S7 Fig. Mutational landscape of The Cancer Genome Atlas (TCGA) cohort. (A) Overall mutational landscape of 181 upper tract urothelial carcinoma (UTUC) samples of the TCGA cohort is depicted. The most frequently altered genes are $FGFR3$ (40%), $KMT2D$ (36%), $KDM6A$ (30%), $TP53$ (28%), and $ARID1A$ (25%). (B) Differentially mutated genes (p < 0.05) between invasive and noninvasive UTUC were noted in $NOTCH2$ (19/137 vs. 0/44 cases), $NOTCH4$ (14/137 vs. 0/44 cases), $BRCA1$ (15/137 vs. 0/44 cases), $EPHB1$ (13/137 vs. 0/44 cases), $DNMT1$ (12/137 vs. 0/44 cases), $TP53$ (50/137 vs. 1/44 cases), $FGFR3$ (44/137 vs. 28/44 cases), and $STAG2$ (16/137 vs. 14/44 cases).