

Supplemental Figure 5



Supplemental Figure 5. Effect sizes of significantly enriched metagenome pathways.

Putative functional profiles of all samples were generated using PICRUSt. KEGG pathways that were enriched across CST were ordered by p-value across all sites and CST. The top 8 pathways for each site and CST were tabulated, which all had FDR-adjusted p-values below 10%. The LDA effect size, providing a measure of discriminatory power, was used to perform hierarchical clustering of tabulated pathways across all sites' CST simultaneously.