Supplementary file 1: The relative abundance of major taxa in three canine breeds

Classification	Percentage of Total Sequences[2]				SEM	*p*-Value	No. of pigs With detectable taxon
	Collective data[1]	Control	DON	ZEN			
zFirmicutes	56.8	56.7	54.7	57.8	0.31	0.72	14
Lactobacillus	4.0	1.1[b]	6.5[a]	3.8[a]	0.13	**0.005**	14
Faecalibacterium	4.4	5.5	3.6	4.2	0.08	0.25	14
Dialister	2.3	2.3	1.2	3.4	0.57	0.67	14
Megasphaera	2.0	0.9[b]	3.0[a]	1.8[a]	0.18	**0.05**	14
Lachnospira	1.9	2.5	2.3	1.0	0.17	0.11	14
Phascolarctobacterium	1.7	1.8	1.6	1.7	0.09	0.91	14
Ruminococcus	1.3	1.7	1.1	1.3	0.09	0.14	14
Bulleidia	1.2	1.4	0.8	1.3	0.09	0.38	14
Blautia	1.1	1.2	0.7	1.3	2.2	0.34	14
Anaerovibrio	0.9	0.9	1.2	0.7	0.12	0.15	14
Coprococcus	0.9	1.1	0.8	0.8	0.04	0.15	14
Oscillospira	0.9	0.8	1.1	0.8	0.09	0.44	14
Catenibacterium	0.7	1.0	0.3	0.9	0.38	0.60	13
p-75-a5	0.6	0.7	0.4	0.8	0.28	0.85	12
Clostridium	0.5	0.5	0.2	0.9	0.14	0.11	14
Dorea	0.5	0.4	0.5	0.6	0.08	0.46	14
Megamonas	0.4	0.0	0.0	1.1	0.61	0.36	6
Shuttleworthia	0.3	0.8	0.2	0.1	0.40	0.44	14
Acidaminococcus	0.3	0.3	0.3	0.3	0.43	0.84	14
Butyrivibrio	0.3	0.1	0.1	0.6	0.19	0.18	14
Selenomonas	0.2	0.0	0.5	0.1	0.39	0.38	14
Roseburia	0.2	0.2	0.3	0.1	0.17	0.21	14
Mitsuokella	0.2	0.2	0.2	0.2	0.19	0.89	14
Streptococcus	0.2	0.3	0.0	0.2	0.26	0.40	14
Peptococcus	0.2	0.2[a]	0.0[b]	0.1[b]	0.11	**0.02**	14
Pelosinus	0.2	0.0[b]	0.2[a]	0.1[a]	0.06	**0.005**	14
Bacteroidetes	35.6	35.9	38.8	32.0	0.04	0.34	14
Prevotella	21.4	25.4	22.2	17.5	0.09	0.39	14
Bacteroides	4.1	2.0[b]	4.6[a]	5.3[a]	0.06	**0.001**	14
CF231	0.6	0.6	0.7	0.5	0.20	0.67	14
Parabacteroides	0.4	0.3	0.6	0.3	0.22	0.44	14
Paludibacter	0.3	0.2[b]	0.4[a]	0.4[a]	0.07	**0.001**	14
Proteobacteria	4.3	4.1	3.1	5.7	0.09	0.23	14
Campylobacter	1.4	1.5[a]	0.0[b]	2.8[a]	0.44	**0.01**	14
Succinivibrio	0.6	0.6	0.6	0.6	0.20	0.81	14

Actinobacillus	0.2	0.1[a]	0.0[b]	0.4[a]	0.38	**0.006**	12
Desulfovibrio	0.2	0.3	0.2	0.2	0.19	0.95	14
Dechloromonas	0.1	0.0[b]	0.2[a]	0.1[a]	0.06	**0.001**	14
Spirochaetes	0.9	0.7	0.8	1.3	0.35	0.74	14
Treponema	0.9	0.7	0.8	1.3	0.36	0.79	14
Cyanobacteria	0.9	0.7	1.0	0.9	0.08	0.39	14
Actinobacteria	0.8	0.8	0.4	1.3	0.29	0.19	14
Collinsella	0.2	0.2	0.1	0.3	0.18	0.24	14
Turicibacter	0.2	0.3[a]	0.0[b]	0.2[a]	0.29	**0.001**	13
TM7	0.4	0.4	0.4	0.3	0.26	0.58	14
Tenericutes	0.3	0.3	0.4	0.3	0.18	0.71	14
Verrucomicrobia	0.2	0.1[b]	0.2[a]	0.2[a]	0.05	**0.001**	14
Akkermansia	0.1	0.0[b]	0.1[a]	0.1[a]	0.04	**0.001**	14
Fusobacteria	0.1	0.1	0.1	0.1	0.07	0.41	14

[1] Sequences obtained from all cecum samples
[2] Values represent means.
[a,b] Within a row, means with a different subscript were different ($p < 0.05$).