**Supplementary Table S4**

**Manuscript:**

Houtkamp, I., Van Zijll Langhout, M., Bessem, M., Pirovano, W., & Kort, R. (2023). Multiomics characterization of the of the zoo-housed gorilla gut microbiome reveals bacterial community compositions shifts, fungal cellulose-degrading, and archaeal methanogenic activity. *Gut Microbiome,* 1-25. doi:10.1017/gmb.2023.11

|  |  |  |
| --- | --- | --- |
|  | **Top 10 eukaryotic genera in zoo- housed metatranscriptome** | **Relative abundance (%)** |
| 1 | *Piromyces* | 9.4 |
| 2 | *Pecoramyces* | 5.3 |
| 3 | *Neocallimastix* | 4.2 |
| 4 | *Melampsora* | 0.5 |
| 5 | *Mitosporidium* | 0.3 |
| 6 | *Hirsutella* | 0.2 |
| 7 | *Aspergillus* | 0.1 |
| 8 | *Anaeromyces* | 0.1 |
| 9 | *Amorphotheca* | < 0.1 |
| 10 | *Saccharomyces* | <0.1 |

**Table S4: Relative abundances of the top 10 eukaryotic genera in zoo-housed gorilla gut metatranscriptome.**