***Supplementary Figure Legends***

**Fig. S1** Biological and mutational landscape of PCD-related features in CM. (a, b) Enrichment analysis of the 56 PCD-related features via (A) GO and (B) KEGG database. (c-f) The significant pathways between the low- and high-CDI group via GSEA. (g) The oncoplot exhibited the SNV mutation landscape of the PCDrelated features in CM.

**Fig. S2** Interaction relationship of the 7 crucial PCD-related features in the CDI signature. (a) Co-expression and functional network of the 7 crucial PCD-related features in the CDI signature established via GeneMANIA. (b) Correlation heatmap of the 7 crucial PCD-related features in the CDI signature.

**Fig. S3** KM curves exhibited the significant prognostic role of each PCD-related features. The blue line represents the low expression of the genes in CDI model while the red line means the high expression of this gene.

**Fig. S4** Scatter plots exhibited the expression difference of each PCD-related features between tumor samples in the TCGA-SKCM cohort and normal samples in the GTEx cohort. The pink represent normal samples and the purple means tumor samples. \*\*, p < 0.01; \*\*\*\*, p < 0.0001.

**Fig. S5** The differential pattern of our prognostic model between the two PCD-related clusters. (a) The difference of CDI between the two PCD-related clusters. (b-h) The difference of the relative mRNA expression of (b) CD28, (c) CYP1B1, (d) LAMP3, (e) SFN, (f) JAK3, (g) STAT4, and (h) TRAF1 between the two PCD-related clusters. The red represents cluster 1 (C1) and the blue represents cluster 2 (C2). \*, p < 0.05; \*\*\*, p < 0.001; \*\*\*\*, p < 0.0001.

**Fig. S6** The specific expression level of 7 crucial PCD-related features in the single cell level. UMAP plot exhibited the distribution of (a) CD28, (c) CYP1B1, (e) JAK3, (g) LAMP3, (i) SFN, (k) STAT4, and (m) TRAF1 across all the cell types. Scatter plot exhibited the distribution of (b) CD28, (d) CYP1B1, (f) JAK3, (h) LAMP3, (j) SFN, (l) STAT4, and (n) TRAF1 across each cell type in detail. (o) Bubble plot revealed the expression levels of all 7 crucial PCD-related features and CDI in each cell type.

**Fig. S7** Scatter plots exhibited the IC50 difference of the 13 potential drugs between the low- and high-CDI group. The green represents samples with high CDI and the orange represents samples with low CDI. \*\*\*\*, p < 0.0001.

***Supplementary Table Legends***

**Supplementary Table 1.** The introduction of 1515 genes related to each PCD pattern.

**Supplementary Table 2.** The gene set of the 28 immune cells used for the ssGSEA algorithm in immune infiltration.