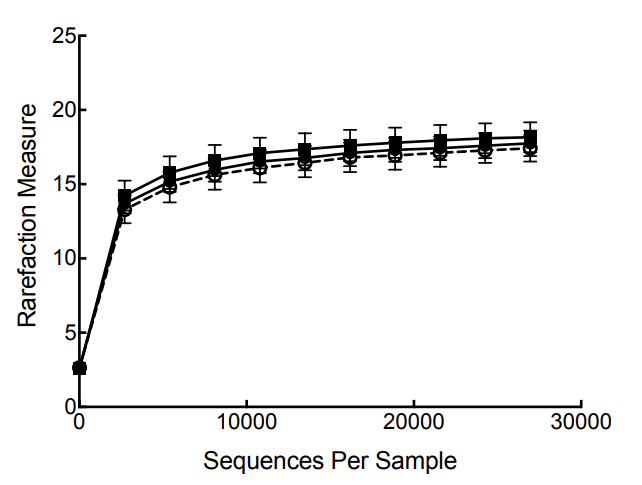
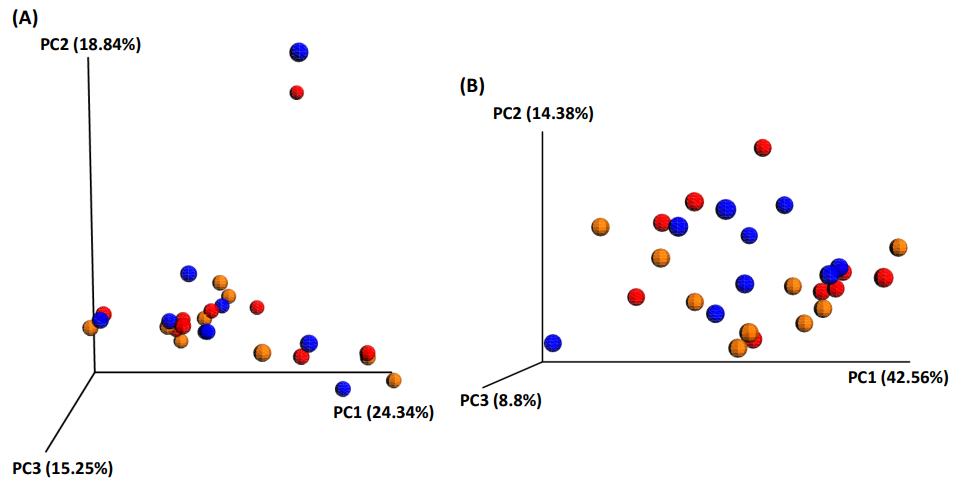
**SUPPLEMENTARY MATERIAL**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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.