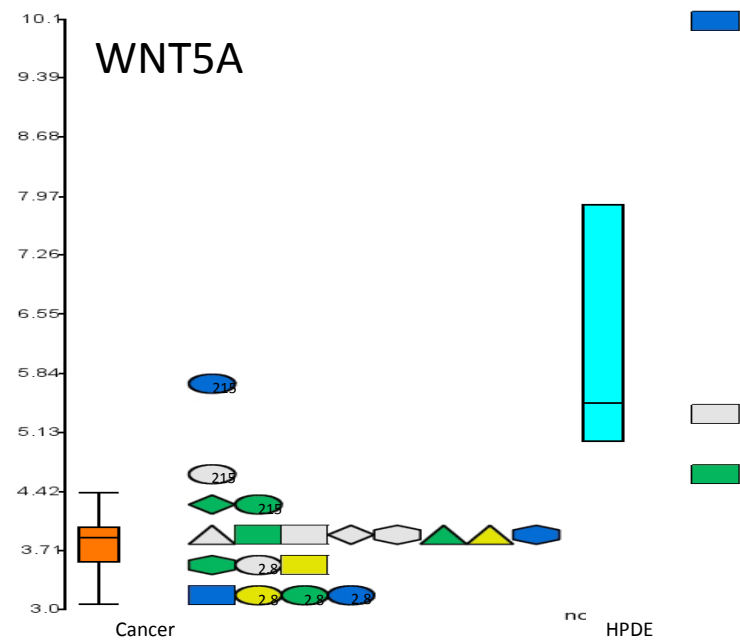
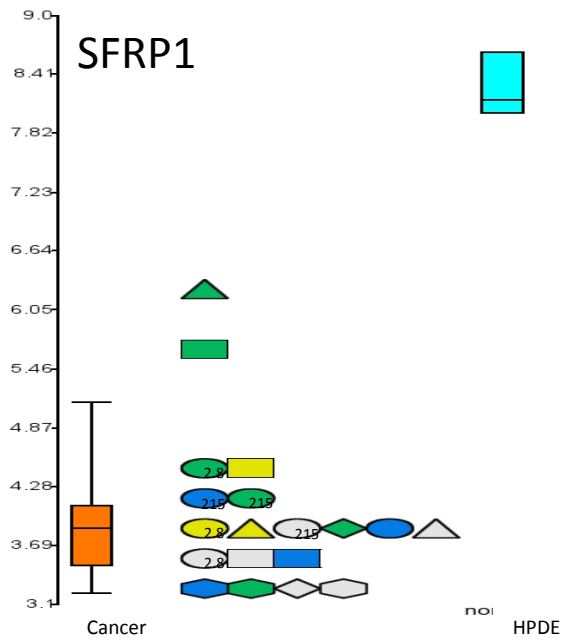
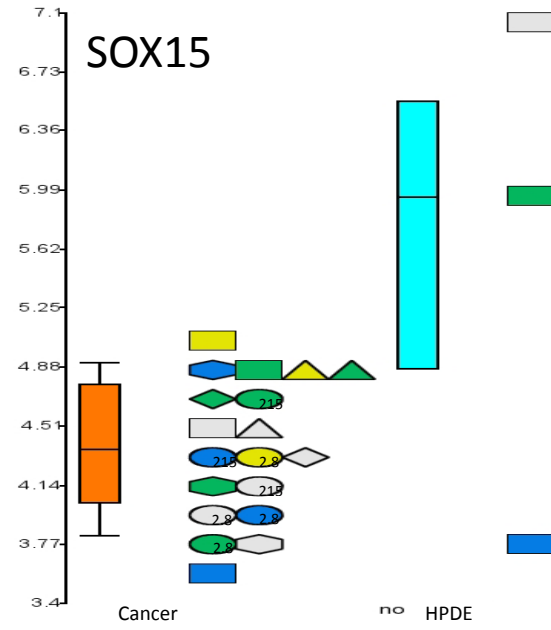
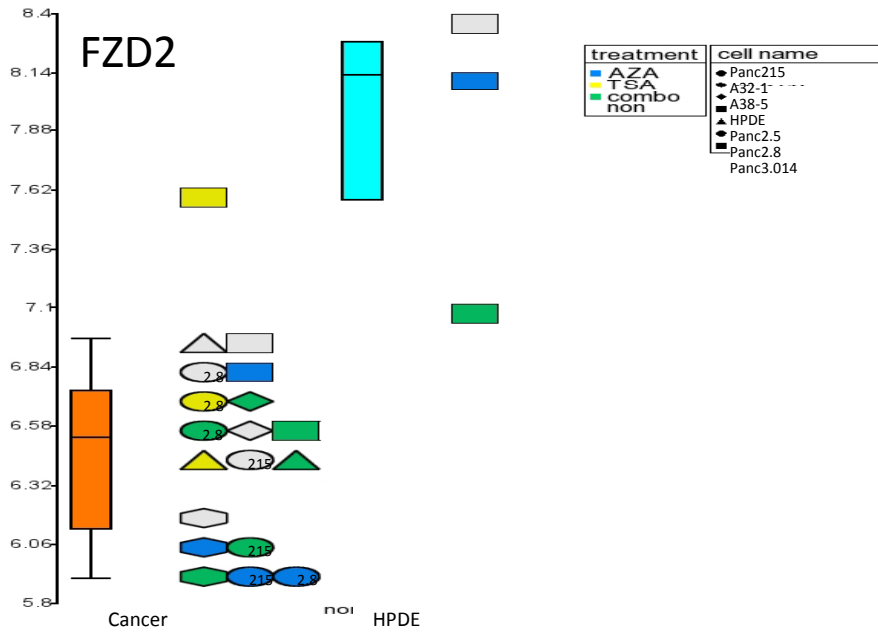
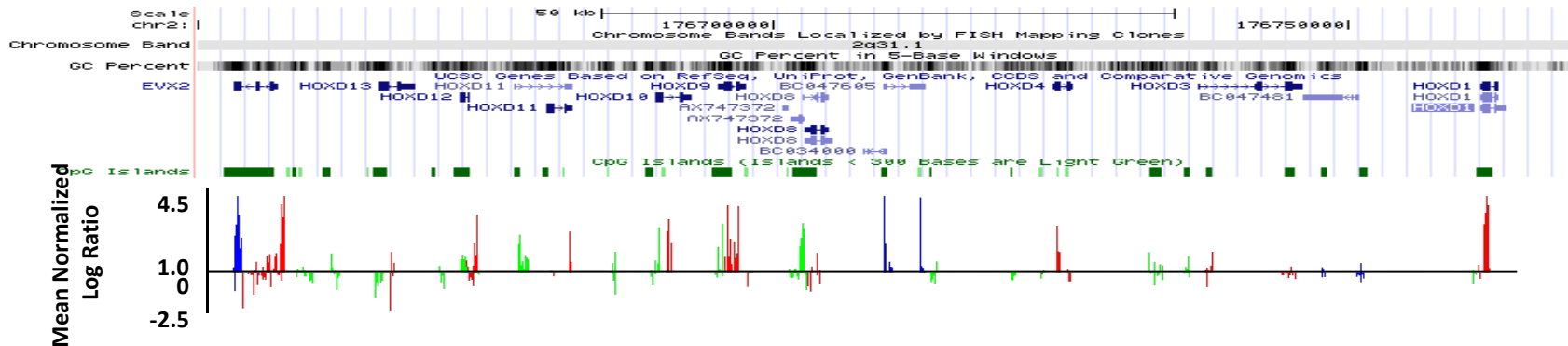
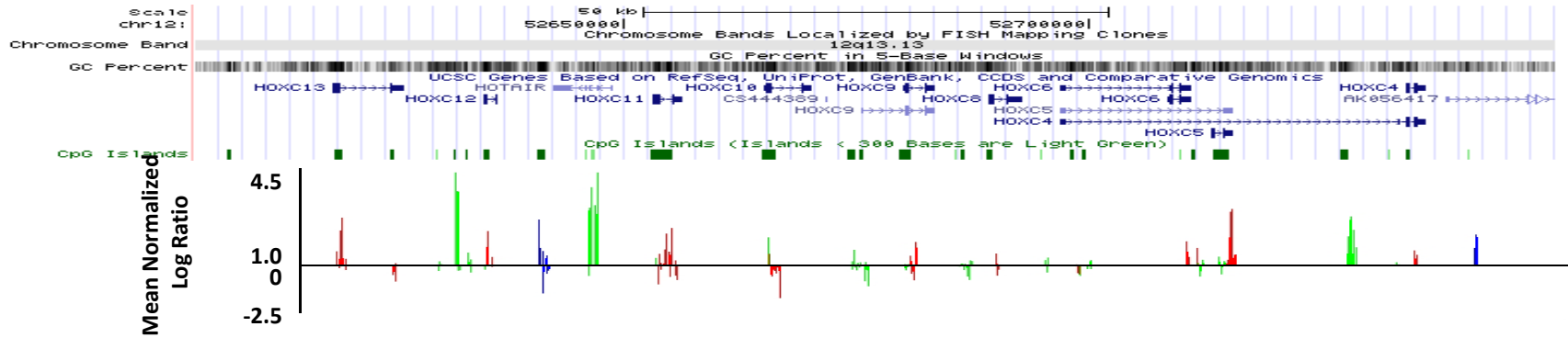
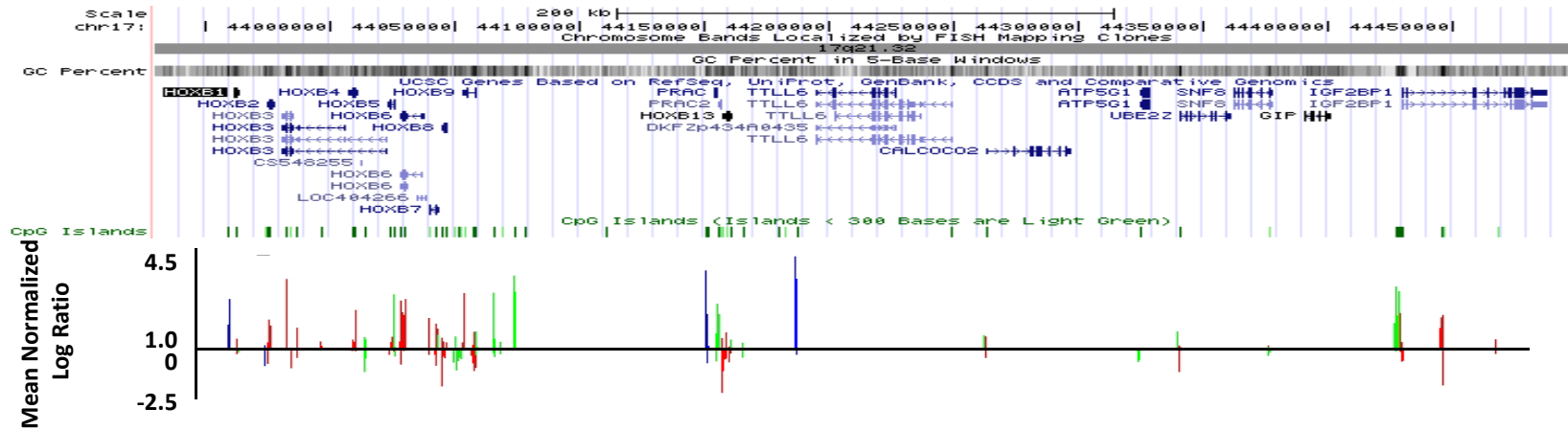


# Supplemental figure 1

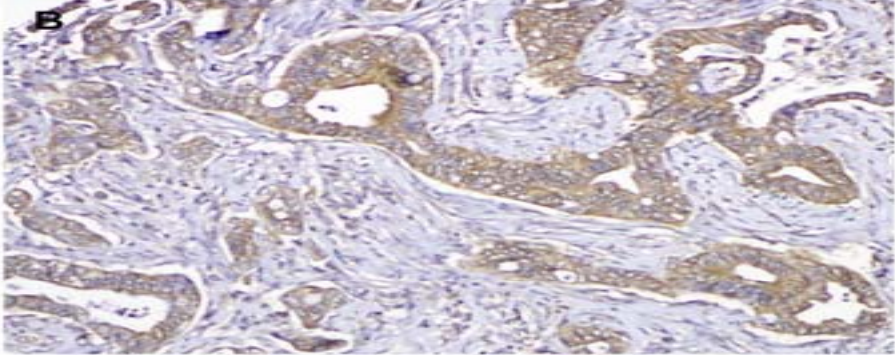
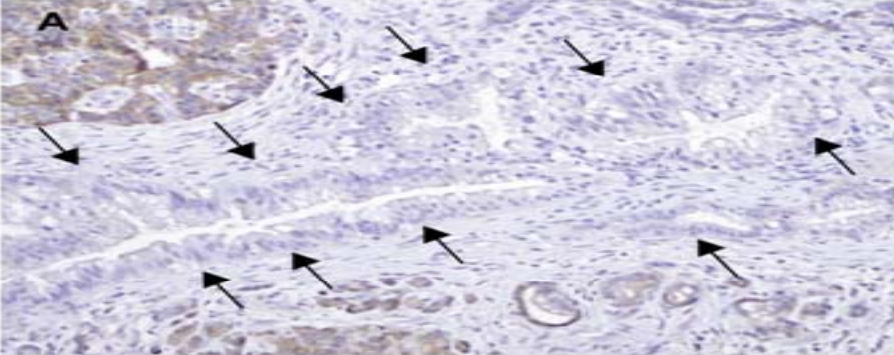


# Supplemental Figure 2

■ DOWNSTREAM ■ INSIDE ■ PROMOTER



Supplemental Figure 3



**Supplementary Figure S1.** FZD2, SFRP1, SOX15 and WNT5A expression profile by Affymetrix exon array. Each cell line was treated with 5-aza-dC (blue), TSA (yellow), the combination (green), or mock treated (white). Each symbol represents one sample and each cell line is represented by a different symbol. The box plot shows the variance among each type of sample (cancer cell lines vs HPDE). Signal intensity is plotted in log 2 scale.

**Supplementary Figure S2.** CpG island methylation cluster at the *HOXB*, *HOXC* and *HOXD* locus. The upper panel shows the gene localization within the cluster. CpG islands represented as green boxes (UCSC Genome Browser). The lower panel shows MCAM data as the mean NLR from nine pancreatic cancer/normal pancreas methylomes. The colors of the peaks indicate the genes probe localization.

**Supplementary Figure S3.** Immunohistochemical labeling of ZBTB16 **(A-B)** Labeling with anti-ZBTB16 antibody revealed **(A)** a loss of expression in the cancer cells (arrows) (x10 magnification), **(B)** A minority of pancreatic cancers retain ZBTB16 expression (x10).