SI\_Figure\_1:

PCoA plot of unweighted UniFrac distances including the 7 outlier Brookfield samples.

SI\_Figure\_2:

Phylum-level taxonomic barplots including the 7 outlier Brookfield samples

SI\_Figure\_3:

PCoA plots of weighted UniFrac distances for captive and wild samples

SI\_Figure\_4:

PCoA plots of weighted UniFrac distances for the different populations of wild samples.

SI\_Table\_1:

Pairwise Kruskal-Wallis test results for Faith’s phylogenetic diversity metric comparisons between populations.

SI\_Table\_2:

Pairwise Kruskal-Wallis test results for observed features (richness) metric comparisons between populations.

SI\_Table\_3:

SINA alignment results of the most abundant core ASVs in SHNWs.

SI\_Table\_4:

SourceTracker2 results testing the estimated proportion of faecal bacteria coming from soil. https://doi.org/10.25909/12979157

SI\_File\_1:  
QIIME2 qzv file of taxonomic bar plots per sample.

SI\_File\_2:

QIIME2 qzv file of ANCOM test at family level (captive and wild samples).

SI\_File\_3:

QIIME2 qzv file of ANCOM test at the ASV level (captive and wild samples).

SI\_File\_4:

QIIME2 qzv file of ANCOM test at family level (between different wild populations).

SI\_File\_5:

QIIME2 qzv file of ANCOM test at the ASV level (between different wild populations).