SUPPLEMENTAL FIGURES AND TABLES

Supplemental Table 1: Total reads per sample

The Illumina assembled total paired end ssu rDNA amplicon reads for 192 gastrointestinal tract samples for the 32 study animals is presented. The individual amplicon reads are sorted by anatomical section and experimental condition (with or without antibiotics, and with and without *Giardia* infection). Total reads are summarized in Figure 1, and deposited in GenBank with the Sequence Read Archive accession number SRP075733.

Supplemental Figure 1: Overall alpha diversity by intestinal site is not significantly changed during giardiasis in animals lacking antibiotic treatment.

Sampling adequacy was assessed using rarefaction plots for all samples using the Chao1 estimate during the course of giardiasis (uninfected, day 3, day 7, and day 14) in untreated animals (A). Alpha diversity measures of species richness, evenness, and phylogenetic distance were used to summarize community ecology of regions of the murine gut (proximal small intestine (pSI), distal small intestine (dSI), cecum contents (CEC) and colonic contents (COL) in animals with (days 3, 7, and 14) and without giardiasis (U). For these analyses, the OTU tables were rarefied to 3000 reads/sample and analyzed in QIIME (see Methods) to compare the relative read abundances. Species richness (B) was determined using Chao1 estimates and species evenness was estimated using the Shannon index (C). The Phylogenetic Distance (D)

was estimated to describe the extent of diversity in each community. Error bars correspond to variation between gut samples of each of the four animals in that experimental group.

Supplemental Figure 2: Samples cluster based on infection rather than anatomic location.

Unifrac comparisons of beta diversity are shown using Principal Coordinate plots (PCOA) to estimate the variance associated with the diversity of all samples from all anatomical sites in antibiotic treated mice with giardiasis (days 3, 7 and 14 post infection) to uninfected control samples (A). Luminal and mucosal small intestinal samples in antibiotic-treated animals are shown to cluster together (B). The total diversity from cecum and colon samples cluster together (C). Proximal (pSI) and distal (dSI) small intestine samples are shown to cluster based on Giardia infection, rather than anatomic sublocation (C).

Supplemental Figure 3: The proximal small intestine and colonic contents have significant changes in diversity during giardiasis with antibiotic treatment

Principal Coordinate plots (PCOA) of weighted Unifrac analyses of beta diversity for all sequence reads from all anatomical sites from all individuals treated with antibiotics. Control (uninfected) samples are distinct compared with *Giardia* infected samples at day 14 for each of the anatomical segments of the foregut (pSI* and dSI*) and hindgut (CEC* and COL). * = $p<0.05$, as calculated by ADONIS.

Supplemental Figure 4: Alterations in gut microbiome diversity in the proximal small intestine and colon contents during giardiasis without antibiotic treatment

Fourteen days post infection without antibiotics, the relative read abundance (%) of the most abundant bacterial divisions and phyla are shown in the mouse foregut: (A) proximal small intestine (pSI), (B) distal small intestine (dSI); and hindgut: (C) cecum contents (CEC) and (D) colon contents (COL) samples with each anatomic section compared to the cognate uninfected sample.

Supplemental Figure 5: The proximal small intestine and fecal pellets have significant changes in diversity during giardiasis without antibiotic treatment

As in C. Principal Coordinate plots (PCOA) of weighted Unifrac analyses of beta diversity for all sequence reads from all anatomical sites from all individuals not treated with antibiotics. Control (uninfected) samples are distinct compared with *Giardia* infected samples at day 14 for each of the anatomical segments of the foregut (pSI* and dSI*) and hindgut (CEC* and COL). * = $p<0.05$, as calculated by ADONIS.

Supplemental Figure 6: Significant shifts in beta diversity occur in the murine foregut and hindgut during giardiasis without antibiotic treatment

Using multivariate statistics, taxa that were significantly enriched or depleted after fourteen days of *Giardia* infection were identified. Taxa that changed significantly after two weeks of

Giardia infection were plotted as the fold change in relative abundance between uninfected and infected animals by sampling site (Foregut = proximal small intestine (pSI) in red and distal small intestine (dSI) in blue; Hindgut = cecum contents (CEC) in green, and colonic contents (COL) in orange. The taxonomy of each species is indicated, where α-Prot = alpha-Proteobacteria, beta-Prot = beta-Proteobacteria gammaProt = gamma-Proteobacteria, BacF = Bacilli (Firmicutes), EryF = Erysipelotrichi (Firmicutes), ClosF = Clostridia (Firmicutes). *Melainabacteria* were categorized as Cyanobacteria-Chloroplast in QIIME. Underlined taxa are used to calculate the Murine Giardiasis Dysbiosis Index (see Figure 7 and Supplemental Figure 7).

Supplemental Figure 7: The Murine Giardiasis Dysbiosis Index during the time course of giardiasis in animals not treated with antibiotics.

As in Figure 5, the average MGDI per body site over the infection time course is shown (A). Bars are missing (CEC Day 7, FP, Uninfected) when no MGDI could be calculated due to the absence of Proteobacteria from the sample. In B, a PCOA analysis is shown using the infection time course as an explicit axis. Samples are colored according to their calculated MGDI, with increased color intensity representing higher MGDI values. There is increased color intensity with increased infection duration, representing a higher MGDI over the course of infection. The circled samples (hindgut) did not show dramatically increased GMDI and clustered distinctly from the other samples.