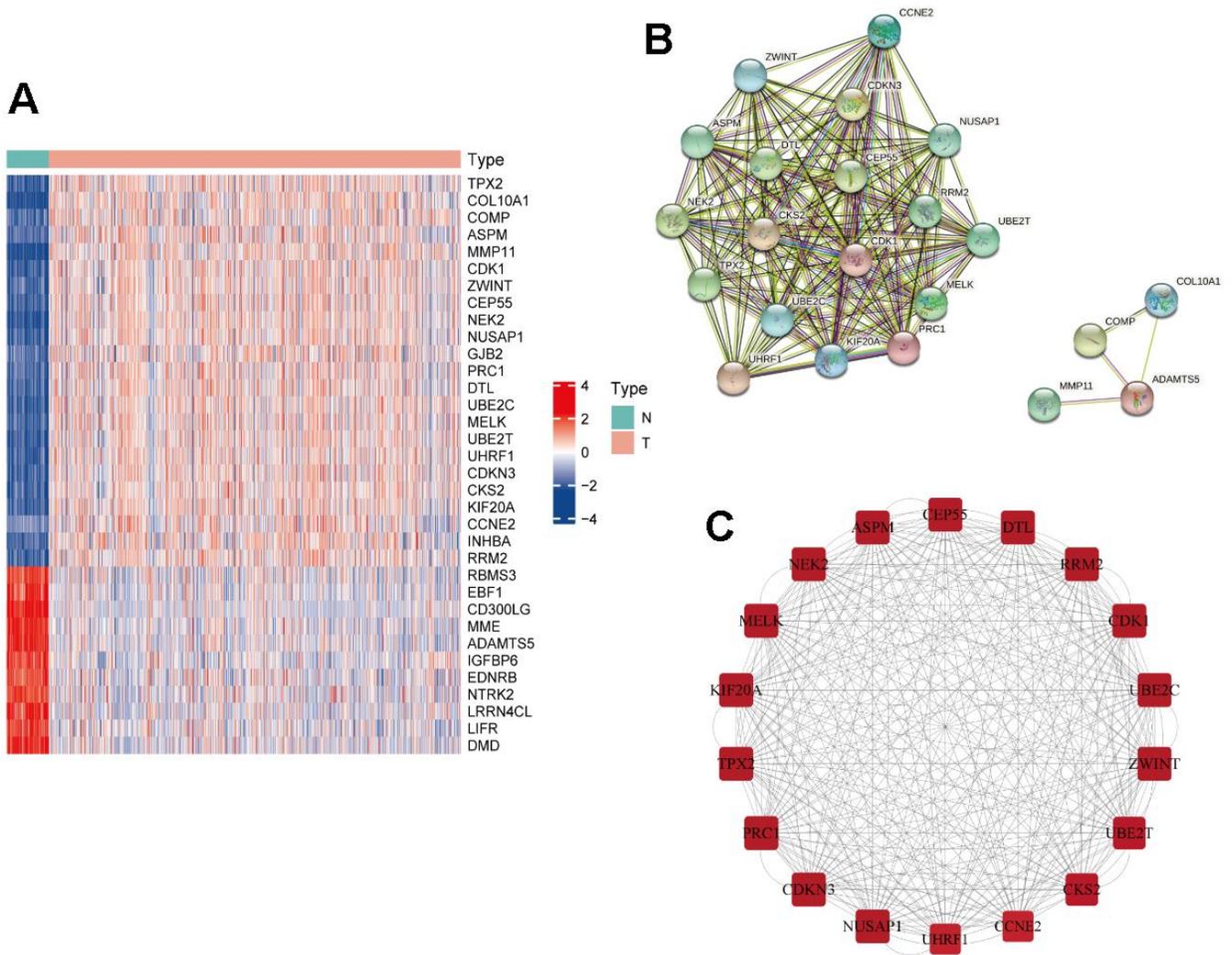
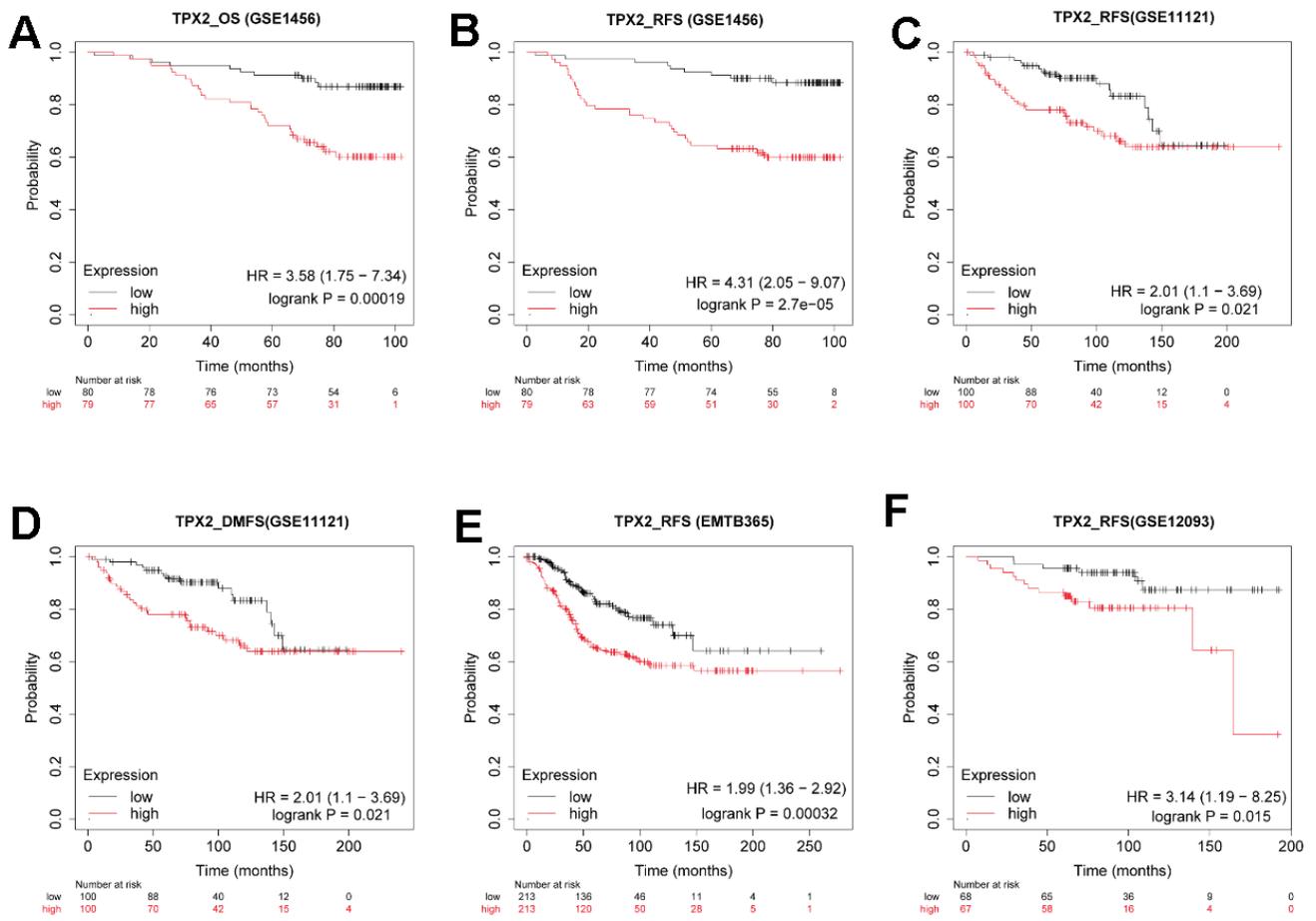


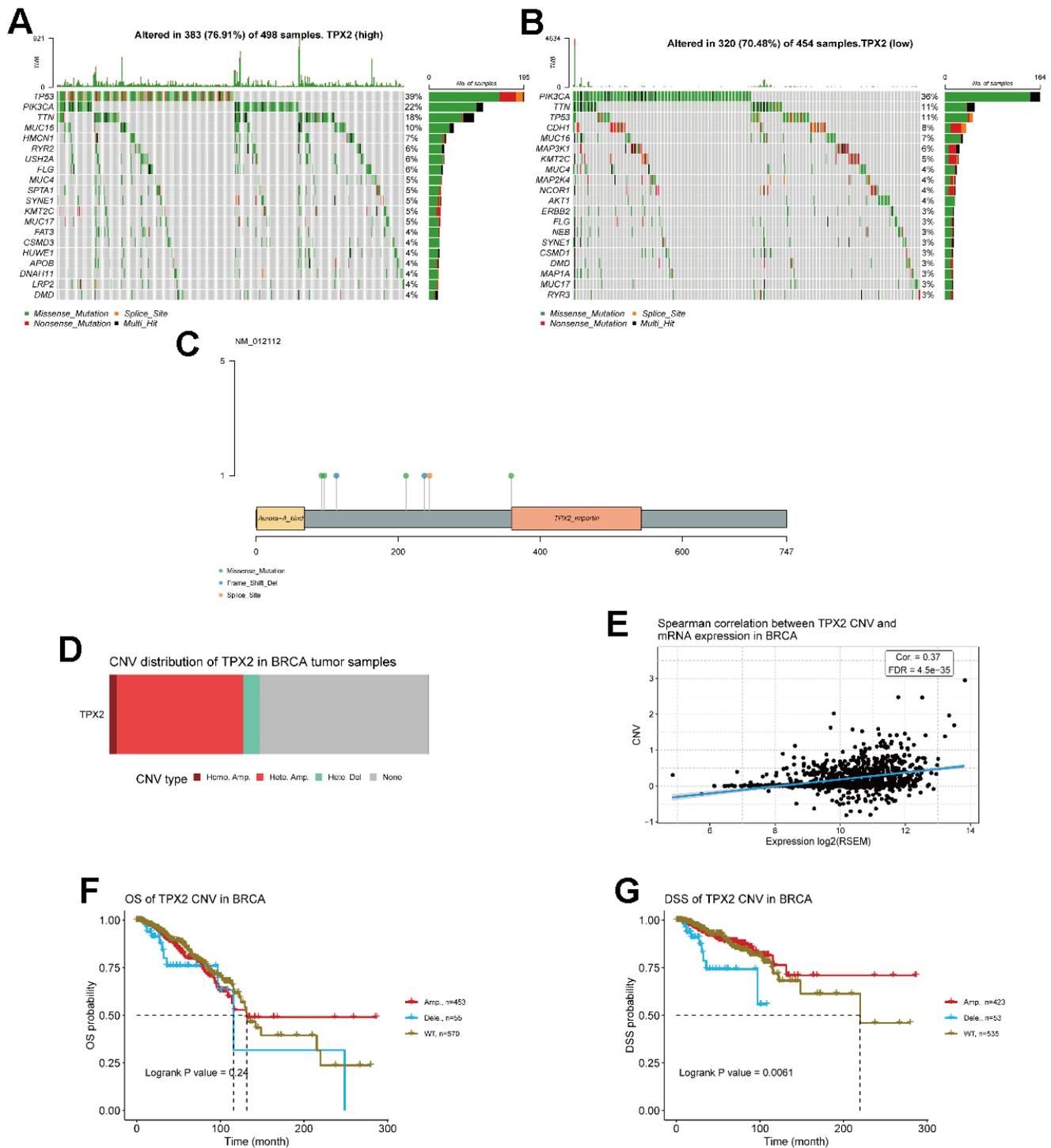
SUPPLEMENTARY FIGURES



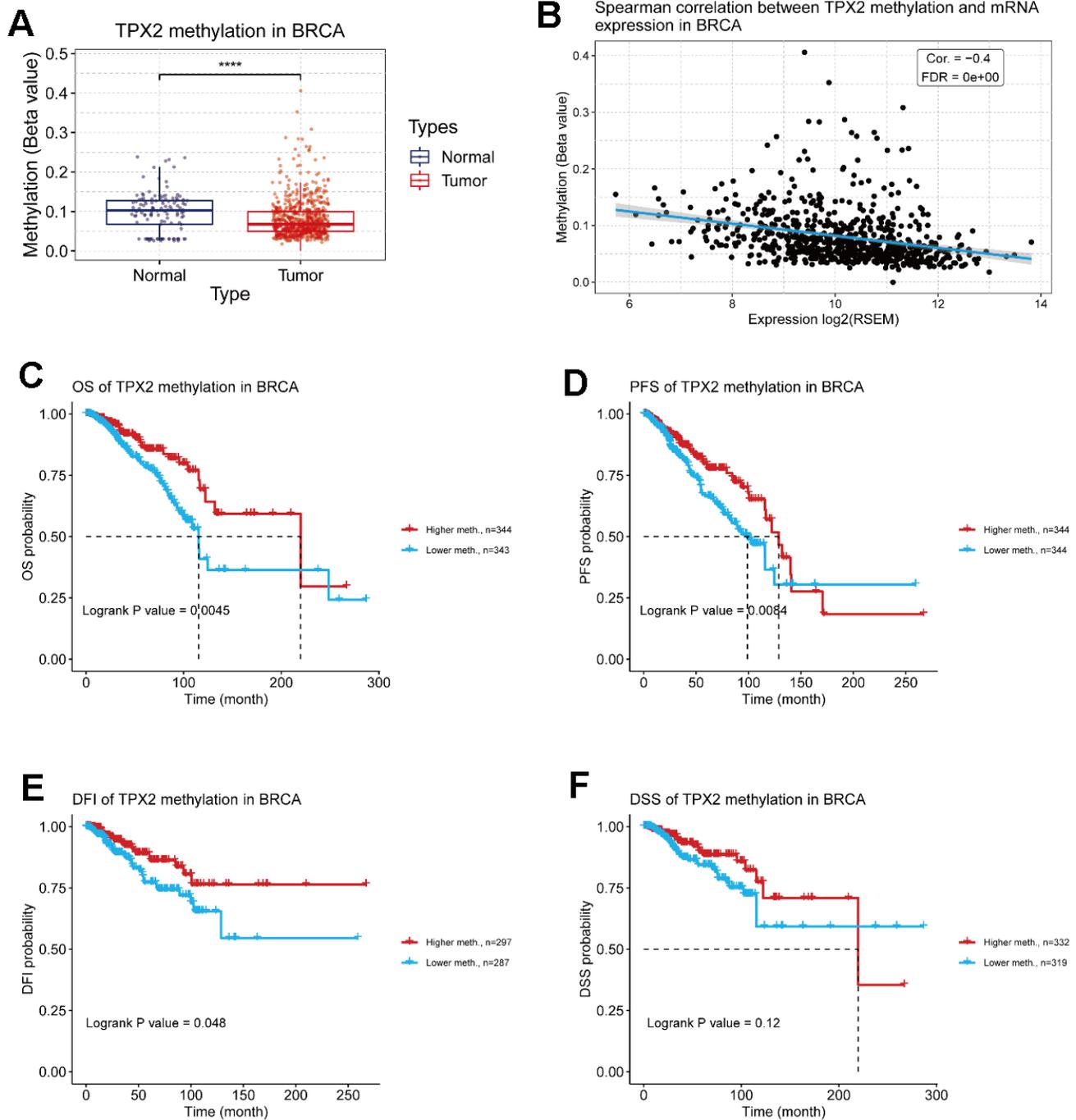
Supplementary Figure 1. PPI network construction and module analysis. (A) The heatmap illustrating the expression landscape of these DEGs in tumor and normal samples. (B) PPI network of these 34 DEGs. Nodes that were not associated with other nodes were hidden. (C) Extraction crucial module by MCODE plugin. Red dots represent interaction genes with a level of high degree.



Supplementary Figure 2. The survival analysis of TPX2 with overall survival (OS), recurrence free survival (RFS), distant Metastasis Free Survival (DMFS) indicators respectively through various datasets (A–F). P < 0.05 was considered significant.

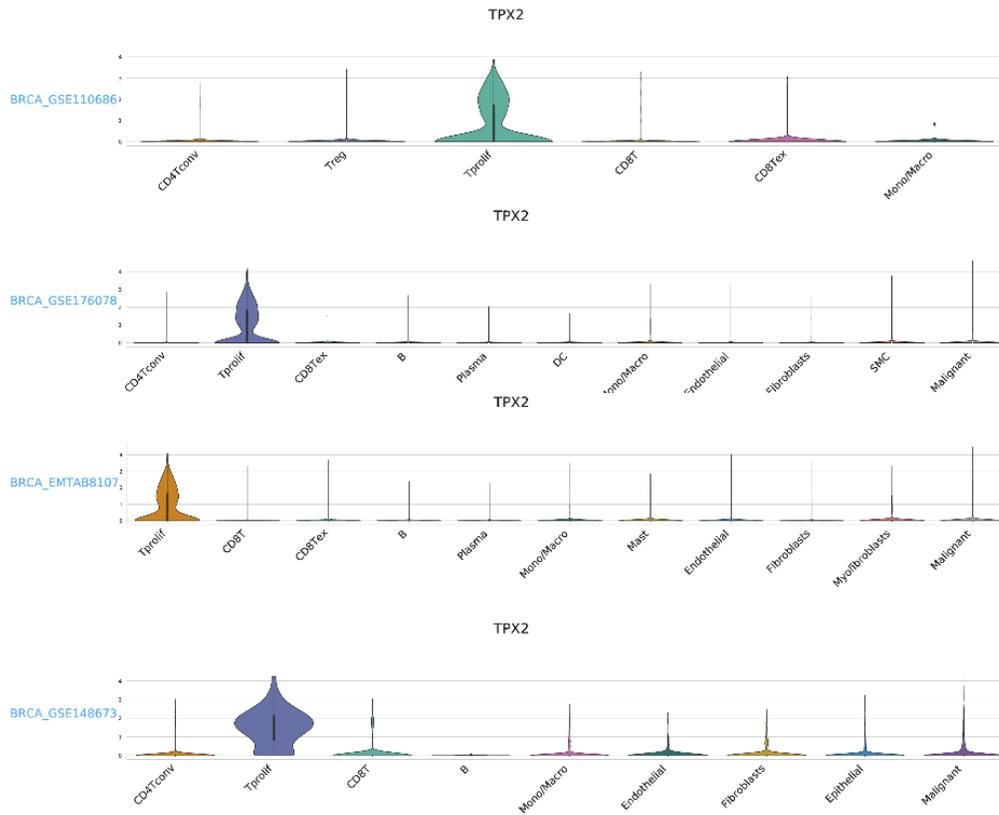


Supplementary Figure 3. The mutation landscape of TPX2 in TCGA-BRCA dataset. (A, B) The differential mutation genes in high TPX2 expression samples (n=498) and low TPX2 expression samples (n=454). (C) The mutation sites of TPX2 gene, different dots represent various mutation form. Green represents missense mutation, blue represents frame shift del, orange represents splice site. (D) The CNV distribution of TPX2 in BRCA tumor samples. (E) The correlation between TPX2 CNV and mRNA expression in BRCA. (F, G) The survival analysis of TPX2 CNV with overall survival (OS) and disease specific survival (DSS) indicators via TCGA-BRCA dataset. P<0.05 was considered significant.

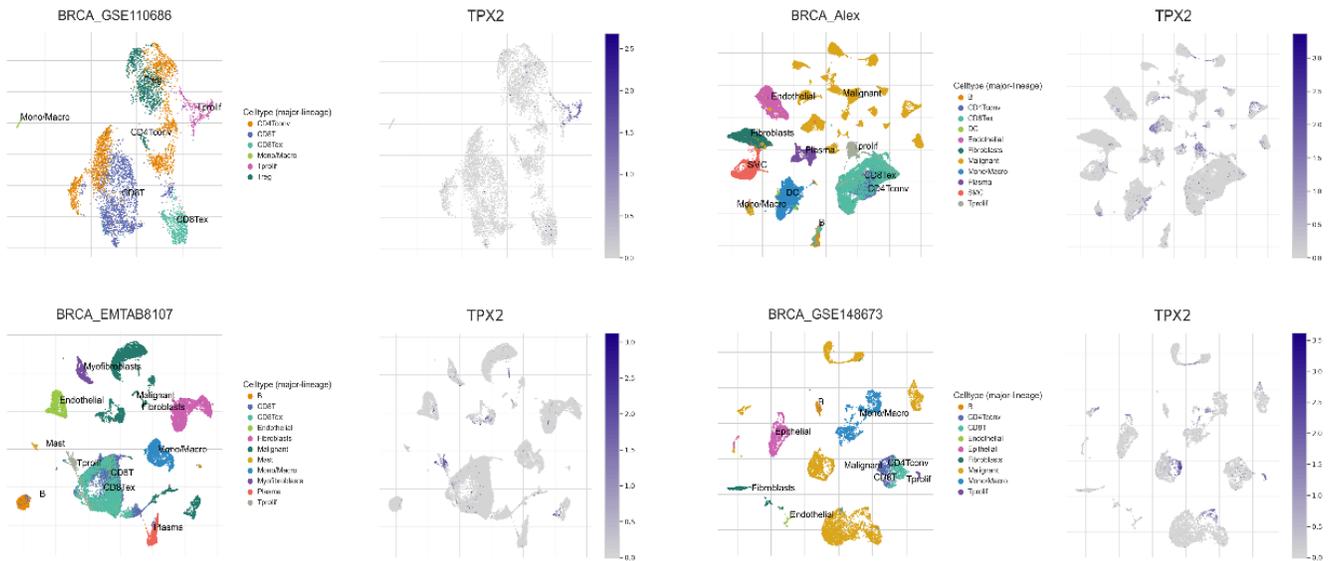


Supplementary Figure 4. The methylation level of TPX2 in TCGA-BRCA dataset and its relationship with prognosis. (A) The methylation of TPX2 in BRCA dataset. **(B)** The correlation between TPX2 methylation and mRNA expression. **(C–F)** The survival analysis of TPX2 methylation with overall survival (OS), progression free survival (PFS), disease free interval (DFI), disease specific survival (DSS) indicators, respectively. $P < 0.05$ was considered significant.

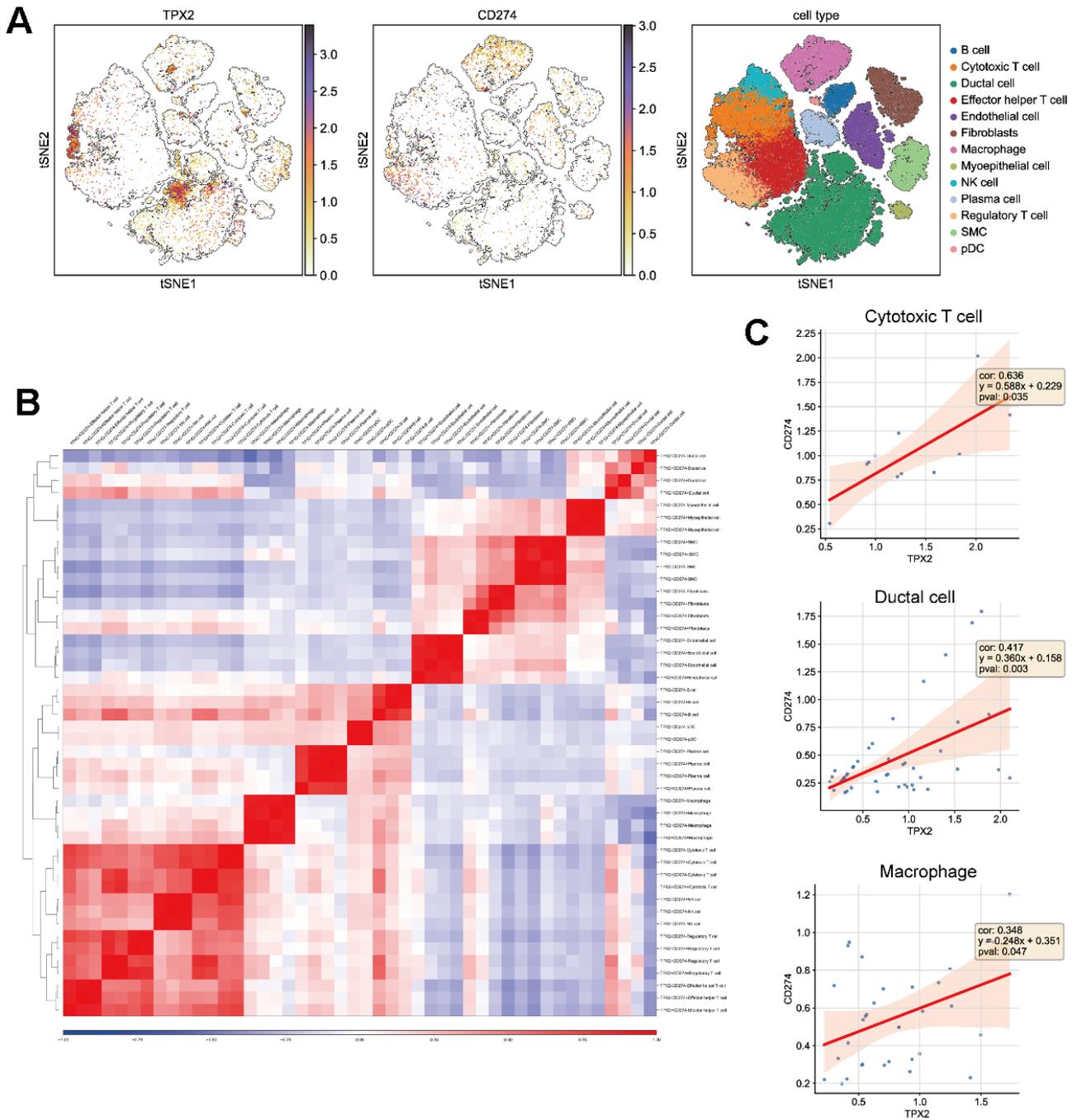
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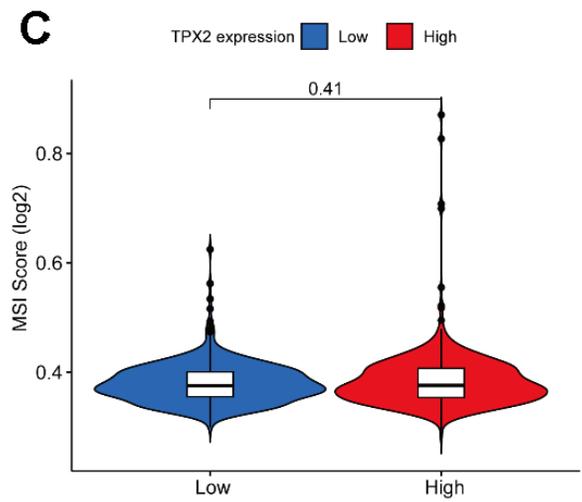
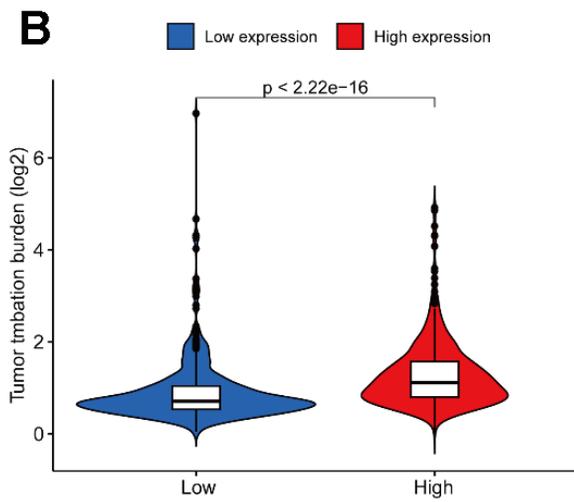
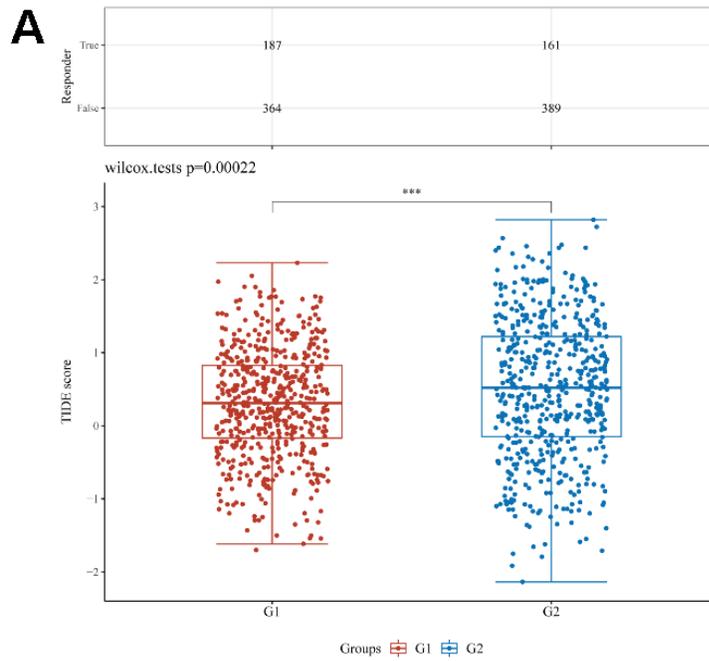
B



Supplementary Figure 5. The distribution of TPX2 expression in different cell types from the four GEO datasets. (A) The Violin plot illustrating the association between TPX2 expression and various cell types in each GEO dataset. **(B)** The t-SNE plot showing the cell types identified in BRCA with different colors, and performing the distribution of TPX2 in these cells.



Supplementary Figure 6. (A) The t-SNE plot showing the cell types identified in BRCA with different colors, and performing the distribution of TPX2 and CD274 in these cells through GSE176078 single cell dataset. (B) The heatmap illustrating the association between TPX2 and CD274 in different cells. (C) The correlation analysis between TPX2 and CD274 in cytotoxic T cell, ductal cell and macrophage cell.



Supplementary Figure 7. (A) The relationship between TPX2 expression and immune response and TIDE score. G1: TPX2-high, G2: TPX2-low. (B, C) The correlation analysis between TPX2 expression and TMB and MSI.