Figure S5

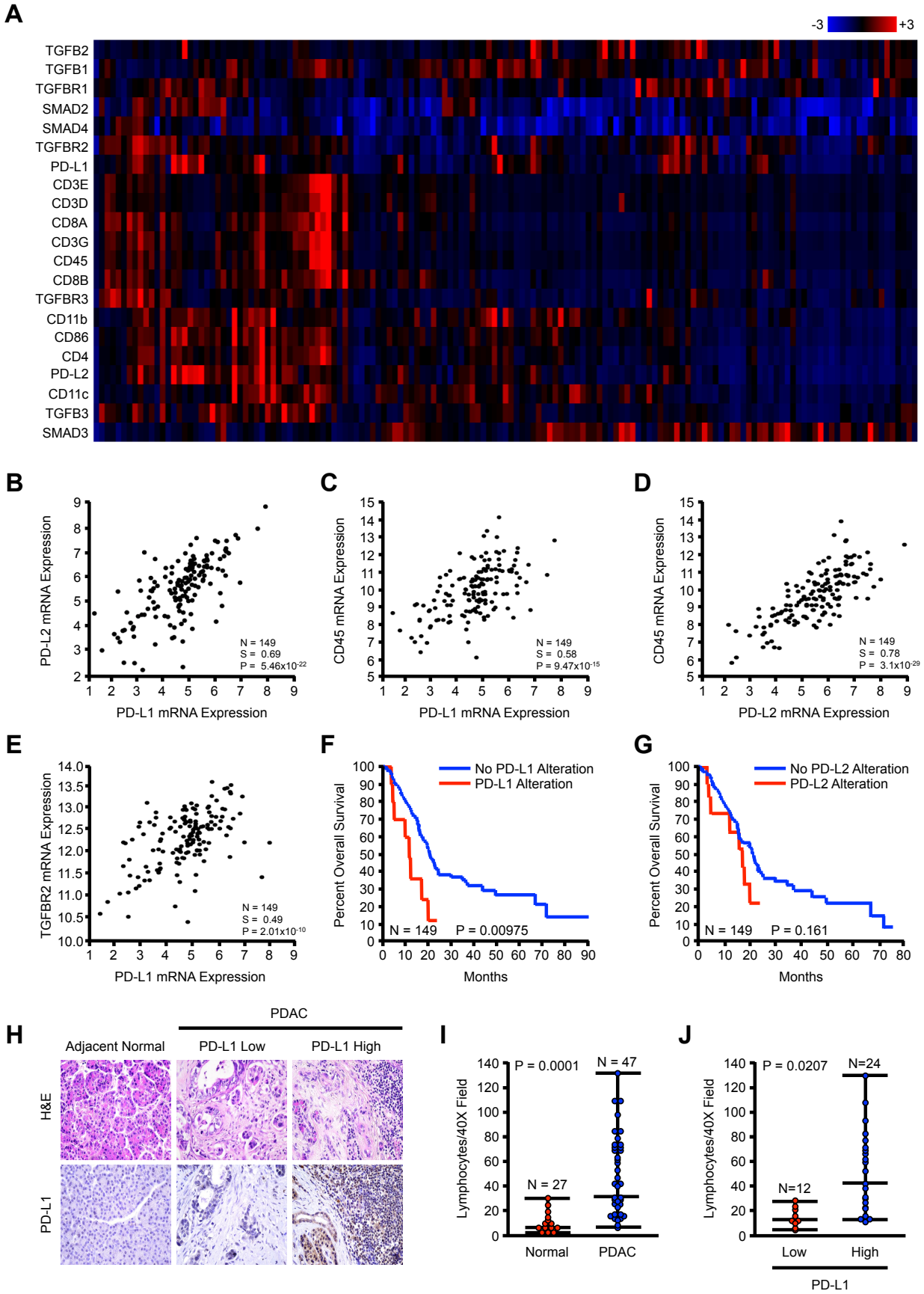

Figure S5. PD-L1/PD-L2 expression is associated with increased immune and TGFβ gene signatures.
(A) Representative heatmap of mRNA expression in the TCGA genomic databases of pancreatic cancer patients (N=186) for expression of PD-L1 (*CD247*), PD-L2 (*PCDCLG2*), genes associated with the TGFβ signaling pathway, and several leukocyte specific genes including CD3D, CD3E, CD3G, CD4, CD8A, CD8E, and CD45. The relationship between mRNA expression of individual genes was plotted evaluating **(B)** PD-L1 (*CD247*) and PD-L2 (*PCDCLG2*) **(C)** PD-L1 (*CD247*) and CD45 **(D)** PD-L2 (*PCDCLG2*) and CD45 **(E)** and PD-L2 (*PCDCLG2*) and TGFBR2. S = Spearman correlation coefficient. **(F,G)** Kaplan-Meier curve indicating the survival of patients with genomic alteration (i.e. amplification) to PD-L1 (*CD247*) or PD-L2 (*PCDCLG2*). **(H)** Excisional biopsies of both adjacent normal (N=27) and PDAC (N=47) tissue sections were stained with H&E or via immunohistochemistry for PD-L1. **(I)** Lymphocytes per 40X field were quantified by two investigators, or stained, and results displayed above. Horizontal lines represent high, low, and median values. **(J)** PD-L1 expression was assessed by two investigators, both of whom assigned a score of 0 (no expression), 1+ (uniform dim expression or focal areas of moderate expression), 2+ (uniform moderate expression or focal areas of strong expression), or 3+ (uniform strong expression). Patients were then stratified into either low (0 or 1+ staining) or high (2+ or 3+ staining) expression groups, and the number of tumor-infiltrating lymphocytes displayed above. Horizontal lines represent high, low, and median values.