**Functional shifts in the core subgingival microbiome during various dentition states.** Figure 3A shows a Bland-Altman plot of changes in the relative abundances of core functional genes in the subgingival microbiome between the different dentitions. Each point is a functional gene. Points above and below the red median line represent genes demonstrating higher abundances in the specified dentition. Red points indicate genes with significantly different abundances (p<0.05, FDR adjusted Wald test). Figure 3B shows the number of functional genes that were different between two subsequent dentitions. For example, the bar “Primary” represents genes that were different between predentate and primary dentitions, while “Mixed” represents number of genes differing between primary and mixed dentitions. Figures 3C and 3D represent the functions encoded by these genes in the primary and permanent dentitions respectively.