

Supplementary Materials

Supplemental Methods: Detailed DNA Extraction Protocol

The Puritan swab samples were thawed, and 0.5 μ L of Ready-Lyse Lysozyme (Epicentre Biotechnologies, Madison, WI) was added to each tube and incubated for 1 h with shaking at 600 rpm and 37°C. The swab was re- moved, placed into a spin basket, and centrifuged for 1 min at 9,400 \times g to extract any remaining liquid. The sample was then added to a glass bead tube (0.5 mm; MO BIO, Carlsbad, CA) and vortexed for 10 min at maximum setting. The samples were then incubated in a heat block for 30 min at 65°C and 600 rpm, followed by ice for 5 min and a brief spin. A 150 μ L of Protein Precipitation Buffer (Epicentre Biotechnologies, Madison, WI) was added, and the samples were vortexed briefly, then centrifuged at 22,000 \times g for 10 min. The supernatant was removed and the protein pellet was discarded. The supernatant was mixed with 500 μ L isopropanol and inverted to mix. The mixture was added to a spin column from the Genomic DNA Isolation Kit (Life Technologies, Grand Island, NY), and the remaining steps were followed according to manufacturer's protocol. The samples were eluted with 50 μ L Elution Buffer (Life Technologies, Grand Island, NY).

Supplemental Table 1A: 16S rRNA gene Sequencing Library Results

Read Counts				
Sample	Min	Mean	Median	Max
Total	1	10736	13342	21890
Child N	164	11639	14100	19430
Dog All	711	12559	14448	21890
N	711	9315	8598	21890
MO	4980	14144	14989	16502
I	941	11389	13140	17373
R	12745	15207	14967	18503
Environment	1	12051	13048	16109
Field Blank	520	4676	4307	10064
Controls				
Extraction	189	2357	2296	5207
Sequence	1	26.2	8	117
Mock	1	4.5	3.5	10
Total DNA Concentration (ng/ul)				
Total	0.04	8.517	3	41.39
Child N	0.05	5.434	2.25	31.67
Dog All	0.16	11.001	7.05	41.39
N	0.16	3.92	0.975	18.5
MO	0.6	18.8	19	41.1
I	0.18	3.19	2.14	9.46
R	1.49	16.9	13.9	41.39
Environment	0.07	19.77	19.98	38.82
Field Blank	0.2	0.7717	0.745	1.61
Controls				
Extraction	0.06	0.327	0.31	0.67
Sequence	0.08	0.2267	0.16	0.7
Mock	0.04	0.105	0.08	0.22
qPCR 16S gene copies (/ul DNA)				
Total	43	1.42e6	4570	6.26e7
Child N	111	16073	2470	2.58e5
Dog All	208	1.41e6	10850	6.26e7
N	208	7630	1730	70100
MO	1080	1.72e6	2.24e5	2.52e7
I	314	10782	3940	77600
R	838	3.69e6	95000	6.26e7
Environment	185e5	7.94e6	5.91e6	2.45e7
Field Blank	88	481	405	1040
Controls				
Extraction	56.6	460	273	1400
Sequence	61.9	344	293	729
Mock	42.8	233	181	475

Supplemental Table 1B: Microbial Community Sequencing Library Decontamination

Decontamination Stage	Number Contaminants (% removed)	Common Genera	Prevalence
Starting Taxa	14183 total ASVs		
Sequencing Controls	166 contaminants (1.17%)	<i>Corynebacterium</i> , <i>Sphingomonas</i> , <i>Streptococcus</i> , <i>Bacillus</i>	832 nd most abundant
Extract Controls	149 contaminants (1.06%)	<i>Corynebacterium</i> , <i>Streptococcus</i> , <i>Staphylococcus</i> <i>Sphingomonas</i>	591 st most abundant
Field Blanks	188 contaminants (1.36%)	<i>Corynebacterium</i> , <i>Streptococcus</i> , <i>Staphylococcus</i> <i>Sphingomonas</i>	705 th most abundant
Final Taxa	13680 total ASVs (3.55%)		

Using 'decontam' package

Supplemental Table 2: AAI Behavioral Observations and Patient-Therapy Dog Contact Scores

Observed Interaction Behaviors	Patients Observed
N *	46
Total time spent with dog, in minutes mean (range)	14 (2-42)
Interact with Dog N (%)	44 (95.7)
Sat on Floor N (%)	28 (61.9)
Touch Head N (%)	43 (93.5)
Touch Back N (%)	27 (58.7)
Touch Belly N (%)	13 (28.2)
Touch Paws N (%)	11 (23.9)
Feed Dog N (%)	24 (52.2)
Walk Dog N (%)	10 (21.7)
Kiss Dog N (%)	2 (4.3)
Hug Dog N (%)	5 (10.9)
Contact Score Level Calculation	
Interact Score+ mean (range)	7.89 (0-17)
Interact Score x Time ^ mean (range) median (IQR)	127 (0-403) 108 (56.25-197.75)
Contact Score Level High (\geq median) N (%) Low ($<$ median) N (%)	25 (51%) 24 (49%)

* observations not recorded for 3 patients

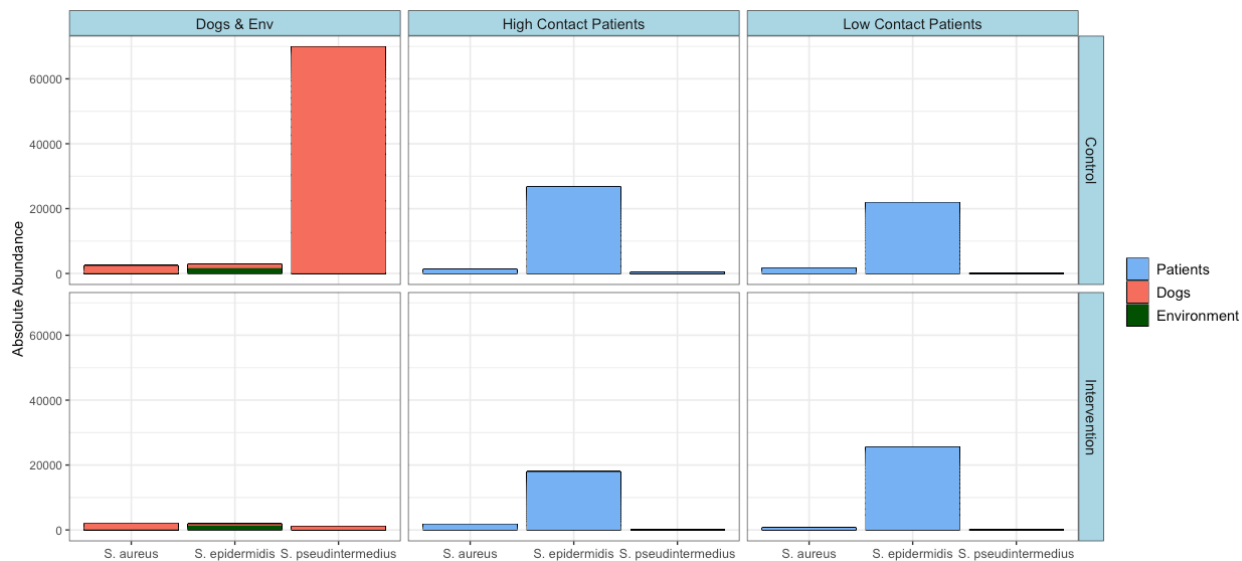
+ score based on total tally of individual behaviors, weighted based on closeness of contact: 1 point for interact with dog, walk dog, and sat on floor, 2 points touches, 3 points for feed, hug, or kiss dog.

^ score multiplied by total time with dog

Supplemental Table 3: Relative Abundance by Host and Site by Phyla and Genus
(Taxa > 3% total abundance)

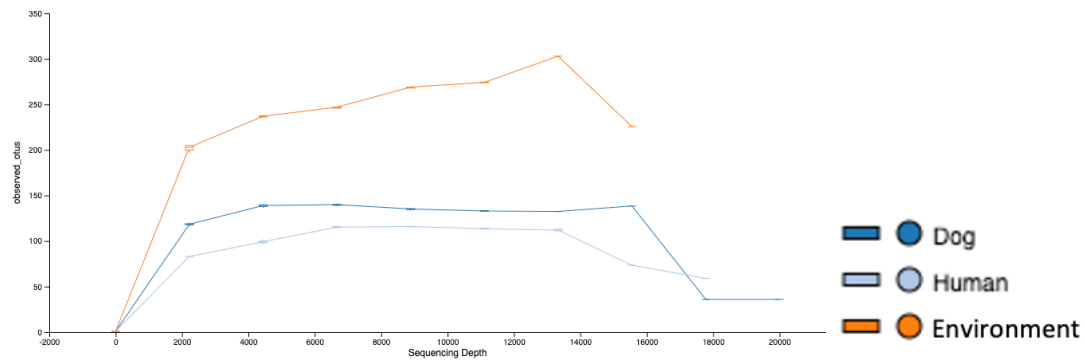
Taxon (Phyla & Genus)	Patient Nasal	Dog Nasal	Dog Oral	Dog Perineal	Dog Inguinal	Environment
<i>Actinobacteria</i>	0.0483	0.0330	0.0432	0.2035	0.0197	0.0522
<i>Corynebacterium</i>	0.1130	0.0330	0.0922	0.2035	0.0431	0.1968
<i>Micrococcus</i>						0.0313
<i>Actinomyces</i>						
<i>Bacteroidetes</i>	0.0137	0.0213	0.0893	0.0704	0.0236	0.0248
<i>Porphyromonas</i>		0.0602	0.1604	0.1065	0.0673	
<i>Capnocytophaga</i>			0.0883			
<i>Bacteroides</i>				0.0734		
<i>Prevotella</i>				0.0312		0.0365
<i>Firmicutes</i>	0.0667	0.1147	0.0212	0.0360	0.0341	0.0633
<i>Staphylococcus</i>	0.2714	0.2886	0.0333	0.0649	0.0453	0.0465
<i>Streptococcus</i>	0.1834	0.0411		0.0952	0.0432	0.1011
<i>Faecalibacterium</i>						0.0688
<i>Blautia</i>				0.0433		
<i>Alloiococcus</i>	0.0382					
<i>Lactobacillus</i>						0.0369
<i>Dorea</i>				0.0317		
<i>Fusobacteria</i>		0.0120	0.0415	0.0370	0.0103	
<i>Fusobacterium</i>			0.0415	0.0370		
<i>Proteobacteria</i>	0.0368	0.0832	0.0559	0.0420	0.0191	0.0204
<i>Moraxella</i>	0.0572	0.1927	0.0396	0.0386		
<i>Conchiformibius</i>		0.0462	0.1879			
<i>Lautropia</i>			0.0741			
<i>Campylobacter</i>				0.0648		
<i>Escherichia</i>				0.0435		
<i>Pantoea</i>						0.0427
<i>Neisseria</i>			0.0408			
<i>Sphingomonas</i>					0.0349	
<i>Pseudomonas</i>					0.0345	
<i>Spirochaetes</i>			0.0274			

Supplemental Figure 1: Absolute Abundance of Key *Staphylococcus* Species

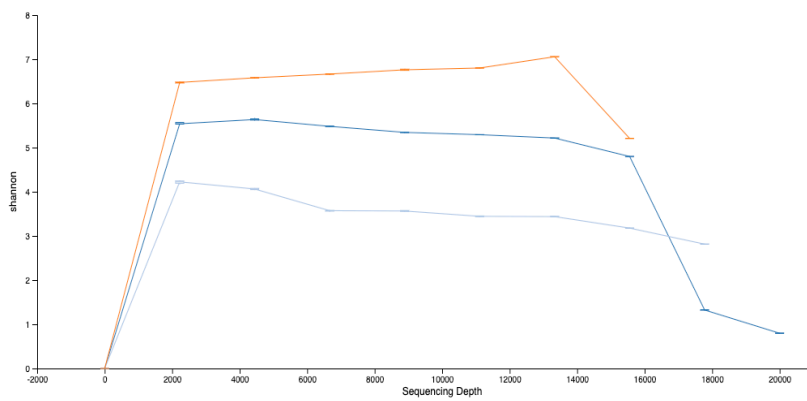


Supplemental Figure 2: Alpha Diversity Curves by Host

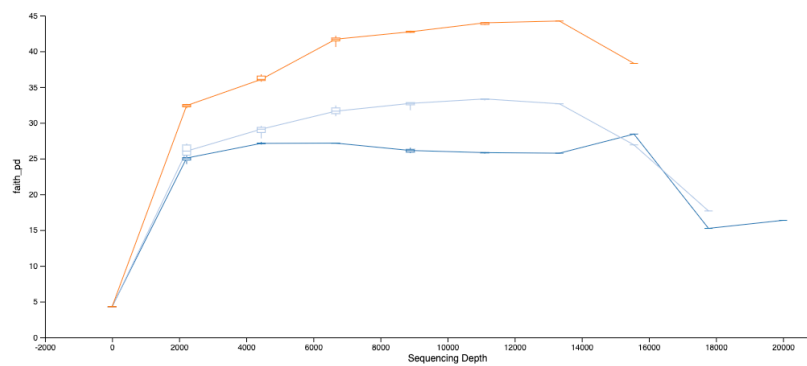
A. Total Taxa



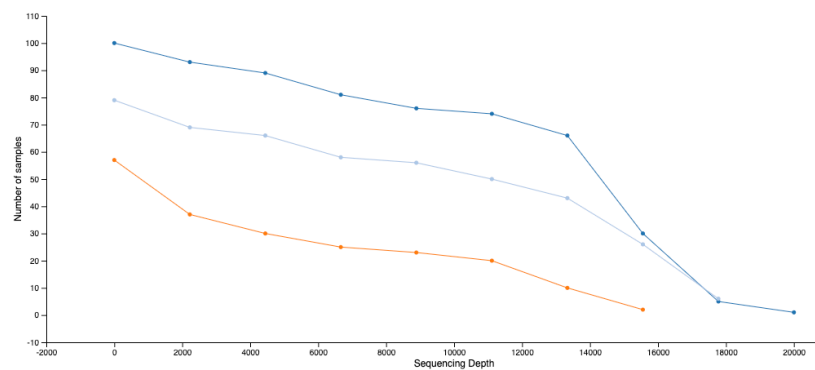
B. Shannon Diversity



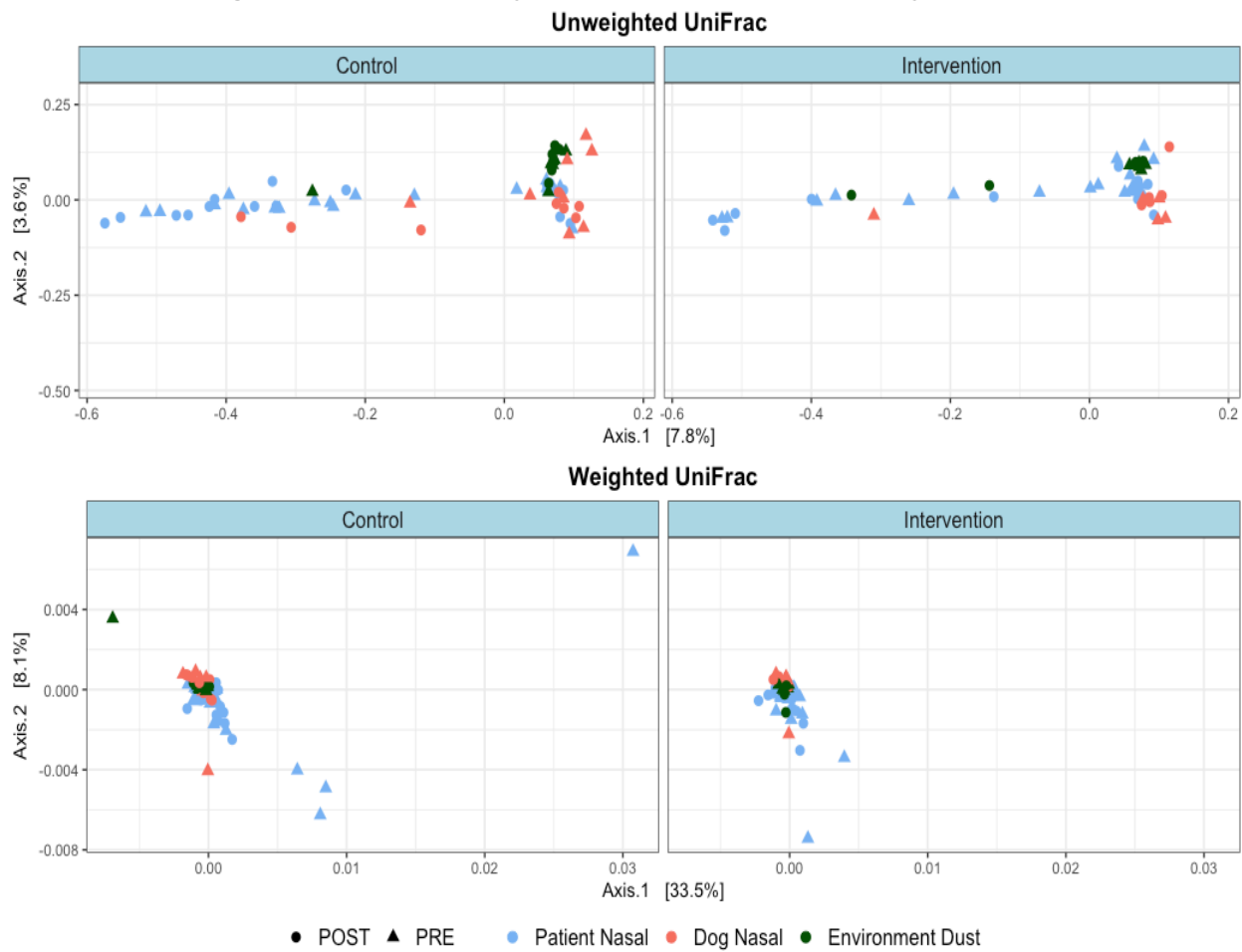
C. Faith's Phylogenetic Diversity



D. Number of Samples

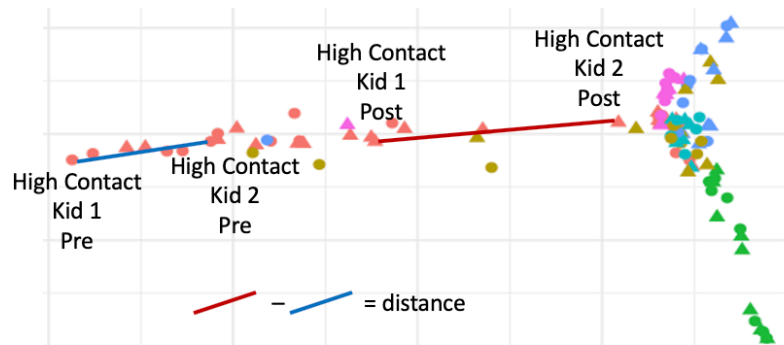


Supplemental Figure 3: Beta Diversity Principle Coordinates Analysis Plots

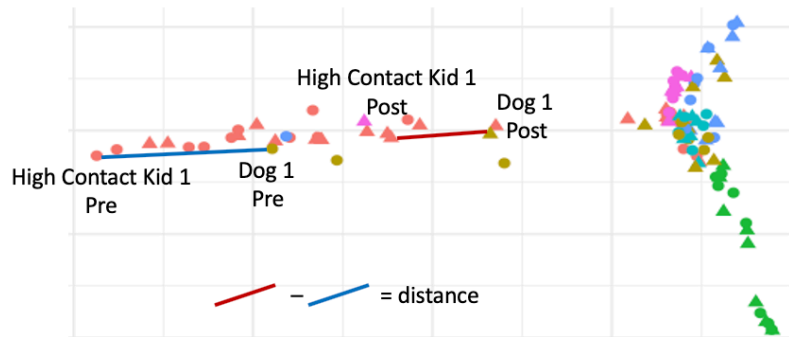


Supplemental Figure 4: Graphical Example for Calculations of Beta Distance in Figure 4

A. Kid-Kid Distance Example

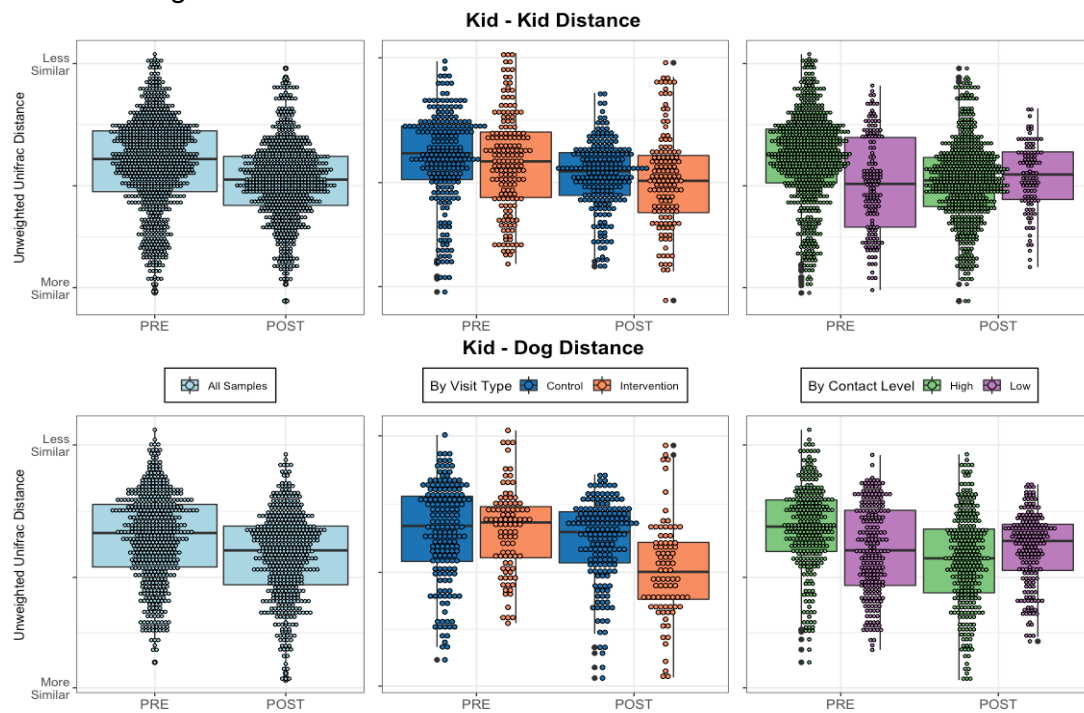


B. Kid-Dog Distance Example

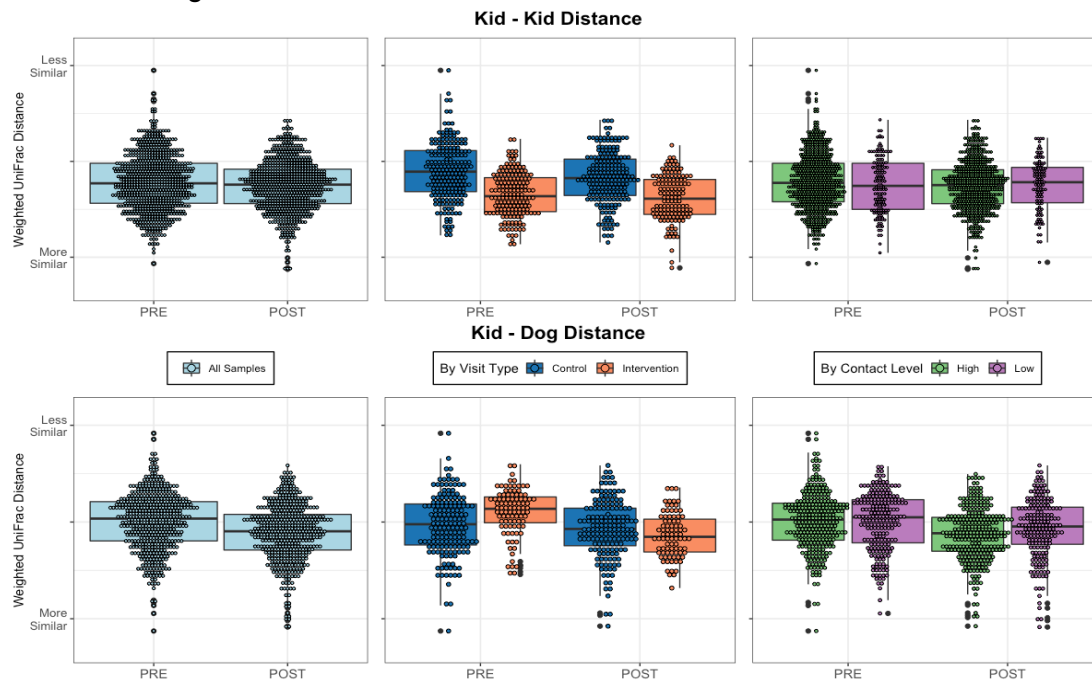


Supplemental Figure 5: Visit Type and Contact Level in Microbial Composition Differences Between Patients and Between Patients and Therapy Dogs

A. Unweighted UniFrac Distance



B. Weighted UniFrac Distance



Supplemental Table 4: Microbial Composition Differences between Patients and Between Patients and Therapy Dogs Before the Visit Compared to After Visit, Based on Visit Type and Contact Score

Results for Beta Distance via PERMANOVA model

Group	Metric	Kid-Kid Distance		Kid-Dog Distance	
		F-statistic	p	F-statistic	p
Unadjusted Effect Pre versus Post					
All Samples	Unweighted UniFrac	47.068	0.0001	38.168	0.0001
	Weighted UniFrac	19.33	0.0001	36.378	0.0001
Control Visits	Unweighted UniFrac	15.926	0.0002	2.294	0.128
	Weighted UniFrac	17.78	0.0001	4.274	0.025
Intervention Visits	Unweighted UniFrac	8.737	0.003	35.188	0.0001
	Weighted UniFrac	1.049	0.313	44.689	0.0001
High Contact	Unweighted UniFrac	89.538	0.0001	82.758	0.0001
	Weighted UniFrac	16.017	0.0001	28.701	0.0001
Low Contact	Unweighted UniFrac	2.418	0.118	0.067	0.829
	Weighted UniFrac	0.474	0.514	9.766	0.001
Multivariate Adjusted Effect					
Pre versus Post visit	Unweighted UniFrac	47.642	0.0001	38.626	0.0001
	Weighted UniFrac	20.962	0.0001	36.422	0.0001
Contact Level	Unweighted UniFrac	10.317	0.0002	2.245	0.135
	Weighted UniFrac	6.691	0.0003	0.829	0.328
Visit Type	Unweighted UniFrac	1.325	0.263	4.728	0.011
	Weighted UniFrac	58.887	0.0001	2.138	0.094

PERMANOVA FDR-corrected **p<0.001**, *p 0.01-0.001*

Unadjusted Effect = difference in microbial composition distance between patients in pre-visit samples compared to microbial composition distance between patients in post-visit samples (kid-kid distance), or significant difference in microbial composition distance between patients and therapy dogs in pre-visit samples compared to microbial composition distance between patients and therapy dogs in post-visit samples (kid-dog distance) within each exposure group.

Example interpretation – In control visits, there is a significant difference in the microbial composition between patients before the visits compared to after the visit (p=0.0002 unweighted, 0.0001 weighted)

Adjusted Effect = independent effect of each exposure of the microbial composition distance between patients (kid-kid distance) or microbial composition distance between patients and therapy dogs (kid-dog distance).

Example interpretation – There is a significant difference in the microbial composition between patients with high contact compared to microbial composition between patients with low contact, independent of collection time (pre versus post) or visit type (control versus intervention) (p=0.0002 unweighted, 0.0003 weighted)