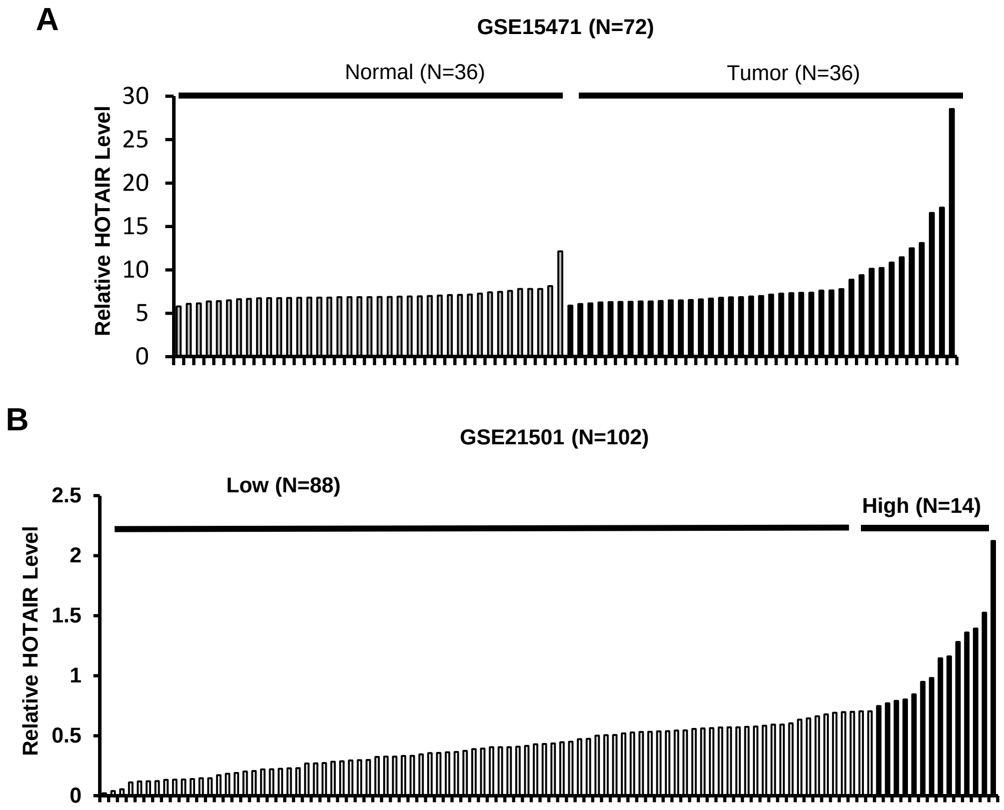
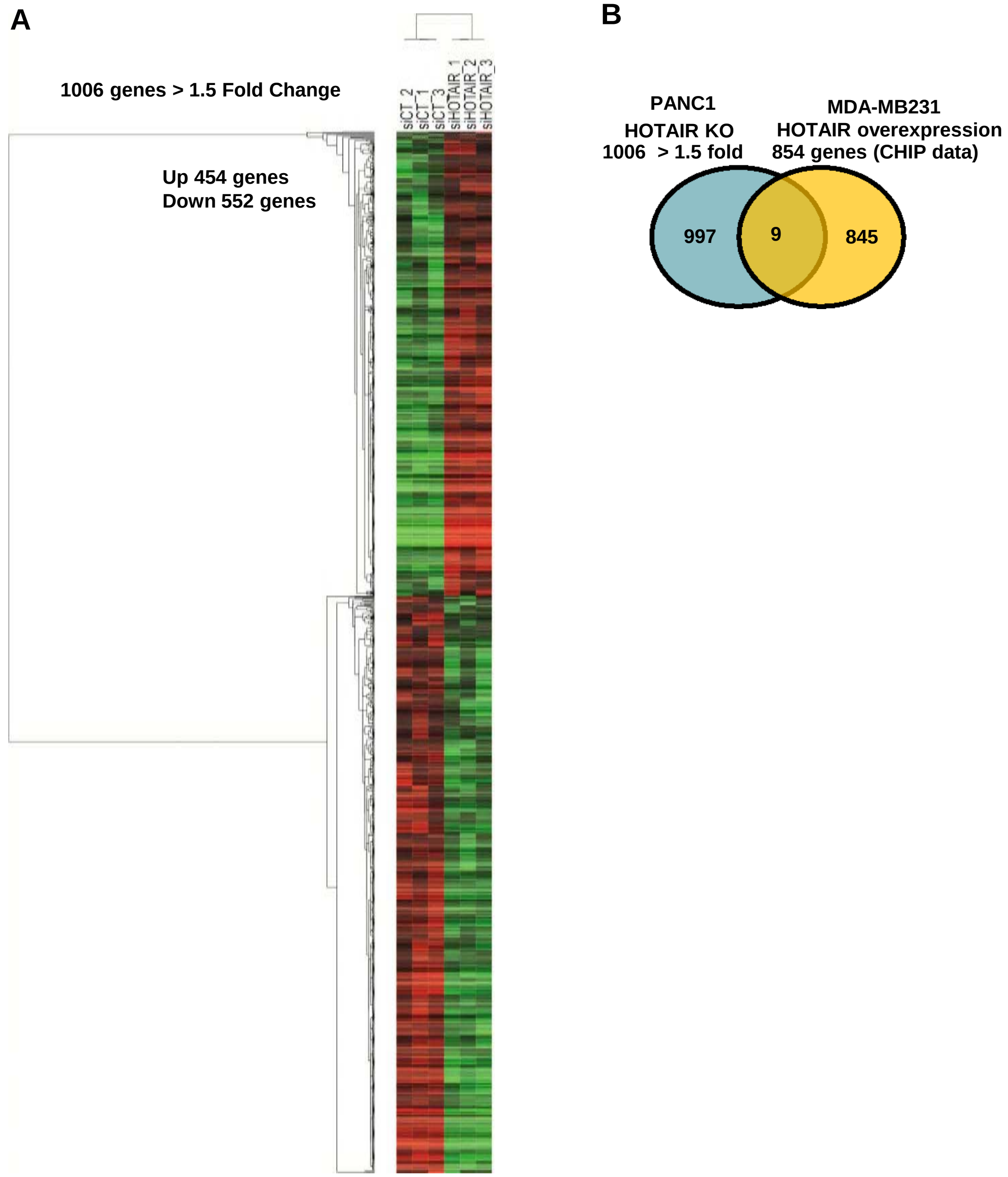
Supplemental Figure S1



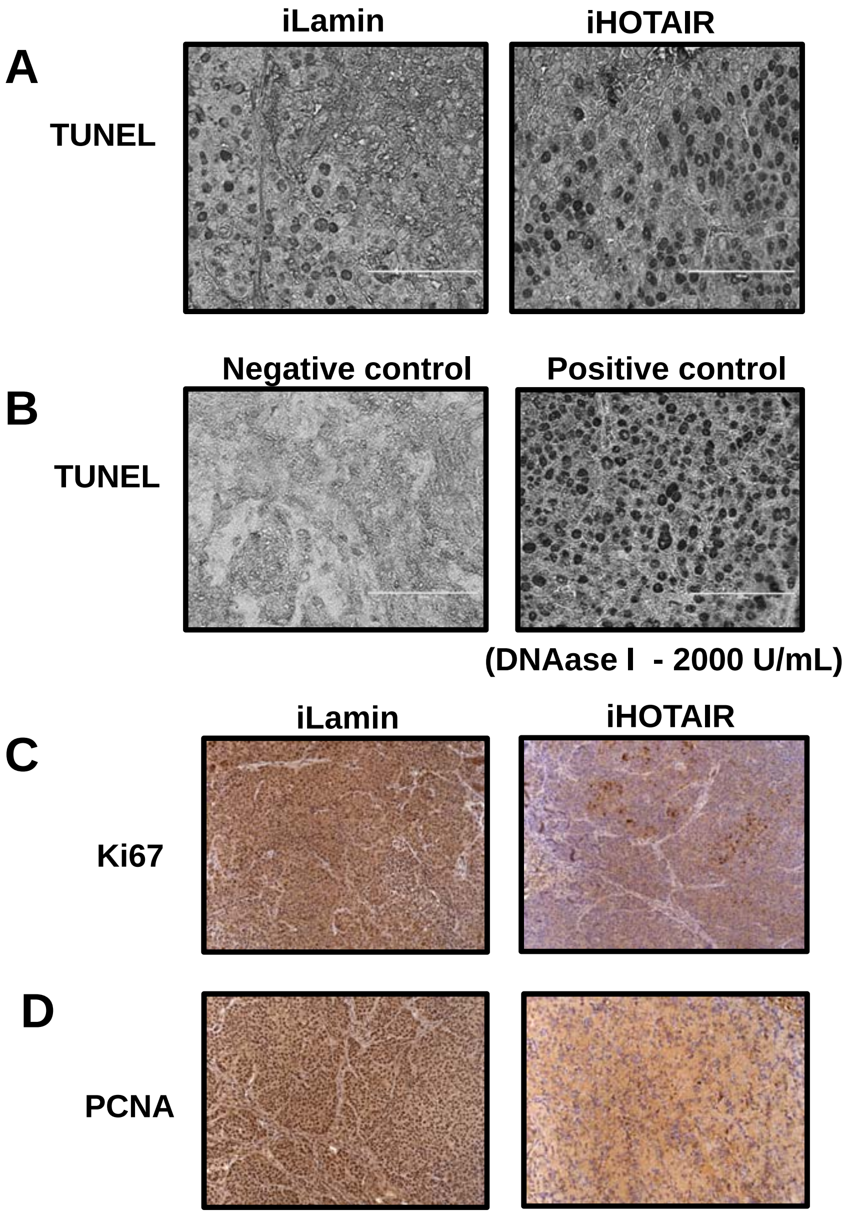
Supplemental Figure S1. Relative HOTAIR expression in patients from two different gene profiling data sets was shown. (A) Normal vs. pancreatic tumor tissue expression. The relative expression of HOTAIR in pancreatic and tumor vs. non-tumors in 36 patients from each group.[25] (B) Relative HOTAIR expression in different subsets of pancreatic cancer patients is given.[24]

Supplemental Figure S2



Supplemental Figure S2. Heat map for 1006 genes (>1.5 fold change) resulted from HOTAIR KO in Panc-1 cell (A) and Venn Diagram for nine common genes between HOTAIR overexpression (MDA-MB-231 cells) and HOTAIR KO (Panc-1 cells) (B).

Supplemental Figure 3



Supplemental Figure 3. Tumor samples from siCT and siHOTAIR treatments (L3.6pL cells) were stained for TUNEL expression (A and B), Ki67 (C) and PCNA (D) as outlined in the Materials and Methods. An unstained negative control and a DNAase-1 treated positive control (B) were included in the TUNEL staining.