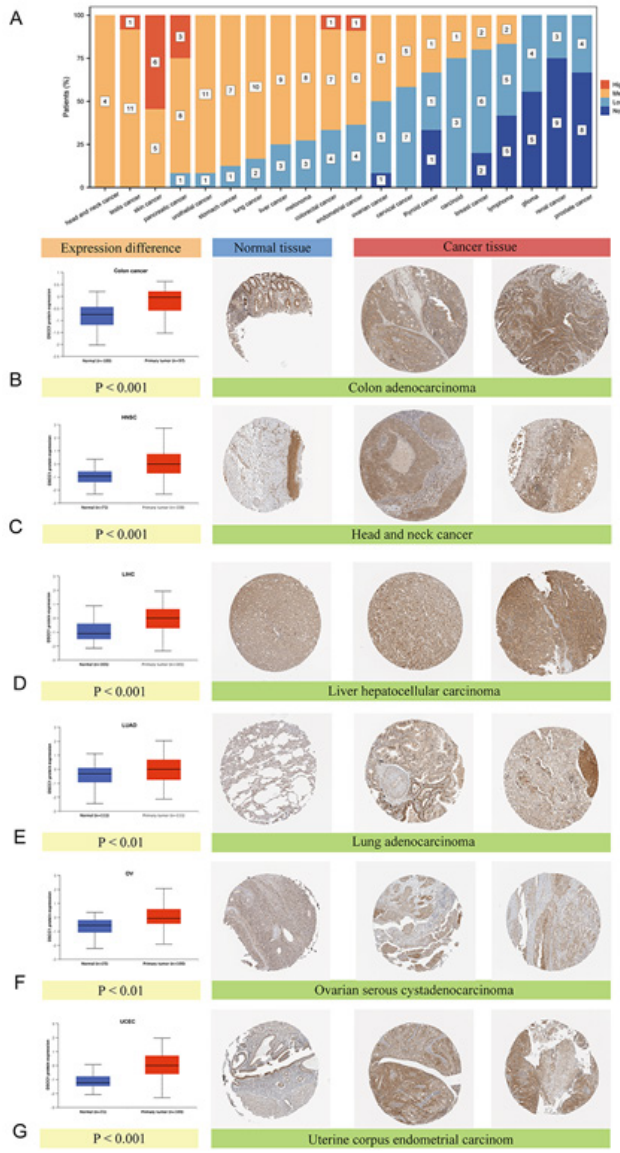

Fig. S1. Protein expression of DSCC1 in the pan-cancer analysis. (A) Percentage of patients with cancer who have different intensities of DSCC1 protein staining. Comparison of DSCC1 protein levels between normal (left) and tumor tissues (right) in COAD (B), HNSC (C), LIHC (D), LUAD (E), OV (F), and UCEC (G). Differences in DSCC1 protein expression between tumor and normal tissues quantified using data from the UALCAN database (yellow bars below). DSCC1, DNA replication and sister chromatid cohesion 1.

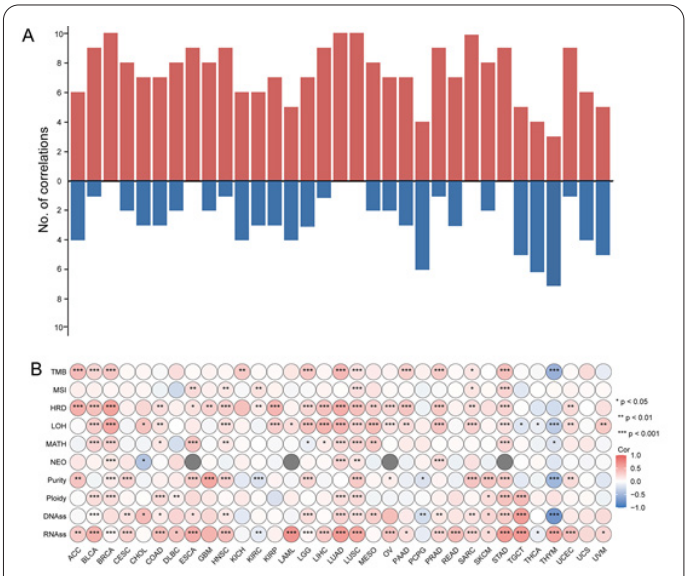

Fig. S2. Association between DSCC1 expression and genomic instability in the pan-cancer analysis. (A) Bar chart showing the number of positive and negative correlations in each tumor. (B) Heatmap showing in detail the correlations between DSCC1 and genomic instability indicators. The darker the color, the stronger the correlation. *P<0.05; **P<0.01; ***P<0.001. DNAss, DNA stemness; DSCC1, DNA replication and sister chromatid cohesion 1; HRD, homologous recombination deficiency; LOH, loss of heterozygosity; MATH, mutant-allele tumor heterogeneity; MSI, microsatellite instability; NEO, neoantigen; RNAss, RNA stemness; TMB, tumor mutational burden.

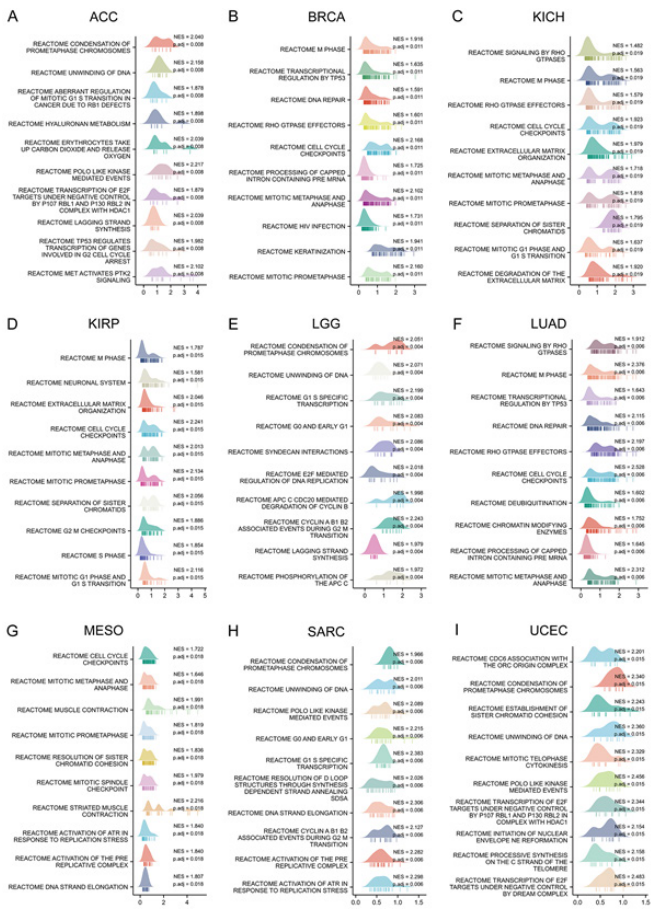

Fig. S3. GSEA functional enrichment analysis demonstrates significantly enriched pathways in the DSCC1 high-expression phenotype. The top 10 Reactome pathways of DSCC1 in ACC (A), BRCA (B), KICH (C), KIRP (D), LGG (E), LUAD (F), MESO (G), SARC (H), and UCEC (I) are displayed as ridge plots. The Y-axis denotes each gene set, and the X-axis denotes the distribution of logFC corresponding to the core molecules in each gene set. The small vertical lines under the ridge represent the core molecules. DSCC1, DNA replication and sister chromatid cohesion 1; GSEA, gene set enrichment analysis; NES, normalized enrichment score.

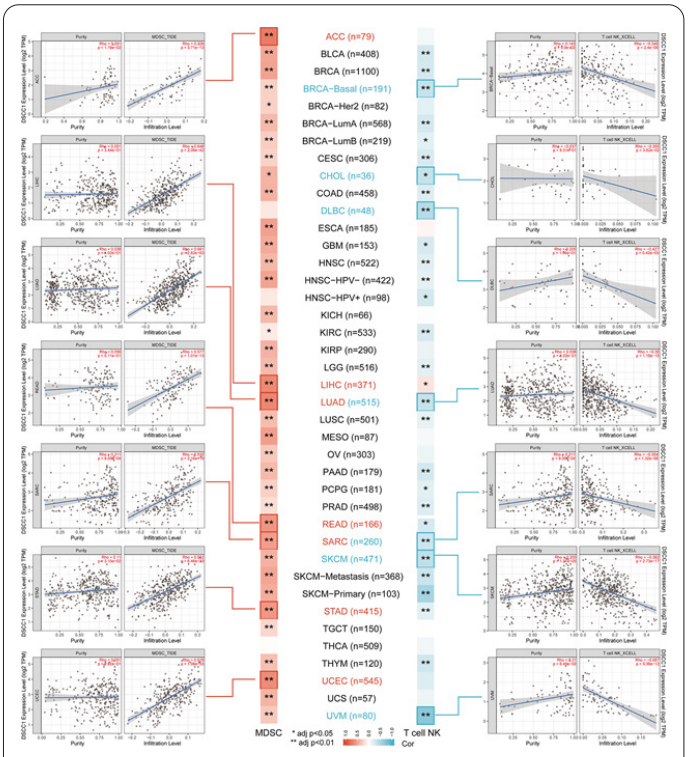

Fig. S4. The Spearman correlation between DSCC1 expression and the immune infiltration level of MDSC (left), and T-cell NK (right) in the pan-cancer analysis. The top seven cancer types in terms of correlation are shown as scattergrams of the results. *P<0.05; **P<0.01. Red represents a positive correlation. Blue represents a negative correlation. The darker the color, the stronger the correlation. DSCC1, DNA replication and sister chromatid cohesion 1; MDSC, myeloid-derived suppressor cell; NK, natural killer.

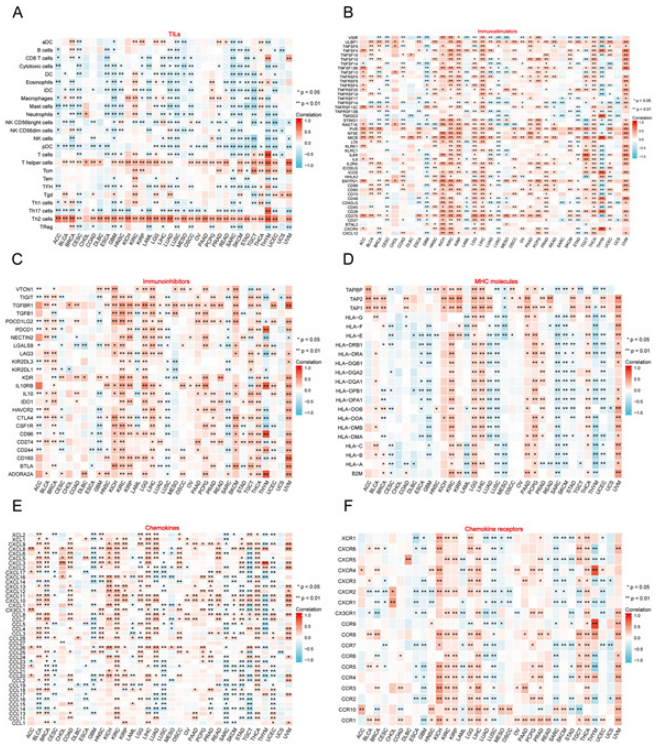

Fig. S5. Relationship of DSCC1 with TILs and immunoregulatory genes in the pan-cancer analysis. DSCC1 expression significantly correlates with TILs (A), immunostimulators (B), immunoinhibitors (C), MHC molecules (D), chemokines (E), and chemokine receptors (F) in most cancers. Color shade is associated with the strength of the correlation. *P<0.05; **P<0.01. aDC, activated dendritic cell; DSCC1, DNA replication and sister chromatid cohesion 1; iDC, immature dendritic cell; MHC, major histocompatibility complex; pDC, plasmacytoid dendritic cell; Tcm, central memory T cell; Tem, effector memory T cell; TFH, T follicular helper cell; Tgd, T gamma delta; TIL, tumor-infiltrating lymphocyte; Treg, regulatory T cell.

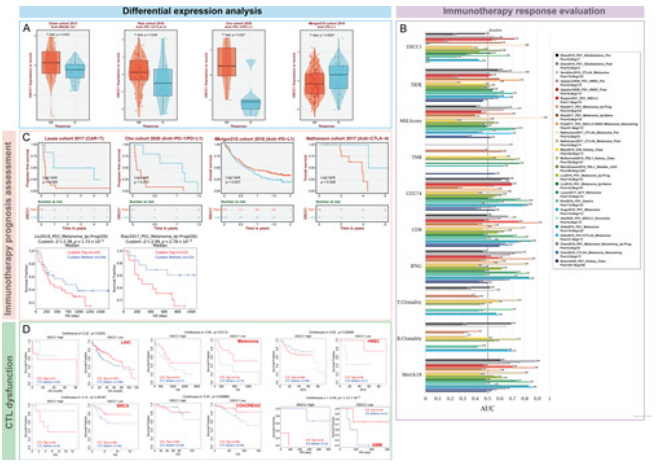

Fig. S6. Assessing the value of DSCC1 in immunotherapy. (A) DSCC1 is differentially expressed in the immunotherapy-responsive (R) and immunotherapy-nonresponsive (NR) groups. (B) Comparison of DSCC1 with other existing biomarkers in predicting ICB treatment efficacy. (C) DSCC1 influences the prognosis of patients receiving ICB treatment. (D) Relationship between DSCC1 expression and CTL dysfunction in six types of cancer. CTL. Cytotoxic T lymphocyte; DSCC1, DNA replication and sister chromatid cohesion 1; ICB, immune checkpoint blockade.

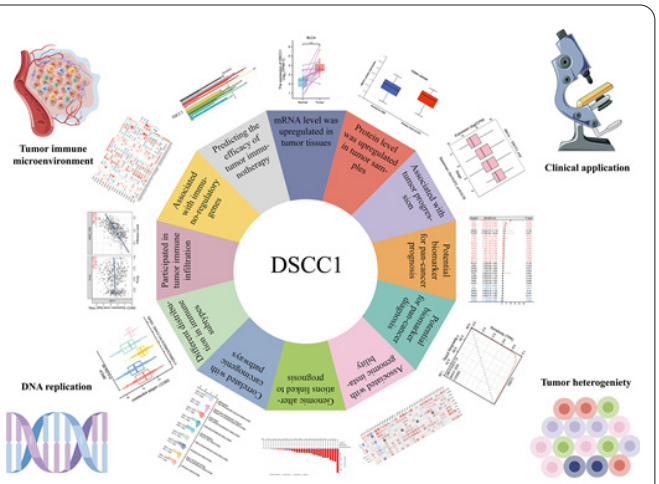

Fig. S7. A summary of the main findings of this work.