

**A Midgut**

Alpha Diversity Measure

Chao1

Shannon

Habitat Region

Region 1

Region 2

Region 3

0.051

0.073

0.55

0.1

0.15

0.66

**B Hindgut**

Alpha Diversity Measure

Chao1

Shannon

Habitat Region

Region 1

Region 2

Region 3

0.64

1

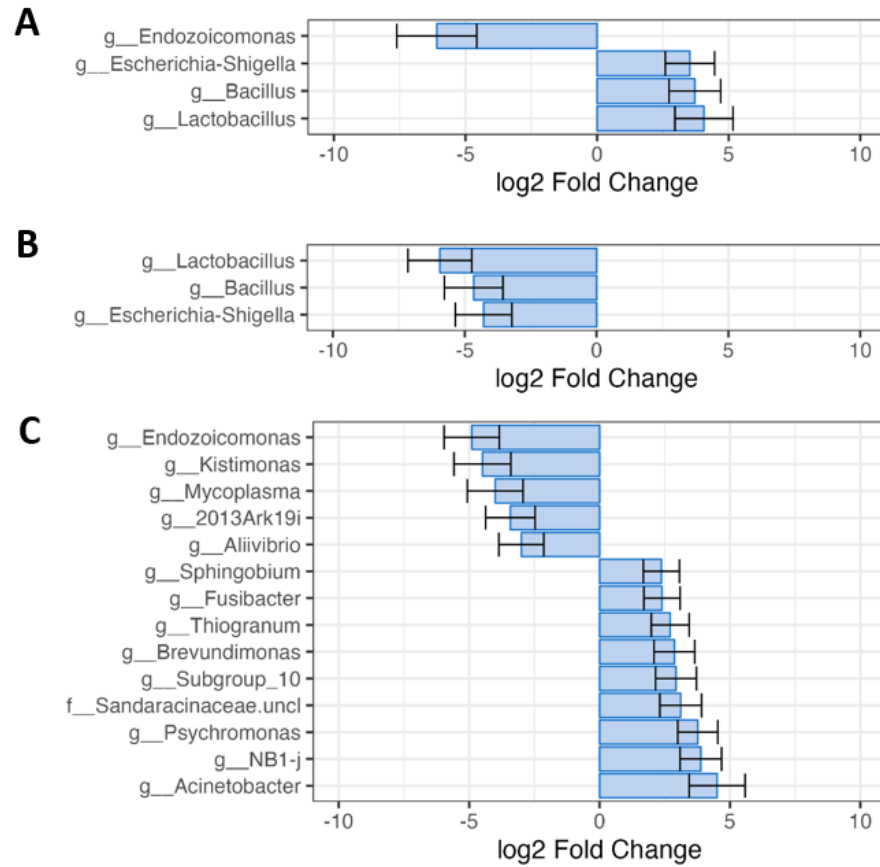
1

0.64

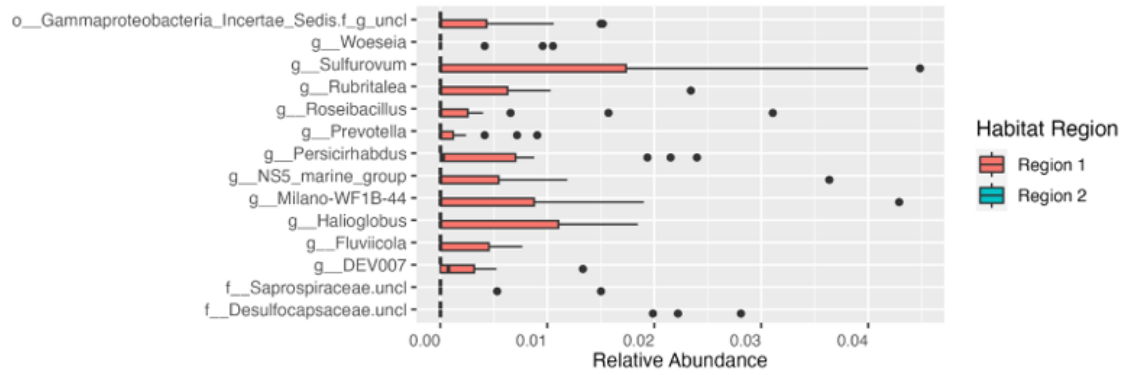
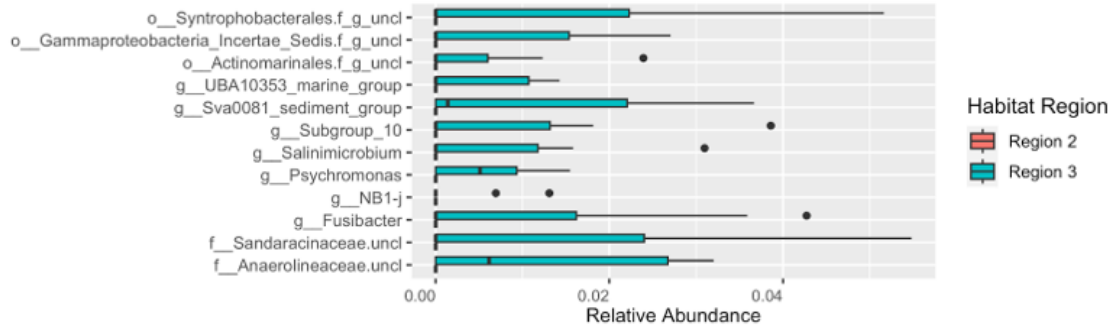
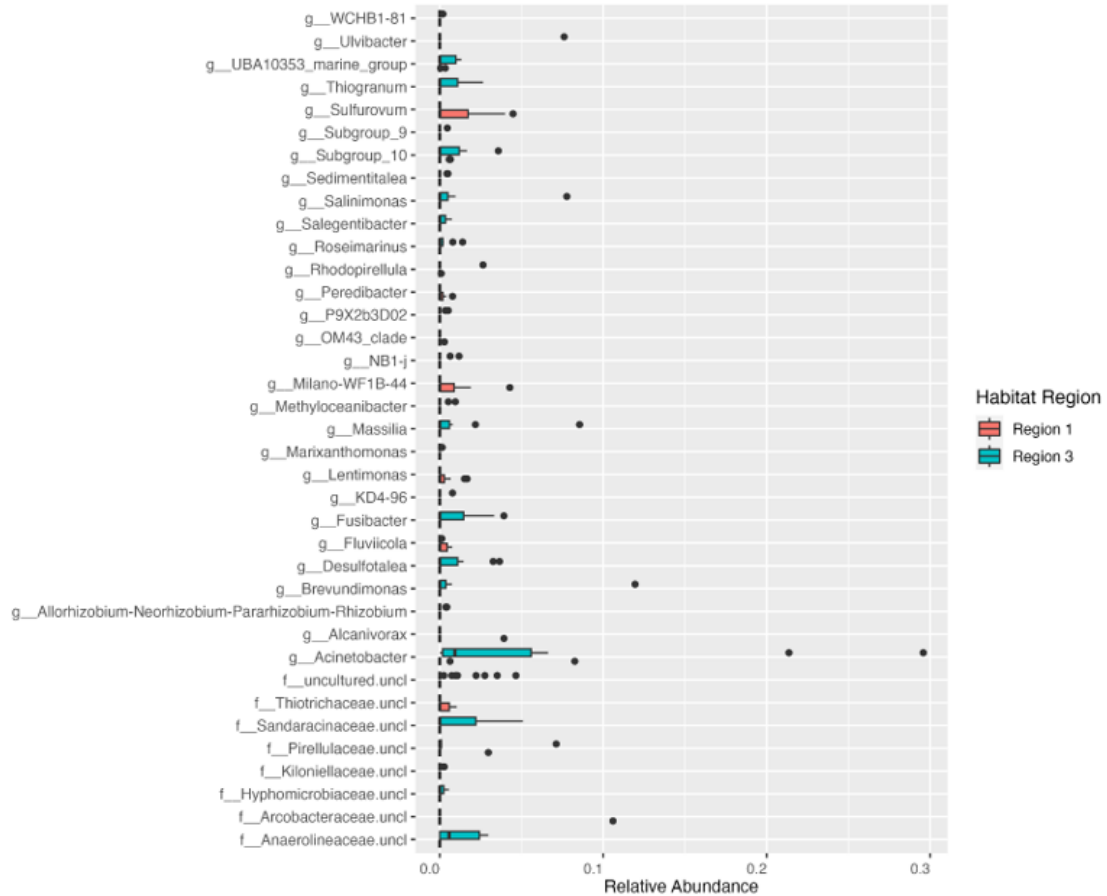
0.86

0.74

**Figure S1. Alpha diversity does not significantly differ by habitat region in the midgut or hindgut.** Chao1 and Shannon Diversity Indices were determined for midgut (A) and hindgut (B) microbiomes collected from Regions 1, 2, and 3. Chao1 considers a count of how many unique taxa there are per rarified sample, and Shannon diversity considers both richness or evenness. Boxplots and error bars represent mean  $\pm$  SEM. Statistical significance ( $p < 0.05$ ) was determined via Wilcoxon test.



**Figure S2. Few differentially abundant taxa are observed in different habitat regions in the hindgut.** Differentially abundant taxa in Region 2 compared to Region 1 (**A**), Region 3 compared to Region 2 (**B**), and Region 3 compared to Region 1 (**C**) were assessed by differential abundance analysis using DESeq2/Phyloseq. Significance was defined as differentially abundant genera with an adjusted Wald Chi-Squared Test p-value of <0.01.

**A****B****C**

**Figure S3. Relatively abundant taxa are observed in different habitat regions in the midgut.** Relative abundance of differentially abundant taxa between regions: Region 2 compared to Region 1 (**A**), Region 3 compared to Region 2 (**B**), and Region 3 compared to Region 1 (**C**) were prepared using ggplot2 and phyloseq, using differentially abundant taxa identified using DESeq2.