



Figure S4

Gene expression in untreated and IFN- γ treated PDACCs

Figure S4 continued

(a) Gene Set Enrichment Analysis (GSEA) was performed in the standalone GSEA java application (1). GSEA enrichment plots of ‘Interferon gamma signaling’ and ‘class I MHC mediated antigen processing presentation’ based on the REACTOME database analysis. Both genesets showed statistically significant enrichment (FDR q value < 0.001; p < 0.001; see inset). (b) We also performed GSEA using MSigDB immunological signatures (Broad Institute, Inc., Massachusetts Institute of Technology, and Regents of the University of California). We summarized here the top 30 leading-edge genes (core genes accounting for the statistical significance of a given geneset) across all statistically significant immunological signatures (FDR < 0.05). Gene names are shown on the y-axis while the total number of genesets where a given gene was part of the leading-edge is shown on the x-axis.

1. Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A*. 2005;102:15545-50.