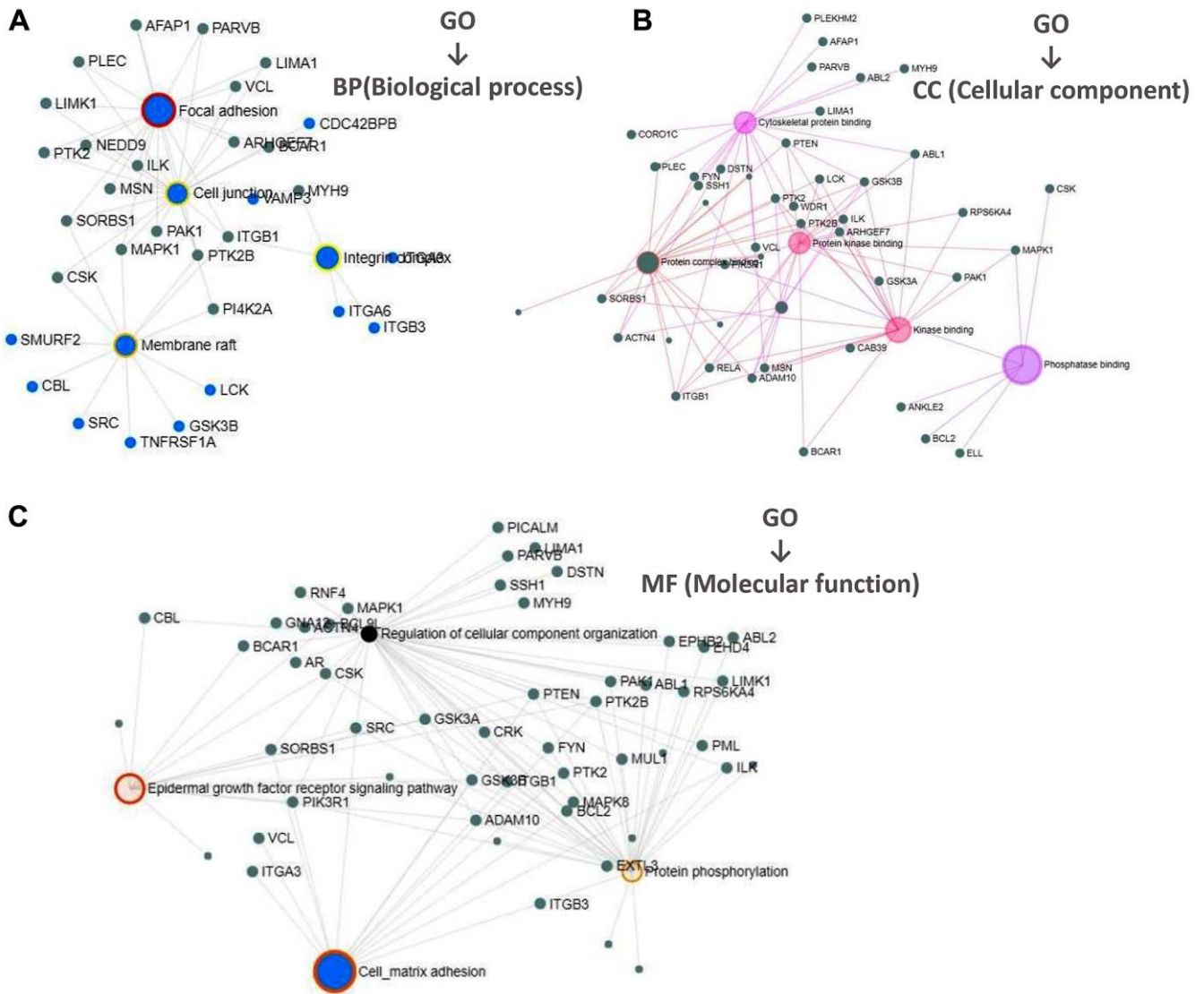


SUPPLEMENTARY FIGURES

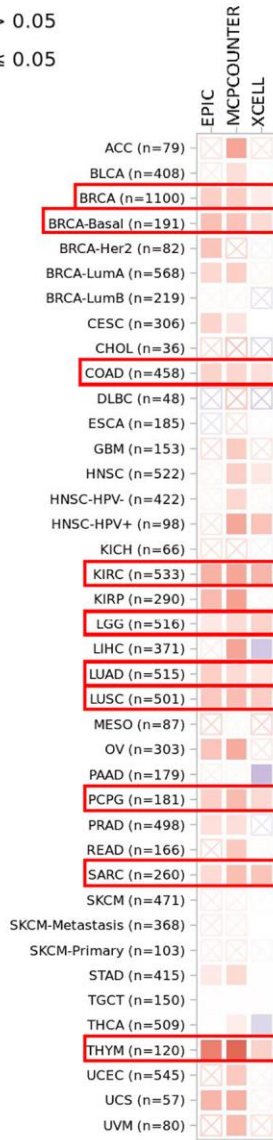
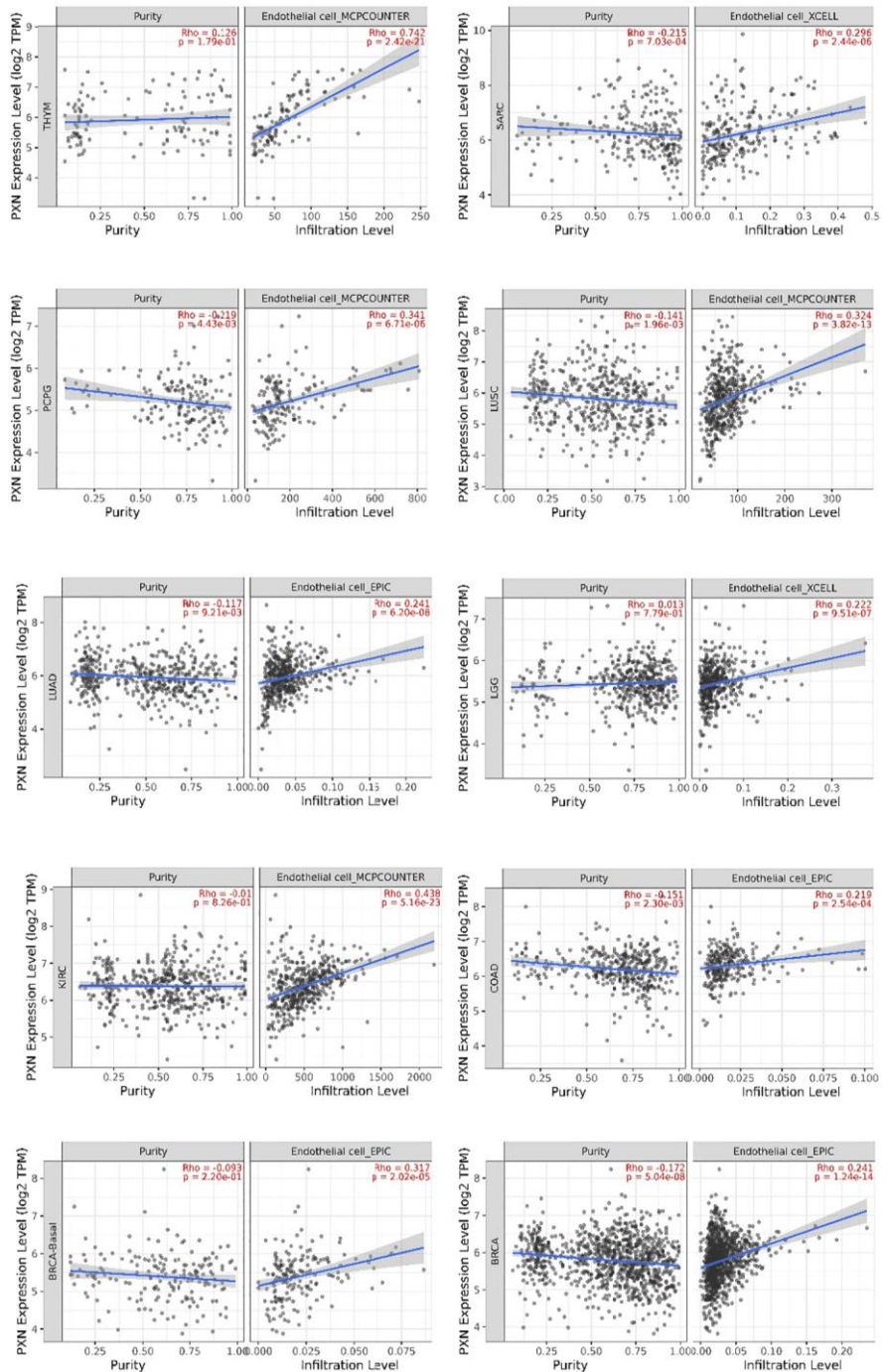


Supplementary Figure 1. Gene Ontology (GO) biological process/cellular component analysis of *PXN*-related genes in tumors. The “cnetplots” models from GO enrichment analysis for (A) the biological process, (B) the cellular component, and (C) the molecular function data are shown.

A

☒ $p > 0.05$
 ■ $p \leq 0.05$

Partial
 1
 0
 -1

Endothelial cells**B**

Supplementary Figure 2. Correlation analysis between *PXN* gene expression and immune infiltration of endothelial cells. Different algorithms explored potential correlations of (A) the expression level of the *PXN* gene and (B) the infiltration level of endothelial cells across all types of cancer in The Cancer Genome Atlas.