**SUPPLEMENTARY MATERIAL**

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| **Supplemental Table 1.** Fecal microbiota populations of prebiotic-supplemented dogs using qPCR (LS means) |
|  | Treatment |  |  |
| Taxa | Control | Low | High | SEM | p-value |
|  Universal | 12.12 | 12.16 | 12.11 | 0.02 | 0.35 |
| **Genera** |  |  |  |  |  |
|  *Faecalibacterium* | 8.29 | 8.42 | 8.30 | 0.09 | 0.42 |
|  *Turicibacter* | 6.68a | 6.76a | 7.34b | 0.24 | **0.04** |
|  *Streptococcus* | 5.26 | 5.50 | 5.31 | 0.30 | 0.82 |
|  *E. coli* | 5.64 | 5.60 | 5.42 | 0.40 | 0.80 |
|  *Blautia* | 9.77 | 9.90 | 9.88 | 0.11 | 0.68 |
|  *Fusobacterium* | 10.17 | 10.11 | 10.16 | 0.06 | 0.48 |
|  *C. hiranonis* | 6.45 | 6.55 | 6.42 | 0.06 | 0.12 |
|  *Lactobacillus* | 5.70 | 6.08 | 6.12 | 0.45 | 0.71 |
|  *Bifidobacterium* | 6.52 | 6.50 | 6.41 | 0.23 | 0.88 |
|  *C. perfringens* | 4.85 | 4.61 | 4.77 | 0.32 | 0.84 |
| **Families** |  |  |  |  |  |
|  Ruminococcaceae | 8.02 | 8.07 | 7.97 | 0.11 | 0.79 |

a,b Means within a row with unlike superscripts were different (P<0.05).



**Supplemental Figure 1.** Rarefaction plot of fecal microbial communities of prebiotic-supplemented dogs. Microbial species richness (alpha diversity) among treatment groups was not different. Control: closed circles, solid line; Low-dose prebiotic: closed squares, solid line; High-dose prebiotic: open circles, dashed line.



**Supplemental Figure 2.** Unweighted (A) and weighted (B) principal coordinates analysis (PCoA) plots of fecal microbial communities of prebiotic-supplemented dogs. Neither unweighted nor weighted UniFrac distances of fecal microbial communities performed on the 97% OTU abundance matrix revealed any differences among treatments. Control: red, Low-dose prebiotic: orange, High-dose prebiotic: blue.