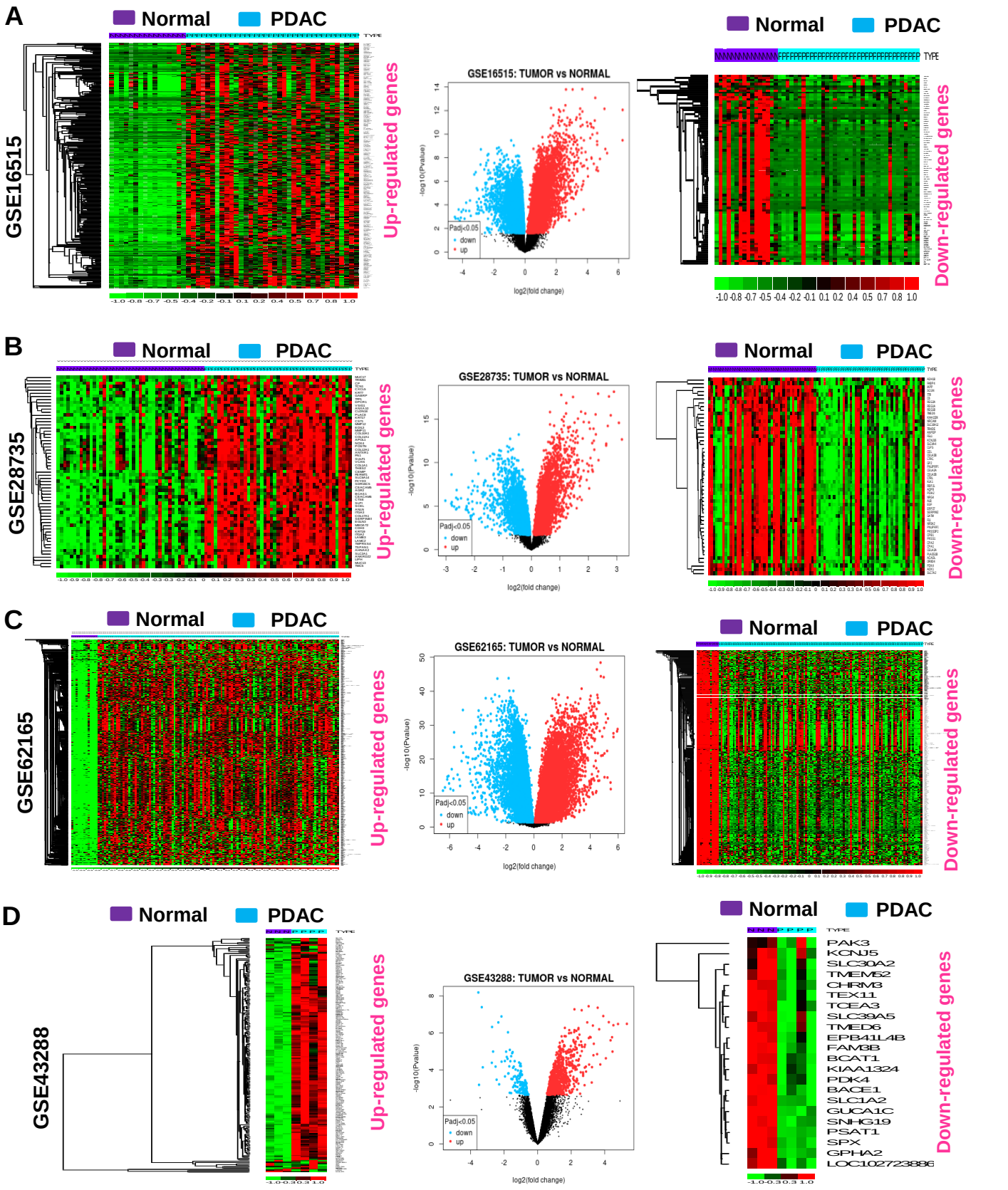

Figure S1. Pancreatic adenocarcinoma mRNA expression profiles GSE16515, GSE28735, GSE62165, and GSE43288 were utilized to analyze the differentially expressed genes. **A-D**) The heat maps show the expression pattern of differentially dysregulated genes and the volcano plot of DEGs in their profiles.

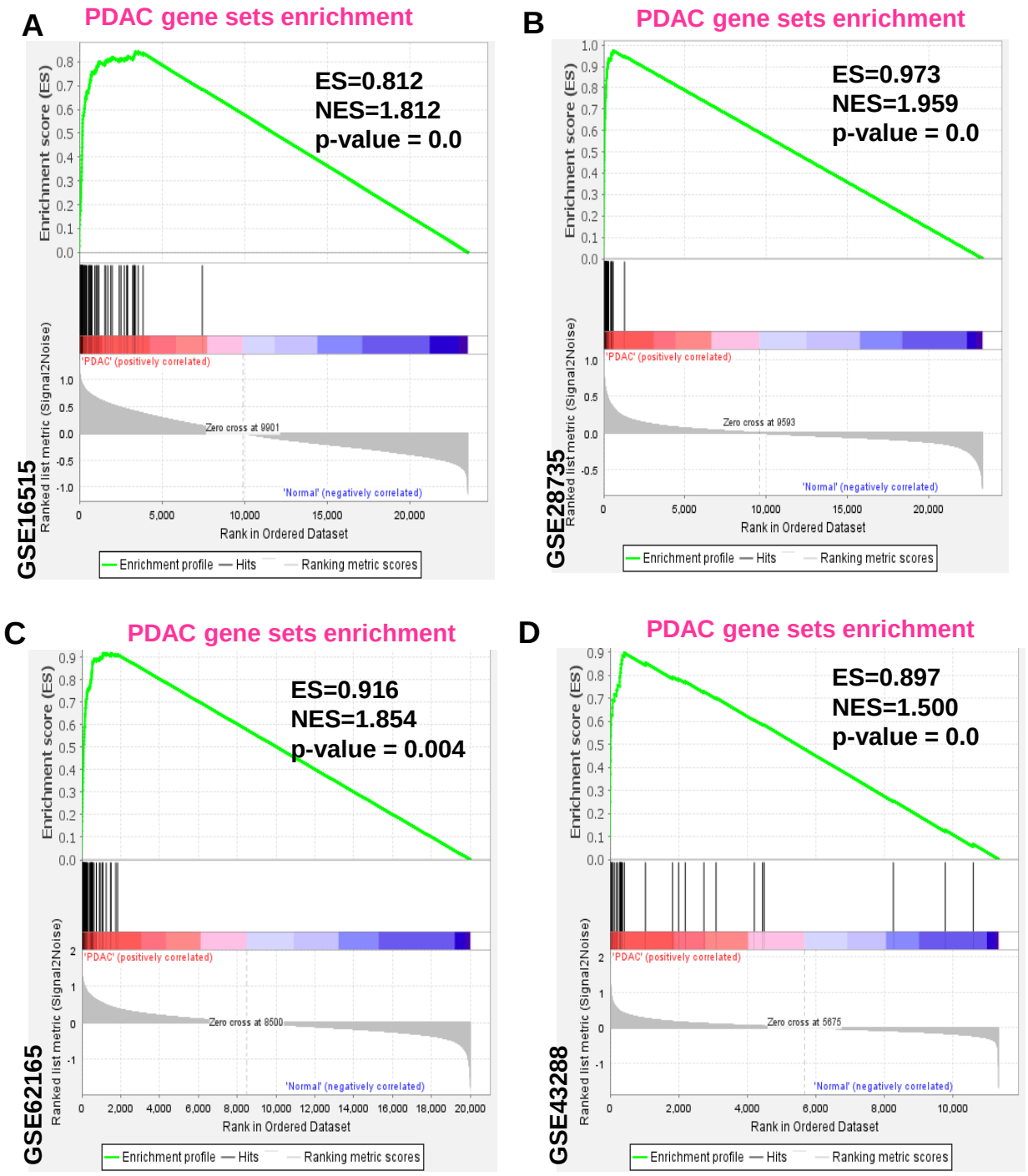

Figure S2. The PDAC hub genes were further confirmed with gene set enrichment analysis in those profiles. **A-D)** The results indicate greater and normalized enrichment scores with significant p values ($p<0.05$).

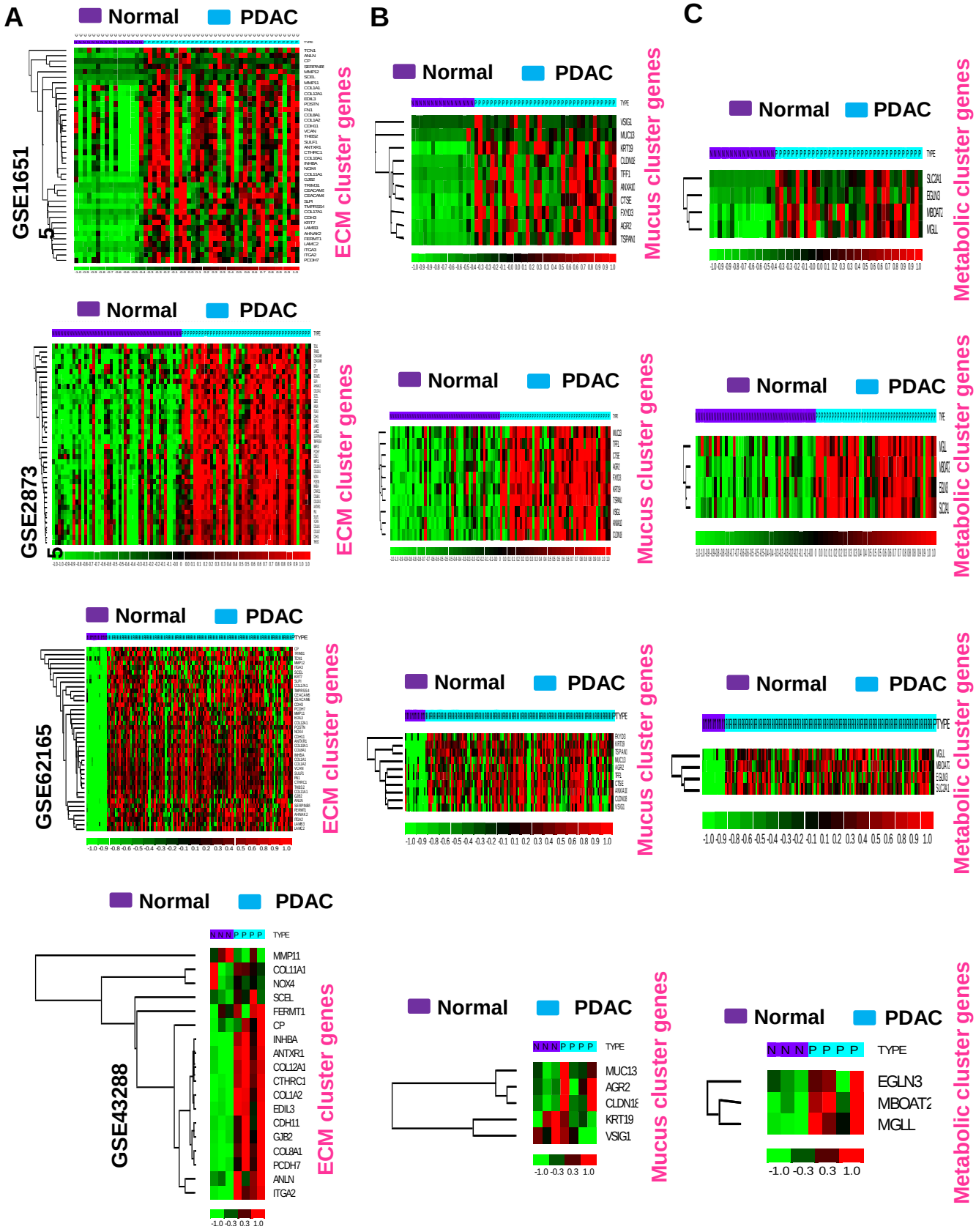

Figure S3. The expression patterns of the three cluster genes in four datasets. **A-C**) Each derived cluster is significantly enriched in PDAC tumors.

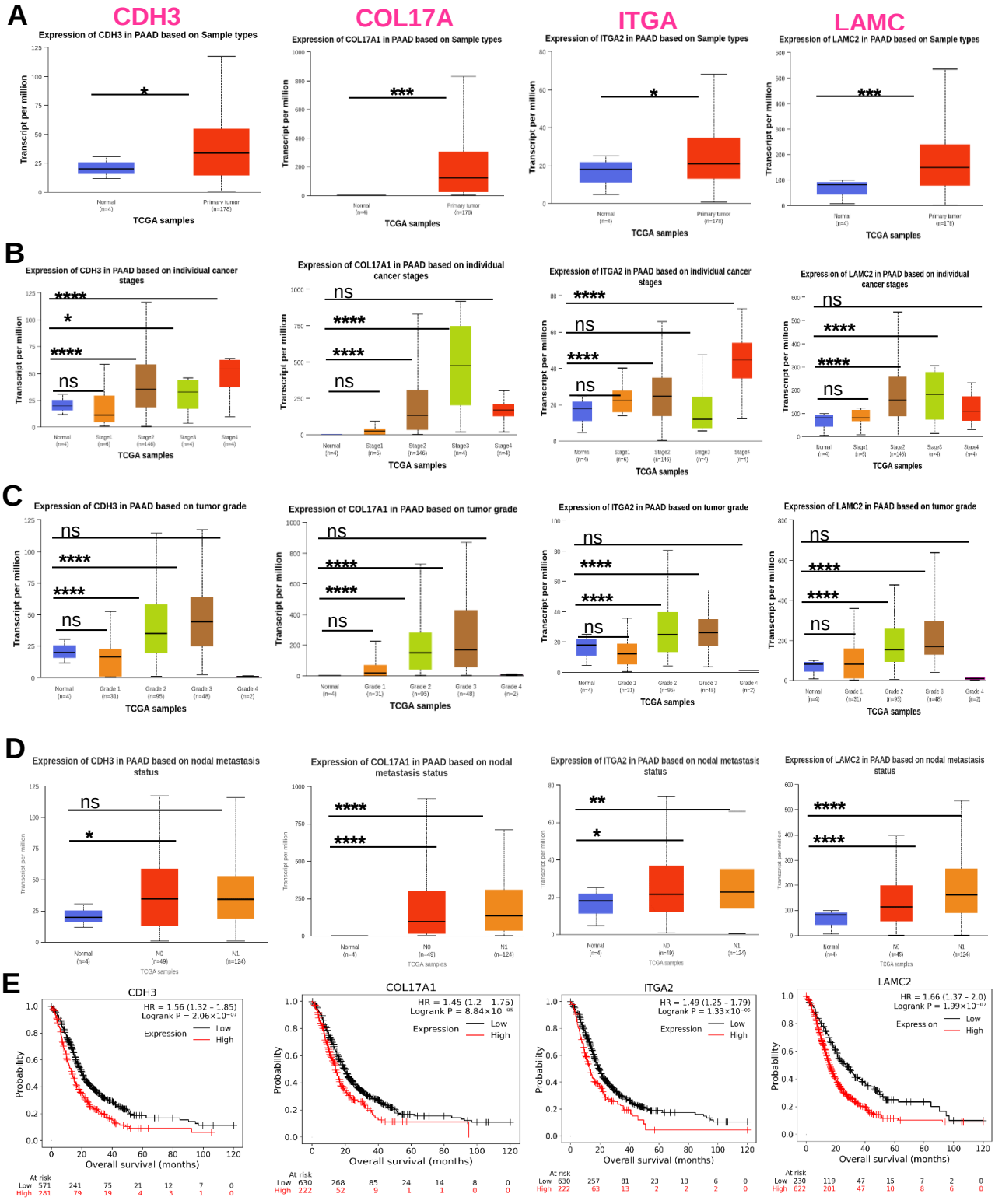

Figure S4. Validation of the ECM cluster genes' expression using TCGA dataset. **A-D**) The ECM genes' mRNA levels are elevated in primary tumors (A), late stage (B), high grade (C), and node N1 metastasis sample (D) compared with normal. **E)** High expression of ECM genes is corelated with poor survival in PDAC patients (****: p<0.0001, ***: p<0.001, **: p<0.01, and *: p<0.05).

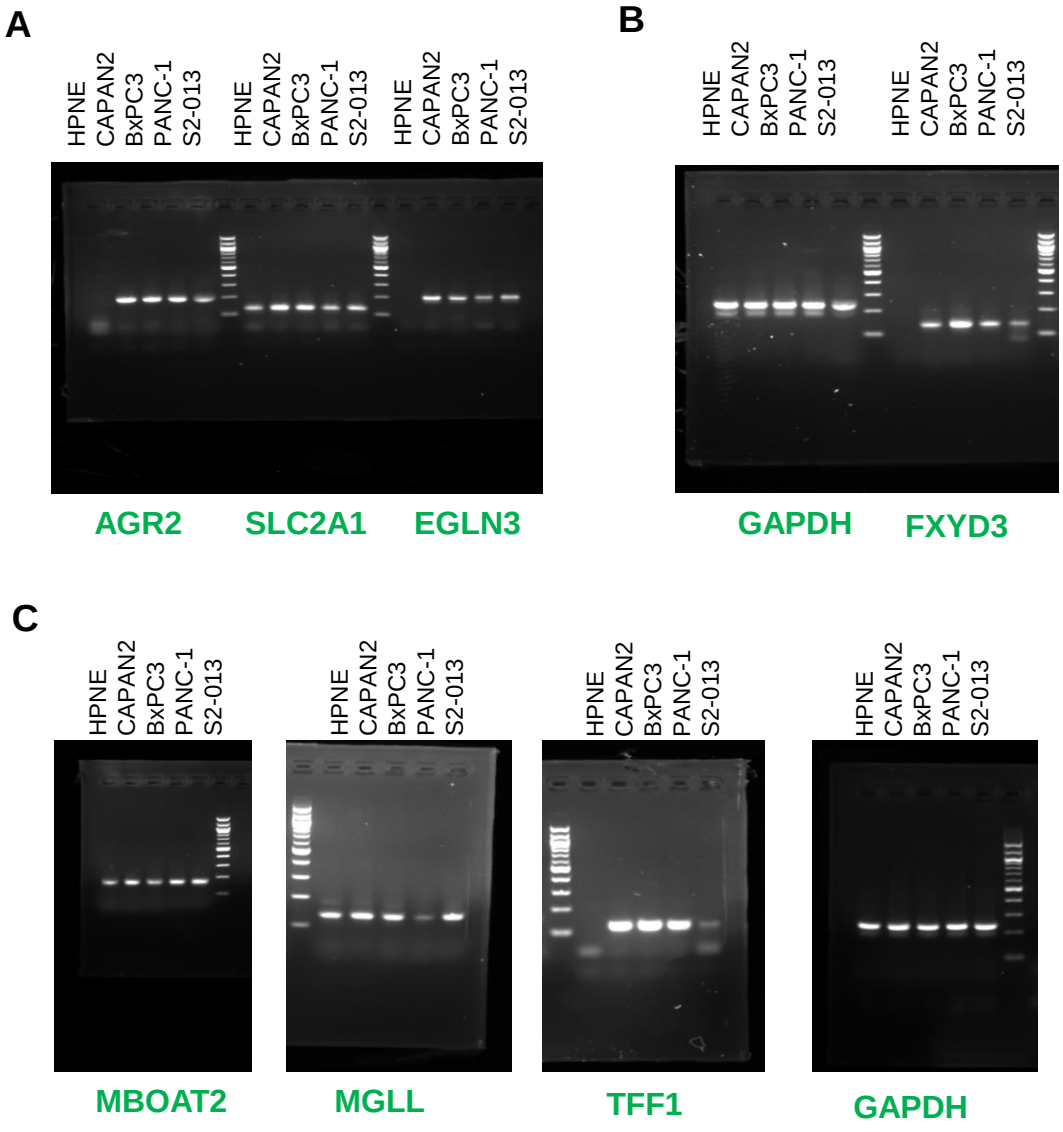

Figure S5. A-C) The uncropped original gel images for the validated genes of RT- PCR products.