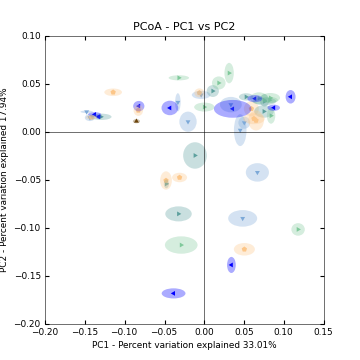
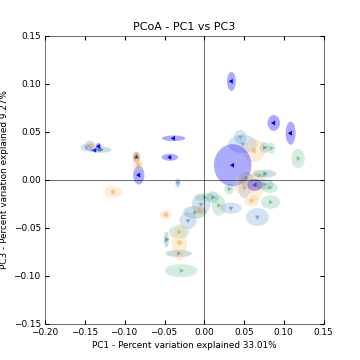
|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary table 1.** Predominant bacterial species (expressed as a percentage of total sequences) in faeces of dogs fed diets containing graded potato fibre (PF) concentrations§ | | | | | | | | |
|  | % PF | | | | | |  |  |
| Species | 0 | 1·5 | 3 | 4·5 | | 6 | SEM | P-Value |
| *Bifidobacterium pseudolongum* | 0·21ab | 0·24ab | 0·15ab | 0·50b | 0·09a | | 0·17 | 0·04 |
| *Prevotella copri*‡ | 0·68b | 0·24a | 0·40ab | 0·52ab | 0·22a | | 0·36 | 0·02 |
| *Clostridium bifermentans* | 0·40 | 0·37 | 0·56 | 0·75 | 0·40 | | 0·27 | 0·59 |
| *C. citroniae*‡\* | 0·06 | 0·09 | 0·15 | 0·17 | 0·15 | | 0·03 | 0·05 |
| *C. disporicum* | 0·01 | 0·02 | 0·02 | 0·03 | 0·03 | | 0·01 | 0·89 |
| *C. hiranonis*\* | 19·57b | 16·64ab | 19·64b | 19·29b | 10·42a | | 4·37 | 0·02 |
| *C. incertae sedis*† | 0·18 | 0·37 | 0·33 | 0·48 | 0·14 | | 0·17 | 0·18 |
| *C. lactatifermen*† | 0·01 | 0·06 | 0·06 | 0·11 | 0·02 | | 0·03 | 0·12 |
| *C. metallolevans* | 0·03 | 0·05 | 0·08 | 0·07 | 0·04 | | 0·03 | 0·39 |
| *C. spiroforme* | 0·42 | 0·36 | 0·52 | 0·22 | 0·21 | | 0·14 | 0·25 |
| *Allobaculum stercoricanis*#† | 2·51 | 3·42 | 3·83 | 2·72 | 2·45 | | 0·84 | 0·16 |
| *Catenibacterium mitsuokai* | 0·13 | 0·11 | 0·06 | 0·06 | 0·03 | | 0·05 | 0·64 |
| *Coprobacillus cateniformis* | 0·12 | 0·15 | 0·16 | 0·15 | 0·11 | | 0·04 | 0·86 |
| *Turicibacter sanguinis* | 0·70 | 0·55 | 0·77 | 0·80 | 0·55 | | 0·23 | 0·62 |
| *Eubacterium biforme* | 0·20 | 0·35 | 0·29 | 0·46 | 0·34 | | 0·15 | 0·62 |
| *E. dolichum* | 0·15 | 0·18 | 0·10 | 0·09 | 0·04 | | 0·06 | 0·24 |
| *Blautia producta*† | 6·33 | 7·81 | 7·61 | 7·56 | 5·98 | | 1·34 | 0·31 |
| *Ruminococcus obeum* | 1·29ab | 0·81a | 1·44ab | 2·32b | 0·97ab | | 0·51 | 0·03 |
| *R. gnavus* | 1·04 | 0·94 | 0·83 | 1·06 | 0·60 | | 0·38 | 0·38 |
| *R. torques* | 0·33 | 0·32 | 0·52 | 0·35 | 0·49 | | 0·18 | 0·84 |
| *Lactobacillus acidophilus* | 0·11 | 0·05 | 0·09 | 0·07 | 0·09 | | 0·07 | 0·96 |
| *L. johnsonii* | 0·68 | 3·54 | 0·66 | 2·04 | 3·45 | | 1·82 | 0·62 |
| *L. reuteri (strain F275)* | 0·19 | 0·68 | 0·17 | 0·54 | 0·53 | | 0·34 | 0·72 |
| *Faecalibacterium prausnitzii*‡\* | 4·15a | 8·67a | 8·89a | 9·63a | 14·88b | | 2·00 | 0·01 |
| *Lactococcus lactis lactis* | 0·14 | 0·46 | 0·05 | 0·12 | 0·01 | | 0·16 | 0·36 |
| *Fusobacterium varium* | 15·51 | 16·77 | 14·21 | 12·34 | 18·35 | | 2·76 | 0·22 |
| §Genera included have LSMEANs of 0·01 or higher.  abMeans in the same row with unlike superscript letters differ (*P* < 0·05).  ‡ Difference between 0% PF vs. all other PF diets (*P* < 0·05).  \*Linear effect (*P* < 0·05).  †Quadratic effect (*P* < 0·05). | | | | | | | | |







Supplementary figure 1: PCoA plots of faecal samples collected from dogs fed diets containing graded potato fibre (PF) concentrations. Violet: 0% PF; green: 1.5% PF; light blue 3% PF; orange: 4.5% PF; light green: 6% PF.



**Supplementary figure 2.** *E. coli* and *C. Perfringens* scatter plots for qPCR data. Horizontal line denotes the median value.