**Supporting information** **captions**

**Figure Legends**

**Figure S1.** Analysis of methylation data obtained by ERRBS in oral tissues of mice treated with DBP and fed control diet *vs.* mice treated with DBP and fed 5% BRB diet. (**A**) Differential methylation annotation. (**B**) Unsupervised analysis of DNA methylation using hierarchical clustering (distance = 1-Pearson correlation, Ward's agglomeration method) Cluster: filtered (count >= 10, coverage <= 99.9th percentile), normalized, destranded. (**C**) Principal component analysis (PCA) of methylated data. (**D)** Stacking bar plots showing percentage of hyper and hypomethylated differential methylated sites out of all covered CpGs per chromosomes (Chr): filtered, normalized, destranded, *q* < 0.01, % methylation difference > 25%.

**Figure S2**. A representative H&E staining showing the histological features identified in the oral tissues of mice. The box indicates the area magnified for the inset. The inset shows epithelial hyperplasia with atypia.

**Supporting Information Table Legends**

**Table S1.**  List of (**A**) hypermethylated and (**B**) hypomethylated loci identified in oral tissues of mice treated with DBP and fed control diet or mice treated with DBP and fed 5% BRB diet.

**Table S2.** Top canonical pathways generated using IPA® on aberrantly methylated genes identified in oral tissues of mice treated with DBP and fed control diet *vs.* mice treated with DBP and fed 5% BRB diet.

**Table S3.** Histological feature in the oral tissues of mice treated with DBP and DBP + BRB.