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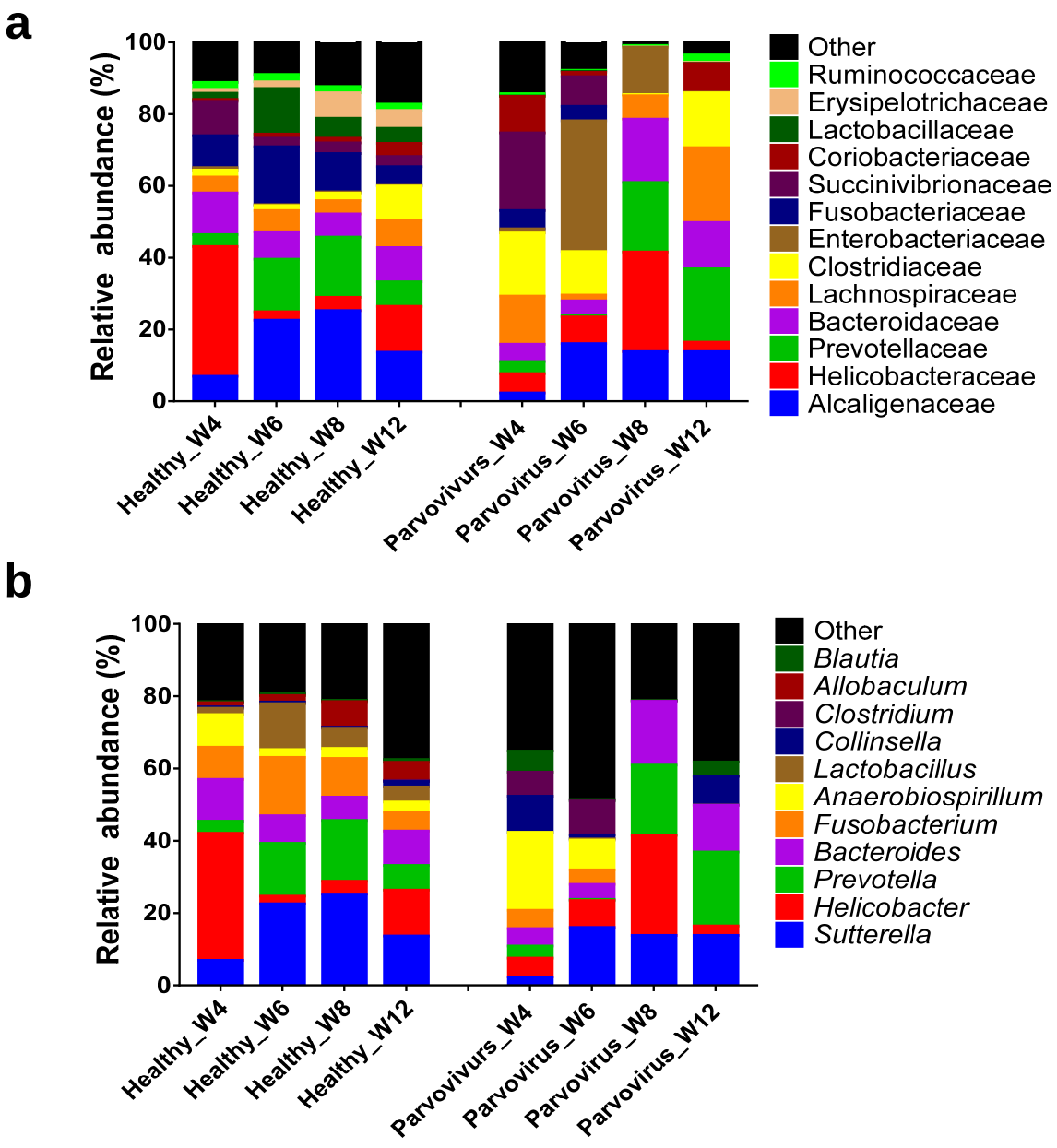

Fig. S1. Taxa summary plots for healthy and CPV infected dogs. Stacked bar plots represent the predominant bacteria taxa present within a group at weeks 4, 6, 8 and 12 at the family (a) and (b) genus level. The relative abundance of predominant bacteria taxa was averaged across all dogs in each health status group. W represents week and number represents the week number.

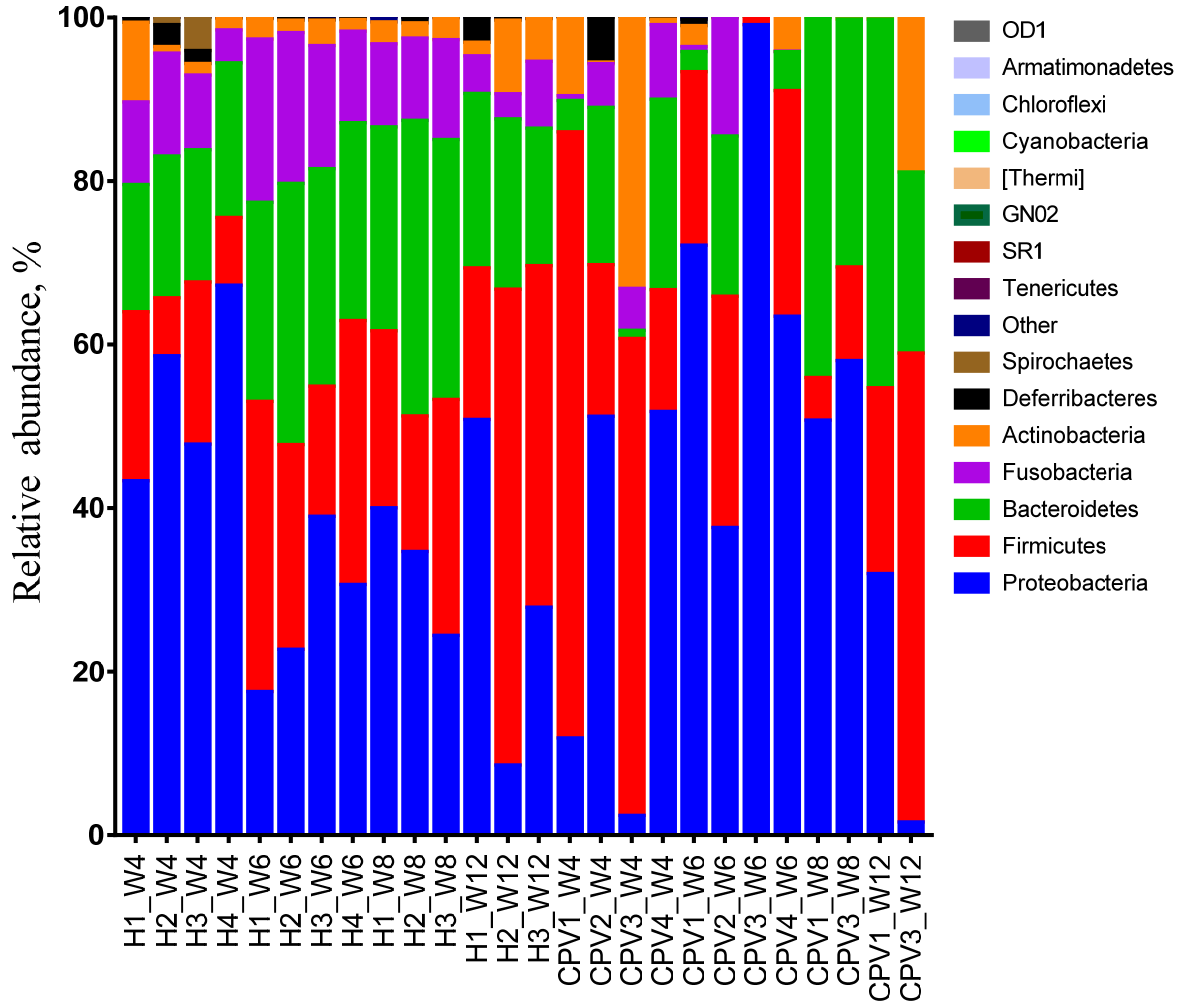

Fig. S2. Stacked bar plot representing the relative abundance of taxa at the phylum level of individual fecal samples from healthy and CPV infected dogs. H represents healthy dogs and CPV represents dogs with canine parvovirus infection. W denotes week at 4, 6, 8 and 12.

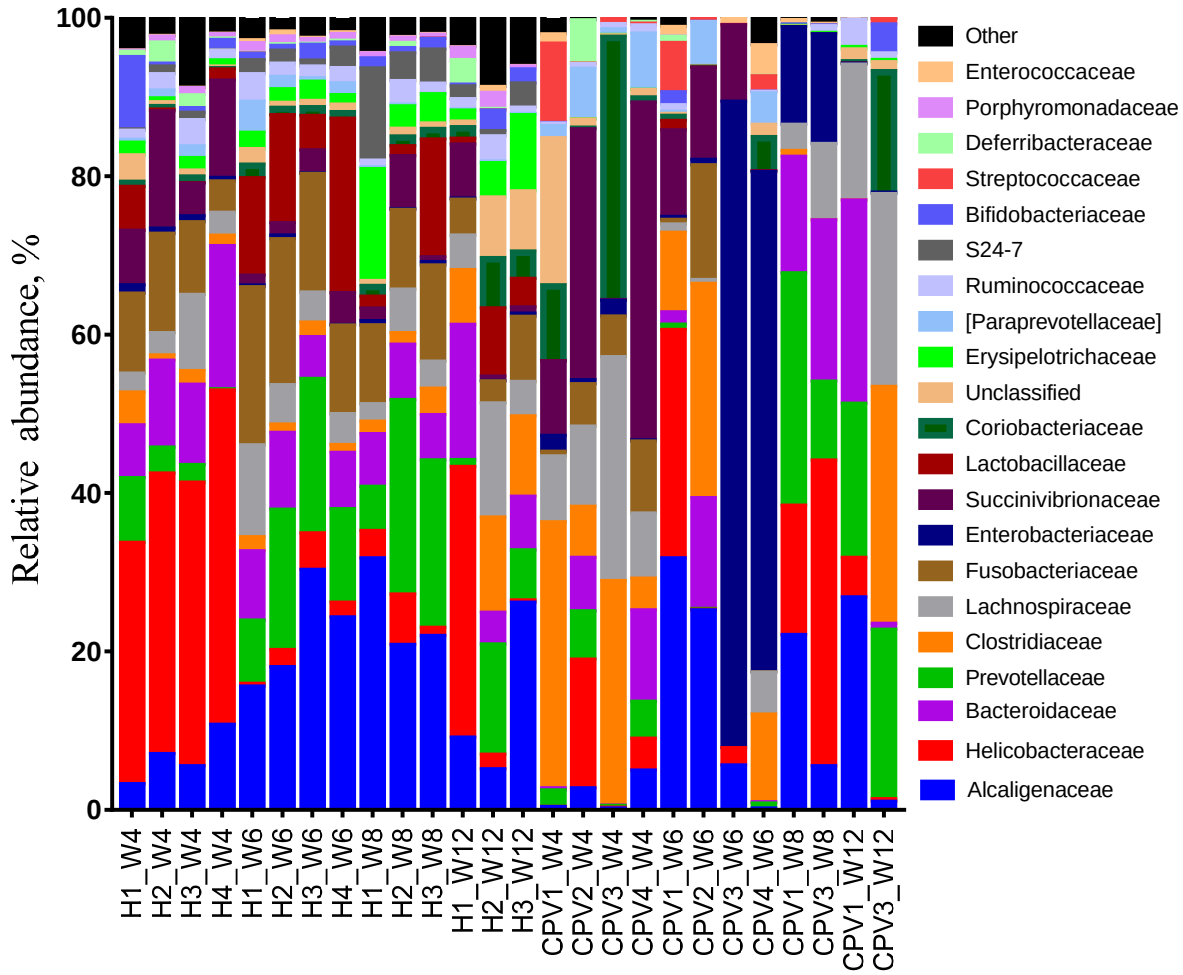

Fig. S3. Stacked bar plot representing the relative abundance of taxa at the family level of individual fecal samples from healthy and CPV infected dogs. H represents healthy dogs and CPV represents dogs with canine parvovirus infection. W denotes week at 4, 6, 8 and 12.

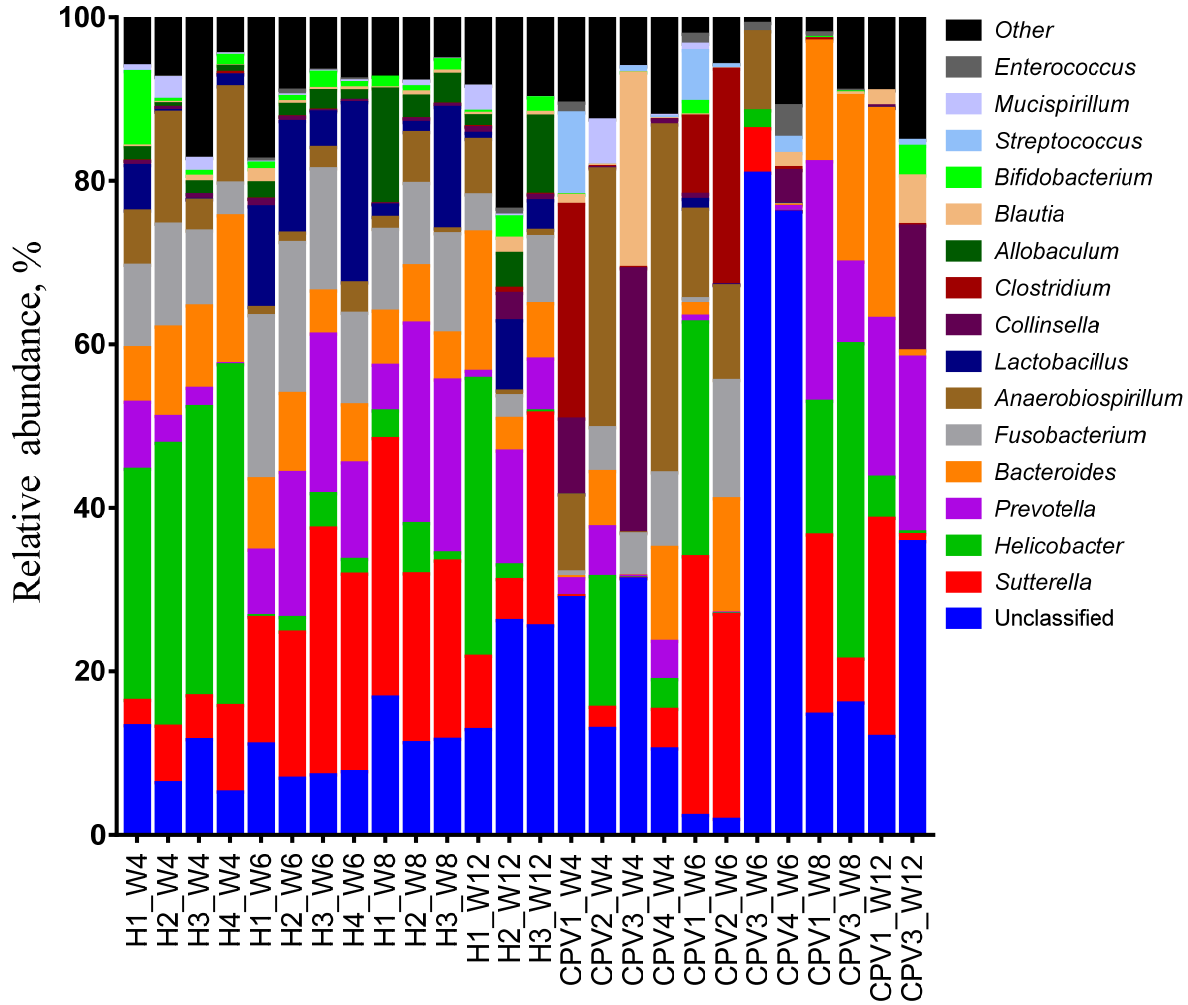

Fig. S4. Stacked bar plot representing the relative abundance of taxa at the genus level of individual fecal samples from healthy and CPV infected dogs. H represents healthy dogs and CPV represents dogs with canine parvovirus infection. W denotes week at 4, 6, 8 and 12.

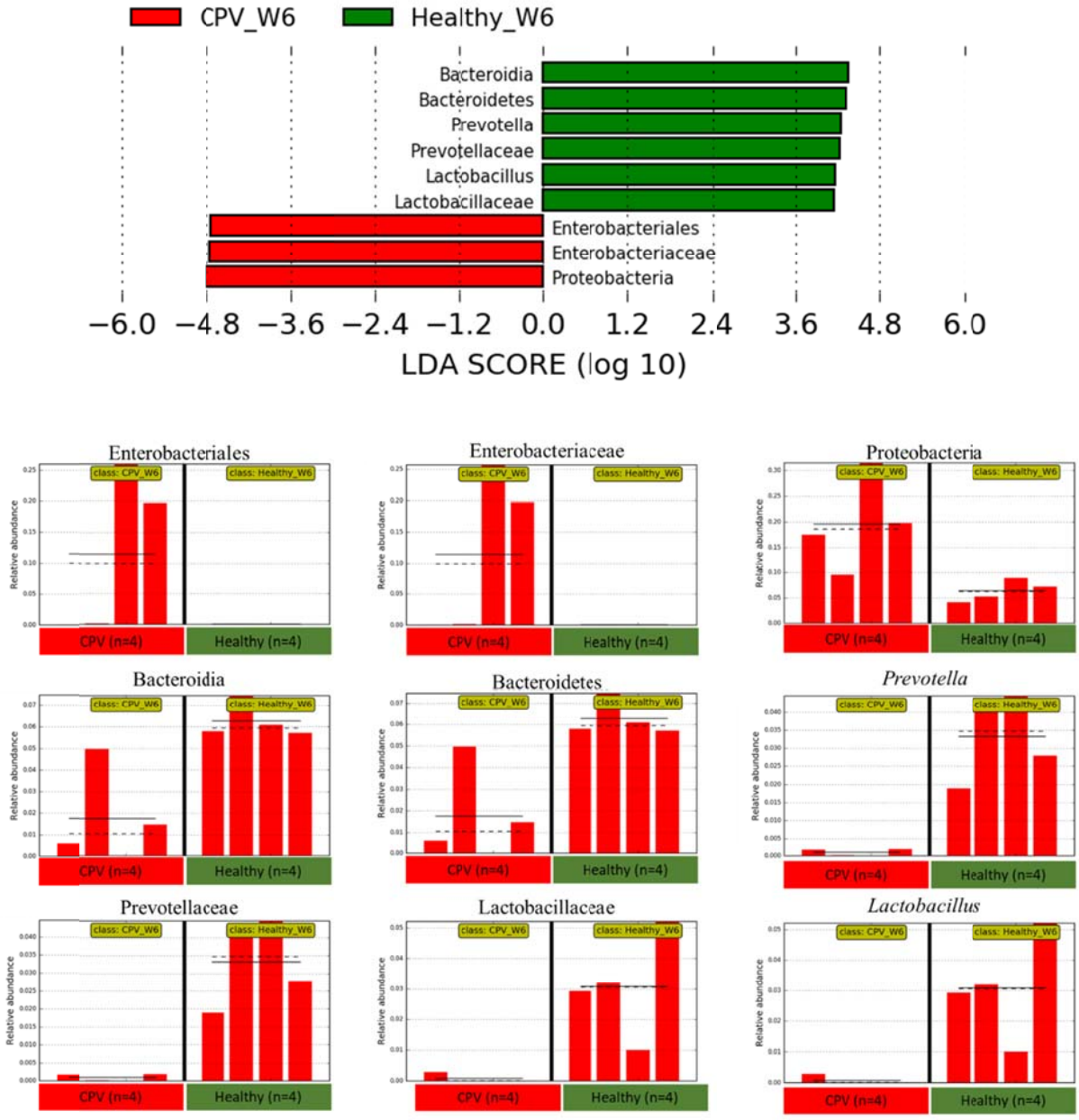

Fig. S5. Linear Discriminant Analysis (LDA) Effect Size (LEfSe) plot of taxonomic biomarkers identified in the gut microbiome between healthy dogs and dogs with CPV at week 6 during the canine parvoviral infection. The LEfSe algorithm, emphasizing both statistical and biological relevance was used for biomarker discovery. A p-value of < 0.05 were considered significant in Kruskal-Wallis and pairwise Wilcoxon tests, respectively. The threshold on the logarithmic discriminant analysis (LDA) score for discriminative features was 4. The length of the histogram represents the LDA score which explains the degree of influence of species with significant difference between the two groups.

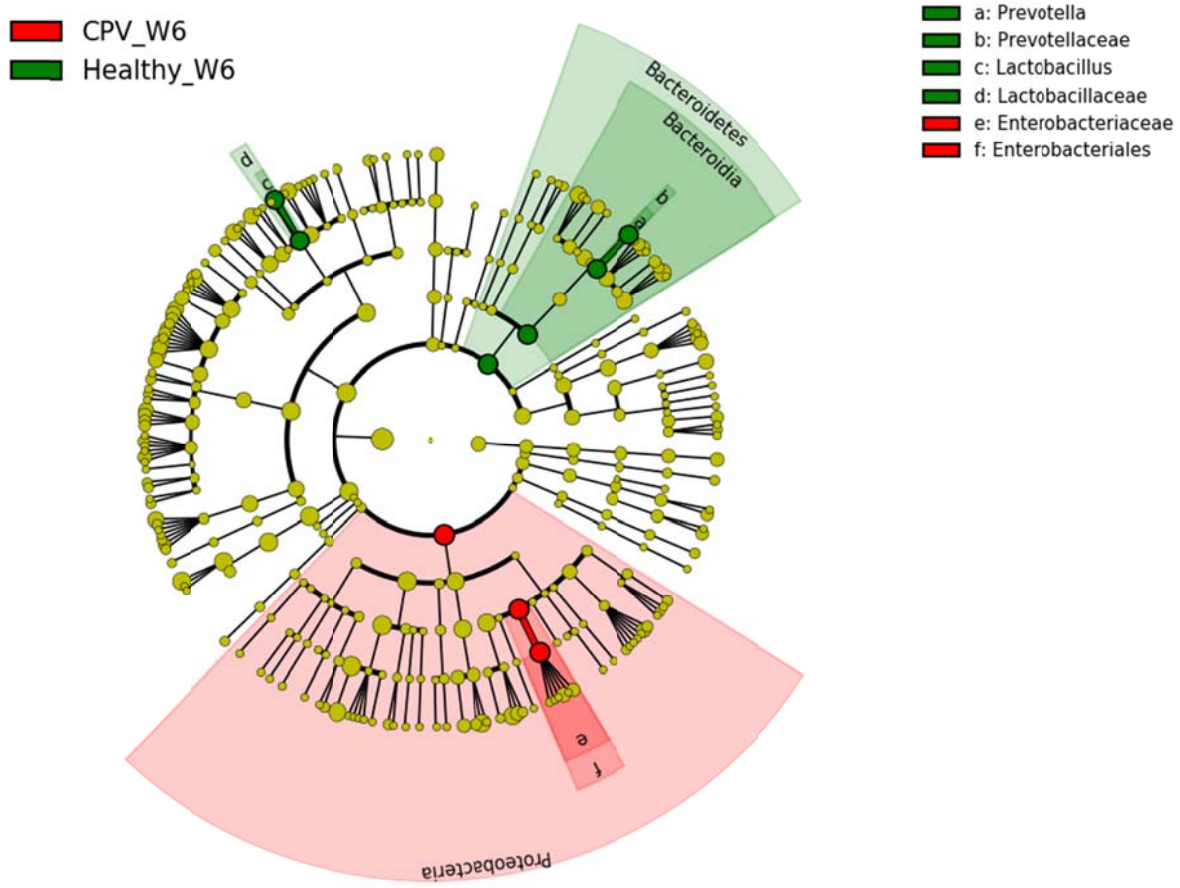

Fig. S6. Cladogram showing differentially abundant taxonomic clades with an LDA score > 4.0 between healthy dogs and dogs with CPV at week 6 during the infection. Red and green indicate the CPV and healthy groups, respectively. The taxonomic classification at the phylum, class, order, family and genus levels were shown from the outside to the inside. The red and green nodes in the phylogenetic tree denote microbial species that play an important role in the CPV and healthy groups, respectively. Yellow nodes represent species with no significant difference based on the LEfSe analysis. A p-value of < 0.05 were considered significant in Kruskal-Wallis and pairwise Wilcoxon tests, respectively.

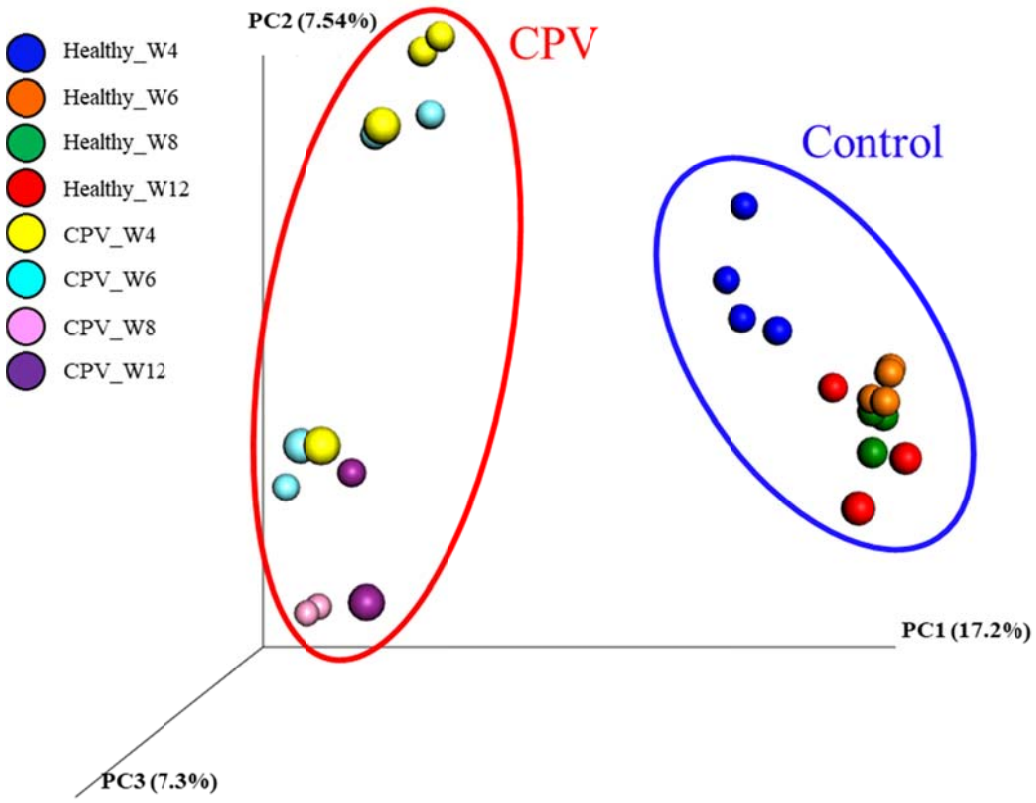

Fig. S7. Principal Coordinates Analysis (PCoA) of unweighted UniFrac distances of 16S rRNA genes. Ellipses denote clustering of the fecal microbial communities in dogs with CPV (red) and healthy control (blue) group, respectively. Statistical analysis revealed a significant separation between samples obtained from CPV and healthy group (ANOSIM; P = 0.029).

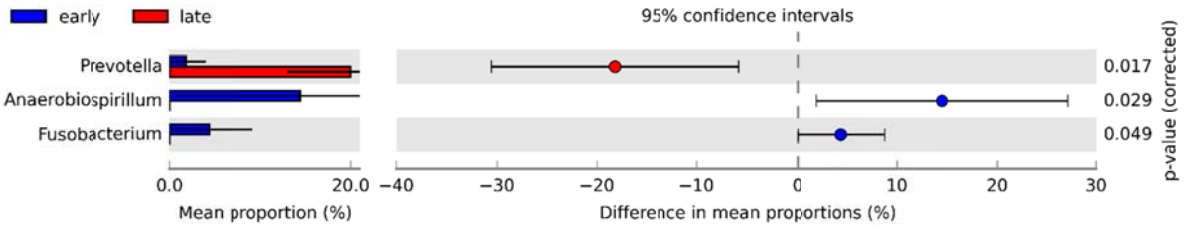

Fig. S8. Extended error plot identifying the significantly different genera between the microbiota of dogs with CPV during the early and late stage of infection. W4 and W6 were designated as early (blue) and W8 and W12 were indicated as late group (red). Corrected *P*-values are shown at the right. A two-sided Welch's t-test was used in the measurement of differences in the relative abundance of microbial taxa and a *P*-value < 0.05 was considered significant.

Table S1. Number of sequences before and after quality control in DNA samples extracted from feces of healthy dogs and dogs with canine parvoviral enteritis at different time points.

Sample ID	Group	Week	Number of sequences	
			Pre-QC	Post-QC
TC2_3	Healthy	W4	197255	130038
TC2_4	Healthy	W6	203498	120089
TC2_5	Healthy	W8	203204	140864
TC2_6	Healthy	W12	191920	128358
TC3_3	Healthy	W4	206382	139376
TC3_4	Healthy	W6	210623	137002
TC3_5	Healthy	W8	201488	133728
TC3_6	Healthy	W12	195105	114960
TC4_3	Healthy	W4	212614	141844
TC4_4	Healthy	W6	222625	147664
TC4_5	Healthy	W8	191221	124243
TC4_6	Healthy	W12	184179	118416
TC5_3	Healthy	W4	212564	144073
TC5_4	Healthy	W6	191122	123327
TC5_5	Healthy	W8	-	-
TC5_6	Healthy	W12	-	-
TT3_3	CPV	W4	223683	133930
TT3_4	CPV	W6	208594	146964
TT3_5	CPV	W8	203061	150368
TT3_6	CPV	W12	179186	131779
TT5_3	CPV	W4	205592	143059
TT5_4	CPV	W6	224254	164334
TT5_5	CPV	W8	-	-
TT5_6	CPV	W12	-	-
TT6_3	CPV	W4	206413	123771
TT6_4	CPV	W6	196484	163292
TT6_5	CPV	W8	211138	158421
TT6_6	CPV	W12	198967	137832
TT7_3	CPV	W4	203688	136027
TT7_4	CPV	W6	196591	142240
TT7_5	CPV	W8	-	-
TT7_6	CPV	W12	-	-

- dead

Table S2. Body weights of each individual dog enrolled in the study at weeks 4, 6, 8 and 12.

Individual animal	W4	W6	W8	W12
CPV_1	1.3	1.65	1.85	-
CPV_2	1.45	1.82	2	3.8
CPV_3	1.35	1.65	1.9	-
CPV_4	1.6	1.85	2.15	4.3
Healthy_1	1.6	1.9	2.3	3.5
Healthy_2	1.45	1.6	1.8	3.7
Healthy_3	1.5	1.75	1.9	3.8
Healthy_4	1.5	1.8	1.95	4.2

Table S3. Vital signs of each individual dog enrolled in this study at week 6.

Individual animal	Body temperature (^{o}C)	Pulse rate (bpm)	Respiration rate (bpm)
CPV_1	40.6	220	68
CPV_2	40.1	228	64
CPV_3	41.5	212	72
CPV_4	41.3	224	72
Healthy_1	38.8	180	32
Healthy_2	38.6	168	36
Healthy_3	38.7	184	28
Healthy_4	38.6	172	28

Table S4. Electrolyte analysis of each individual dog enrolled in this study at week 6.

Individual animal	Na	K	Cl
CPV_1	138.9	3.24	106.4
CPV_2	140.6	3.04	110.1
CPV_3	141.7	3.31	104.1
CPV_4	134.7	2.89	98.9
Healthy_1	146.5	3.57	110.9
Healthy_2	148.7	3.69	112.1
Healthy_3	146.1	3.48	105.5
Healthy_4	148.3	3.51	109.2

Na (sodium), K (potassium), Cl (chloride)

Table S5. Complete blood count (CBC) analysis of each individual dog enrolled in this study at week 6.

Individual animal	WBC	PCV	PLT	Neutrophil	Lymphocyte	Monocyte	Eosinophil
CPV_1	0.3	28.7	70	0.2	0.1	-	-
CPV_2	0.5	30.2	69	0.2	0.2	-	0.1
CPV_3	5.3	35.4	253	3.7	0.9	0.4	0.3
CPV_4	4.5	36.1	177	2.9	1.1	0.3	0.2
Healthy_1	7.6	34.8	265	5.2	1.4	0.8	0.2
Healthy_2	8.7	36.6	301	5.5	2.1	0.9	0.2
Healthy_3	9.2	35.7	254	6.4	1.9	0.7	0.2
Healthy_4	7.5	40.2	290	5.8	1.3	0.3	0.1

PCV (packed cell volume), WBC (white blood cell), PLT (platelet)

Table S6. Serum chemistry analysis of each individual dog enrolled in this study at week 6.

Individual animal	AST	ALT	ALP	GGT	TBIL	TP	ALB	Crea	BUN	Glucose	LIP	IP	Amylase	Chol
CPV_1	12	33	539	7	0.2	2.9	1.4	0.2	3.7	107	6.3	4.6	228	157
CPV_2	25	150	586	8	0.3	4	2.5	0.1	4.3	115	12.5	5.3	398	212
CPV_3	67	352	627	11	1.6	3	1.5	0.4	5.4	118	10.2	3.1	321	251
CPV_4	80	524	688	10	0.5	3.2	1.7	0.3	5.1	90	11.7	4.1	286	142
Healthy_1	26	61	257	3	0	4.5	2.6	0.3	10	151	12.7	3.4	241	201
Healthy_2	29	62	312	2	0	4.9	2.8	0.3	8.8	121	13.8	4.2	329	186
Healthy_3	15	50	270	2	0	5.1	2.7	0.2	8.9	109	9.7	3.5	263	219
Healthy_4	15	58	354	4	0	4.7	2.6	0.2	11.4	105	10.3	4.5	381	180

AST (aspartate aminotransferase), ALT (alanine aminotransferase), ALKP (alkaline phosphatase), GGT (gamma-glutamyl transferase), Tbil (total bilirubin), TP (total protein), ALB (albumin), Crea (creatinine), BUN (blood urea nitrogen), LIP (lipase), IP (phosphorus-inorganic), Chole (cholesterol)

Mothur scripts

- make.file(inputdir=/path/to/working_directory, type=fastq)
- make.contigs(file=current, processors=8)
- trim.seqs(fasta=current, qfile=current, qaverage=27, maxambig=0, maxhomop=8, minlength=200, maxlength=700)
- list.seqs(fasta=current)
- get.seqs(accnos=current, name=current, fasta=current)

QIIME scripts

- validate_mapping_file.py –m mappingfile.txt –o validate_mapping_file_output
- pick_de_novo_otus.py –i $PWD/sequences.fna –o otus
- biom summarize-table –i otus/otu_table.biom
- summarize_taxa_through_plots –i otus/out_table.biom –o taxa_summary –m mappingfile.txt
- alpha_rarefaction.py –i otus/otu_table.biom –m mappingfile.txt –o alpha_rarefaction –p alpha_params.txt –t otus/rep_set.tre
  alpha_params.txt contains the following:
  alpha_diversity:metrics shannon,PD_whole_tree,chao1,observed_otus
- beta_diversity_through_plots.py –i otus/otu_table.biom –m mappingfile.txt –o beta_diversity –t otus/rep_set.tre –e 114960