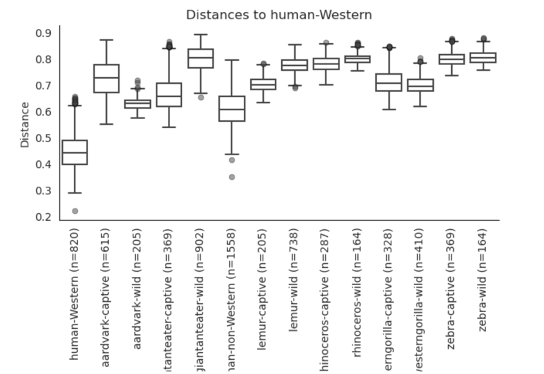
A B

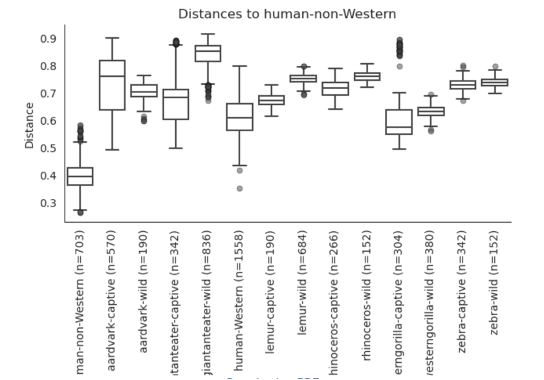
 



C

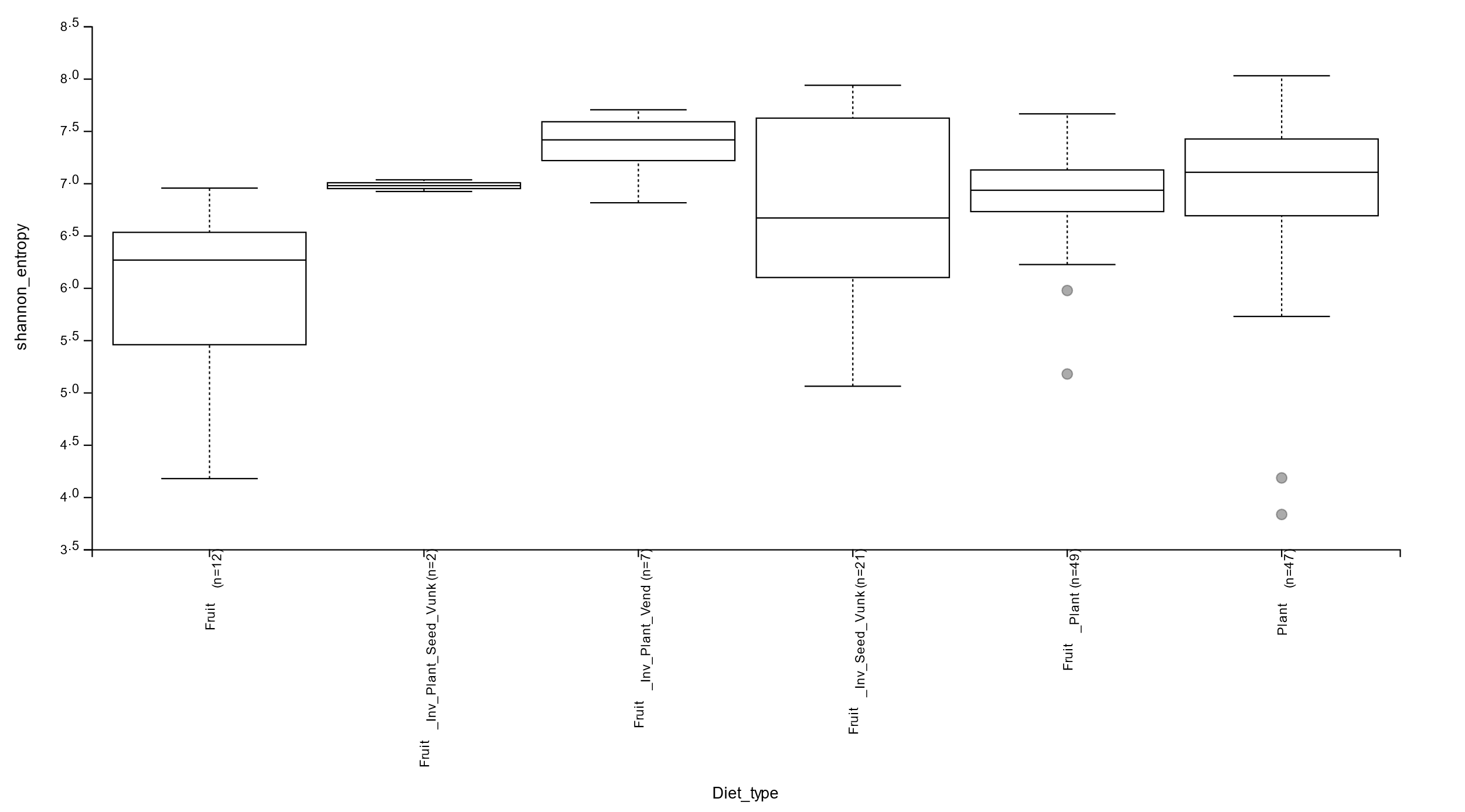
**Figure S1. Principal coordinate analysis in taxonomic groups do not have a clear pattern with location.** PCoA plots using the Bray-Curtis dissimilarity index show diversity across various locations. (A) family *Rhinocerotidae* and (B) genus *Equus* exhibit a pattern in regards to location. (C) *Gorilla gorilla* do not exhibit any clustering in regards to location. PERMANOVA testing did not exhibit statistical significance.





**Figure S2.** Unweighted UniFrac distance metric comparing distances of captive and wild animals to Western and non-Western humans. Captive animals are more similar to humans than wild animals are, and to non-Western humans than to Western humans.

A



B

|  |  |  |
| --- | --- | --- |
| **Diet composition** |  | *p*-value |
| Fruit (n=12) | Fruit\_Inv\_Plant\_Seed\_Vunk (n=2) | 0.067889 |
|  | Fruit\_Inv\_Plant\_Vend (n=7) | 0.000723 |
|  | Fruit\_Inv\_Seed\_Vunk (n=21) | 0.02474 |
|  | Fruit\_Plant (n=49) | 7.65E-05 |
|  | Plant (n=47) | 0.000223 |
| Fruit\_Inv\_Plant\_Seed\_Vunk (n=2) | Fruit\_Inv\_Plant\_Vend (n=7) | 0.143235 |
|  | Fruit\_Inv\_Seed\_Vunk (n=21) | 0.827259 |
|  | Fruit\_Plant (n=49) | 0.734095 |
|  | Plant (n=47) | 0.686041 |
| Fruit\_Inv\_Plant\_Vend (n=7) | Fruit\_Inv\_Seed\_Vunk (n=21) | 0.144556 |
|  | Fruit\_Plant (n=49) | 0.004925 |
|  | Plant (n=47) | 0.125462 |
| Fruit\_Inv\_Seed\_Vunk (n=21) | Fruit\_Plant (n=49) | 0.594819 |
|  | Plant (n=47) | 0.377381 |
| Fruit\_Plant (n=49) | Plant (n=47) | 0.109281 |

**Figure S3. Shannon diversity demonstrate a significant decrease in bacterial abundance compared to other composition.** Alpha diversity of each diet composition is computed using QIIME2 and plotted in (A) boxplot visualized with QIIME2 view tested for statistical significance, (B) statistical significance in *p*-value of each composition to one another.

**Table S1.** Indicator family of giant anteaters (*Myrmecophaga tridactyla*)

|  |  |  |
| --- | --- | --- |
| Taxonomic Classification | Indicator Statistic | *p*-value |
| National Zoo (number of indicator families = 2)  Bacteria Tenericutes Mollicutes Anaeroplasmatales Anaeroplasmataceae  Bacteria Verrucomicrobia Verrucomicrobiae Verrucomicrobiales Verrucomicrobiaceae | 1.0000  0.993 | 0.005  0.010 |
| Zurich Zoo (number of indicator families = 8)  Bacteria Actinobacteria Actinobacteria Actinomycetales NA  Bacteria Proteobacteria NA NA NA  Bacteria Firmicutes Bacilli Lactobacillales Leuconostocaceae  Bacteria Firmicutes Bacilli Turicibacterales Turicibacteraceae  Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae  Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae  Bacteria Firmicutes Clostridia Clostridiales NA  Bacteria Firmicutes Clostridia Clostridiales Peptococcaceae | 1.000  0.995  0.970  0.967  0.924  0.899  0.877  0.875 | 0.015  0.020  0.010  0.015  0.010  0.010  0.020  0.030 |

**Table S2.** Indicator family of aardvarks (*Orycteropus afer*)

|  |  |  |
| --- | --- | --- |
| Taxonomic Classification | Indicator Statistic | *p*-value |
| Cincinnati Zoo (number of indicator families = 3)  Bacteria Proteobacteria Gammaproteobacteria Aeromonadales Succinivibrionaceae  Bacteria Bacteroidetes Bacteroidia Bacteroidales Prevotellaceae  Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae | 0.991  0.964  0.836 | 0.005  0.010  0.020 |
| Colchester Zoo (number of indicator families = 5)  Bacteria Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales Micrococcaceae  Bacteria Proteobacteria Gammaproteobacteria Pseudomonadales Moraxellaceae  Bacteria Firmicutes Clostridia Clostridiales [Tissierellaceae]  Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae | 0.934  0.911  0.902  0.871  0.862 | 0.010  0.005  0.010  0.015  0.005 |
| London Zoo (number of indicator families = 8)  Bacteria Bacteroidetes Bacteroidia Bacteroidales RF16  Bacteria TM7 TM7-3 CW040 F16  Bacteria Firmicutes Bacilli Bacillales Alicyclobacillaceae  Bacteria Tenericutes Mollicutes RF39 NA  Bacteria Bacteroidetes Bacteroidia Bacteroidales NA  Bacteria Firmicutes Clostridia Clostridiales [Mogibacteriaceae]  Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae  Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae | 0.988  0.942  0.920  0.892  0.870  0.837  0.831  0.807 | 0.010  0.015  0.005  0.030  0.040  0.020  0.045  0.035 |
| TdR Nature Reserve (number of indicator families = 32)  Bacteria Actinobacteria Actinobacteria Actinomycetales Geodermatophilaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales Thermomonosporaceae  Bacteria Planctomycetes Planctomycetia Gemmatales Isosphaeraceae  Bacteria Bacteroidetes NA NA NA  Bacteria Proteobacteria Gammaproteobacteria NA NA  Bacteria Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae Bacteria Firmicutes Bacilli Bacillales Bacillaceae  Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae  Bacteria Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae  Bacteria Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales NA  Bacteria Firmicutes Bacilli Lactobacillales Aerococcaceae  Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Brucellaceae  Bacteria Proteobacteria Gammaproteobacteria Xanthomonadales Xanthomonadaceae  Bacteria Firmicutes Bacilli Bacillales NA  Bacteria Actinobacteria Actinobacteria Actinomycetales Promicromonosporaceae  Bacteria Proteobacteria Betaproteobacteria Burkholderiales Alcaligenaceae  Bacteria NA NA NA NA  Bacteria Actinobacteria Actinobacteria Actinomycetales Actinomycetaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales Bogoriellaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales Mycobacteriaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales Streptosporangiaceae  Bacteria Gemmatimonadetes Gemm-3 NA NA  Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae  Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Methylobacteriaceae  Bacteria Proteobacteria Gammaproteobacteria  Bacteria Proteobacteria Gammaproteobacteria Chromatiales Ectothiorhodospiraceae  Bacteria Proteobacteria NA NA NA  Bacteria Tenericutes Mollicutes RsaHF231 NA  Bacteria TM7 TM7-3 I025 NA  Bacteria Fusobacteria Fusobacteriia Fusobacteriales Fusobacteriaceae  Bacteria Actinobacteria Actinobacteria Actinomycetales Yaniellaceae | 1.000  1.000  1.000  1.000  1.000  0.998  0.997  0.997  0.985  0.984  0.984  0.983  0.982  0.979  0.975  0.974  0.973  0.959  0.866  0.866  0.866  0.866  0.866  0.866  0.866  0.866  0.866  0.866  0.866  0.866  0.855  0.852 | 0.005  0.005  0.005  0.005  0.005  0.005  0.005  0.005  0.030  0.005  0.005  0.005  0.005  0.005  0.005  0.005  0.005  0.005  0.015  0.015  0.015  0.015  0.030  0.020  0.015  0.020  0.010  0.030  0.015  0.015  0.040  0.035 |

**Table S3.** **Indicator taxa at the genus level.** Indicator taxa analysis showing bacterial taxa present in humans and captive animals that are absent in wild animals. Most notable genera include *Blautia, Streptococcus, Coprococcus, Ruminococcus, Oscillospira, Faecalibacterium, Lachnospira, Roseburia* and *Clostridium*. A represents the specificity of each taxon to the group (human-captive animals), B the fidelity and stat the indicator value (A\*B). Asterisks represent different p-values (‘\*\*\*’ - 0, ‘\*\*’ - 0.001, ‘\*’ - 0.01, ‘.’ - 0.05, ‘ ’ - 0.1).

|  |  |  |
| --- | --- | --- |
| Giant anteater |  |  |

A picture containing text, newspaper, screenshot

Description automatically generated

|  |  |  |
| --- | --- | --- |
| Rhinoceros |  |  |

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Description automatically generated

|  |  |  |
| --- | --- | --- |
| Lemur |  |  |

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Description automatically generated

|  |  |  |
| --- | --- | --- |
| Western gorilla |  |  |

Text

Description automatically generated

**Table S4. Differentially abundant classes based on diet composition.** Differential abundance was computed in R using the phyloseq package at class level based on the diet composition. The significance is reported with adjusted *p*-value.

|  |  |
| --- | --- |
| **Class** | **Adjusted *p*-value** |
| Opitutae | 0.017170242 |
| Epsilonproteobacteria | 0.00609561 |
| Gammaproteobacteria | 0.002797558 |
| Planctomycetia | 0.006412206 |
| Erysipelotrichi | 2.20E-05 |
| Anaerolineae | 6.27E-27 |
| Clostridia | 0.000469216 |