Figure S1 – *ANTXR1/TEM8* is overexpressed in PDAC

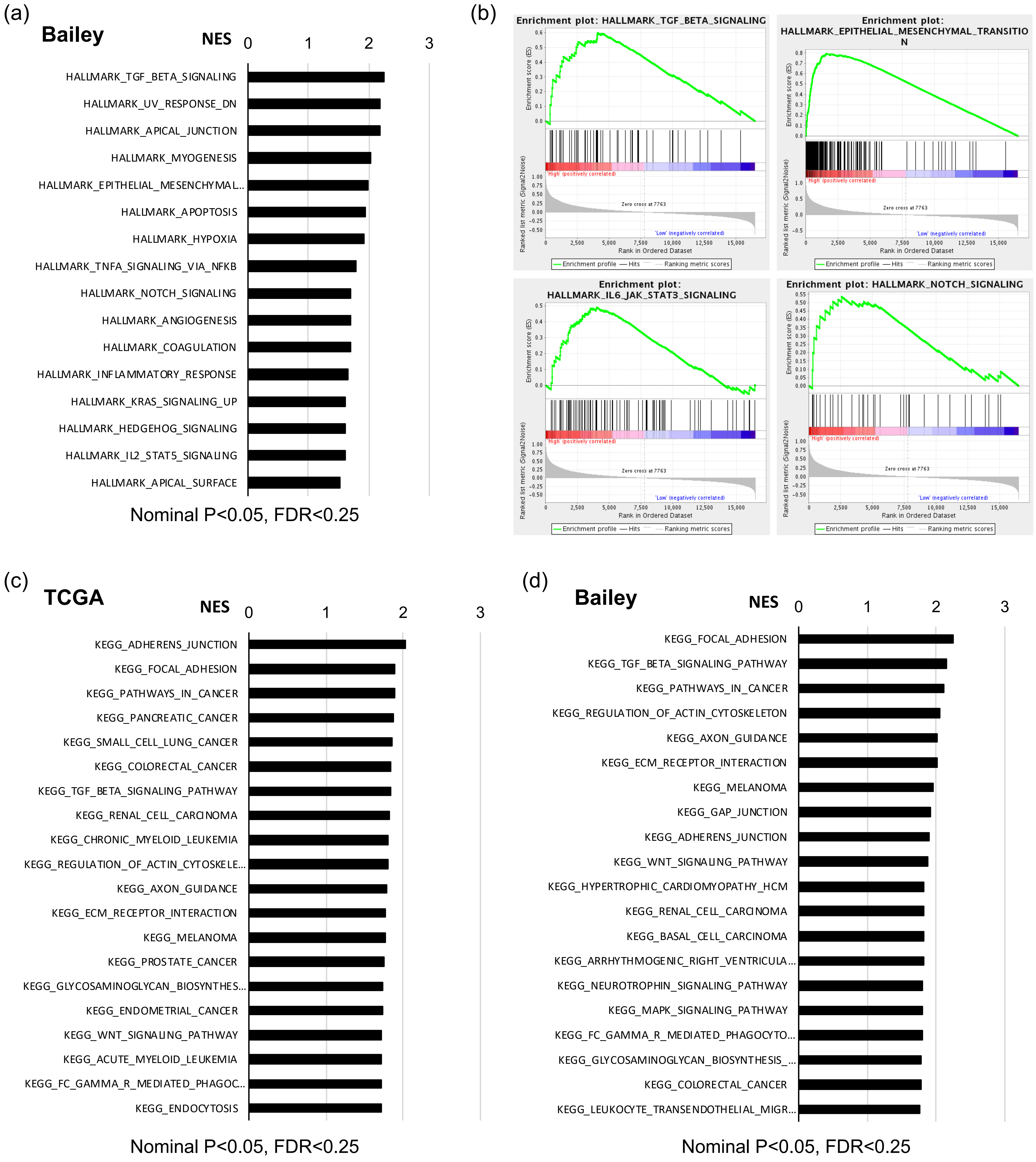

Figure S1. *ANTXR1/TEM8* is overexpressed in PDAC. (a-b) Genesets enriched in the transcriptional profiles of tumors belonging to the top *ANTXR1* high expression group, compared with the bottom expression group in the Bailey *et al.* dataset. A nominal p value of <0.05, FDR<25% is considered statistically significant. Shown are the NES values for each pathway using the Hallmark genesets (a) and example enrichment plots for TGF-beta, EMT, Notch, and IL-6/JAK6/STAT3 signaling (b). (c-d) Kegg genesets enriched in the transcriptional profiles of tumors belonging to the top *ANTXR1* high expression group, compared with the bottom expression group in the (c) TCGA and (d) Bailey *et al.* datasets. A nominal p value of <0.05, FDR<25% is considered statistically significant. Shown are the NES values for each pathway.