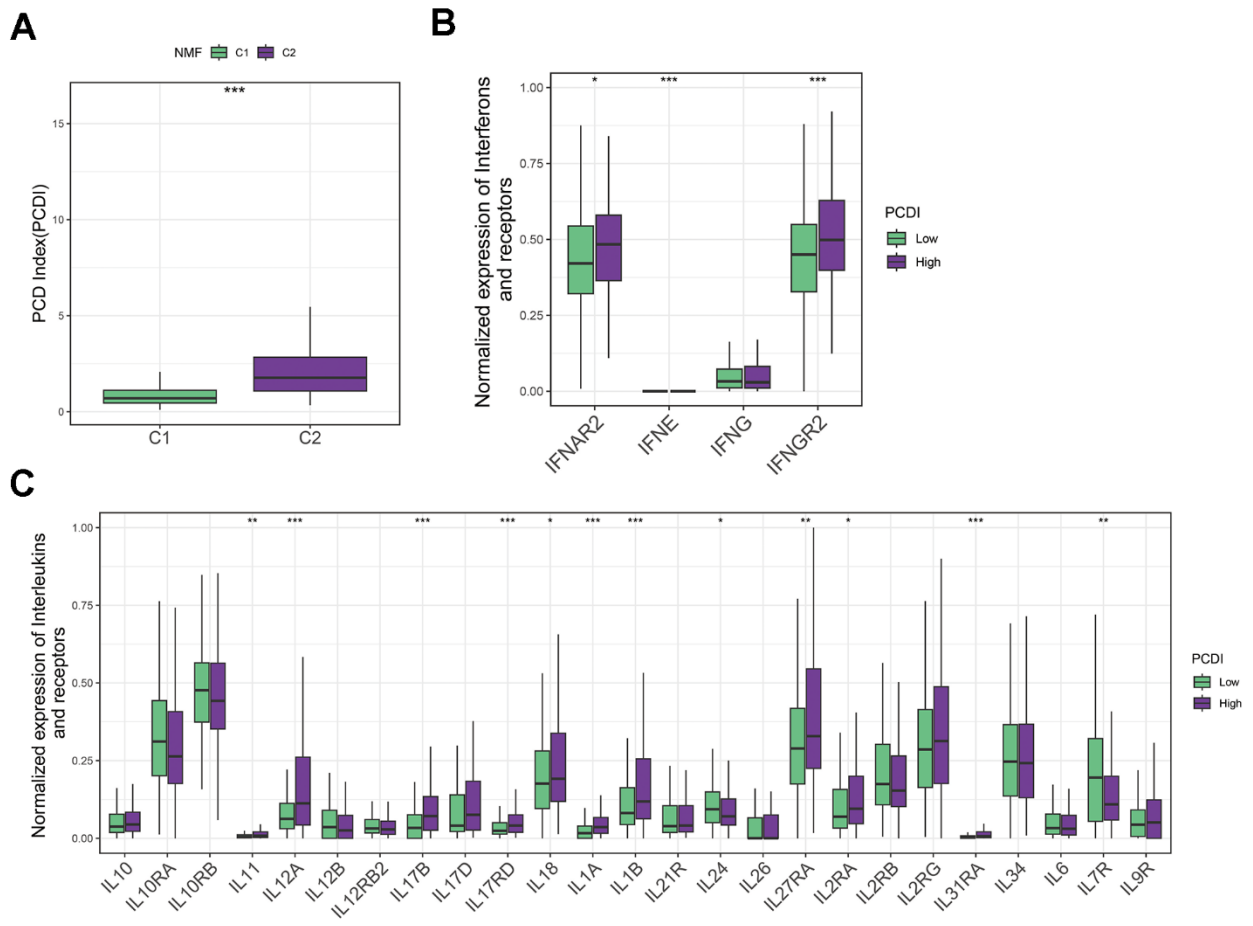


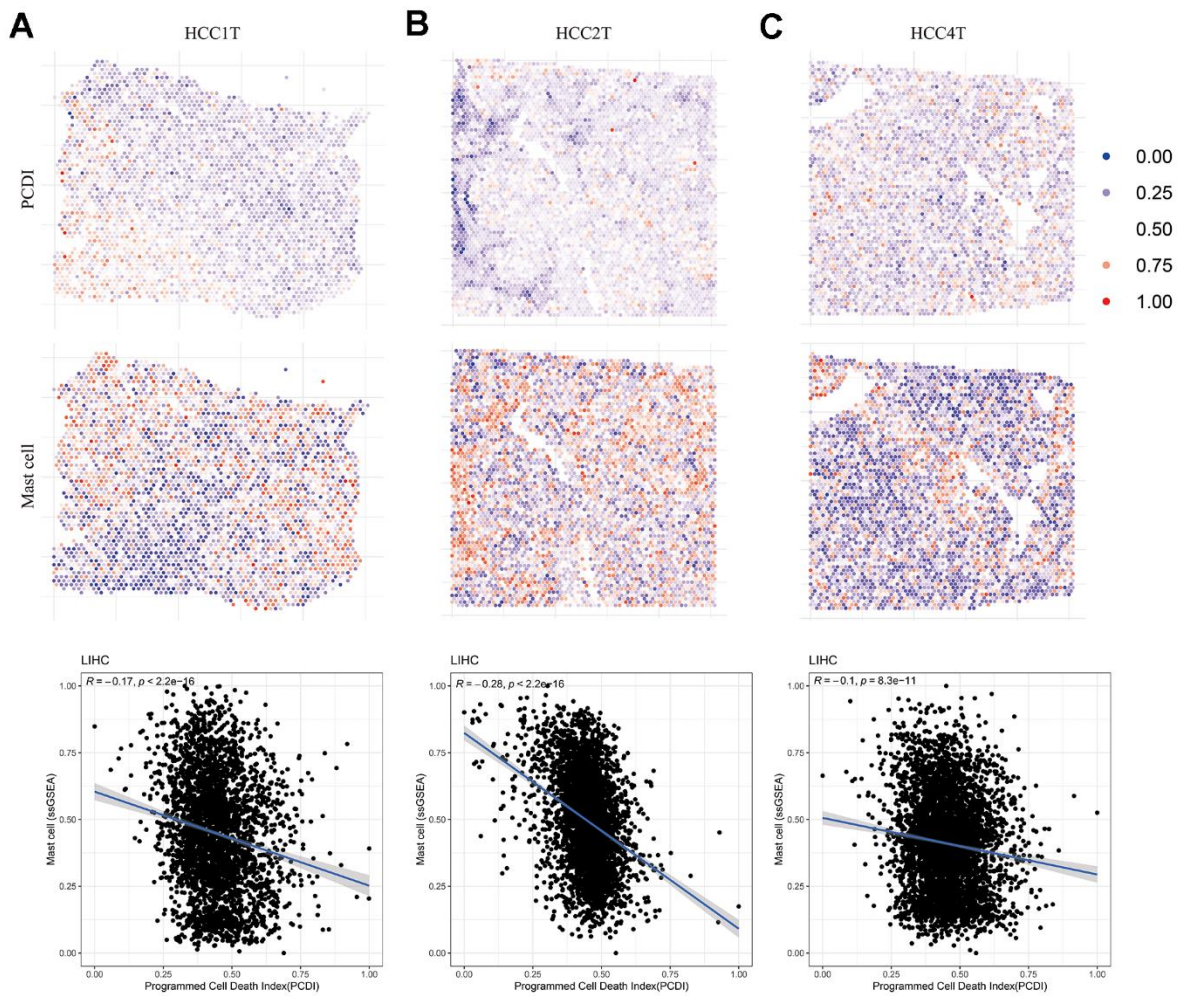
those without significant change. **(B)** A Venn diagram depicts the intersection of PCD-related DEGs and those linked to patient outcomes. **(C)** A Circos plot presents the genomic location and expression of 45 PCD genes across five datasets. **(D)** GO analysis of PCD-associated DEGs. **(E)** KEGG analysis centered on PCD-related DEGs. **(F)** Summary of mutation landscape in the TCGA-LIHC dataset. **(G)** Oncoplot illustrating genes associated with PCD in the TCGA-LIHC dataset. **(H)** Circos plot demonstrate the CNV of selected 45 PCD genes on the genome in TCGA-LIHC. **(I–J)** Dot plot presents the results of KEGG enrichment analysis for both clusters. **(K)** Gene set enrichment analysis (GSEA) highlights hallmark pathways within each cluster.



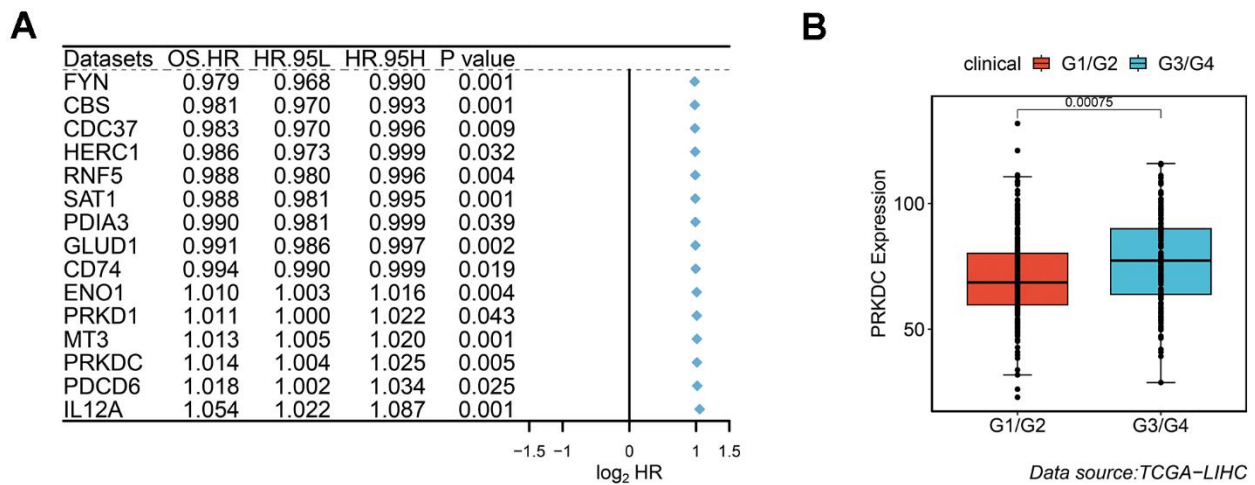
Supplementary Figure 2. Somatic diversification of two groups. **(A)** Comparative box plots contrasting Tumor Immune Dysfunction and Exclusion (TIDE) scores between C1 and C2. **(B)** Box plot illustrating normalized fraction level of leukocyte in C1 and C2. **(C)** Box plot showing the normalized score of intratumor heterogeneity between C1 and C2. **(D)** Box plot depicting the normalized score of homologous recombination defects in C1 versus C2. **(E)** Box plot presenting normalized score of BCR Shannon and Richness between C1 and C2. **(F)** Box plot contrasting normalized score of TCR Shannon and richness in C1 versus C2. (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$ determined by two-way ANOVA test).



Supplementary Figure 3. Immune landscape of high and low PCDI groups. (A) Comparative box plots demonstrating PCDI in C1 and C2 groups. (B) Comparative box plots showcasing normalized expression levels of interferons and their receptors in two groups. (C) Comparative box plots demonstrating normalized expression levels of interleukins and receptors in two groups. (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$ determined by Wilcoxon test).



Supplementary Figure 4. Immune landscape of PCDI in two-dimensional spatial level. (A) PCDI score of each spatial plot in three LIHC spatial transcriptome samples. (B) GSEA score of mast cell of each spatial plots in three LIHC spatial transcriptome samples. (C) Correlation between mast cell score and PCDI in LIHC spatial transcriptome samples.



Supplementary Figure 5. Clinical correlation of PCD genes. (A) Univariate Cox regression analysis of PCD associated genes in PCDI. (B) The expression of PRKDC in G1/G2 and G3/G4 stage.