**Supplementary Figure S6**

**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

**Figure S6: CBM families in the gut metagenome and metatranscriptome of a zoo-housed gorilla (DNA vs RNA).** Percentages represent the percentual contribution of each Carbohydrate Binding Module (CBM) family to the total number of CBM families found by shotgun metagenomics (DNA, left) and RNA-seq (RNA, right) on fecal samples of a zoo-housed gorilla. 