



**SUPPLEMENTARY FIG. S3.** Cluster analysis. K-means cluster analysis was done as an exploratory visual approach. We analyzed the gene set from array 1 and called that dataset 1, and from array 2 and called that dataset 2. Distribution plots of the expression of genes is shown for data sets 1 and 2. The y-axis shows the ratio of relative expression levels in different crypt subsections. **(A)** Expression plot of all genes in data set 1. Left side of x-axis is B versus T (B/T). Right side of x-axis is M/T. **(B)** Expression plot of all genes in data set 2. Left side of x-axis is B/T. Right side of x-axis is M/T. **(C)** K-means clustering of data set 1. Left side of x-axis is B/M. Middle of x-axis is B/T. Right side of x-axis is T/M. Four distinct expression clusters emerged from the data. **(D)** K-means clustering of data set 2. Left side of x-axis is B/M. Middle of x-axis is B/T. Right side of x-axis is T/M. Four distinct expression clusters emerged from the data. Expression profiles are similar for each data set. No unique cellular pathway was apparent from this analysis. But, we did find that each dataset could be partitioned into the same 4 clusters (C, D). B, crypt bottom; M, crypt middle; T, crypt top.