Legend of Supplementary Tables

Table S1. Taxonomic composition of the gelada gut at the phylum, class, order, family and genus levels. The mean relative abundance and prevalence (% of the samples with each taxon) of bacterial taxa are indicated.

Table S2. Taxonomic composition of the core ASVs (i.e. present in at least 90% of samples) in the gelada gut at the order level.

Table S3. Predictors of observed richness and Faith's phylogenetic diversity (PD). Estimates with p-values <0.05 are highlighted in bold.

Table S4. Loading scores of ASVs on the first principal component. Positive loadings correspond to wetter periods, while negative loadings correspond to drier periods.

Table S5 Taxonomic distribution of seasonally differentially abundant taxa. Only taxa with a PC loading scores > 0.4 and <-0.4 are included.

Table S6. Differential abundance results for all taxa. Results were obtained by fitting negative binomial GLMMs for each taxa, controlling for individual identity and unit membership. The estimate and p-values of fixed effects are reported. Due to some negative binomial models that did not converge, taxa preceded by a "*" were modeled with a binomial GLMM, with presence/absence as the outcome variable.

Table S7. Differential abundance results for KEGG pathways level 2. Model results were obtained by fitting LMMs on each pathway, while controlling for individual identity and unit membership. The estimate and p-value of the fixed effects are reported.

Table S8. Differential abundance results for KEGG pathways level 3. Model results were obtained by fitting LMMs on each pathway, controlling for individual identity and unit membership. The estimate and p-value of the fixed effects are reported.

Table S9. Predictors of Shannon index, observed richness and Faith's phylogenetic diversity (PD) in females only. Estimates with p-values <0.05 are highlighted in bold.

Table S10. Predictors of the structure of the female gelada gut microbiome. We carried out a PERMANOVA using 10,000 permutations and the Aitchison dissimilarity distance between samples.

Table S11. Number of differentially abundant taxa for each predictor in the female samples.

Table S12. Differential abundance results for female samples at five taxonomic levels.

Table S13. Differential abundance results for KEGG pathways level 2 for female samples. Model results were obtained by fitting LMMs on each pathway, while controlling for individual identity and unit membership. The estimate and p-value of the fixed effects are reported.

Table S14. Differential abundance results for KEGG pathways level 2 for female samples. Model results were obtained by fitting LMMs on each pathway, while controlling for individual identity and unit membership. The estimate and p-value of the fixed effects are reported.

Table S15. Predictors of Shannon index, observed richness, and Faith's phylogenetic diversity (PD) on (1) all samples and (2) female samples on a rarefied dataset. Parameters and tests are based on 758/439 samples and 131/70 individuals in all models. The LMMs were performed controlling for individual identity and unit membership. The 95% confidence intervals that do not cross zero and p-values of statistically significant results are highlighted in bold.

Table S16. Results of PERMANOVA testing for the effects that significantly structure the gut microbiome of geladas on a rarefied dataset for (1) all samples or (2) female samples only. We used Bray Curtis, unweighted Unifrac or weighted Unifrac distances to assess between-sample dissimilarity. 10000 permutations were carried out and individual identity was

added as a strata in the model. The R-squared values indicate the amount of between-sample variation explained by each variable