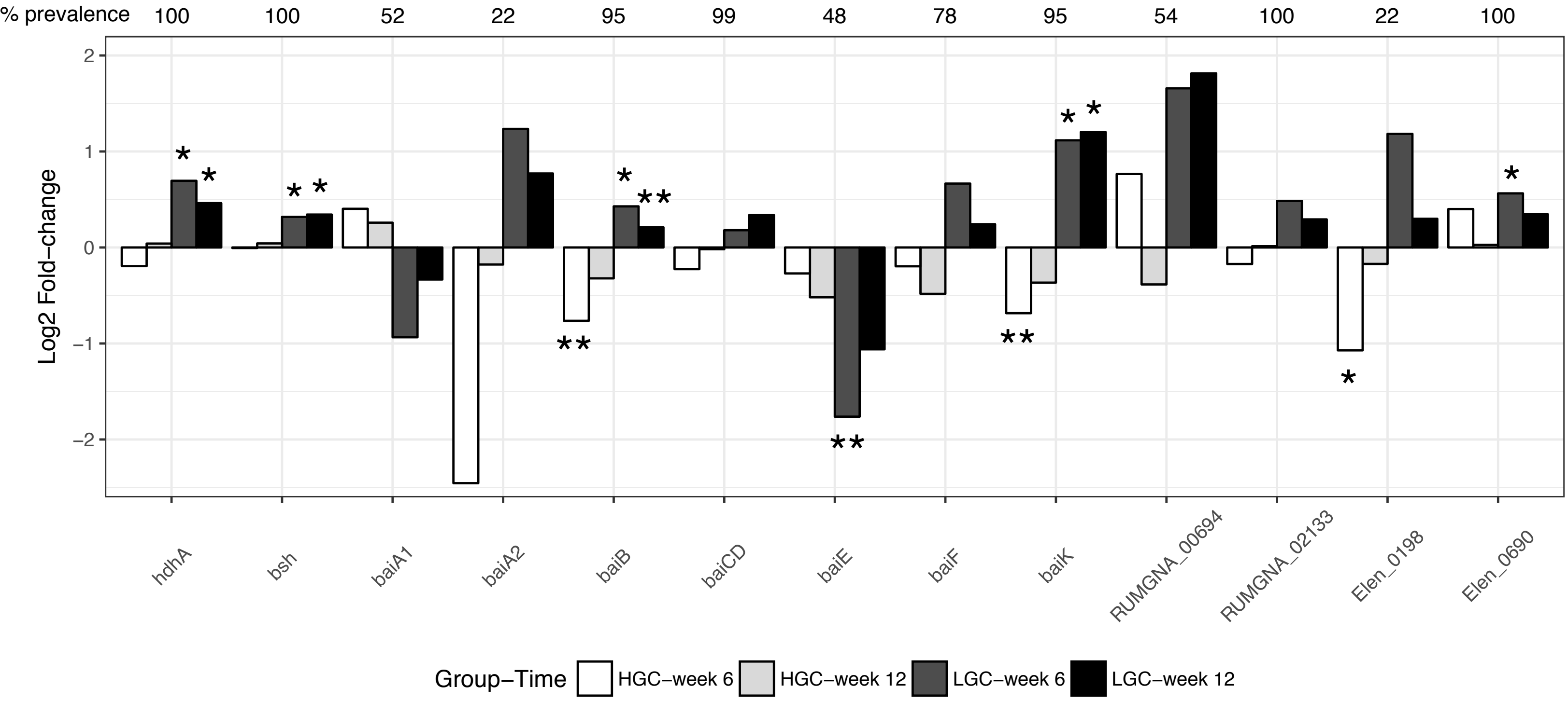

**Supplementary Figure 2.** Fold change (on log base 2 scale) of each bile acid gene between baseline and weeks 6 and 12, stratified by baseline gene richness. Prevalence is number of metagenome samples (subject 1 at baseline is a different sample from subject 1 at week 6) with abundance greater than 0. Statistical significance was determined by paired Wilcoxon tests with *P<0.05 and **P<0.01. Fold-change of means was calculated because too many zeros were present in some genes to calculate fold-change with median (resulted in infinity or undefined ratios).