**Table S1.** Parameter estimates for 28 generalized linear mixed models testing the role of different covariates on the rarefied number of reads for each taxonomic group in each fecal sample. Parameter estimates are reported as mean ± standard error and are on the log-scale. In all models, the intercept represents the contrast for samples from high elevation birds tested at middle elevations. Parameter estimates in bold represent significant results using a Benjamini-Hochberg adjustment with a false discovery rate of 0.05.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Taxonomic Level** | **Taxonomic Group** | **Intercept** | **Effect of high elevation site** | **Effect of captivity** | **Effect of originating at low elevation** | **Effect of originating at middle elevation** |
| Phylum | Actinobacteria | **7.86 ± 0.15** | 0.11 ± 0.19 | 0.00 ± 0.01 | 0.15 ± 0.19 | 0.05 ± 0.20 |
| - | Bacteroidetes | **1.98 ± 0.48** | 0.63 ± 0.36 | 0.05 ± 0.03 | 0.20 ± 0.59 | 0.29 ± 0.59 |
| - | Cyanobacteria | **1.67 ± 0.39** | 0.55 ± 0.39 | -0.03 ± 0.03 | -0.19 ± 0.53 | **1.85 ± 0.55** |
| - | Firmicutes | **8.22 ± 0.25** | **-1.28 ± 0.34** | -0.01 ± 0.01 | -0.22 ± 0.34 | -0.18 ± 0.35 |
| - | Fusobacteria | **4.28 ± 0.35** | **1.94 ± 0.32** | **0.06 ± 0.02** | 0.78 ± 0.40 | 0.91 ± 0.40 |
| - | Proteobacteria | **7.16 ± 0.25** | -0.38 ± 0.24 | 0.02 ± 0.01 | -0.05 ± 0.30 | 0.12 ± 0.30 |
| Genus | *Acinetobacter* | 2.02 ± 1.73 | -1.73 ± 0.98 | -0.07 ± 0.07 | -1.95 ± 0.89 | 0.27 ± 1.09 |
| - | *Asaia* | -0.45 ± 1.07 | **-5.79 ± 1.94** | 0.04 ± 0.10 | 1.77 ± 1.35 | 4.06 ± 1.61 |
| - | *Bergeyella* | 0.09 ± 0.61 | 0.33 ± 0.47 | **0.10 ± 0.03** | -0.3 ± 0.68 | 0.54 ± 0.65 |
| - | *Coenonia* | -1.38 ± 0.98 | -0.65 ± 0.65 | **0.16 ± 0.06** | -1.7 ± 1.02 | **-4.75 ± 1.48** |
| - | *Corynebacterium* | **7.76 ± 0.19** | 0.17 ± 0.24 | -0.01 ± 0.01 | 0.21 ± 0.24 | 0.08 ± 0.25 |
| - | *Enterococcus* | **4.83 ± 0.37** | 0.03 ± 0.48 | 0.04 ± 0.02 | -0.62 ± 0.53 | -0.43 ± 0.62 |
| - | *Escherichia Shigella* | **5.08 ± 0.67** | -0.87 ± 1.18 | -0.05 ± 0.06 | -0.28 ± 0.9 | 2.11 ± 1.29 |
| - | *Fructobacillus* | **7.38 ± 0.72** | **-3.32 ± 0.62** | -0.04 ± 0.04 | -1.00 ± 0.97 | -1.38 ± 1.06 |
| - | *Gluconobacter* | -0.95 ± 2.53 | **-4.05 ± 1.29** | 0.10 ± 0.10 | 2.22 ± 2.94 | -4.19 ± 3.52 |
| - | *Klebsiella* | **6.59 ± 0.31** | **-3.78 ± 0.44** | 0.05 ± 0.02 | 0.09 ± 0.44 | -0.53 ± 0.43 |
| - | *Lactobacillus* | -1.97 ± 1.08 | -1.03 ± 0.74 | 0.10 ± 0.05 | -0.13 ± 1.36 | 0.37 ± 1.34 |
| - | *Lactococcus* | **3.78 ± 0.64** | **-1.56 ± 0.60** | -0.02 ± 0.03 | -0.09 ± 0.90 | 2.29 ± 0.92 |
| - | *Leuconostoc* | **7.60 ± 0.43** | **-1.76 ± 0.47** | -0.01 ± 0.03 | -0.01 ± 0.58 | -0.89 ± 0.6 |
| - | *Moraxella* | **3.61 ± 0.33** | -0.10 ± 0.34 | 0.03 ± 0.020 | -0.32 ± 0.38 | -0.30 ± 0.36 |
| - | *Neokomagataea* | 1.34 ± 1.05 | -7.40 ± 3.28 | 0.22 ± 0.12 | 1.06 ± 1.12 | 0.20 ± 1.38 |
| - | *Riemerella* | **2.24 ± 0.35** | 0.87 ± 0.42 | 0.05 ± 0.04 | 0.29 ± 0.39 | -0.69 ± 0.41 |
| - | *Rothia* | **5.27 ± 0.26** | **-0.60 ± 0.23** | **0.05 ± 0.01** | -0.44 ± 0.35 | -0.25 ± 0.36 |
| - | *Stenotrophomonas* | 1.45 ± 0.89 | -1.57 ± 1.50 | 0.06 ± 0.08 | -0.43 ± 1.15 | -0.45 ± 1.60 |
| - | *Streptobacillus* | **4.28 ± 0.35** | **1.93 ± 0.33** | **0.06 ± 0.02** | 0.78 ± 0.39 | 0.92 ± 0.40 |
| - | *Streptococcus* | 0.96 ± 0.48 | 0.80 ± 0.40 | -0.01 ± 0.02 | -0.61 ± 0.42 | 0.60 ± 0.45 |
| - | *Suttonella* | **3.31 ± 0.34** | -0.63 ± 0.37 | **0.08 ± 0.02** | -0.75 ± 0.39 | -0.87 ± 0.38 |
| - | *Weissella* | **5.48 ± 0.80** | **-1.59 ± 0.57** | -0.06 ± 0.04 | -1.28 ± 1.17 | **-3.34 ± 1.18** |