

Supplementary Figure 2. Comparison of hyper- and hypomethylated CpG loci among each of the patient methylation subgroups. Differential methylation was determined by subtracting tumor beta values at each CpG locus from the mean locus value in normal head and neck tissues (n=18). Significant loci were identified by a Cox-Wilcoxon rank sum test where q<0.05 and  $|\Delta\beta|$ >0.2.