

Canine oral microbiome transplant - Preliminary Report v3

(all data were re-analyzed according to the revised metadata;

All figures are updated; changes in text are highlighted in cyan color)

Prepared by Yuki Chan and Rory Watt (May ??, 2018)

A) Technical Overview of how the Illumina MiSeq sequencing data was processed and taxonomy was assigned:

(1) Primer sequences were trimmed from the clean reads using cutadapt

Ref: Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet.journal*, 17(1), pp-10.

(2) Sequences were processed using the DADA2 R package

Ref: Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: high-resolution sample inference from Illumina amplicon data. *Nature Methods*, 13(7), 581.

Ref: Callahan, B. J., McMurdie, P. J., & Holmes, S. P. (2017). Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. *The ISME Journal*, 11(12), 2639.

“DADA2 is a software package that models and corrects Illumina-sequenced amplicon errors. DADA2 infers sample sequences exactly, without coarse-graining into OTUs, and resolves differences of as little as one nucleotide...”

DADA2 implements a new quality-aware model of Illumina amplicon errors. Sample composition is inferred by dividing amplicon reads into partitions consistent with the error model. The full workflow involves: filtering, error learning and modeling, dereplication, merging paired-end reads, and chimera identification” (Quote from Callahan et al. 2016)

Data stats after DADA2 pipeline:

SampleID	RawReads	clean	filtered	denoised	merged	nonchim	%output
MT-A-1	50265	35144	34247	34247	24877	20685	41.2%
MT-A-2	50968	35500	34708	34708	25757	20851	40.9%
MT-A-3	54617	35000	34061	34061	27890	24538	44.9%
MT-A-4	49865	34805	33956	33956	25122	20178	40.5%
MT-B-1	49589	34992	34160	34160	25570	21456	43.3%
MT-B-2	53257	35478	34450	34450	28033	24079	45.2%
MT-B-3	55239	35060	34231	34231	27703	23592	42.7%
MT-B-4	49250	34646	33925	33925	27474	23103	46.9%
MT-C-1	53289	34817	34269	34269	26331	20717	38.9%
MT-C-2	60002	34883	34239	34239	29144	25740	42.9%
MT-C-3	57681	34992	34470	34470	28566	23427	40.6%
MT-C-4	51699	34849	34314	34314	26374	21686	41.9%
MT-D-1	51900	35000	34393	34393	26761	21670	41.8%
MT-D-2	51878	35009	34387	34387	26129	20253	39.0%
MT-D-3	54702	34617	33961	33961	26869	20929	38.3%
MT-D-4	47834	34408	33849	33849	25489	20566	43.0%

MT-E-I-1	51331	34772	33987	33987	25426	20800	40.5%
MT-E-II-1	54934	34848	34011	34011	27058	19876	36.2%
MT-E-III-1	51587	34949	34087	34087	26424	19000	36.8%
MT-E-IV-1	51141	34941	33998	33998	25444	19443	38.0%
MT-E-V-1	56223	35034	34177	34177	27120	19545	34.8%
MT-E-V-2 removed	59157	34975	34252	34252	29908	22116	37.4%
MT-F-1	53046	34633	34083	34083	27705	23819	44.9%
MT-F-2	52271	34933	34305	34305	26367	19841	38.0%
MT-F-3	52542	35009	34373	34373	26276	20763	39.5%
MT-F-4	51180	35169	34549	34549	26088	20615	40.3%
MT-G-1	51628	35246	34628	34628	26390	21473	41.6%
MT-G-2	52810	34549	33977	33977	25882	19090	36.1%
MT-G-3	49457	34389	33817	33817	25868	19570	39.6%
MT-G-4	55495	34808	34175	34175	27205	22848	41.2%
MT-H-1	52976	35244	34612	34612	26429	21923	41.4%
MT-H-2	52791	35304	34571	34571	26487	21527	40.8%
MT-H-3	52368	34638	34047	34047	26388	20480	39.1%
MT-H-4	51536	35280	34631	34631	25986	22714	44.1%
MT-I-1	52996	35289	34608	34608	26597	21711	41.0%
MT-I-2	55780	34808	34115	34115	26696	20330	36.4%
MT-I-3	49221	34732	34293	34293	26238	21201	43.1%
MT-I-4	51675	35017	34359	34359	26118	22772	44.1%
MT-J-1	54336	35135	34479	34479	27661	22780	41.9%
MT-J-2	53817	35060	34351	34351	27544	21665	40.3%
MT-J-3	56563	34899	34138	34138	29498	25406	44.9%
MT-J-4	55658	35560	34805	34805	28791	24203	43.5%
MT-K-1	54890	35518	34645	34645	27321	23256	42.4%
MT-K-2	54327	35051	34362	34362	26543	22164	40.8%
MT-K-3	51341	34807	34169	34169	27723	23614	46.0%
MT-K-4	53320	35026	34277	34277	26154	21370	40.1%
MT-L-1	50316	34672	33911	33911	25401	19924	39.6%
MT-L-2	51657	35102	34263	34263	26928	21030	40.7%
MT-L-3	58197	35043	34052	34052	29715	27059	46.5%
MT-L-4	53352	35552	34848	34848	27182	21792	40.8%
MT-M-1	52059	35035	34049	34049	25566	20515	39.4%
MT-M-2	53180	34589	33788	33788	26763	20618	38.8%
MT-M-3	50304	34984	34350	34350	27257	21687	43.1%
MT-M-4	51884	34580	33777	33777	25292	19853	38.3%
MT-N-1	52130	35457	34721	34721	25555	20643	39.6%
MT-N-2	55280	35432	34608	34608	27423	19635	35.5%
MT-N-3	52272	34831	33986	33986	26424	19408	37.1%
MT-N-4	56101	35630	34656	34656	28763	24902	44.4%
MT-O-1	53803	35605	34687	34687	26806	22185	41.2%
MT-O-2	55477	35085	34204	34204	26594	19698	35.5%

MT-O-3	51406	34705	34086	34086	26953	20183	39.3%
MT-O-4	57804	30635	29707	29707	29442	29353	50.8%
MT-P-1	49664	34687	33925	33925	24797	21097	42.5%
MT-P-2	53456	35255	34454	34454	27137	20575	38.5%
MT-P-3	51636	35196	34306	34306	26042	19996	38.7%
MT-P-4	50803	35690	34867	34867	26050	20257	39.9%
MT-Q-1	49872	35359	34365	34365	25526	21759	43.6%
MT-Q-2	56068	35296	34422	34422	27882	24249	43.2%
MT-Q-3	49932	34747	34019	34019	27181	20859	41.8%
MT-Q-4	49970	34400	33805	33805	24521	19718	39.5%
MT-R-1	49775	34750	34182	34182	24948	19961	40.1%
MT-R-2	50983	34825	34290	34290	26408	20666	40.5%
MT-R-3	51757	35202	34644	34644	26760	20644	39.9%
MT-R-4	50754	35236	34708	34708	26132	20203	39.8%
MT-S-1	53333	34874	34275	34275	27725	25310	47.5%
MT-S-2	49249	34300	33739	33739	26851	20475	41.6%
MT-S-3	47863	34909	34372	34372	25541	20172	42.1%
MT-S-4	50925	34430	33799	33799	24804	19641	38.6%
Transplant-A	54312	34958	34077	34077	26218	19070	35.1%
Transplant-C	54635	34958	34087	34087	26529	19030	34.8%
Transplant-F	62548	34815	33942	33942	30944	29165	46.6%
Transplant-H	53950	34755	33992	33992	27057	18614	34.5%
Transplant-J	56797	34907	34068	34068	28091	21314	37.5%
Transplant-L	56037	35545	34629	34629	27779	21479	38.3%
Transplant-N	57660	35093	34325	34325	27844	20902	36.3%
Transplant-P	57327	34916	33943	33943	28430	20442	35.7%
Transplant-Q	56452	35457	34637	34637	28008	19784	35.0%

Stats on the number of reads in all the samples:

min	18614	18614
max	29353	29353
mean	21525	21532
SD	2110	2098

N.B. The numbers of high-quality sequence reads are quite even across all samples.

These 86 samples resulted in 1759 ASVs (Amplicon Sequence Variants), conceptually equivalent to OTUs defined at 100% identity.

Stats on the number of ASVs in all the samples:

min	169	139
max	439	439
mean	282	281
SD	53	55

(3) Statistical analyses using the phyloseq and other R package

Ref: McMurdie, P. J., & Holmes, S. (2013). phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS one*, 8(4), e61217.

Ref: Callahan, B. J., Sankaran, K., Fukuyama, J. A., McMurdie, P. J., & Holmes, S. P. (2016). Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. *F1000Research*, 5.

"An important first step in analyzing microbiome data is to do unsupervised, exploratory analysis":

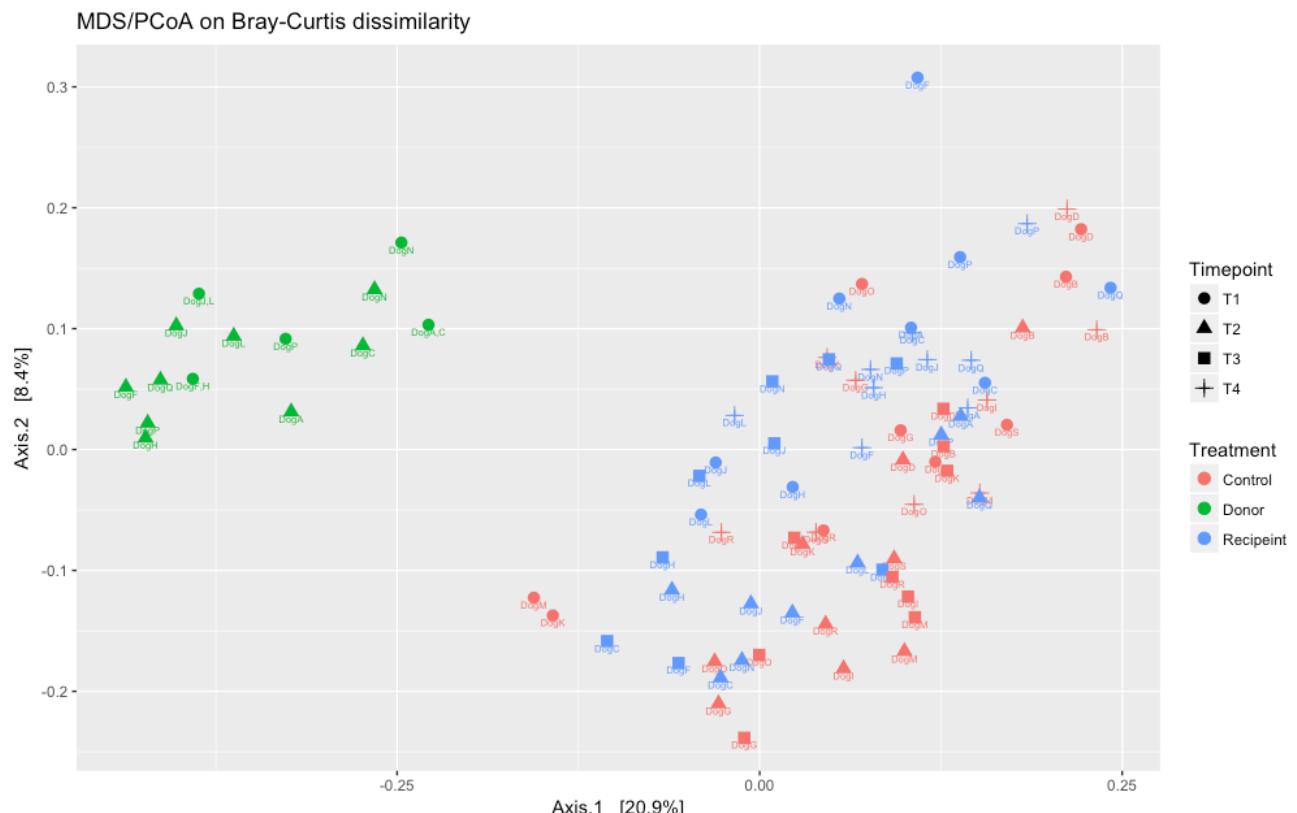


Figure 1 Principal Coordinates Analysis (PCoA) based on the Bray–Curtis dissimilarity measure of the ASV data; which takes into account the composition of taxa/ASVs in the samples.

The Bray Curtis dissimilarity measure compares samples based on the presence/absence of specific taxa (in this case, the presence/absence of ASVs)

This data can then be visualized on an ordination plot, such as a Principal Coordinates Analysis (PCoA plot).

Each dot on the plot represents an individual sample.

Here, the 9 donor dog samples taken at the T2 time-point for transplant (● = Transplant-A, C, F, H, J, L, N, P, Q) and the 5 donor dog samples taken at baseline T1 time-point (● = MT-E-I-1, MT-E-II-1, MT-E-III-1, MT-E-IV-1, MT-E-V-1) cluster together. There is a clear distinction between these 14 samples, and all the control dogs samples, as well as the recipient dogs samples taken at all time-points.



Figure 2 PCoA based on the unweighted UniFrac measure of the ASV data; which takes into account the phylogenetic distance but not the abundances of taxa/ASVs.

The Unifrac Principal coordinates analysis plot is constructed based on a phylogenetic tree, and compares the phylogenetic relatedness of the taxa (ASVs) in each sample. The unweighted analysis does not take account of the relative abundance of the respective taxa, whereas the weighted Unifrac DOES take account of abundance.

The unweighted Unifrac PCoA plot shown above is very similar to the Bray Curtis Dissimilarity plot shown previously.

MDS/PCoA on Weighted UniFrac

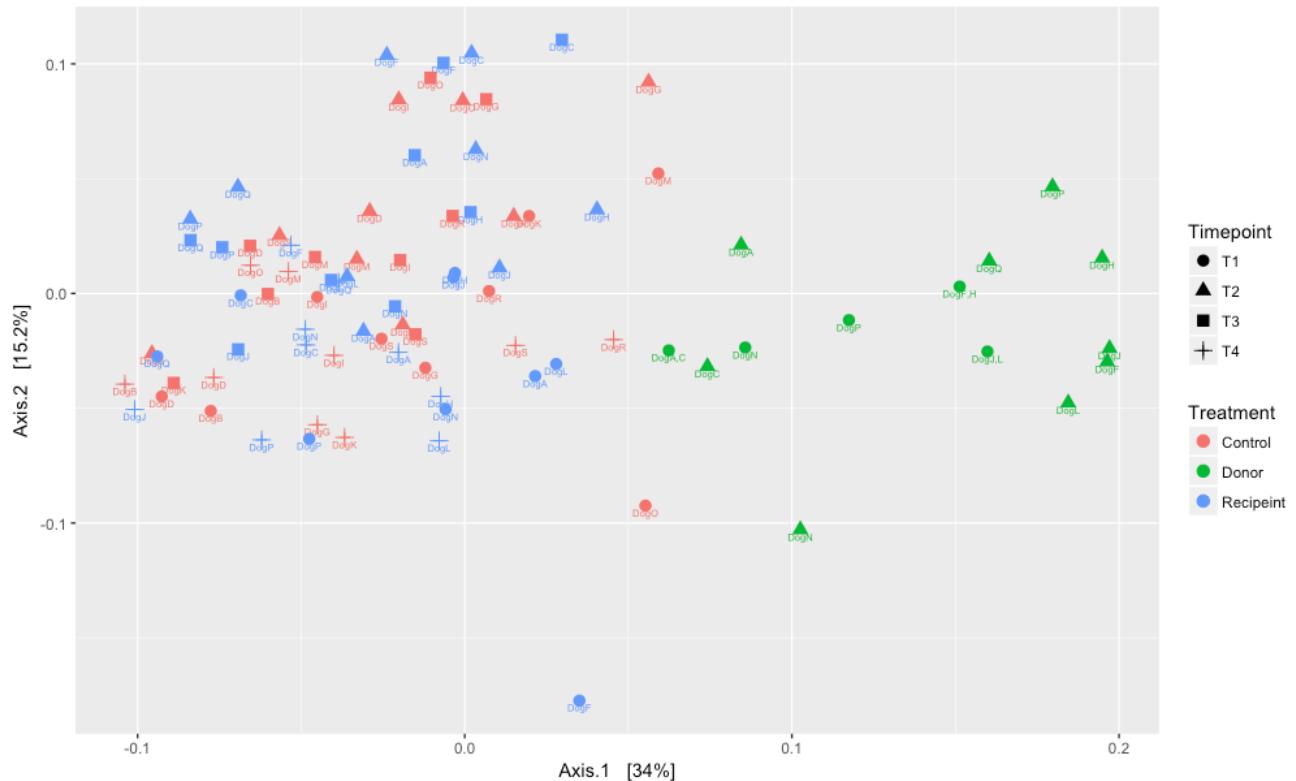


Figure 3 PcoA based on the weighted UniFrac measure of the ASV data; which takes into account the phylogenetic distance AND the abundances of taxa/ASVs.

Here, in the weighted Unifrac analysis, the relationship is somewhat similar to that shown in the previous two ordination plots. The 5 donor dog E samples (\bullet = MT-E-I-1, MT-E-II-1, MT-E-III-1, MT-E-IV-1, MT-E-V-1) taken at the baseline (T1), and the 9 donor dog samples for transplant (\bullet = Transplant-A, C, F, H, J, L, N, P, Q) still cluster together.

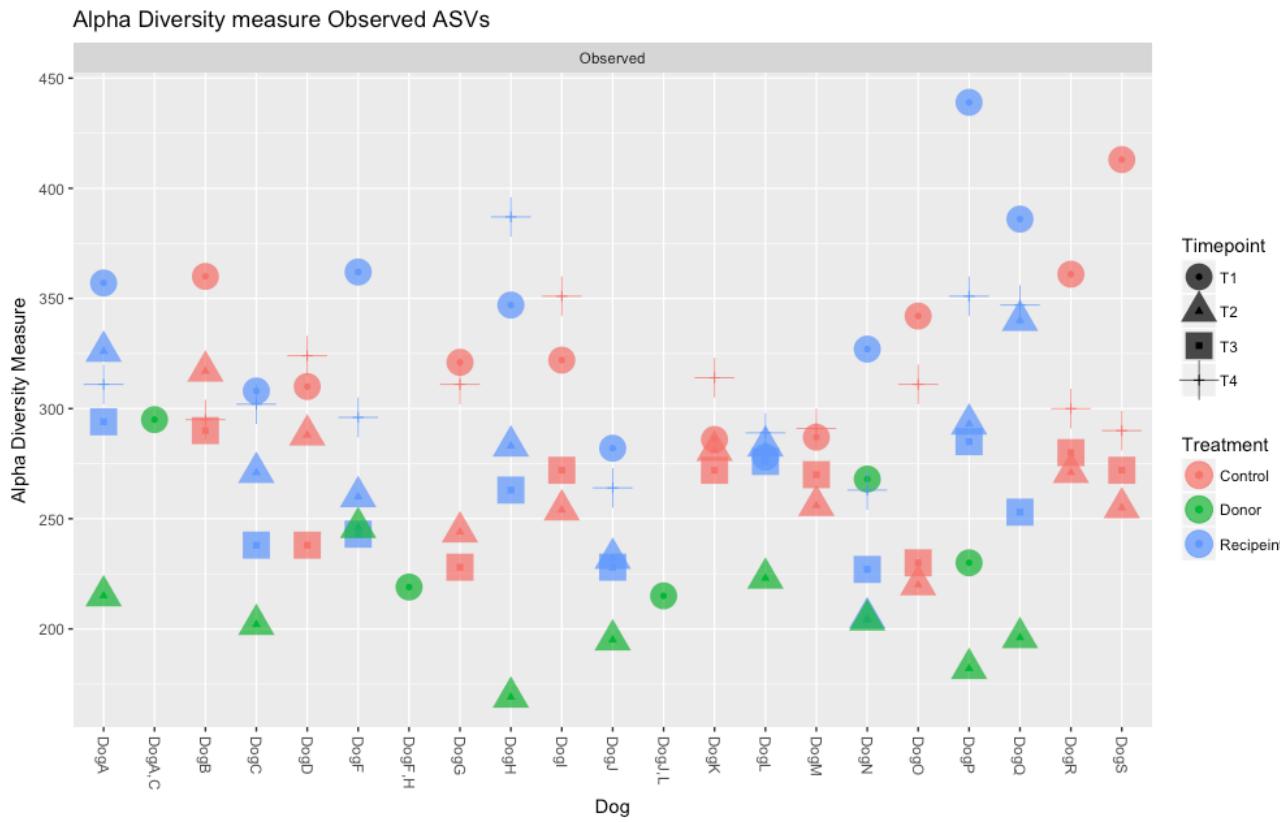


Figure 4 Number of observed ASVs (species richness) in all samples (by individual Dogs)

These two plots show the levels of taxonomic diversity in each of the respective samples. The observed ASVs refer to the species richness in the samples, whereas the Shannon entropy measures both species richness and evenness. This is plotted per dog (x-axis) – showing the respective levels of diversity for each of the 4 time-points for each dog. Noticed that all the transplant samples from donor E dog possess the lowest diversity.

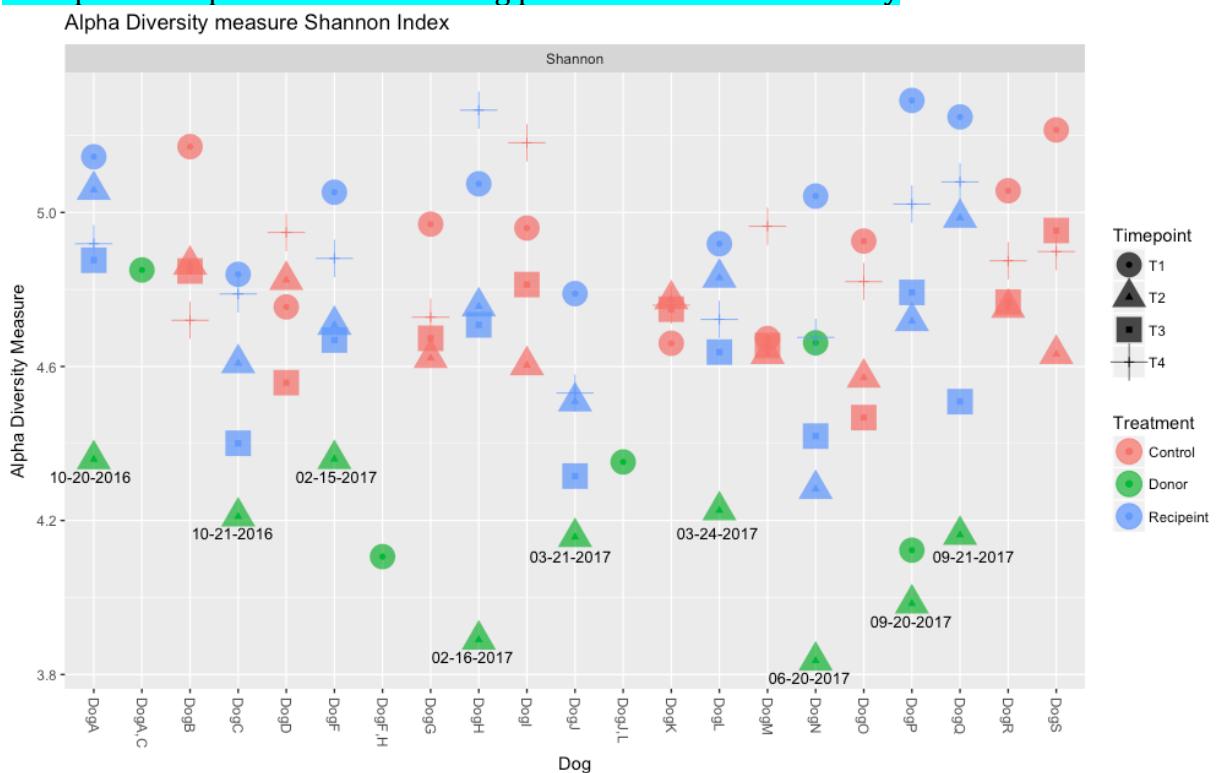


Figure 5 Shannon entropy (alpha diversity measure) in all samples

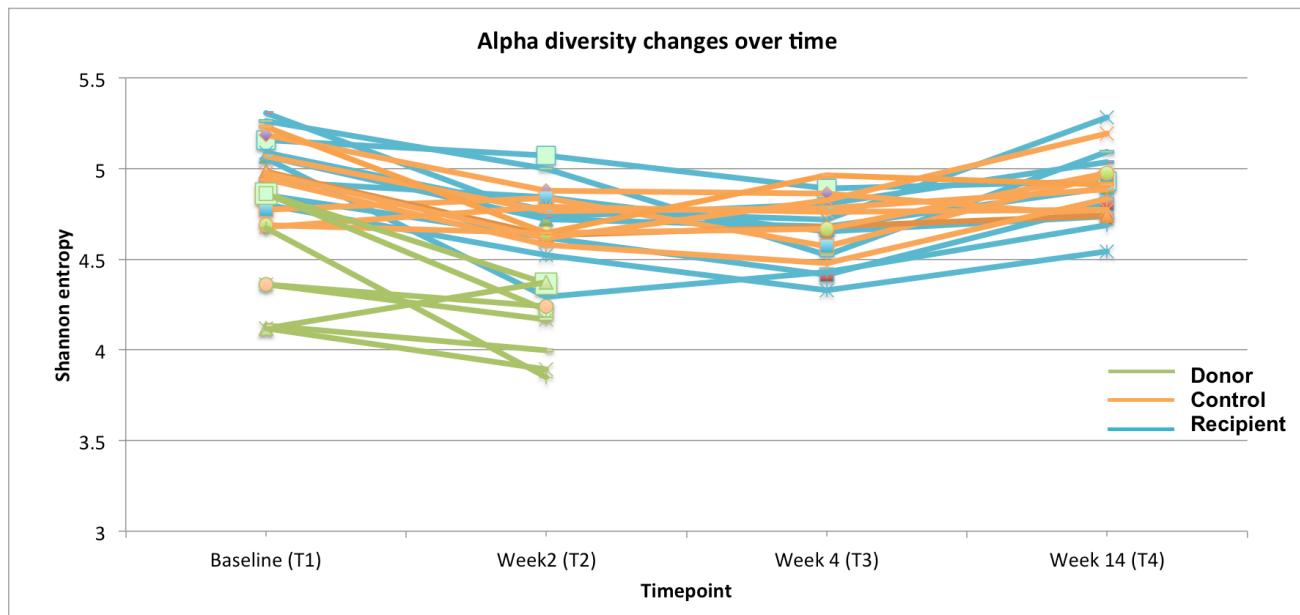
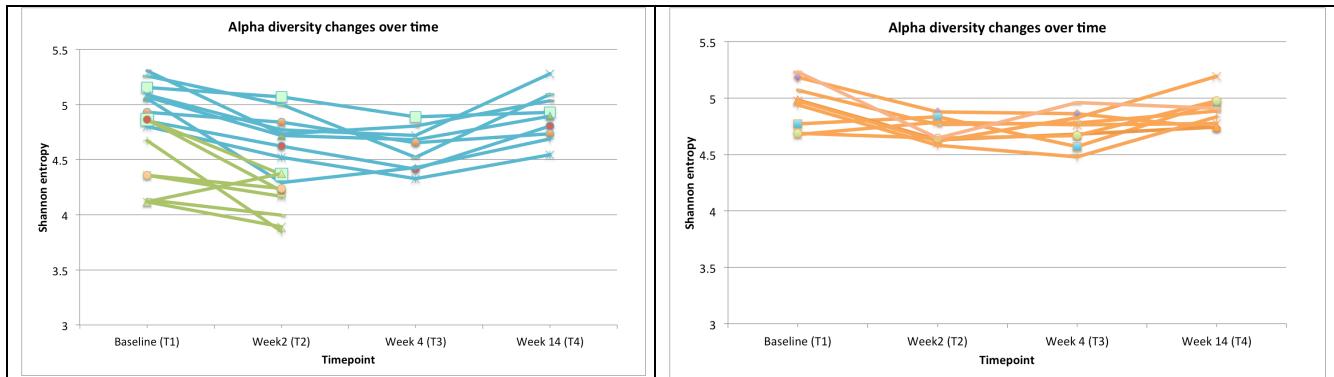


Figure 6 Shannon entropy in all samples (by Time-points)



The 9 samples taken from the donor dog E at T2 for the transplantation were at the lowest diversity

The recipient dogs seem to have decreased diversity in their microbiota after transplantation: comparing T3 to T2, 7/9 dogs have a drop in their shannon entropy. The diversity of the microbiota restored at T4 (8/9 at levels still lower than the baseline).

The total diversity changes in control dogs seem to have slightly different trends. Comparing T3 to T2 microbiota in the same dog, some have decreased diversity (3/9), two of them maintain at the same and four of them have gained diversity. Towards the end, half of the control dogs (5/9) have decreased diversity compared to baseline.

(4) Taxonomy Assignment

"The DADA2 package provides a native implementation of the naive Bayesian classifier method (Wang et al. 2007) for taxonomy assignment. It takes as input a set of sequences to be classified, and a training set of reference sequences with known taxonomy, and outputs taxonomic assignments with at least minBoot (default at 50) bootstrap confidence. The dada2 package also implements a method to make species level assignments based on exact matching between ASVs and sequenced reference strains. Recent analysis (Edgar 2018) suggests that exact matching (or 100% identity) is the only appropriate way to assign species to 16S gene fragments." (Quoted from DADA2 workflow)

We use a curated reference sequence database that comprised of the RDP trainset 16 (Cole 2014, derived from RDP Release 11.5 that consists of 3,356,809 aligned and annotated 16S rRNA sequences, updated 2016-09-30), eHOMD 16S rRNA RefSeq Version 15.1 (Chen et al. 2010, updated 2017-11-16) and the full set of canine oral microbiome 16S rRNA gene sequences (Dewhirst et al. 2012, 416 full-length sequences). Mothur (Schloss 2009) was used to process the reference sequences.

NB. The silva SSU reference database (v132 last updated 2017-12-13) is not used due to the incompatible taxonomy with the NCBI, HOMD, RDP databases, most notably due to the proposed superphylum, Patescibacteria that includes candidate phyla Gracilibacteria (GN02), Microgenomates, Parcubacteria, and Saccharibacteria (TM7)

Ref: Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and environmental microbiology*, 73(16), 5261-5267.

Ref: Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., Hartmann, M., Hollister, E.B., Lesniewski, R.A., Oakley, B.B., Parks, D.H., Robinson, C.J. and Sahl, J.W., 2009. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and environmental microbiology*, 75(23), pp.7537-7541.

Ref: Edgar, R. C. (2018). Updating the 97% identity threshold for 16S ribosomal RNA OTUs. *Bioinformatics*, bty113, <https://doi.org/10.1093/bioinformatics/bty113>.

Ref: Cole, J. R., Q. Wang, J. A. Fish, B. Chai, D. M. McGarrell, Y. Sun, C. T. Brown, A. Porras-Alfaro, C. R. Kuske, and J. M. Tiedje. 2014. Ribosomal Database Project: data and tools for high throughput rRNA analysis Nucl. Acids Res. 42(Database issue):D633-D642; doi: 10.1093/nar/gkt1244 [PMID: 24288368]

Ref: Chen, T., Yu, W-Han, Izard, J., Baranova, O.V., Lakshmanan, A., Dewhirst, F.E. (2010) The Human Oral Microbiome Database: a web accessible resource for investigating oral microbe taxonomic and genomic information. *Database*, Vol. 2010, Article ID baq013, doi: 10.1093/database/baq013

Ref: Dewhirst, Floyd E., Erin A. Klein, Emily C. Thompson, Jessica M. Blanton, Tsute Chen, Lisa Milella, Catherine MF Buckley, Ian J. Davis, Marie-Lousie Bennett, and Zoe V. Marshall-Jones. "The canine oral microbiome." *PloS one* 7, no. 4 (2012): e36067.

The table below provides a general overview of the microbiota composition in all samples at the phylum rank.

Phylum	No. of ASVs	No. of reads
Absconditabacteria (SR1)	33	48369
Acidobacteria	1	7
Actinobacteria	73	25251
Bacteroidetes	392	607403
Chlorobi	19	43700
Chloroflexi	2	18
Cyanobacteria	1	6
Elusimicrobia	3	870
Firmicutes	363	317726
Fusobacteria	61	104684
Gracilibacteria (GN02)	25	15039
Proteobacteria	422	494525
Saccharibacteria (TM7)	67	45025
Spirochaetes	205	93099
Synergistetes	42	37809
Tenericutes	33	9593
WPS-2	1	350
<NA>	16	7662

Table 1 ASVs abundance in each phylum

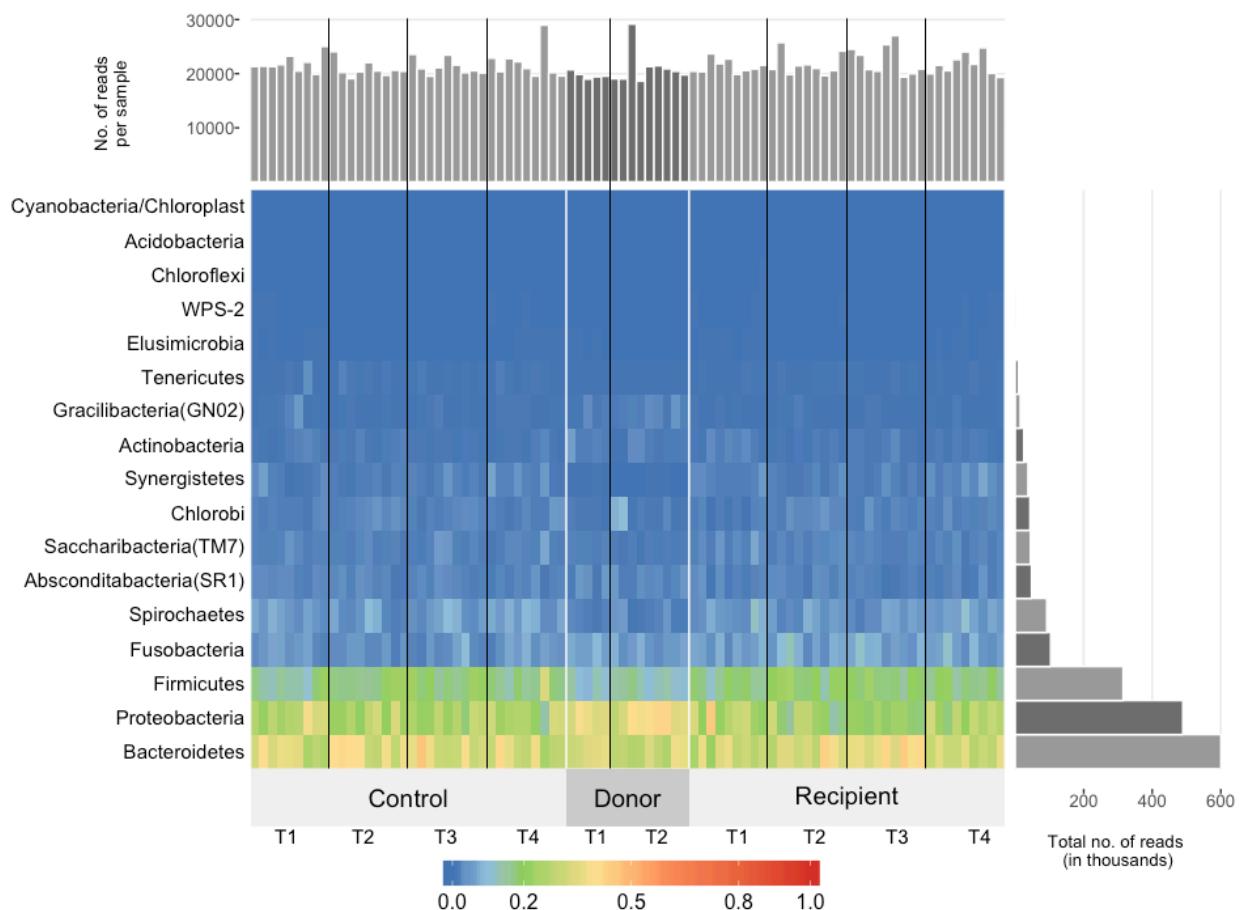


Figure 7 heatmap showing all the phyla detected in all samples (color scale to the relative abundance per sample)

This heatmap provides visualization of the phylum composition in each sample. The three bacterial phyla Bacteroidetes, Proteobacteria and Firmicutes are dominant and prevalent in all samples.

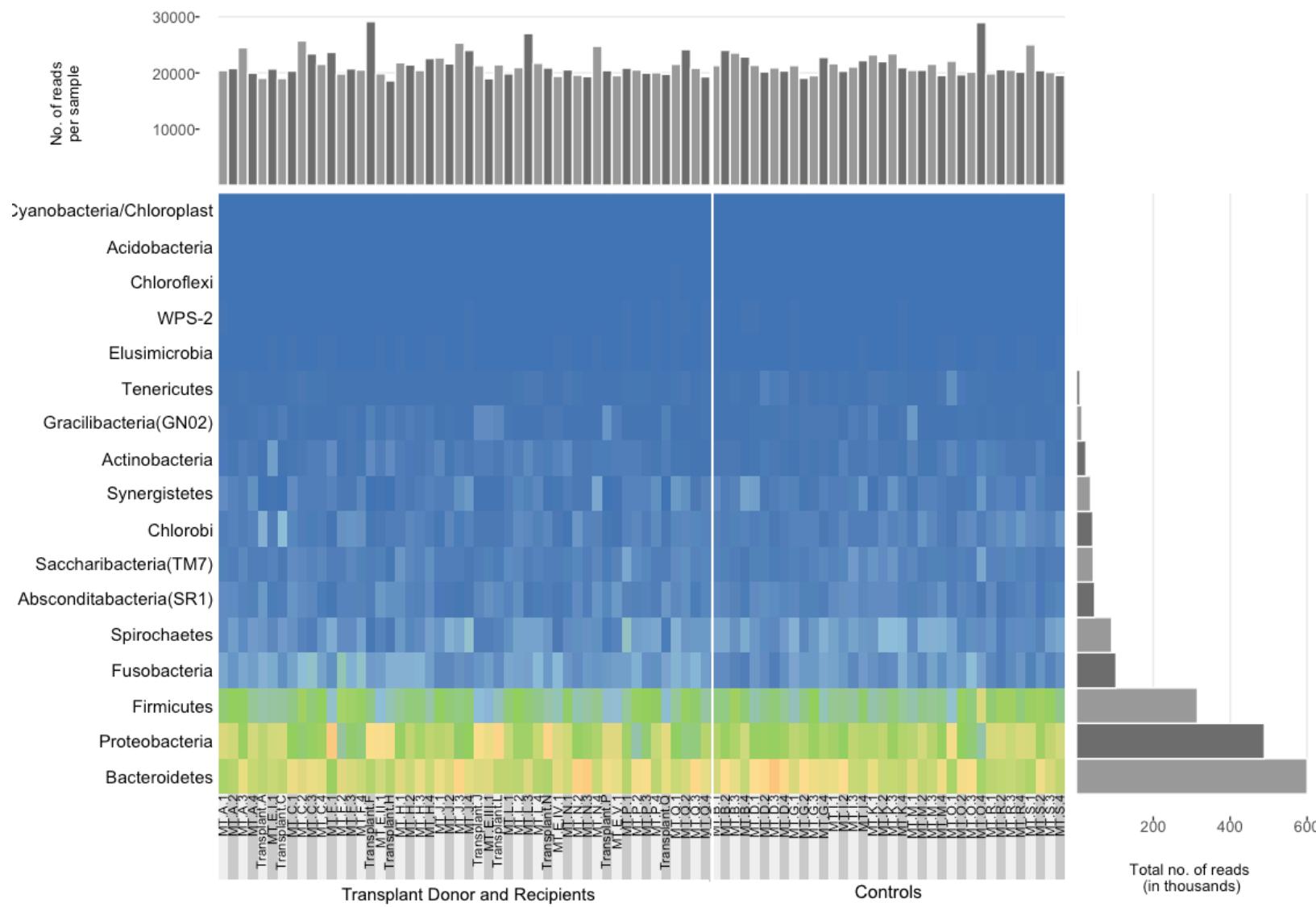


Figure 8 heatmap at Phylum rank (samples arranged by Dog)

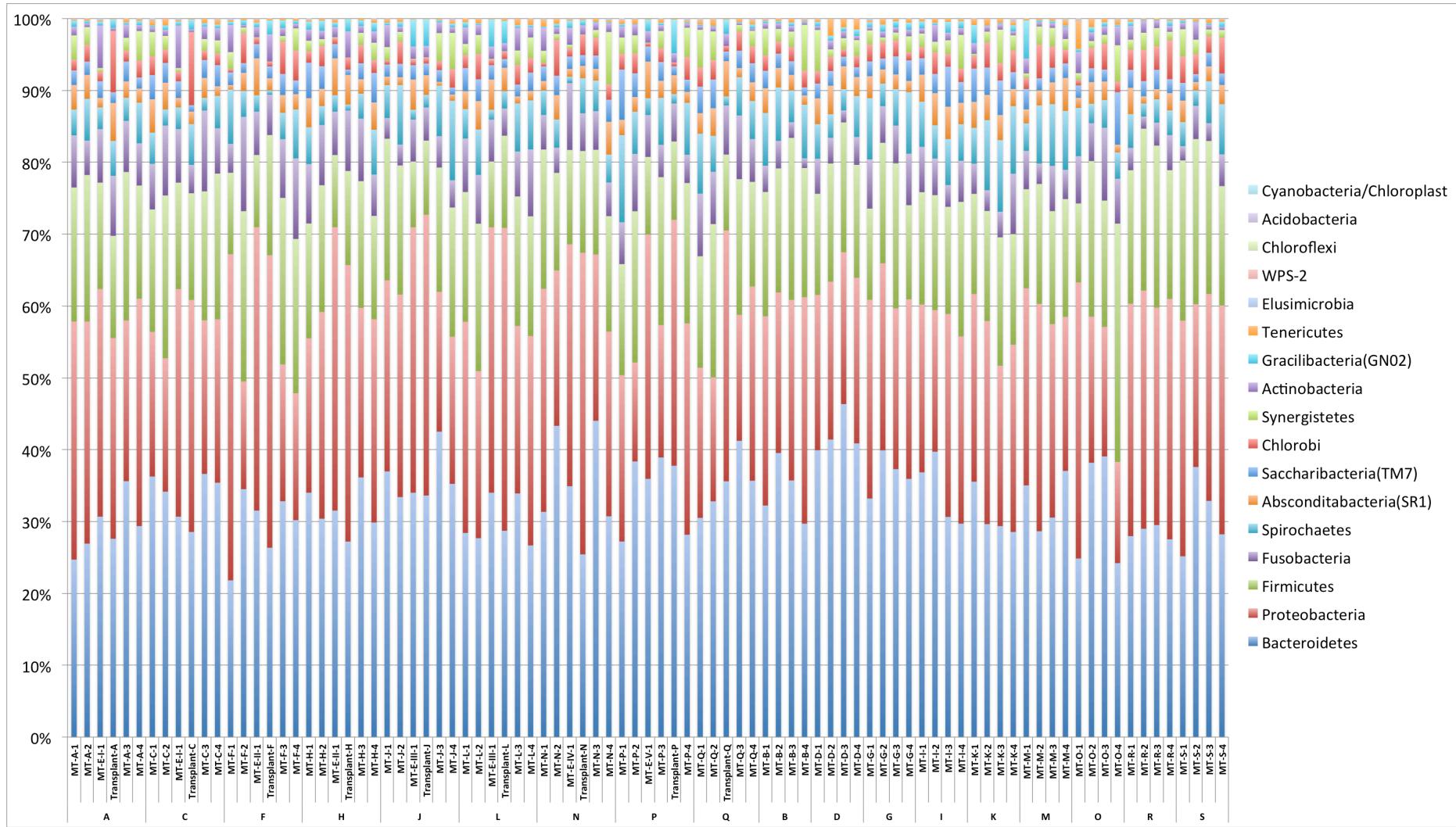


Figure 9 Barchart showing the relative abundances of the microbiota at the phylum rank in all samples

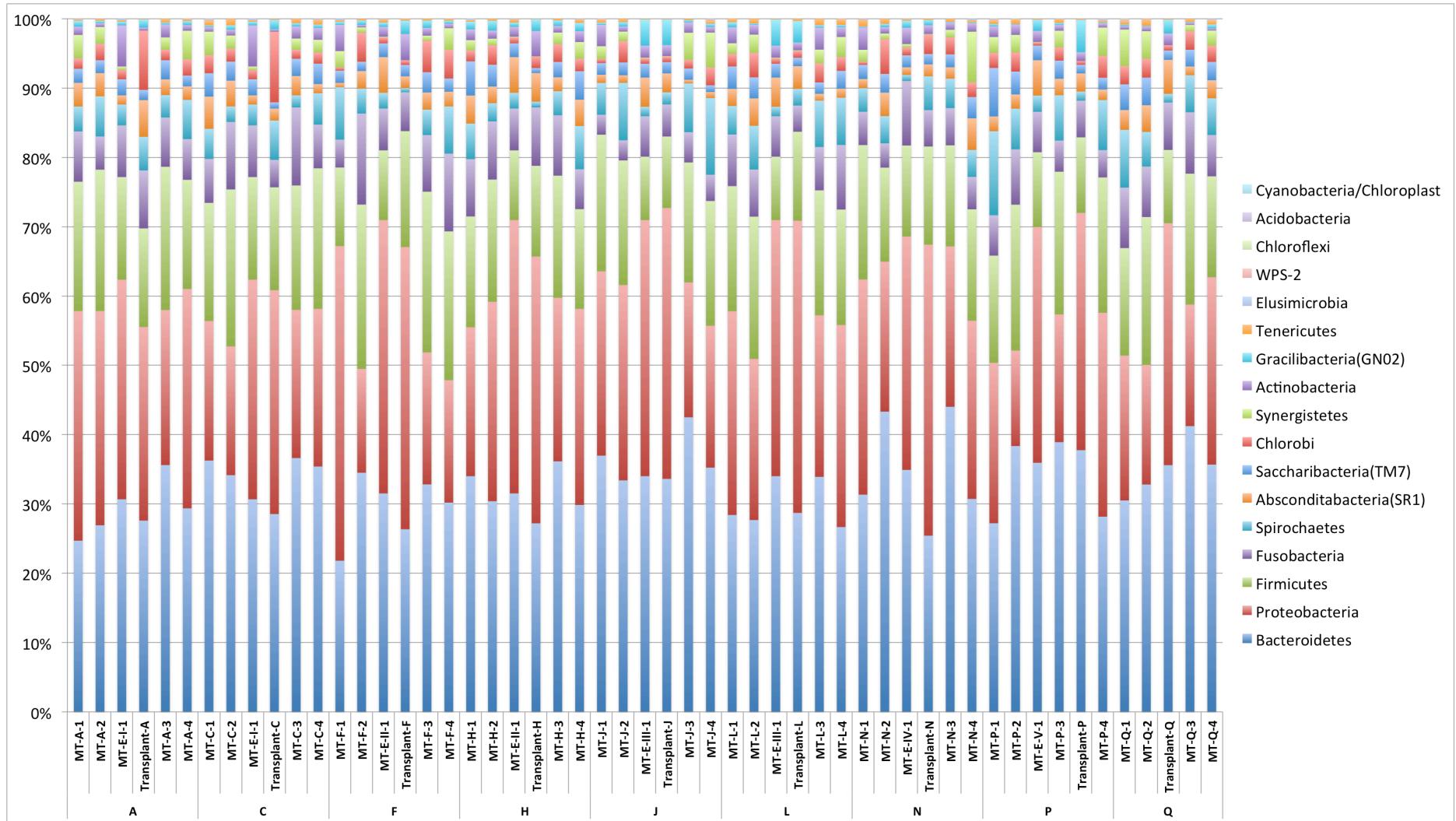


Figure 10 phylum barchart for the transplant donor and recipients

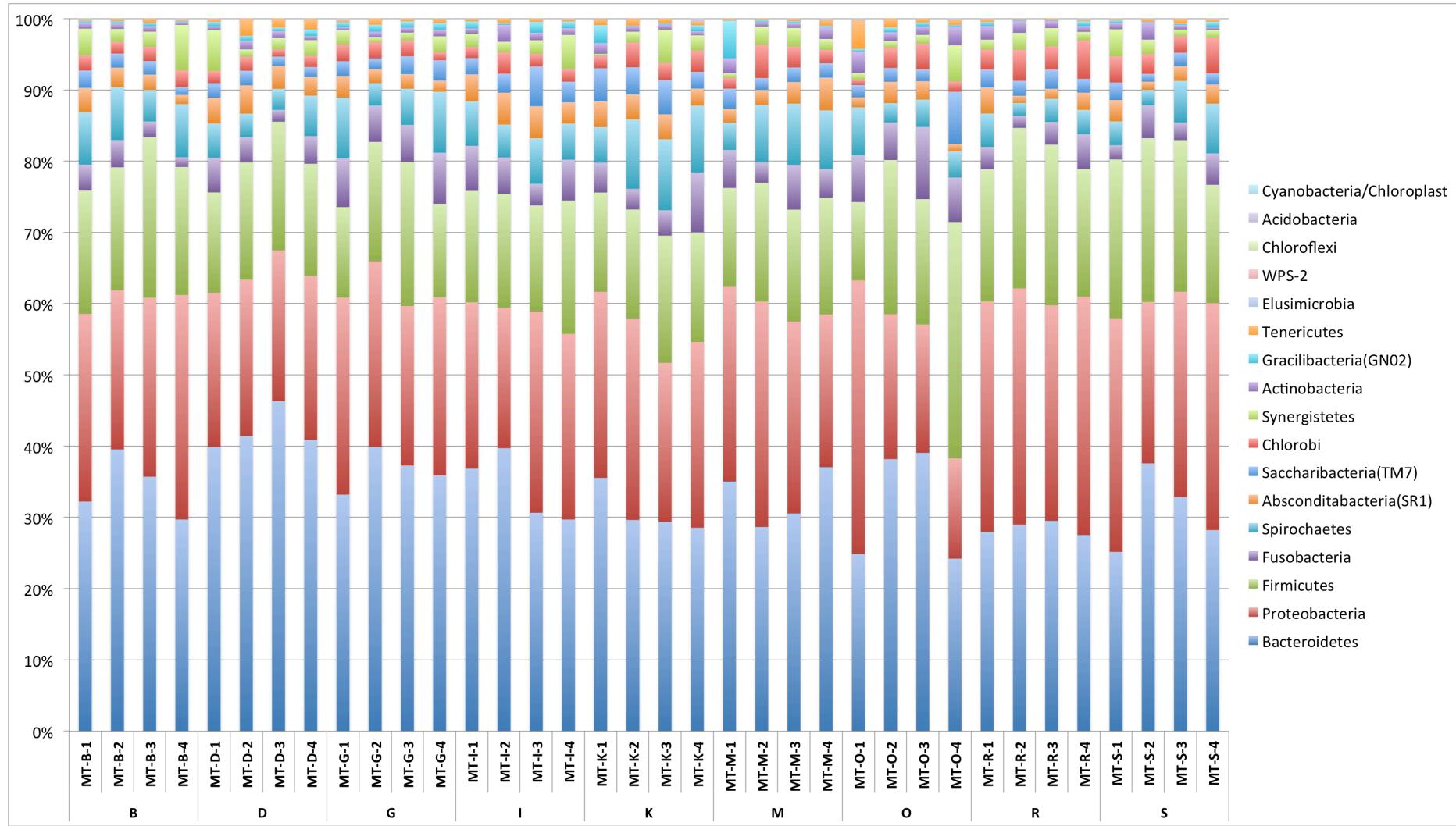


Figure 11 phylum barchart for the controls

Members of microbiota successfully transferred from the donor to the recipients were considered individually for each dog and summarized in the tables below:

	dog	DogA	DogA	DogA,C	DogA	DogA	DogA
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-A-1	MT-A-2	MT-E-I-1	Transplant-A	MT-A-3	MT-A-4
Neisseriaceae	ASV287	0	0	38	45	21	0
Neisseria sp.	ASV290	0	0	22	45	13	0
Neisseria sp.	ASV235	0	0	0	50	25	0
Xenophilus sp.	ASV286	0	0	32	43	31	0
Treponema sp. COT 356	ASV341	0	0	25	42	19	0
Porphyromonas sp.	ASV376	0	0	29	14	38	0
Porphyromonas sp.	ASV176	0	0	60	19	25	0
Porphyromonas sp.	ASV1069	0	0	0	3	0	3
Porphyromonas sp.	ASV123	0	0	39	19	0	15
Porphyromonas sp.	ASV150	0	0	51	19	0	88
TM7 G-2 sp.	ASV193	0	0	24	134	74	0

	dog	DogC	DogC	DogA,C	DogC	DogC	DogC
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-C-1	MT-C-2	MT-E-I-1	Transplant-C	MT-C-3	MT-C-4
Neisseria sp.	ASV665	0	0	16	53	21	0
Fusobacterium sp.	ASV287	0	0	38	66	39	0
Neisseria sp.	ASV738	0	0	0	22	33	0
Leucobacter sp.	ASV286	0	0	32	113	57	27
Pasteurellaceae G-2 sp.	ASV341	0	0	25	121	31	16
Xenophilus sp.	ASV489	0	0	0	16	3	0
Fusobacterium sp.	ASV45	0	0	28	712	0	44
Porphyromonas sp.	ASV44	0	0	30	152	374	224

Porphyromonas sp.	ASV458	0	0	0	21	9	0
Porphyromonas sp.	ASV577	0	0	0	13	0	6
Pasteurellaceae G-1 sp.	ASV575	0	0	5	7	0	3
Propionibacterium sp. COT 296	ASV624	0	0	5	8	0	2
Chlorobi G-1 sp.	ASV145	0	0	18	14	33	0
Bergeyella sp.	ASV218	0	0	0	44	99	0
Alloprevotella sp.	ASV40	0	0	279	1531	233	39
GN02 G-1 sp.	ASV176	0	0	60	14	126	101
Paraprevotella sp.	ASV348	0	0	0	15	35	0
Moraxella sp.	ASV174	0	0	0	97	12	19
Campylobacter mucosalis	ASV123	0	0	39	19	0	39
GN02 G-1 sp.	ASV150	0	0	51	45	65	133
Acholeplasmatales G-4 sp.	ASV651	0	0	5	12	16	6
Neisseria sp.	ASV53	0	0	53	200	38	0
Bacteroidia sp.	ASV162	0	0	143	25	52	83
Porphyromonas sp.	ASV396	0	0	47	4	0	10
Tissierella sp.	ASV828	0	0	0	25	0	26

	dog	DogF	DogF	DogF,H	DogF	DogF	DogF
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-F-1	MT-F-2	MT-E-II-1	Transplant-F	MT-F-3	MT-F-4
Clostridiales F-1,G-4 sp.	ASV271	0	0	80	83	5	4
Peptostreptococcaceae XI G-10 sp.	ASV44	0	0	131	69	67	249
Helcococcus sp. COT 140	ASV356	0	0	44	39	33	0
TM7 G-2 sp.	ASV173	0	0	73	30	62	10
Treponema sp. COT 359	ASV589	0	0	28	18	9	0
Propriionivibrio sp. COT 223	ASV261	0	0	115	47	94	36
Fusobacterium sp.	ASV477	0	0	0	2	28	9
Prevotella sp. COT 372	ASV40	0	0	165	189	570	102

Stenotrophomonas sp. COT 224	ASV326	0	0	9	16	0	9
Capnocytophaga sp.	ASV244	0	0	0	15	18	33
Treponema sp.	ASV403	0	0	13	28	0	4
Chlorobi G-1 sp.	ASV184	0	0	39	33	15	28
Cardiobacterium sp. COT 176	ASV362	0	0	17	4	0	12
Lachnospiraceae XIVa G-2 sp.	ASV640	0	0	4	32	8	0
Bergeyella sp.	ASV431	0	0	0	15	7	4
unclassified Alphaproteobacteria	ASV1058	0	0	0	4	0	3
Erysipelotrichaceae G-2 sp.	ASV146	0	0	33	45	321	211
Lachnospiraceae XIVa G-2 sp.	ASV140	0	0	0	6	47	0

	dog	DogH	DogH	DogF,H	DogH	DogH	DogH
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-H-1	MT-H-2	MT-E-II-1	Transplant-H	MT-H-3	MT-H-4
Peptostreptococcaceae XI G-10 sp.	ASV287	0	0	65	42	36	0
Treponema sp. COT 359	ASV892	0	0	1	3	0	9
Erysipelotrichaceae	ASV278	0	0	30	71	58	0
Treponema sp.	ASV699	0	0	0	4	0	13
Proteocatella sp. COT 032	ASV196	0	0	46	325	0	8
Fusobacterium sp.	ASV700	0	0	0	4	0	5
Capnocytophaga cynodegmi	ASV261	0	0	115	65	62	0
Porphyromonas sp.	ASV40	0	0	165	315	469	32
Catonella sp. COT 257	ASV53	0	0	217	513	37	51
Peptostreptococcaceae XI G-3 sp.	ASV695	0	0	0	5	0	10
Propionibacterium sp. COT 296	ASV396	0	0	7	7	0	19
Chlorobi G-1 sp.	ASV184	0	0	39	23	13	18
Deltaproteobacteria G-1 sp.	ASV221	0	0	29	16	9	8
Moraxella sp.	ASV418	0	0	0	57	4	0
Peptostreptococcaceae XI G-5 sp.	ASV298	0	0	0	15	14	32

Actinomyces sp.	ASV315	0	0	32	22	8	6
Streptococcus sp.	ASV555	0	0	0	18	13	0
Erysipelotrichaceae G-4 sp. COT 381	ASV121	0	0	72	41	24	21
Capnocytophaga sp.	ASV250	0	0	23	14	20	0

	dog	DogJ	DogJ	DogJ,L	DogJ	DogJ	DogJ
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-J-1	MT-J-2	MT-E-III-1	Transplant-J	MT-J-3	MT-J-4
Bacteroidia sp.	ASV331	0	0	0	9	0	12
Porphyromonas sp.	ASV71	0	0	100	83	68	0
Porphyromonas sp.	ASV235	0	0	27	12	69	0
Porphyromonas sp.	ASV286	0	0	29	10	94	12
Porphyromonas sp.	ASV341	0	0	23	14	75	0
Porphyromonas macacae	ASV399	0	0	1	28	0	13
Prevotella sp.	ASV129	0	0	6	31	11	18
Alloprevotella sp.	ASV88	0	0	48	34	0	15
Bergeyella sp.	ASV44	0	0	206	254	960	0
Capnocytophaga sp.	ASV892	0	0	4	3	0	8
Capnocytophaga cynodegmi	ASV278	0	0	96	49	35	0
unclassified Alphaproteobacteria	ASV477	0	0	0	3	65	0
Chlorobi G-1 sp.	ASV40	0	0	144	168	245	43
Stenotrophomonas sp. COT 224	ASV326	0	0	43	66	0	8
Xanthomonadaceae	ASV279	0	0	0	9	0	19
Xenophilus sp.	ASV158	0	0	242	39	41	0
Brachymonas sp.	ASV473	0	0	0	51	35	0
Alcaligenaceae	ASV438	0	0	0	25	43	0
Neisseria sp.	ASV115	0	0	0	57	89	99
Moraxella sp.	ASV144	0	0	0	139	0	5
Moraxella sp.	ASV53	0	0	263	955	36	0

Treponema sp.	ASV863	0	0	0	8	0	9
Peptostreptococcaceae XI G-10 sp.	ASV121	0	0	23	26	0	8

	dog	DogL	DogL	DogJ,L	DogL	DogL	DogL
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-L-1	MT-L-2	MT-E-III-1	Transplant-L	MT-L-3	MT-L-4
Bacteroidia sp.	ASV331	0	0	0	33	8	16
Porphyromonas sp.	ASV287	0	0	50	33	24	0
Porphyromonas sp.	ASV290	0	0	41	31	15	20
Porphyromonadaceae G-1 sp.	ASV422	0	0	0	17	5	10
Porphyromonas sp.	ASV316	0	0	17	13	28	0
Paraprevotella sp.	ASV680	0	0	5	26	0	10
Alloprevotella sp.	ASV88	0	0	48	113	42	9
unclassified Bacteroidetes	ASV461	0	0	12	6	0	9
Bergeyella sp.	ASV44	0	0	206	414	169	137
Capnocytophaga sp.	ASV501	0	0	0	9	0	6
Flavobacteriaceae	ASV427	0	0	0	4	0	4
Capnocytophaga cynodegmi	ASV278	0	0	96	52	41	0
TM7 G-3 sp.	ASV336	0	0	12	27	31	0
GN02 G-1 sp.	ASV577	0	0	0	56	12	0
GN02 G-2 sp.	ASV108	0	0	219	90	12	33
Campylobacterales	ASV777	0	0	2	19	16	2
Globicatella sp.	ASV421	0	0	25	33	0	10
Erysipelotrichaceae	ASV196	0	0	51	73	0	10
Fusobacterium sp.	ASV145	0	0	0	36	0	55
Fusobacterium sp.	ASV261	0	0	53	49	103	35
unclassified Alphaproteobacteria	ASV477	0	0	0	8	67	3
Chlorobi G-1 sp.	ASV40	0	0	144	218	513	186
Stenotrophomonas sp. COT 224	ASV326	0	0	43	32	0	8

Xenophilus sp.	ASV176	0	0	92	44	163	139
Brachymonas sp.	ASV361	0	0	9	25	5	23
Brachymonas sp.	ASV585	0	0	11	1	16	20
Brachymonas sp.	ASV380	0	0	0	14	155	56
Pasteurellaceae G-1 sp.	ASV348	0	0	13	9	14	0
Pasteurellaceae G-2 sp.	ASV174	0	0	0	235	0	61
Pasteurellaceae G-2 sp.	ASV214	0	0	8	69	5	78
Moraxella sp.	ASV53	0	0	263	368	69	0
Actinomyces sp.	ASV134	0	0	121	42	140	0
Treponema sp. COT 233	ASV204	0	0	0	13	55	37
Treponema sp.	ASV362	0	0	0	16	0	15
Spirochaeta sp.	ASV711	0	0	0	5	3	20
Catonella sp. COT 257	ASV298	0	0	11	31	0	15
Peptostreptococcaceae XI G-3 sp.	ASV315	0	0	39	25	7	0
Peptostreptococcaceae XI G-5 sp.	ASV555	0	0	15	26	12	0

	dog	DogN	DogN	DogN	DogN	DogN	DogN
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-N-1	MT-N-2	MT-E-IV-1	Transplant-N	MT-N-3	MT-N-4
Bacteroidia sp.	ASV339	0	0	0	23	0	14
Porphyromonas sp.	ASV290	0	0	0	24	20	0
Paraprevotella sp.	ASV680	0	0	3	26	12	0
Alloprevotella sp.	ASV88	0	0	25	66	174	185
Bergeyella sp.	ASV44	0	0	81	361	536	130
Porphyromonas gulae	ASV141	0	0	69	4	19	4
Porphyromonas sp.	ASV23	0	0	349	72	122	69
GN02 G-1 sp.	ASV577	0	0	0	25	0	10
Fusobacterium sp.	ASV261	0	0	47	71	28	0
Chlorobi G-1 sp.	ASV40	0	0	219	501	364	124

Stenotrophomonas sp. COT 224	ASV326	0	0	50	10	0	11
Xanthomonadaceae	ASV279	0	0	29	5	0	25
Xenophilus sp.	ASV64	0	0	100	31	90	136
Xenophilus sp.	ASV176	0	0	113	29	0	32
Comamonas sp. COT 270	ASV16	0	0	0	103	245	305
Pasteurella sp.	ASV124	0	0	0	83	66	0
Neisseria sp.	ASV206	0	0	71	14	12	14
Neisseria sp.	ASV123	0	0	45	65	0	39
Neisseria sp.	ASV150	0	0	254	12	0	28
Moraxella sp.	ASV53	0	0	181	241	41	0
Actinomyces sp.	ASV134	0	0	20	51	51	35
Treponema sp.	ASV221	0	0	0	44	0	47
Treponema sp. COT 233	ASV204	0	0	0	26	0	52
Spirochaeta sp. COT 314	ASV343	0	0	0	3	5	27
Desulfovibrio sp.	ASV38	0	0	0	63	299	737
Lachnospiraceae XIVa G-4 sp.	ASV357	0	0	29	19	53	0
Peptostreptococcaceae XI G-3 sp.	ASV130	0	0	0	31	0	26
Helcococcus sp. COT 140	ASV146	0	0	17	43	28	13
Peptostreptococcaceae XI G-7 sp.	ASV185	0	0	18	7	0	27

	dog	DogP	DogP	DogP	DogP	DogP	DogP
	timepoint	T1	T2	T1	T2	T3	T4
	treatment	Recipient	Recipient	Donor	Donor	Recipient	Recipient
	Sample	MT-P-1	MT-P-2	MT-E-V-1	Transplant-P	MT-P-3	MT-P-4
Porphyromonas sp.	ASV290	0	0	36	34	27	0
Prevotella sp. COT 372	ASV271	0	0	40	53	3	4
Bacteroidetes	ASV461	0	0	18	9	3	0
Erysipelotrichaceae	ASV917	0	0	4	3	0	4
Xenophilus sp.	ASV176	0	0	65	31	80	0
Neisseria sp.	ASV206	0	0	35	11	21	42

Neisseria sp.	ASV368	0	0	8	9	28	0
Treponema sp. COT 233	ASV204	0	0	39	31	0	48
Catonella sp. COT 025	ASV354	0	0	5	14	7	0

dog	timepoint	DogQ	DogQ	DogQ	DogQ	DogQ
	treatment	T1	T2	T2	T3	T4
		Recipient	Recipient	Donor	Recipient	Recipient
Sample		MT-Q-1	MT-Q-2	Transplant-Q	MT-Q-3	MT-Q-4
Bacteroidia sp.	ASV665	0	0	3	17	19
Paludibacter sp.	ASV531	0	0	11	16	0
Porphyromonas macacae	ASV399	0	0	12	0	49
Paraprevotella sp.	ASV680	0	0	3	5	13
Cloacibacterium sp. COT 320	ASV353	0	0	8	6	0
Capnocytophaga canimorsus	ASV219	0	0	55	10	0
Porphyromonas gulae	ASV195	0	0	94	392	94
SR1 G-1 sp.	ASV351	0	0	26	0	1
Xenophilus sp.	ASV176	0	0	41	31	0
Pasteurella canis	ASV70	0	0	472	0	28
Pasteurellaceae G-2 sp.	ASV110	0	0	206	0	28
Pasteurellaceae G-2 sp.	ASV79	0	0	228	8	0
Pasteurellaceae G-2 sp.	ASV174	0	0	54	0	17
Neisseria sp.	ASV206	0	0	16	0	24
Neisseria sp.	ASV609	0	0	5	0	8
Conchiformibius sp.	ASV127	0	0	27	43	22
Moraxella sp.	ASV144	0	0	52	0	29
Moraxella sp.	ASV53	0	0	672	54	0
Actinomyces sp.	ASV134	0	0	178	15	13
Treponema sp. COT 233	ASV204	0	0	26	27	31
Deltaproteobacteria G-1 sp.	ASV411	0	0	20	5	0
Deltaproteobacteria G-1 sp. COT 266	ASV437	0	0	7	13	0

Lachnospiraceae XIVa G-7 sp.	ASV635	0	0	12	13	0
Lachnospiraceae XIVa G-2 sp.	ASV431	0	0	4	13	0
Lachnospiraceae XIVa G-4 sp.	ASV357	0	0	6	7	0
Peptostreptococcaceae XI G-3 sp.	ASV315	0	0	16	19	7