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.
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.