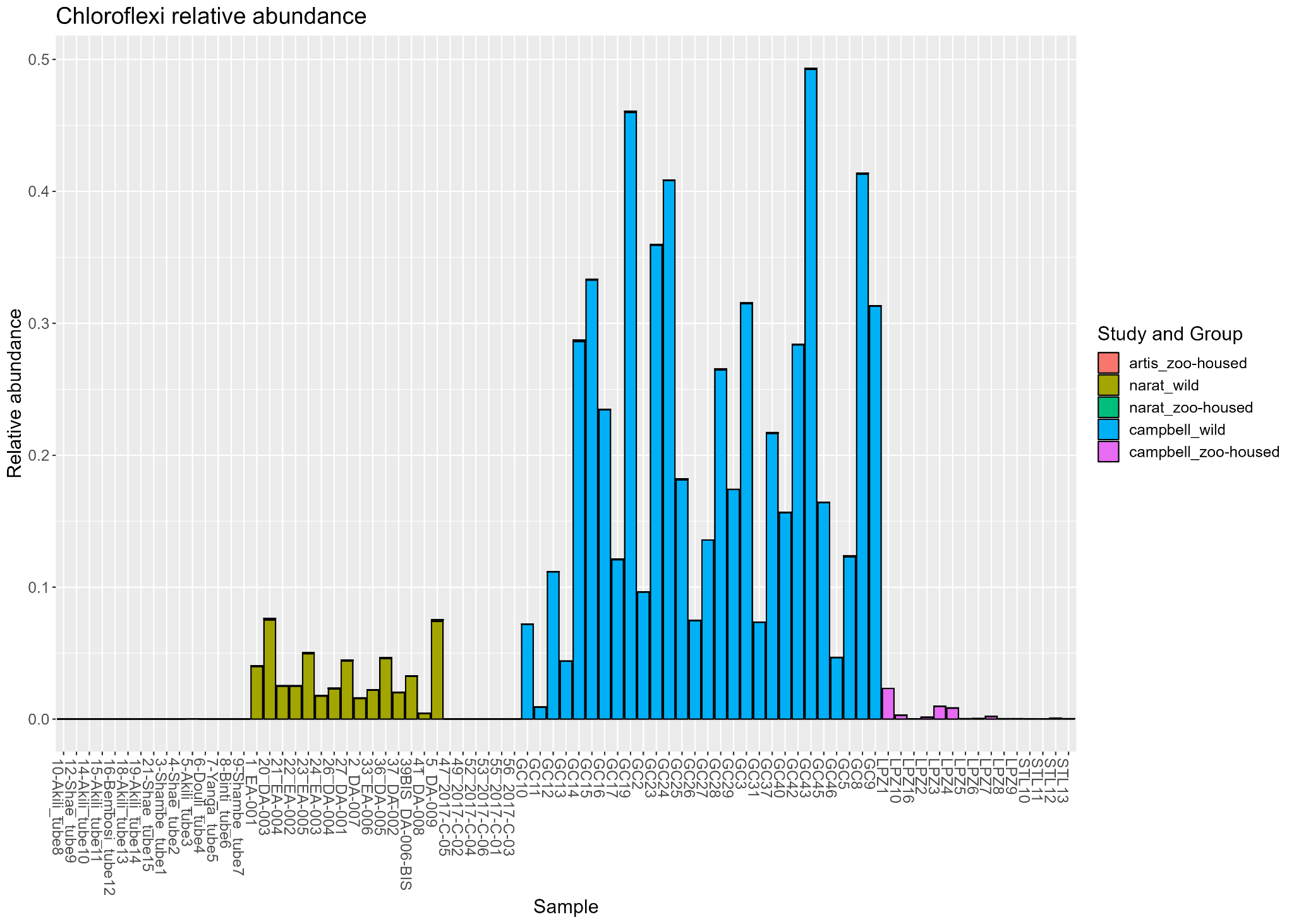
**Supplementary Figure S4**

**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



**Figure S4: Relative abundances of the phylum Chloroflexi.** Relative abundances (between 0 and 1) are shown per sample. Colors indicate which study a fecal sample belongs to and whether it originates from a wild or zoo-housed gorilla.