**Supplementary Table S3**

**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

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| --- | --- | --- |
|  | **Top 10 bacterial genera in zoo- housed metatranscriptome** | **Relative abundance (%)** |
| 1 | *Lactobacillus* | 14.6 |
| 2 | *Limosilactobacillus* | 9.4 |
| 3 | *Muricauda* | 4.2 |
| 4 | *Clostridium* | 2.9 |
| 5 | *Prevotella* | 2.1 |
| 6 | *Treponema* | 2.1 |
| 7 | *Vibrio* | 1.6 |
| 8 | *Streptomyces* | 1.6 |
| 9 | *Ruminococcus* | 1.2 |
| 10 | *Blautia* | 0.8 |

**Table S3: Relative abundances of the top 10 bacterial genera in zoo-housed gorilla gut metatranscriptome.**