



Supplementary Figure 3. Validation of array CpG methylation data by pyrosequencing. Concordance of array and pyrosequencing CpG methylation measurements in 88 HNSCCs are plotted for the (A) *ALDH3A1* and (C) *TAP1* loci. For visualization, dashed lines representing fitted regressions are shown. Spearman's rho indicates the non-parametric correlation between array and pyrosequencing methylation. Kaplan-Meier estimates are plotted for tumor methylation groups based solely on the (B) *ALDH3A1* and (D) *TAP1* CpG loci. Survival of patients with the highest methylation is plotted in green, while those in the lowest group are in black. Vertical tick marks represent censored observations and log-rank test p -values are shown.