Suppl. 6: *Abundance and statistical differences of different bacterial groups in faecal samples analysed with Illumina sequencing.*

Percentage and statistical differences of bacterial groups in faecal samples analysed via Illumina sequencing are reported as median values and range in FRE dogs and HC before and after the dietary trial. *P* values and adjusted *P* values with Bonferroni correction are reported. Significant results are in bold.

FRE, food-responsive enteropathy dog; HC, healthy control dogs; Baseline, before dietary trial with animal protein-free-diet; After, after 30 or 60 days of dietary trial animal protein-free-diet; Min., minimum; Max., maximum.

Bacterial group	**FRE Baseline**	**FRE After**	**HC Baseline**	**HC After**	**FRE Baseline vs HC Baseline**		**FRE Baseline vs FRE After**		**HC Baseline vs HC After**		**FRE After vs HC Baseline**	
					P value	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**
g.Actinomyces	0(0-0.012)	0(0-0.008)	0(0-0.018)	0(0-0.058)	0.514	0.642	0.28	0.611	0.145	0.403	0.904	0.929
g.Corynebacterium	0(0.002-0.036)	0(0.002-0.016)	0(0-0.026)	0(0-1.716)	0.341	0.491	0.374	0.611	0.298	0.494	0.789	0.892
g.Leucobacter	0(0-0.004)	0(0-0.004)	0(0-0.01)	0(0-0.048)	**0.044**	0.127	0.798	0.831	0.201	0.439	0.077	0.263
*f.Micrococcaceae;g_*	0(0-0.04)	0(0-0.006)	0(0-0.006)	0(0-0.018)	0.44	0.579	0.223	0.611	0.095	0.343	0.787	0.892
g.Arthrobacter	0(0-0.004)	0(0-0.008)	0(0-0.006)	0(0-0.136)	0.436	0.579	0.244	0.611	0.247	0.468	0.797	0.892
g.Bifidobacterium	0(0.014-0.668)	0.1(0.016-12.628)	0(0.016-17.826)	0.2(0.01-4.908)	0.334	0.491	0.349	0.611	0.573	0.679	0.66	0.823
*f.Coriobacteriaceae;g_*	0(0-0.034)	0(0-0.008)	0(0-0.118)	0(0-0.032)	**0.048**	0.134	0.323	0.611	0.248	0.468	0.053	0.209
g.Adlercreutzia	0(0.002-0.098)	0(0-0.05)	0(0.002-0.084)	0(0-0.244)	0.131	0.253	0.23	0.611	0.142	0.403	**0.021**	0.12
g.Collinsella	1.4(0.058-7.386)	1.5(0.08-4.656)	4.7(2.312-11.65)	4(1.058-19.668)	**0.006**	**0.048**	0.71	0.783	0.56	0.678	**0.002**	**0.03**
g.Slackia	0(0-0.782)	0(0-0.202)	0.2(0.004-0.548)	0.1(0.004-0.224)	**0.022**	0.098	0.344	0.611	0.054	0.264	**0.015**	0.12
g.Bacteroides	0.4(0.088-15.498)	2.4(0.118-7.41)	5.9(0.21-16.498)	5.8(0.37-19.274)	0.053	0.138	0.645	0.768	0.53	0.652	0.101	0.322
g.Parabacteroides	0(0-3.632)	0(0.002-0.616)	0(0-0.23)	0(0.004-0.388)	0.618	0.736	0.43	0.633	0.181	0.422	0.119	0.343
g.Prevotella	0(0.008-2.012)	0.2(0.006-4.572)	0.1(0.008-1.198)	0.3(0.004-3.928)	0.291	0.455	0.099	0.611	0.051	0.264	0.501	0.749
*f.S24.7;g_*	0(0-0.072)	0(0-0.124)	0(0-0.038)	0(0-0.198)	**0.033**	0.116	0.154	0.611	0.25	0.468	0.545	0.761
*f.Paraprevotellaceae;g_*	0(0-0.006)	0(0-0.034)	0(0-0.088)	0(0-0.03)	0.159	0.285	0.337	0.611	0.159	0.41	0.239	0.561
g.Prevotella.	0(0.002-0.872)	0(0.002-1.614)	0.3(0.006-2.56)	0.2(0.008-2.026)	0.084	0.18	0.518	0.681	0.948	0.961	0.23	0.555
g.Mucispirillum	0(0-0.002)	0(0-0.004)	0(0-0.16)	0(0-0.098)	0.132	0.253	0.726	0.789	0.088	0.343	0.15	0.416

Bacterial group	**FRE Baseline**	**FRE After**	**HC Baseline**	**HC After**	**FRE Baseline vs HC Baseline**		**FRE Baseline vs FRE After**		**HC Baseline vs HC After**		**FRE After vs HC Baseline**	
					P value	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**
g.Bacillus	0(0-0.014)	0(0-0.054)	0(0-0.06)	0(0-0.084)	0.236	0.376	0.601	0.741	0.445	0.579	0.43	0.714
*f.Planococcaceae;g_*	0(0-0.004)	0(0-0.006)	0(0-0.002)	0(0-0.018)	0.333	0.491	0.343	0.611	0.101	0.343	**0.018**	0.12
g.Rummeliibacillus	0(0.002-0.202)	0(0.006-0.122)	0(0.002-0.084)	0(0-10.67)	0.348	0.492	0.47	0.665	0.33	0.494	0.363	0.65
g.Staphylococcus	0(0-0.024)	0(0-0.01)	0(0-0.006)	0(0-0.08)	0.321	0.491	0.382	0.611	0.18	0.422	0.646	0.823
o.Lactobacillales;f_Other;g_Other	0(0-0.102)	0(0-0.006)	0(0-0.006)	0(0-0.006)	0.067	0.158	0.123	0.611	0.336	0.494	0.676	0.823
*f.Aerococcaceae;g_*	0(0-0.006)	0(0-0.006)	0(0-0.014)	0(0-0.004)	0.644	0.743	0.343	0.611	0.256	0.468	0.311	0.619
f.Enterococcaceae;g_Other	0(0-0.09)	0(0-0.006)	0(0-0.004)	0(0-0.02)	0.063	0..152	0.072	0.611	0.094	0.343	0.203	0.525
g.Enterococcus	0.3(0.032-27.068)	0.2(0.042-0.604)	0.1(0.03-0.23)	0.1(0.032-1.358)	0.074	0.163	0.148	0.611	**0.043**	0.264	**0.014**	0.12
g.Lactobacillus	0.2(0.062-1.51)	0.2(0.078-35.124)	0.1(0.048-4.264)	0.1(0.054-52.838)	0.93	0.955	0.337	0.611	0.38	0.538	0.364	0.65
*f.Leuconostocaceae;g_*	0(0-0.006)	0(0-0.056)	0(0-0.004)	0(0-0.024)	0.784	0.84	0.364	0.611	0.311	0.494	0.972	0.977
g.Streptococcus	1.6(0.222-38.236)	7(0.284-60.696)	7.7(0.24-34.172)	6(0.24-60.11)	0.815	0.861	0.36	0.611	0.247	0.468	0.447	0.714
g.Turicibacter	0.3(0.104-23.546)	0.9(0.136-28.192)	0.3(0.1-11.66)	1.8(0.102-6.198)	0.639	0.743	0.676	0.774	0.744	0.797	0.292	0.608
o.Clostridiales;f_Other;g_Other	0.1(0.014-0.734)	0.1(0.04-7.186)	0.2(0.044-4.238)	0.2(0.064-1.418)	**0.04**	0.121	0.349	0.611	0.398	0.552	0.253	0.576
*o.Clostridiales;f_;g_*	0.4(0.056-2.398)	0.5(0.118-1.202)	1.3(0.108-3.79)	0.7(0.194-2.818)	**0.04**	0.121	0.613	0.741	0.13	0.403	**0.022**	0.12
f.Clostridiaceae;g_Other	1.5(0.046-6.21)	0.9(0.226-2.306)	2.4(1.536-3.18)	1.3(0.552-2.404)	0.178	0.304	0.209	0.611	**0.001**	**0.024**	**0.002**	**0.015**
*f.Clostridiaceae;g_*	9.5(0.236-34.324)	10.3(1.998-27.192)	23.1(13.448-27.514)	9.2(4.4-21.298)	**0.014**	0.087	0.596	0.741	**0.001**	**0.024**	**0.001**	**0.025**
g.Candidatus.Arthromitus	0(0-0.01)	0(0-1.066)	0(0-0.396)	0(0.002-0.09)	0.672	0.751	0.168	0.611	0.523	0.652	0.284	0.608
g.Clostridium	2.1(0.094-69.628)	0.4(0.13-23.014)	0.4(0.11-6.9)	0.3(0.106-6.432)	0.412	0.562	0.446	0.643	0.807	0.853	0.447	0.714
g.SMB53	0.1(0.006-0.69)	0.1(0.036-0.432)	0.6(0.246-0.76)	0.3(0.118-0.574)	**0.007**	**0.048**	0.529	0.684	**0.001**	**0.024**	**>0.001**	**0.015**
g.Sarcina	0.1(0.014-0.49)	0.2(0.02-4.83)	0.1(0.012-2.442)	0.1(0.018-2.966)	0.977	0.977	0.27	0.611	0.58	0.679	0.519	0.749
f.Lachnospiraceae;g_Other	0(0.004-0.16)	0.1(0.022-0.218)	0.1(0.024-0.22)	0.1(0.038-0.186)	**0.006**	**0.048**	**0.007**	0.555	**0.046**	0.264	0.519	0.749
*f.Lachnospiraceae;g_*	0.8(0.03-3.312)	1.4(0.506-2.654)	2.8(0.762-15.508)	1.5(1.104-2.244)	**0.001**	**0.038**	0.106	0.611	0.056	0.264	**0.004**	0.061
g.Blautia	3.4(0.238-15.334)	11(1.436-26.83)	11.4(2.29-22.65)	8.4(3.774-18.424)	**0.026**	0.103	0.05	0.611	0.405	0.552	0.815	0.899
g.Coprococcus	0(0.002-0.064)	0.1(0.012-0.886)	0.1(0.01-0.178)	0(0.032-0.07)	0.113	0.231	0.195	0.611	0.448	0.579	0.598	0.787
g.Dorea	0.7(0.048-2.924)	1.1(0.31-3.426)	1.9(0.44-4.856)	1(0.506-2.842)	**0.03**	0.114	0.786	0.83	**0.044**	0.264	**0.022**	0.12
g.Epulopiscium	0(0.004-0.506)	0(0.006-0.272)	0(0.002-0.034)	0(0.002-0.128)	0.536	0.659	0.741	0.794	0.068	0.302	0.462	0.722
g.Roseburia	0(0-0.022)	0(0.002-0.016)	0(0.008-0.506)	0(0.002-0.176)	**0.001**	**0.038**	0.126	0.611	0.469	0.596	**0.017**	0.12
g..Ruminococcus.	0.7(0.084-6.294)	2(0.298-13.148)	1.9(0.87-10.492)	3.7(0.698-7.504)	0.143	0.262	0.407	0.611	0.312	0.494	0.558	0.761

Bacterial group	**FRE Baseline**	**FRE After**	**HC Baseline**	**HC After**	**FRE Baseline vs HC Baseline**		**FRE Baseline vs FRE After**		**HC Baseline vs HC After**		**FRE After vs HC Baseline**	
					P value	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**
g.Peptococcus	0(0.002-1.868)	0(0.008-0.684)	0.3(0.012-1.088)	0.1(0.012-2.212)	**0.021**	0.097	0.373	0.611	0.697	0.769	0.074	0.263
*f.Peptostreptococcaceae;g_*	0.6(0.082-29.942)	3.2(0.36-22.188)	0.7(0.188-12.666)	0.9(0.274-5.178)	0.482	0.613	0.682	0.774	0.638	0.714	0.107	0.322
*f.Ruminococcaceae;g_*	0.2(0.032-2.658)	0.6(0.034-13.972)	0.9(0.12-5.936)	1.4(0.19-7.762)	0.053	0.138	0.236	0.611	**0.04**	0.264	0.38	0.662
g.Faecalibacterium	0(0.002-0.294)	0.1(0.004-1.848)	0.1(0.02-0.812)	0.2(0.01-0.982)	**0.035**	0.119	0.211	0.611	**0.021**	0.26	0.558	0.761
g.Oscillospira	0(0-0.116)	0(0-0.018)	0(0-0.026)	0(0.002-0.092)	0.361	0.502	0.27	0.611	0.053	0.264	0.317	0.619
g.Ruminococcus	0(0-0.168)	0(0-0.014)	0(0-0.046)	0(0-0.104)	0.226	0.368	0.341	0.611	0.602	0.684	0.514	0.749
f.Veillonellaceae;g_Other	0(0-0.002)	0(0-0.008)	0(0-0.008)	0(0-0.022)	0.142	0.262	0.217	0.611	0.136	0.403	0.861	0.91
g.Megamonas	0.1(0.036-6.39)	0.6(0.052-7.814)	0.2(0.064-25.892)	1.1(0.06-13.266)	**0.005**	**0.048**	0.087	0.611	0.415	0.555	0.77	0.892
g.Megasphaera	0(0.006-0.334)	0(0.006-8.538)	0(0.004-0.042)	0(0.004-2.938)	0.701	0.762	0.242	0.611	0.205	0.439	0.681	0.823
g.Phascolarctobacterium	0(0-0.018)	0(0.002-0.696)	0(0.002-0.632)	0(0.004-1.08)	0.06	0.149	0.205	0.611	0.051	0.264	0.977	0.977
f.Mogibacteriaceae	0(0-0.01)	0(0-0.002)	0(0-0.056)	0(0-0.032)	0.975	0.977	0.108	0.611	0.594	0.684	**0.03**	0.149
f.Erysipelotrichaceae	0.2(0.032-2.58)	0.5(0.15-2.908)	2(0.166-10.02)	1.1(0.4-8.456)	**0.006**	**0.048**	0.312	0.611	0.839	0.874	**0.047**	0.205
g.Allobaculum	0.1(0.01-2.194)	0.2(0.014-2.648)	1(0.032-2.03)	0.5(0.018-1.068)	**0.006**	**0.048**	0.865	0.865	**0.001**	**0.024**	**0.005**	0.061
g.Catenibacterium	0.1(0.036-6.684)	2.1(0.072-15.33)	1(0.236-8.93)	3.4(0.16-15.606)	**0.016**	0.088	**0.028**	0.611	0.155	0.41	0.861	0.91
g.Coprobacillus	0(0-0.034)	0(0-0.018)	0(0-0.144)	0(0.004-0.032)	**0.016**	0.088	0.506	0.677	**0.037**	0.264	**0.01**	0.104
g..Eubacterium.	0.3(0.04-8.326)	1.5(0.104-16.904)	1.8(0.124-6.194)	3.6(0.2-10.33)	0.198	0.33	0.112	0.611	0.103	0.343	0.703	0.837
f.Fusobacteriaceae;g_Other	0(0.006-0.436)	0.1(0.008-0.38)	0.2(0.018-0.71)	0.1(0.016-0.284)	**0.018**	0.089	0.607	0.741	**0.017**	0.252	0.107	0.322
g.Fusobacterium	2.9(0.07-16.726)	0.8(0.102-18.356)	5.6(0.158-24.274)	2.5(0.668-14.088)	0.114	0.231	0.849	0.861	0.105	0.343	0.16	0.428
g.Sutterella	0.2(0.044-1.216)	0.2(0.018-0.368)	0.3(0.034-2.4)	0.5(0.056-2.258)	0.578	0.699	0.401	0.611	0.292	0.494	0.219	0.547
g.Campylobacter	0(0.002-1.294)	0(0.002-0.26)	0(0.002-2.122)	0(0.006-1.582)	0.883	0.92	0.398	0.611	0.967	0.967	0.076	0.263
*f.Helicobacteraceae;g_*	0(0-0.018)	0(0-0.004)	0(0-0.02)	0(0-0.014)	0.671	0.751	0.482	0.67	0.868	0.892	0.671	0.823
g.Helicobacter	0(0.01-0.35)	0(0.006-0.44)	0.1(0.01-3.172)	0.4(0.02-3.712)	0.073	0.163	0.82	0.842	0.186	0.422	0.053	0.209
*f.Succinivibrionaceae;g_*	0(0.006-0.058)	0(0.008-0.278)	0(0.002-6.924)	0(0.004-0.864)	0.681	0.751	0.39	0.611	0.265	0.474	0.883	0.92
g.Anaerobiospirillum	0(0-0.468)	0(0-0.74)	0(0-1.534)	0(0-0.572)	0.168	0.292	0.503	0.677	0.306	0.494	0.348	0.65
g.Succinivibrio	0(0-0.004)	0(0-0.006)	0(0-0.202)	0(0-0.006)	0.478	0.613	0.322	0.611	0.331	0.494	0.284	0.608
f.Enterobacteriaceae;g_Other	0(0-0.092)	0(0-0.072)	0(0-0.004)	0(0-0.002)	**0.005**	**0.048**	0.692	0.775	0.72	0.783	0.322	0.619
*f.Enterobacteriaceae;g_*	13.3(0.09-64.676)	0.5(0.1-9.076)	0.3(0.092-4.13)	0.2(0.124-14.256)	**0.004**	**0.048**	**0.023**	0.611	0.367	0.53	0.598	0.787
g.Citrobacter	0(0-0.008)	0(0-0.002)	0(0-0.004)	0(0-0.016)	**0.007**	**0.048**	**0.045**	0.611	0.171	0.422	0.855	0.91

Bacterial group	**FRE Baseline**	**FRE After**	**HC Baseline**	**HC After**	**FRE Baseline vs HC Baseline**		**FRE Baseline vs FRE After**		**HC Baseline vs HC After**		**FRE After vs HC Baseline**	
					P value	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**	***P value***	**Adjusted *P* value**
*f.Pseudomonadaceae;g_*	0(0-0.444)	0(0-0.004)	0(0-0.004)	0(0-0.004)	**0.024**	0.099	0.308	0.611	0.336	0.494	0.447	0.714
g.Anaeroplasma	0(0-0.008)	0(0-0.002)	0(0-0.088)	0(0-0.278)	**0.04**	0.121	0.678	0.774	0.228	0.468	**0.046**	0.205