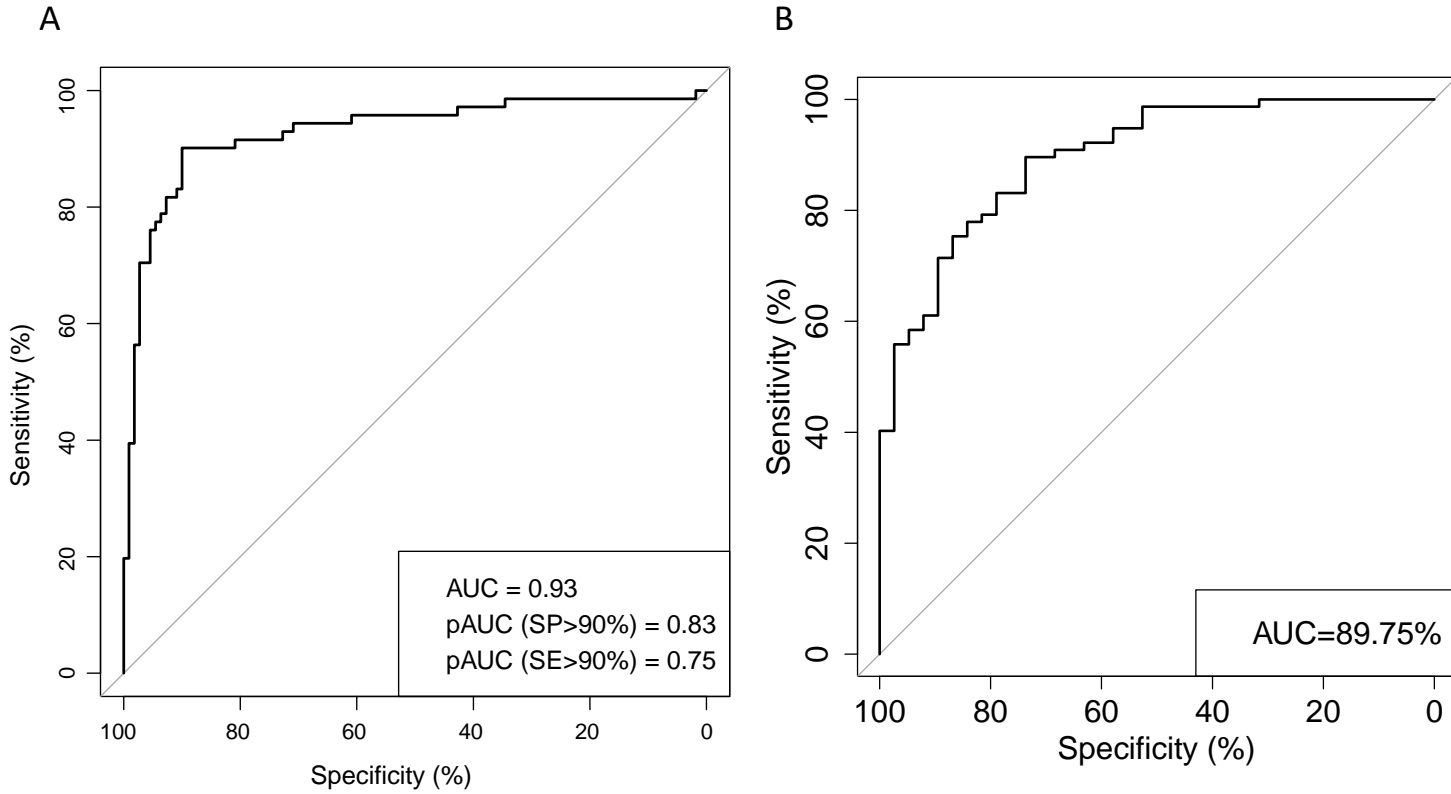


Supplementary Figure 1: Technical training set: Dot-plot graphs of individual markers *Cg6522*, *YPEL3*, and *POU3F1* (A, B, C, respectively) in DNA extracted from biopsy samples. Each sample was defined by histologic diagnosis, shown on x-axis, as determined by pathologist D.R. The y-axis shows the relative methylation percent when compared to the reference gene C-LESS for total DNA, as measured by the MS-ddPCR assay for each marker. One way ANOVA was used to determine statistical significance between histologic groups based on relative methylation percent. P-values < 0.01 when compared to normal tissue are considered significant (*).



Supplementary Figure 2: ROC curve of the model $-3.7459640 + 0.1130 * cg6522 + 0.1926 * POU3F1$ to classify HGD/EAC vs SQ/BE in brushing training set 1 (A) and brushing validation set (B) with the cutoff p value of 0.45.