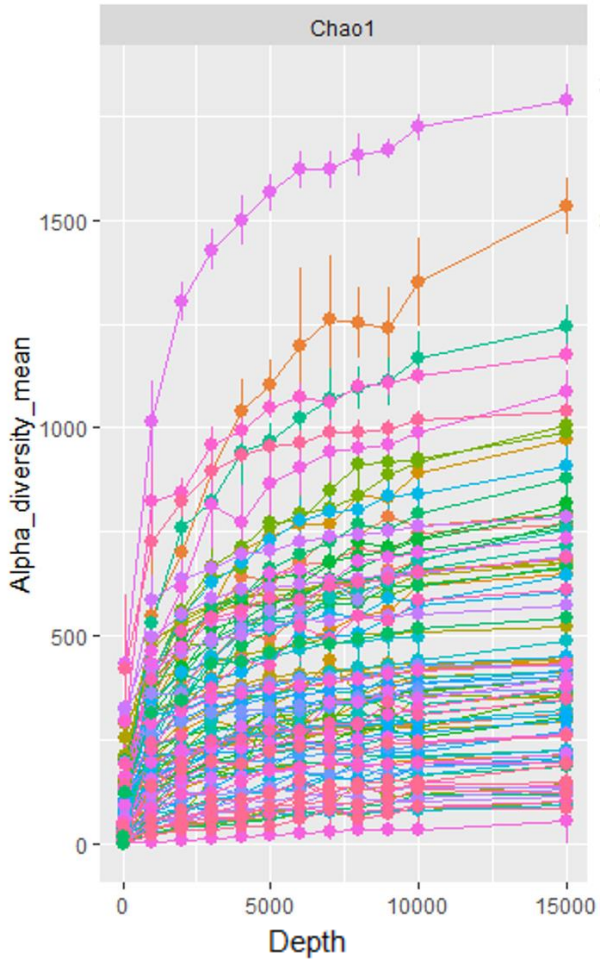
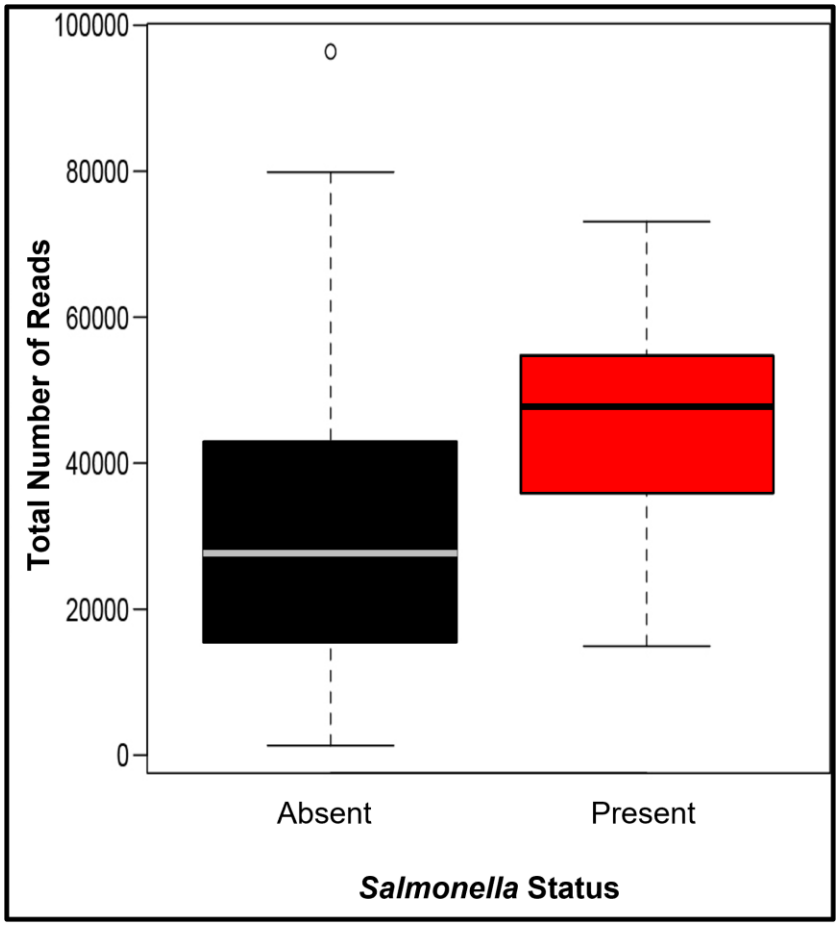
Supplemental Materials

Supplementary Table 1. Locations, coordinates (Lon/Lat), population names, sample sizes (*N*), number of samples with *Salmonella* present in the microbiome (Pos), proportion positive, and *Salmonella* read statistics (mean, standard deviation, maximum and minimum reads) for all barn swallows (*Hirundo rustica*, *n* = 108) sampled in Israel. These data were used in the analyses and to generate the map (Fig. 1). Coordinates are reported for the first location listed in each population.

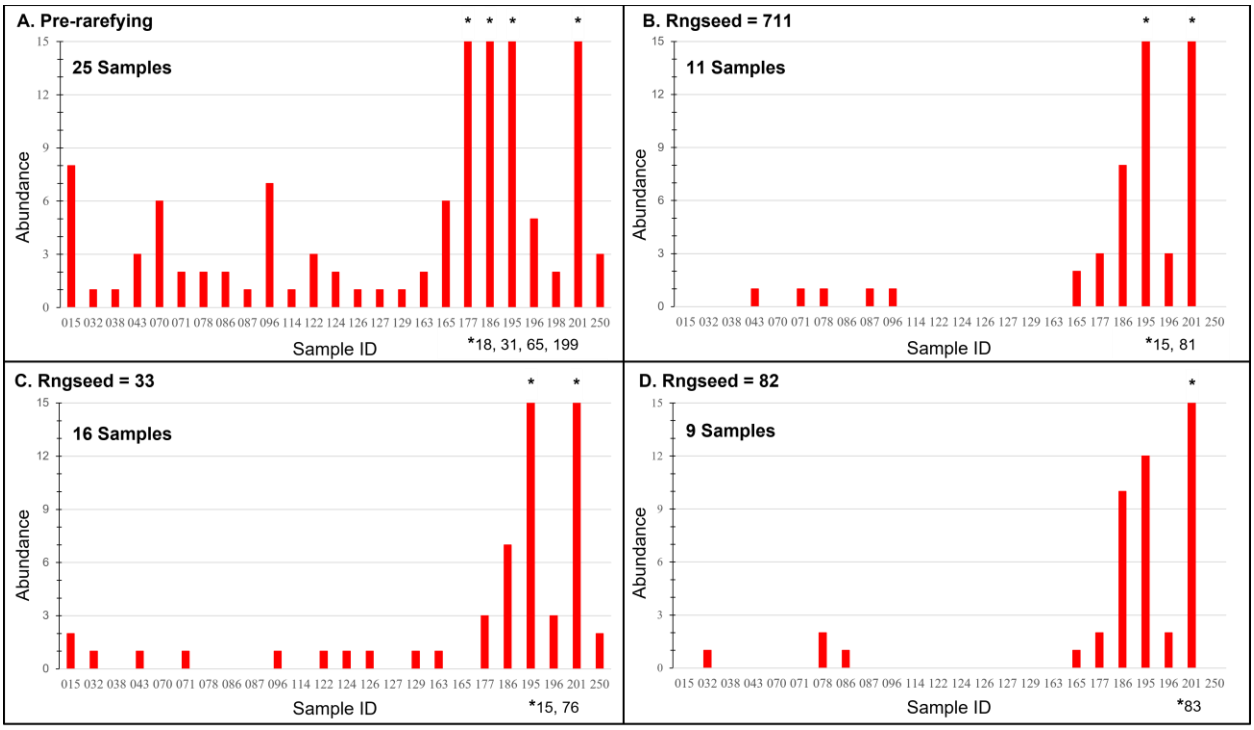
Location	Lon (°E)	Lat (°N)	Population	*N*	Pos	Proportion Positive	Mean *Sal* Reads	Standard Deviation	Max *Sal* Reads	Min *Sal* Reads
Beit_ha_shita, Beit_She'an_mall, Tel-Saharon_Alfalfa_Field	35.438	32.551	Beit_shean	38	7	0.18	53.3	68.4	199	2
Levahot_habashan_fish_ponds, Agamon_ringing_station, Rosh_Pina_mall	35.642	33.138	Hula	34	10	0.29	4.7	2.4	8	3
Shafyaim_parking_lot	34.828	32.222	Shefayim	15	8	0.53	1.9	1.5	6	1
Zichron_mall, Ma'agan_Michael_fish_ponds	34.932988	32.569222	Hof_hacarmel	21	3	0.14	3.3	2.3	7	1



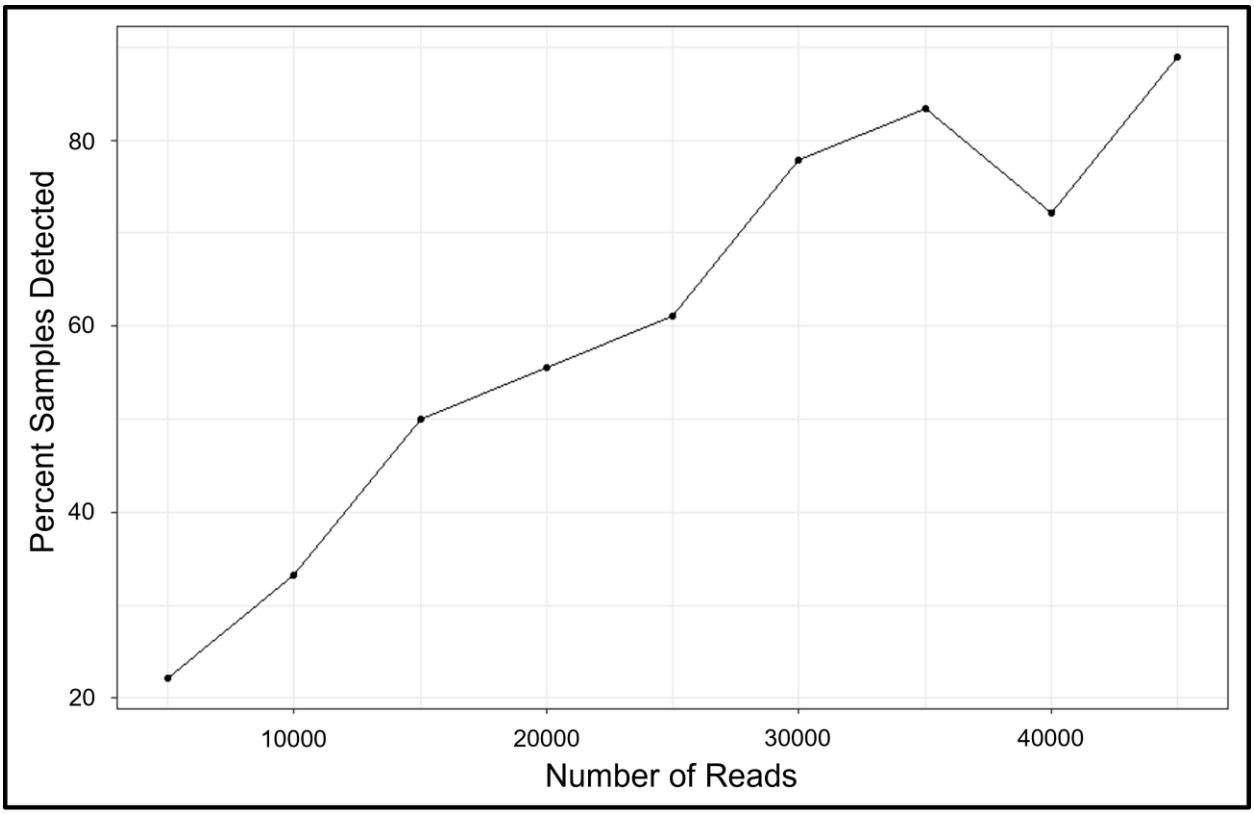
Supplemental Figure 1. Rarefaction curve showing mean Chao1 estimates of bacterial alpha diversity by 16S rRNA gene sequencing depth in barn swallow (*Hirundo rustica*) fecal samples collected in Israel. The error bars represent standard deviation.



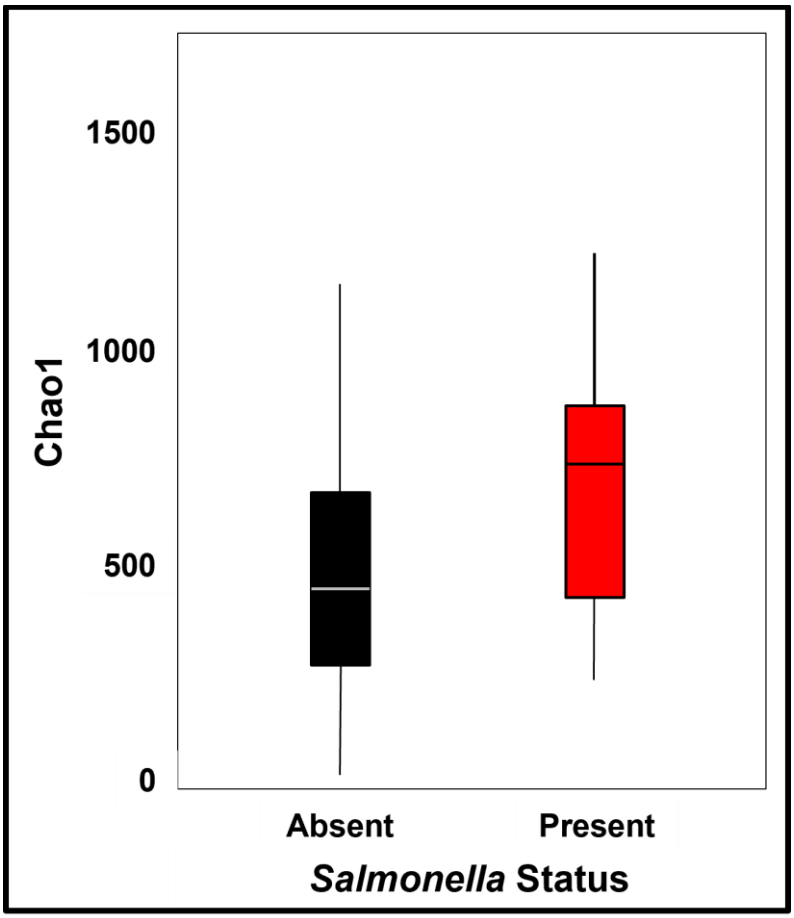
Supplemental Figure 2. Total number of reads in samples absent (black) and present (red) for the presence of *Salmonella* from barn swallow (*Hirundo rustica*) fecal samples collected in Israel. *Salmonella*-present samples had significantly higher numbers of 16S rRNA gene sequence reads than negative samples ($p = 0.002$).



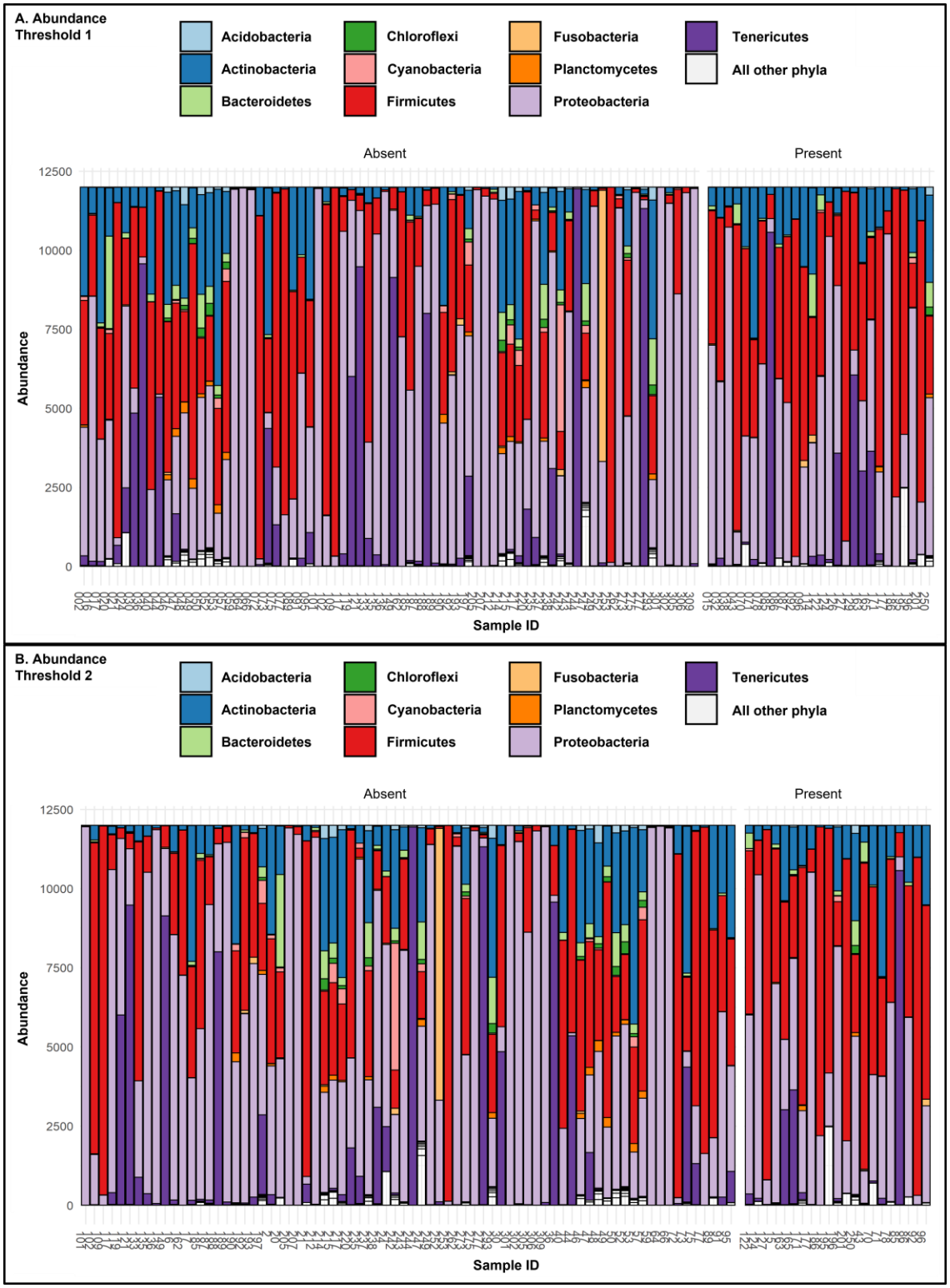
Supplemental Figure S3. *Salmonella* absolute abundance by sample ID in barn swallow (*Hirundo rustica*) fecal samples collected in Israel. Abundance was estimated A) before rarefaction, B) after rarefaction at rngseed = 711, C) after rarefaction at rngseed = 33, and D) and after rarefaction at rngseed = 82. Panels B-D provide examples of the stochasticity of detecting *Salmonella* in a sample. Samples marked with an asterisk had abundance levels greater than 15 reads with actual values listed in the bottom right of each panel following the order of the samples.



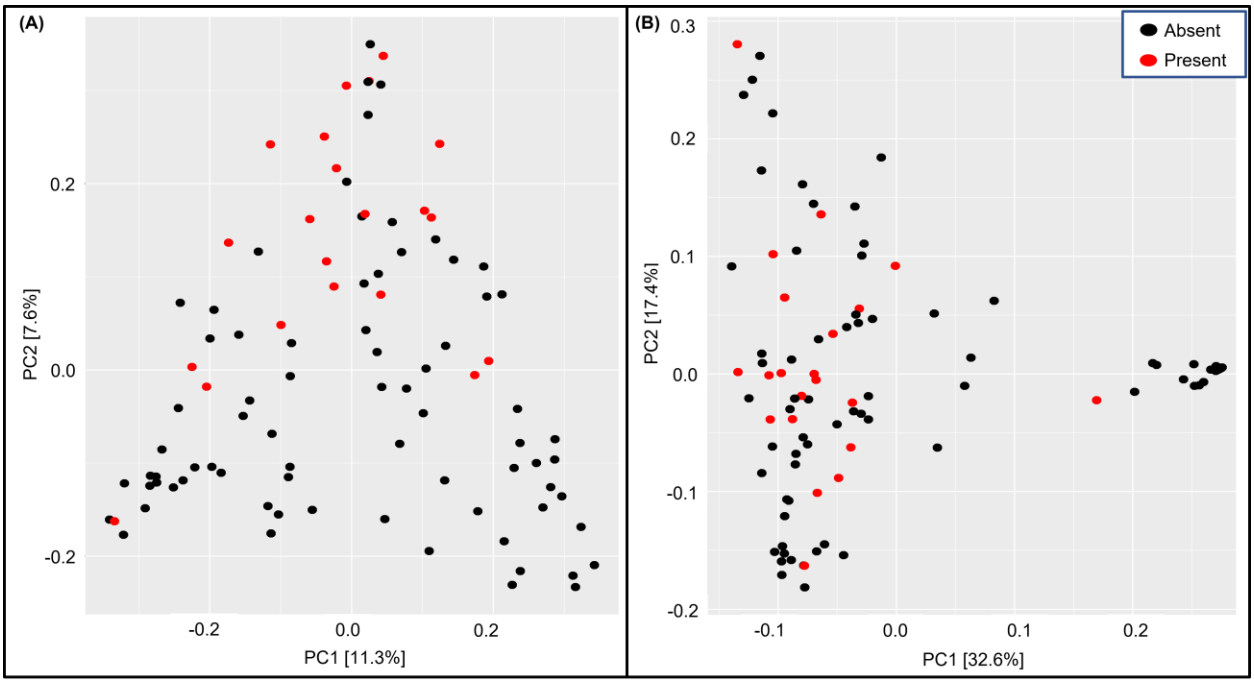
Supplementary Figure 4. The percent of barn swallow (*Hirundo rustica*) fecal samples collected in Israel with greater than 45,000 reads (N = 18) that are positive for the presence of *Salmonella* after rarefying at different 16S rRNA gene sequencing depths (5,000-45,000). All these samples were *Salmonella*-positive when all reads were considered.



Supplementary Figure 5. Bacterial alpha diversity, as estimated by the Chao1 statistic, by *Salmonella* spp. status (absent, present) in barn swallow (*Hirundo rustica*) fecal samples collected in Israel when using a *Salmonella* detection threshold of two reads. *Salmonella* absent samples had significantly lower diversity than positive samples (Mann-Whitney-Wilcoxon test, $p = 0.003$).



Supplementary Figure 6. Proportional abundance of the 10 most abundant bacterial phyla (colors), with all other phyla lumped together (white), showing both *Salmonella* absent (left) and present (right) barn swallows (*Hirundo rustica*) collected in Israel for a *Salmonella* detection threshold of A) one and B) two reads.



Supplementary Figure 7. Principal coordinate analysis plots showing the bacterial communities in barn swallow (*Hirundo rustica*) fecal samples with *Salmonella* (present: red dots) and without (absent: black dots) by **(A)** unweighted UniFrac and **(B)** weighted UniFrac metrics for a *Salmonella* detection threshold of two reads. The amount of the variation explained by each axis is in brackets. Bacterial beta diversity significantly differed for both metrics (unweighted: p = 0.002, weighted: p = 0.013) between *Salmonella*-present and -absent birds. The homogeneity of dispersion was significant for both the unweighted (p = 0.001) and the weighted (p = 0.048) UniFrac metrics.