Figure S1. The immunohistochemical staining shows the peroxisomal biogenesis factor 13 protein expression between tumor tissues and normal tissues in some tumors.
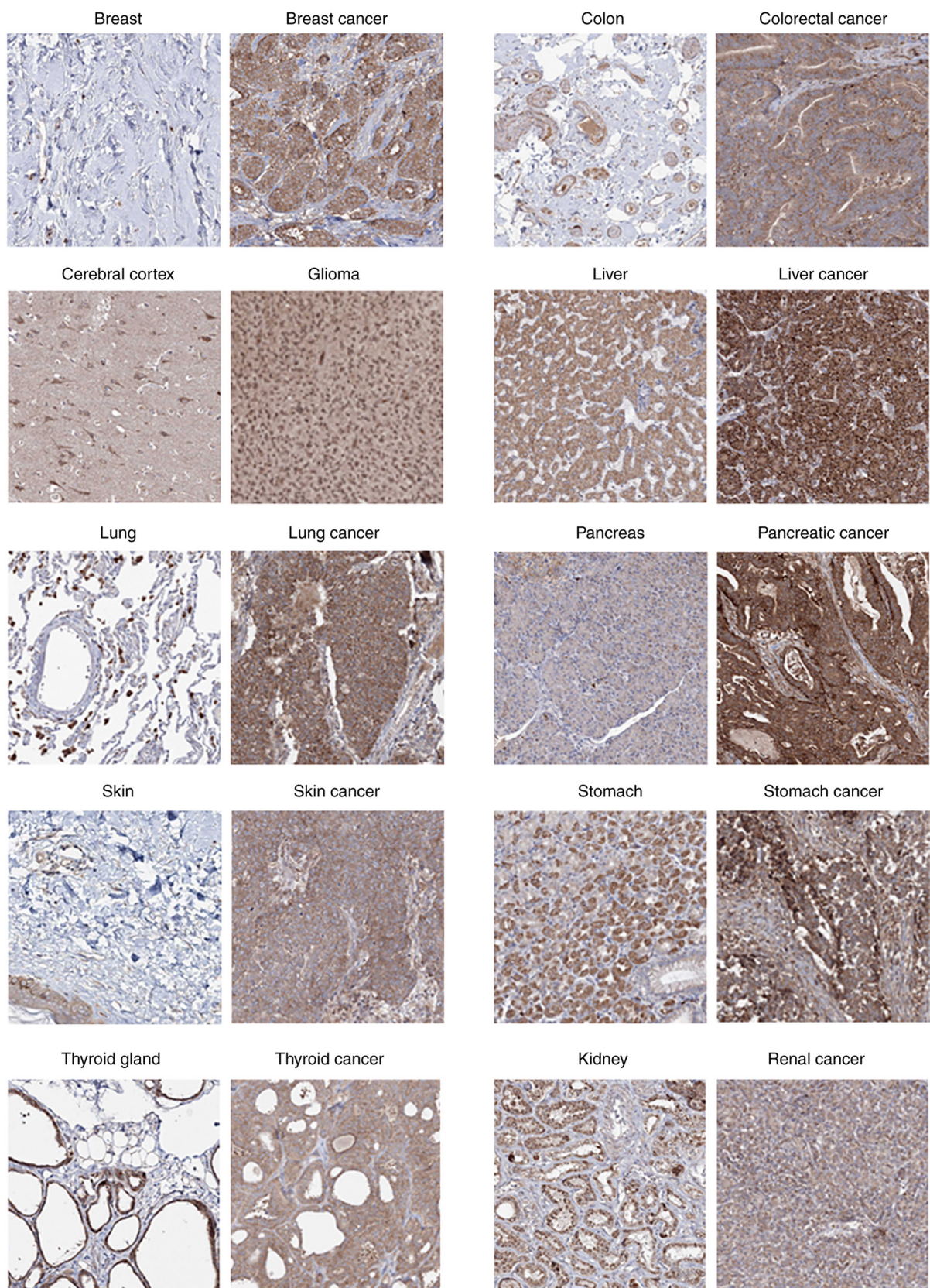
Figure S2. Cox analysis of PEX13 in pan-cancers. The relationships between PEX13 expression level and (A) disease-free interval, (B) progression-free interval and (C) disease-specific survival. DFI, disease-free interval; PFI, progression-free interval; DSS, disease-specific survival.
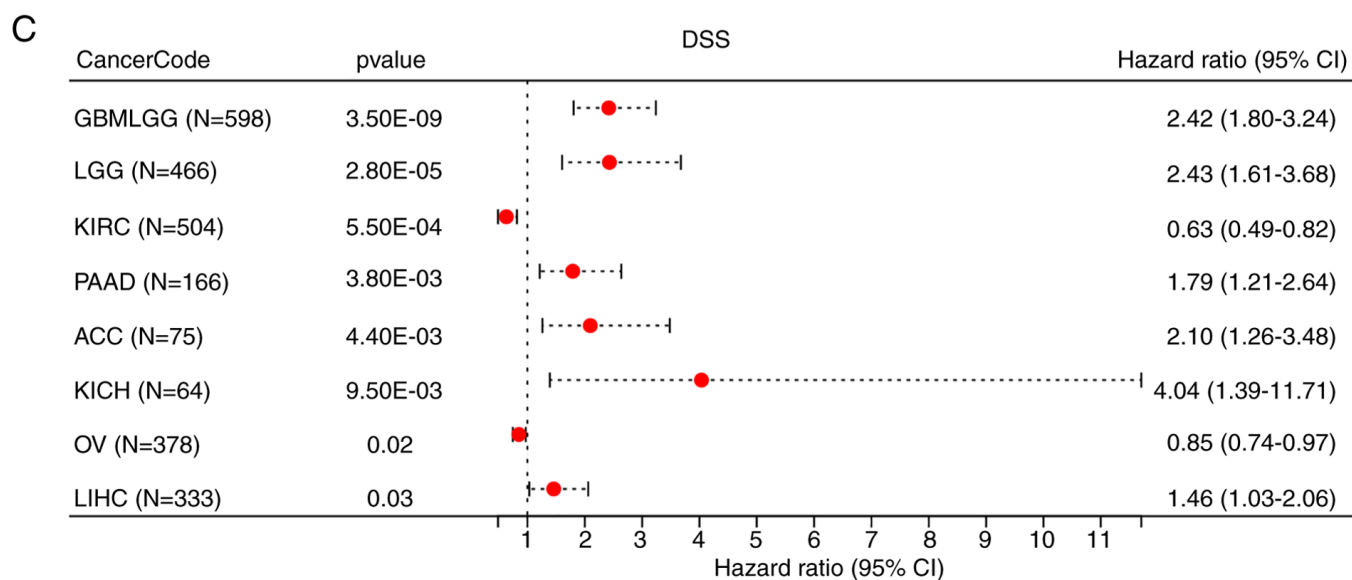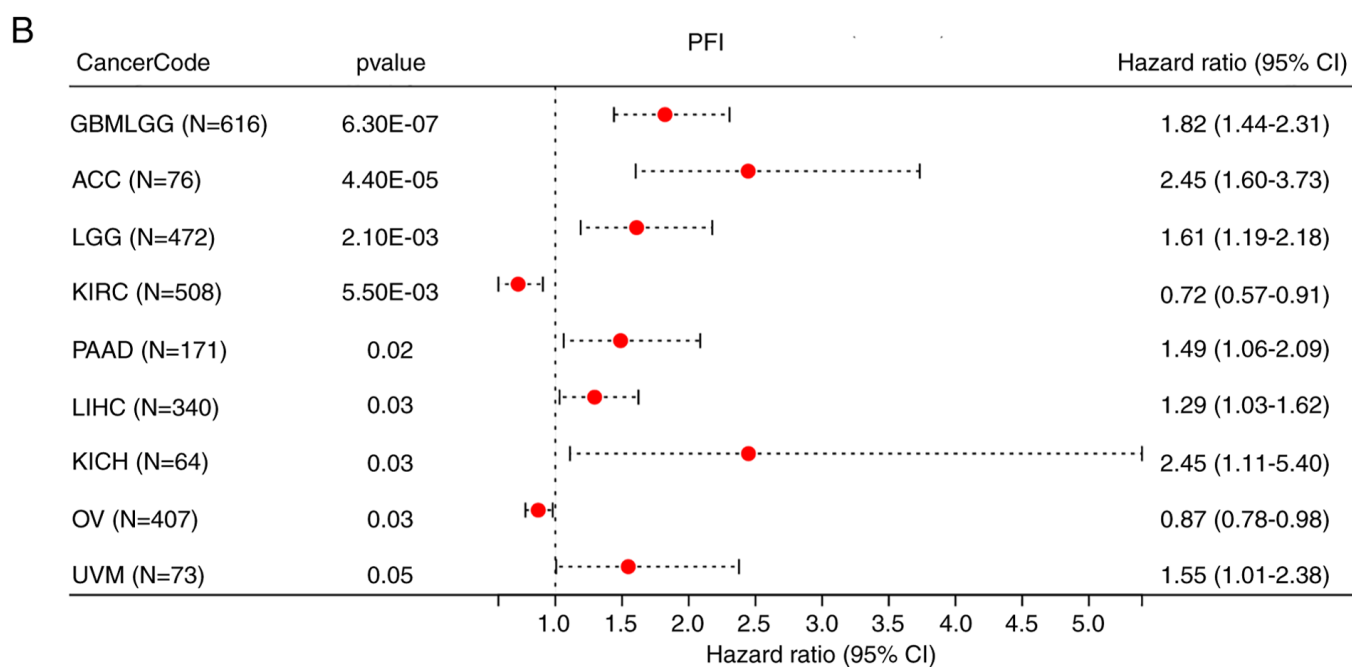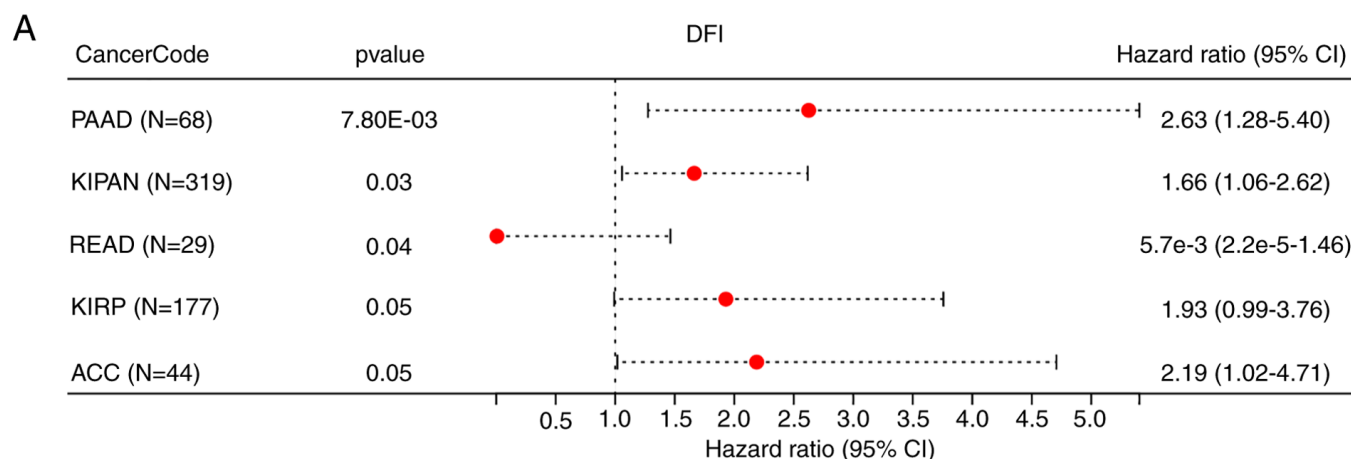
Figure S3. Enrichment analysis of PEX13-related genes in PAAD. (A) Correlation heat map displayed the top 50 PEX13 positively related genes and top 50 PEX13 negatively related genes in PAAD via the LinkedOmics portal. The Gene Ontology-Biological Process analyses of the top (B) 50 PEX13 positively and (C) top 50 PEX13 negatively related genes in PAAD. The (D) KEGG enrichment analyses of the top 50 PEX13 positively related genes and (E) top 50 PEX13 negatively related genes in PAAD. PEX, peroxisomal biogenesis factor; PAAD, pancreatic adenocarcinoma.
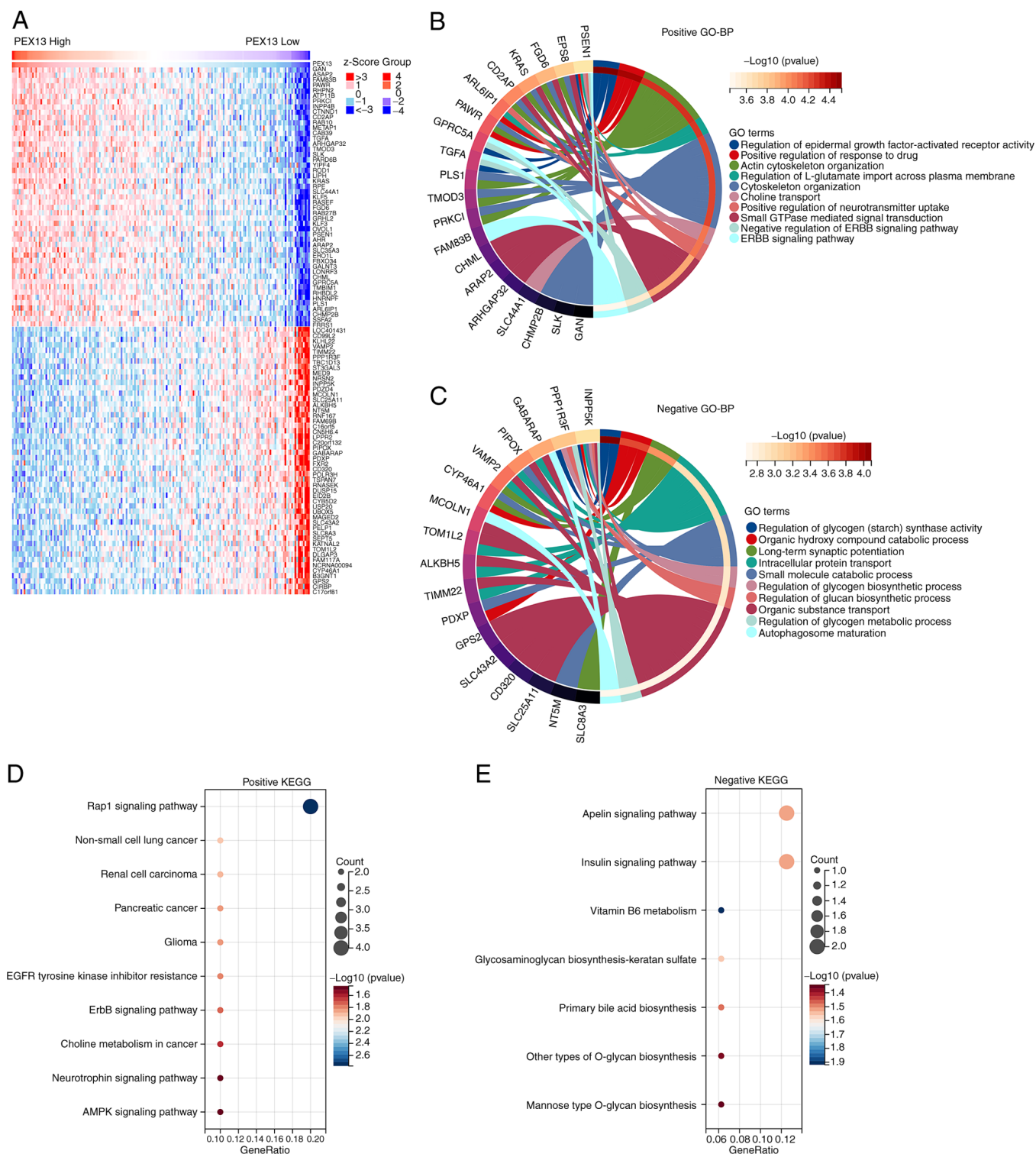
Figure S4. Correlations between PEX13 expression and immune cell infiltration in pan-cancers. (A) Correlations between PEX13 expression and the infiltration level of B cells in various tumors through different algorithms. (B) The correlations between PEX13 expression and tumor purity and the infiltration level of B cells in PAAD via different algorithms. (C) The correlation heat map showed the correlations between PEX13 expression and the infiltration level of macrophages in multiple tumors by different algorithms. (D) The relationships between PEX13 expression level and tumor purity and the infiltration level of macrophages in PAAD via diverse algorithms. PEX, peroxisomal biogenesis factor; UVM, uveal melanoma; UCS, uterine carcinosarcoma; UCEC, uterine corpus endometrial carcinoma; TGCT, testicular germ cell tumors; THCA, thyroid carcinoma; THYM, thymoma; STAD, stomach adenocarcinoma; SKCM, skin cutaneous melanoma; SARC, sarcoma; READ, rectum adenocarcinoma; PRAD, prostate adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PAAD, pancreatic adenocarcinoma; OV, ovarian serous cystadenocarcinoma; MESO, mesothelioma; LUSC, lung squamous cell carcinoma; LUAD, lung adenocarcinoma; LIHC, liver hepatocellular carcinoma; LGG, brain lower grade glioma; KIRC, kidney renal clear cell carcinoma; KICH, kidney chromophobe; HNSC, head and neck cancer; HPV, human papillomavirus; GBM, glioblastoma multiforme; ESCA, esophageal carcinoma; DLBC, lymphoid neoplasm diffuse large b-cell lymphoma; COAD, colon adenocarcinoma; CHOL, cholangiocarcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; BRCA, breast invasive carcinoma; BLCA, bladder urothelial carcinoma; ACC, adrenocortical carcinoma.
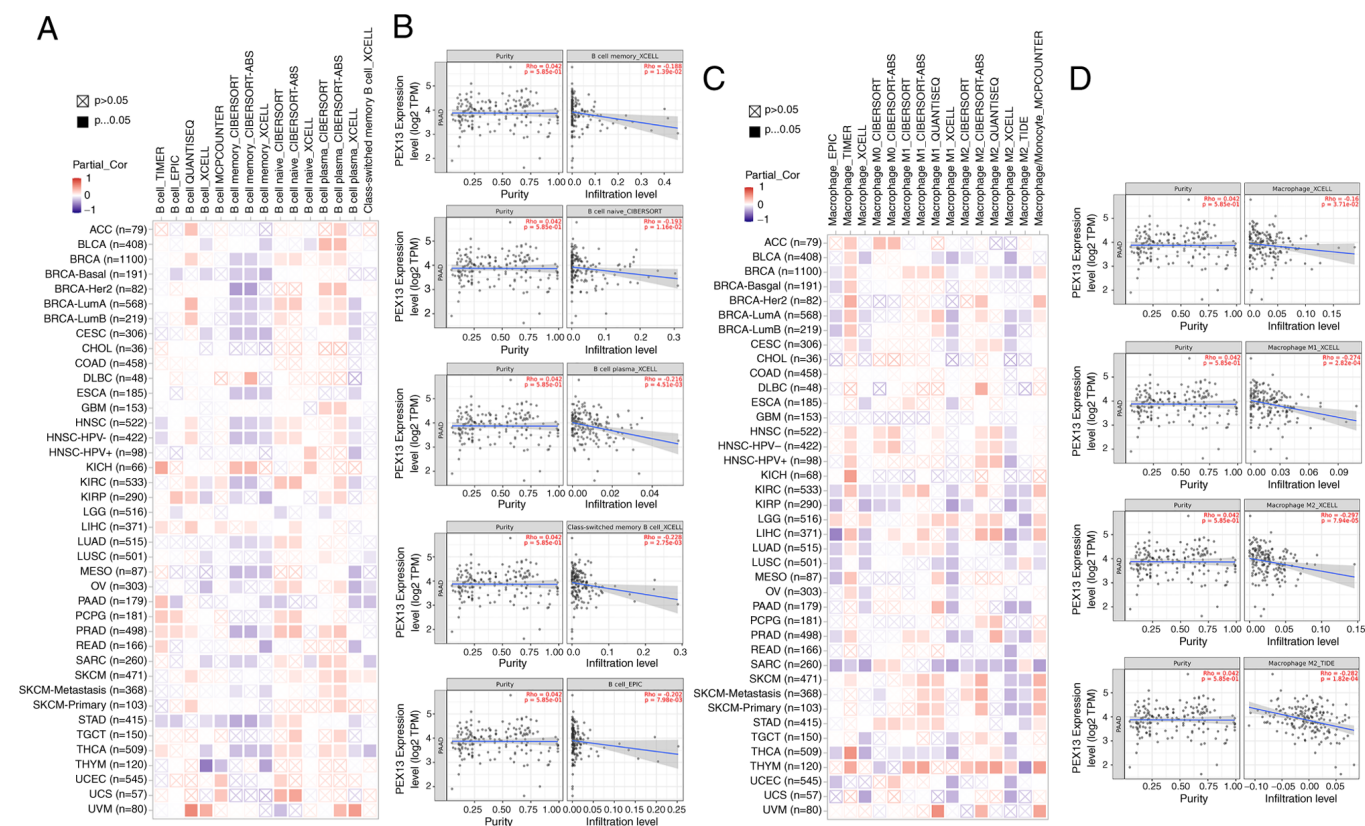
Figure S5. Correlations between PEX13 expression and ESTIMATE score in some tumors. Association between PEX13 expression and (A) ImmuneScore, (B) StromalScore and (C) ESTIMATEScore in lung adenocarcinoma, STES, sarcoma and lung squamous cell carcinoma. LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; SARC, sarcoma; STES, stomach and esophageal carcinoma.