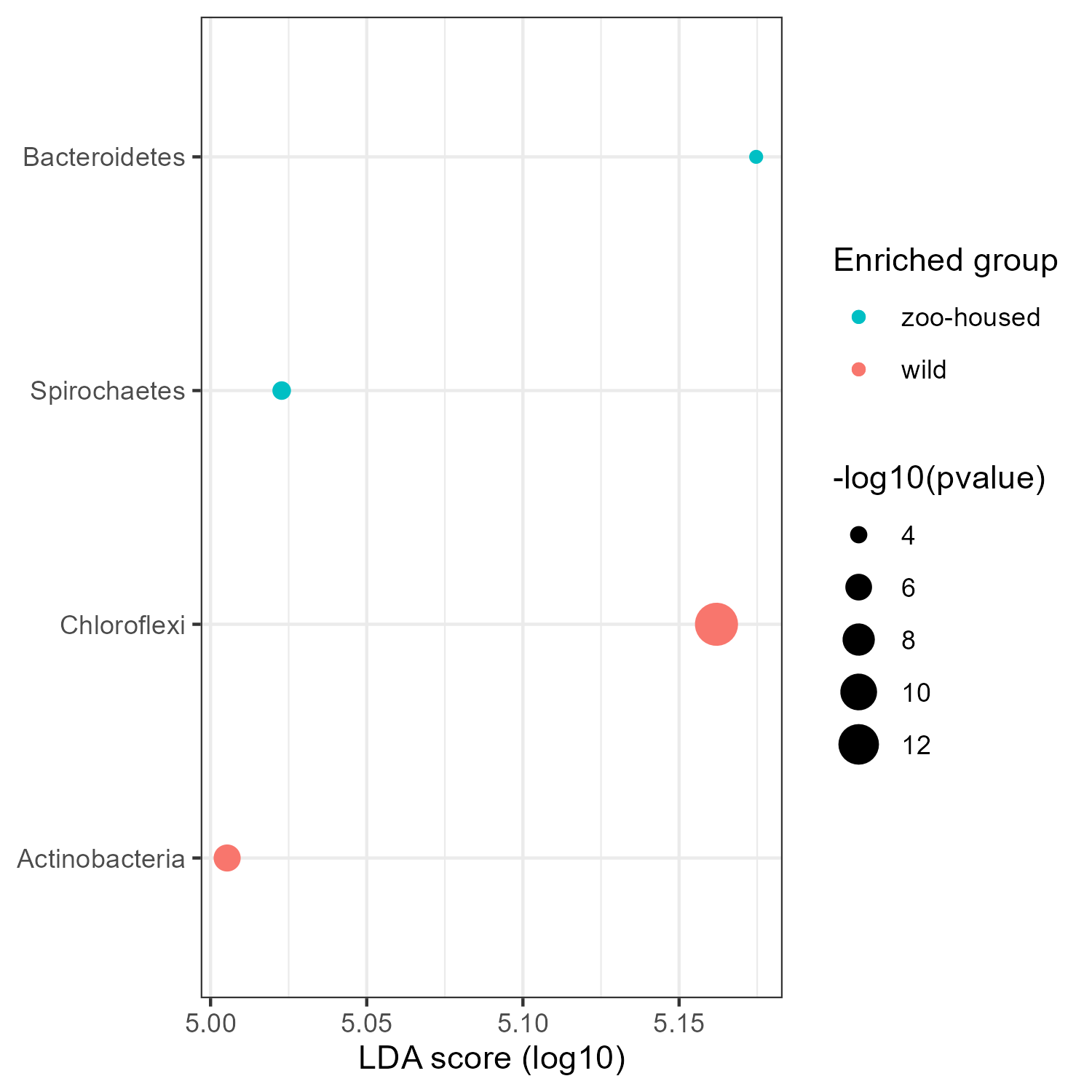
**Supplementary Figure S3**

**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



**Figure S3. Phyla identified as significantly enriched in wild or zoo-housed samples by LEfSE analysis.** Log10 transformed LDA scores above 4 and corresponding log10 transformed p-values, resulting from LefSE analysis at genus level between WG and ZHG samples. Genera with an LDA score > 4.0 and p-value < 0.05 are shown.