

Supplementary Figures

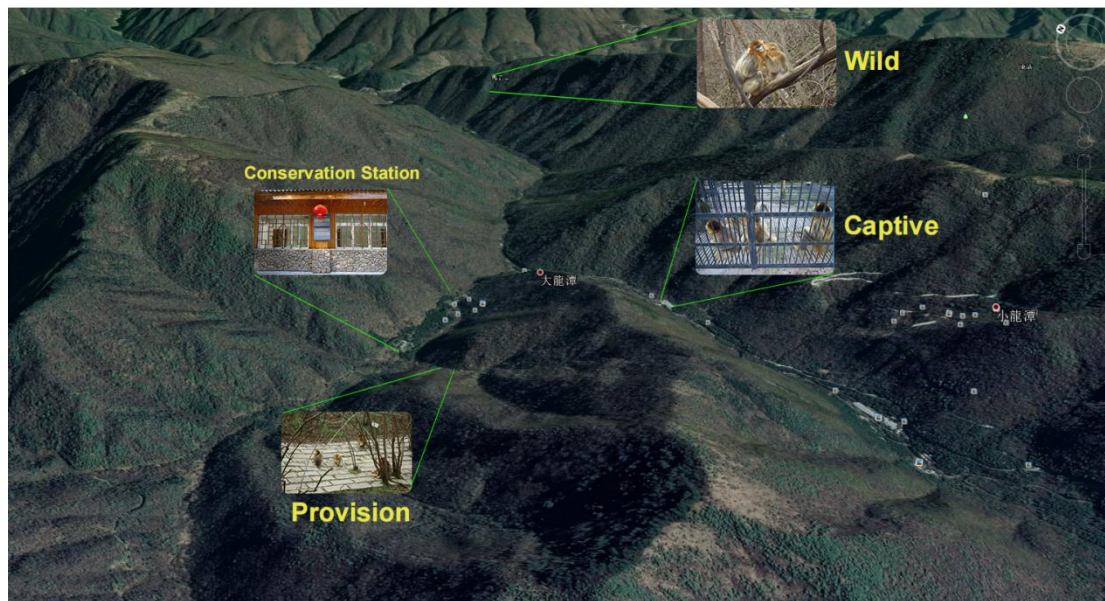


Figure S1. Sampling spots of this study. The google map shows the sampling sites of the wild (W), provision (P), and captive (C) golden snub-nosed monkey in Shennongjia National Park, as well as the position of the conservation station .

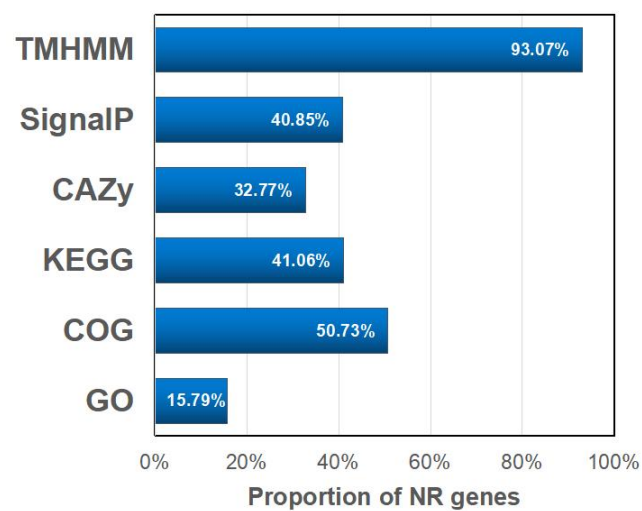


Figure S2. Statistics of functional annotation for the gut microbial reference gene catalog.

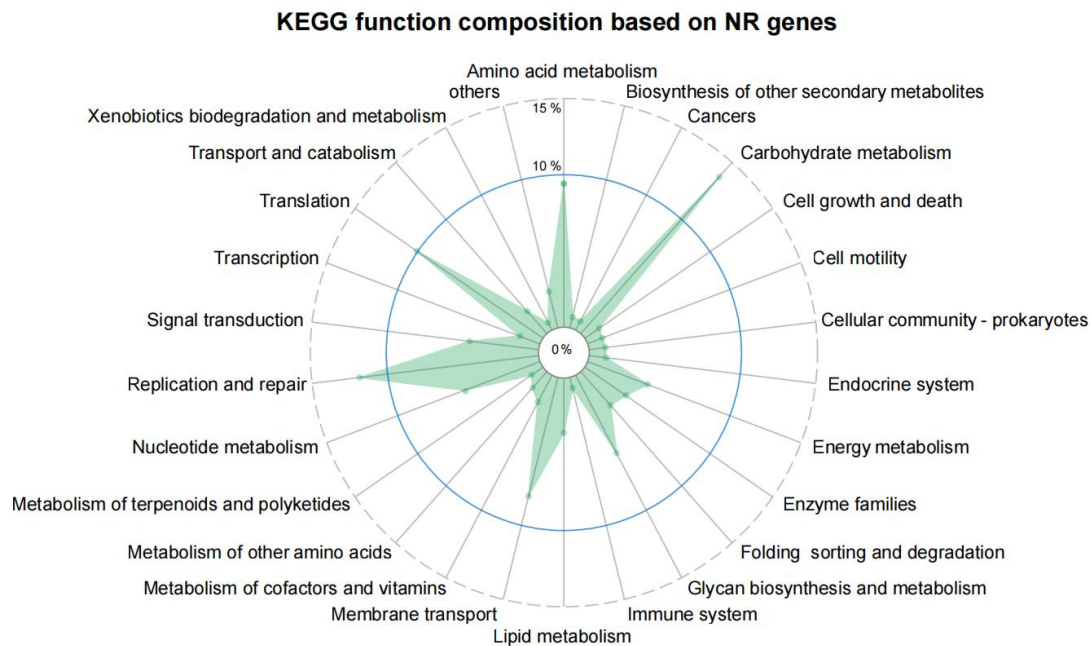


Figure S3. KEGG function composition based on NR genes from the golden snub-nosed monkey gut microbial reference gene catalog.

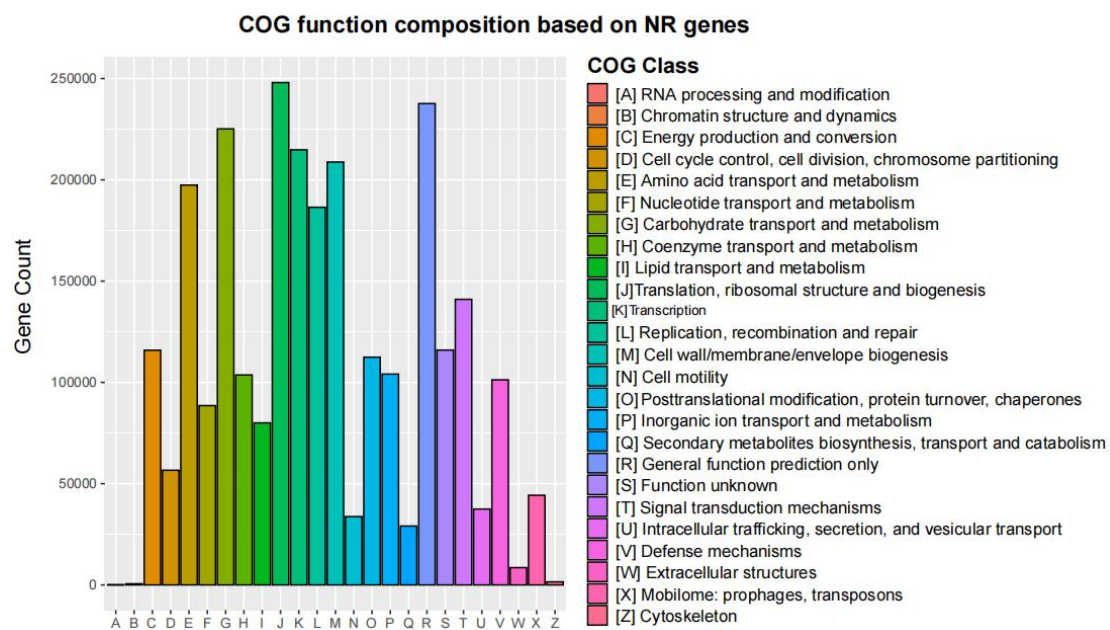


Figure S4. COG function composition based on NR genes from the golden snub-nosed monkey gut microbial reference gene catalog.

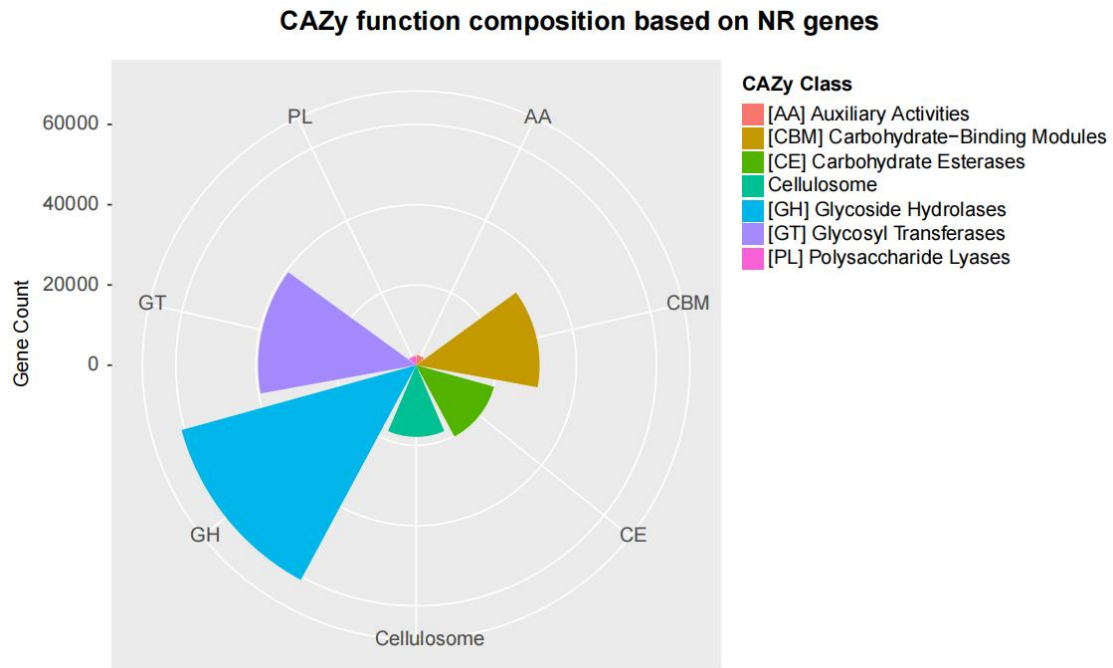


Figure S5. CAZy function composition based on NR genes from the golden snub-nosed monkey gut microbial reference gene catalog.

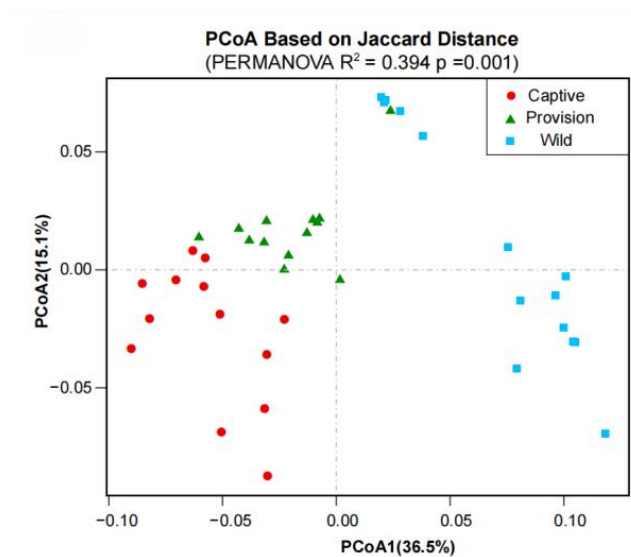


Figure S6. Differences in golden snub-nosed monkey gut microbiome beta-diversity associated with the Captive, Provisioned and Wild. PCoA based on Jaccard distance. The statistical significance among groups was assessed by PERMANOVA. PCoA, principal coordinates analysis; PERMANOVA, permutational multivariate analysis of variance.

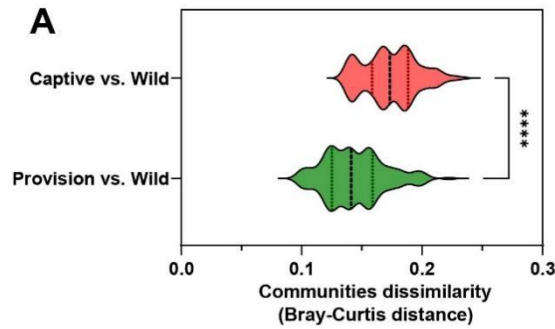


Figure S7. Beta-diversity between the Wild and Captive group and beta-diversity between the Wild and Provisioned group . The statistical significance between groups was assessed by Mann Whitney U test.

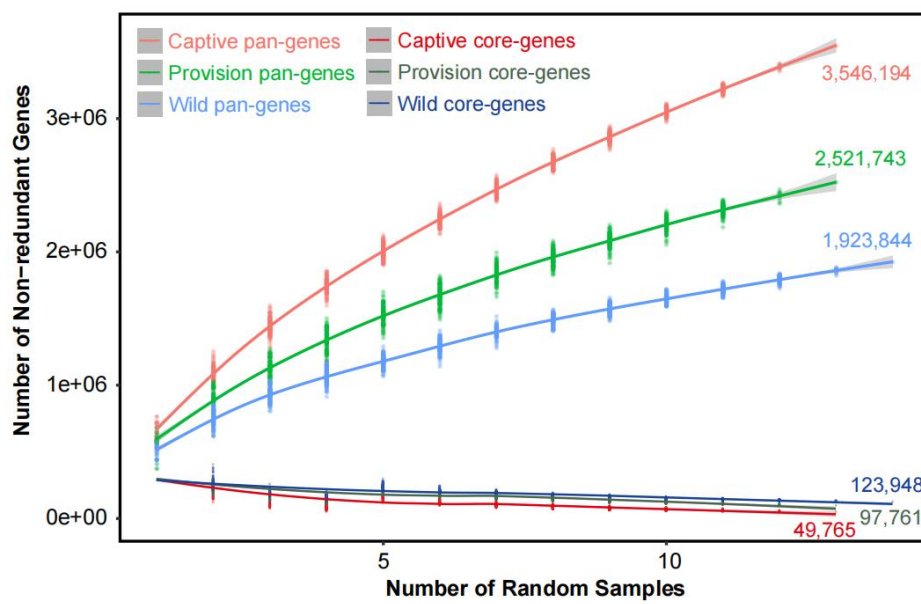


Figure S8. Rarefaction analysis of pan-genes and core-genes on the Captive, Provisioned and Wild golden snub-nosed monkey gut microbiome.

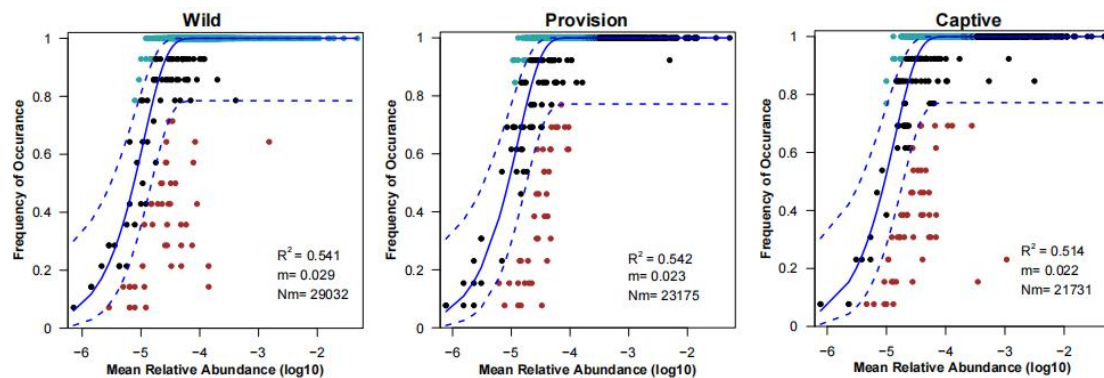


Figure S9. Fit of the neutral community model (NCM) of community assembly. The predicted

occurrence frequencies for Captive, Provisioned and Wild representing microbial communities from Captive, Provisioned and Wild golden snub-nosed monkey, respectively. The solid blue lines indicate the best fit to the NCM as in Sloan et al., and the dashed blue lines represent 95% confidence intervals around the model prediction. Species that occur more or less frequently than predicted by the NCM are shown in different colors. Nm indicates the metacommunity size times immigration, R^2 indicates the fit to this model.

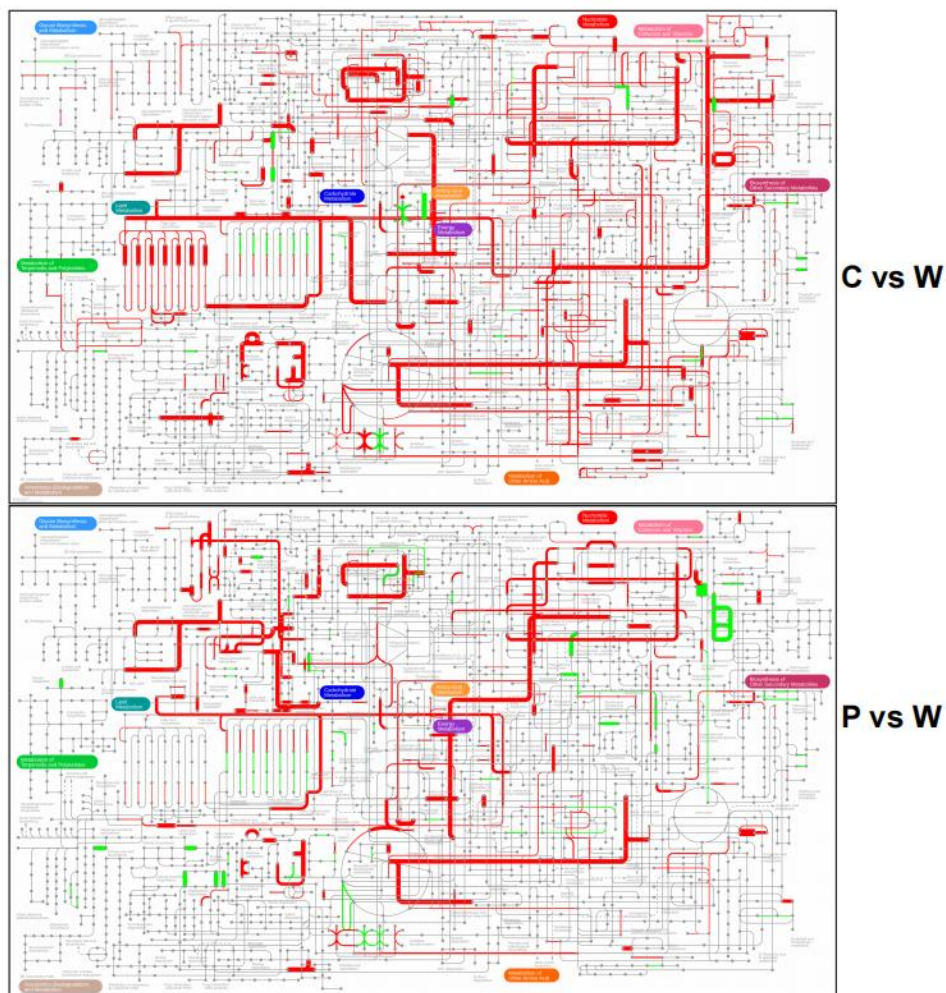


Figure S10. Metabolic pathways analysis based on the KEGG functional differences among the wild (W), provision (P), and captive (C) golden snub-nosed monkey. A pairwise comparison of pathway networks was conducted to screen the significantly regulated metabolic pathways, and IPATH3 was used for visualization. The red lines represent the up-regulated pathways, and the green lines represent the down-regulated pathways, while the gray lines represent the pathways with no difference between groups.

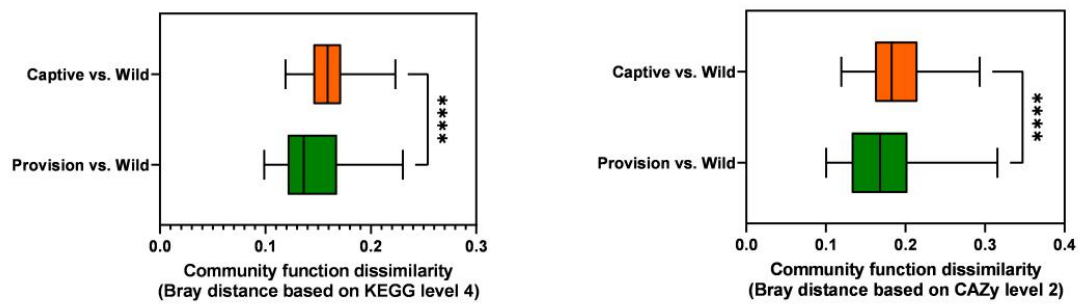


Figure S11. Box plots of beta-diversity between the Wild and Captive groups and beta-diversity between Wild and Provisioned. The statistical significance between groups was assessed by Mann Whitney U test.

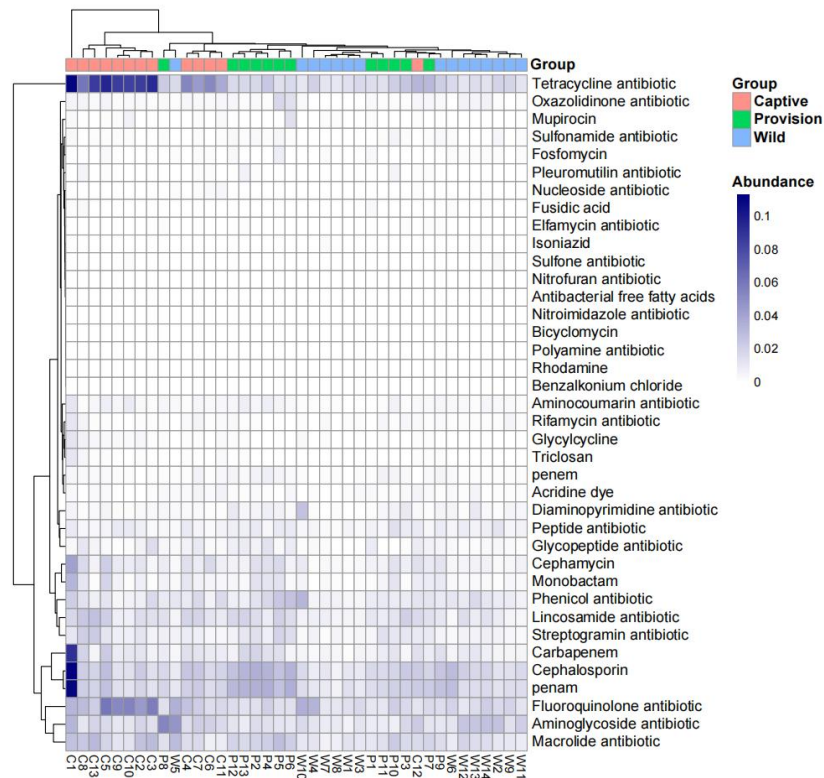


Figure S12. Antibiotic resistance gene analysis of the gut microbiota in the Wild, Provisioned and Captive golden snub-nosed monkey. The abscissa of the heat map represents the sample, and the ordinate represents the type of ARGs.

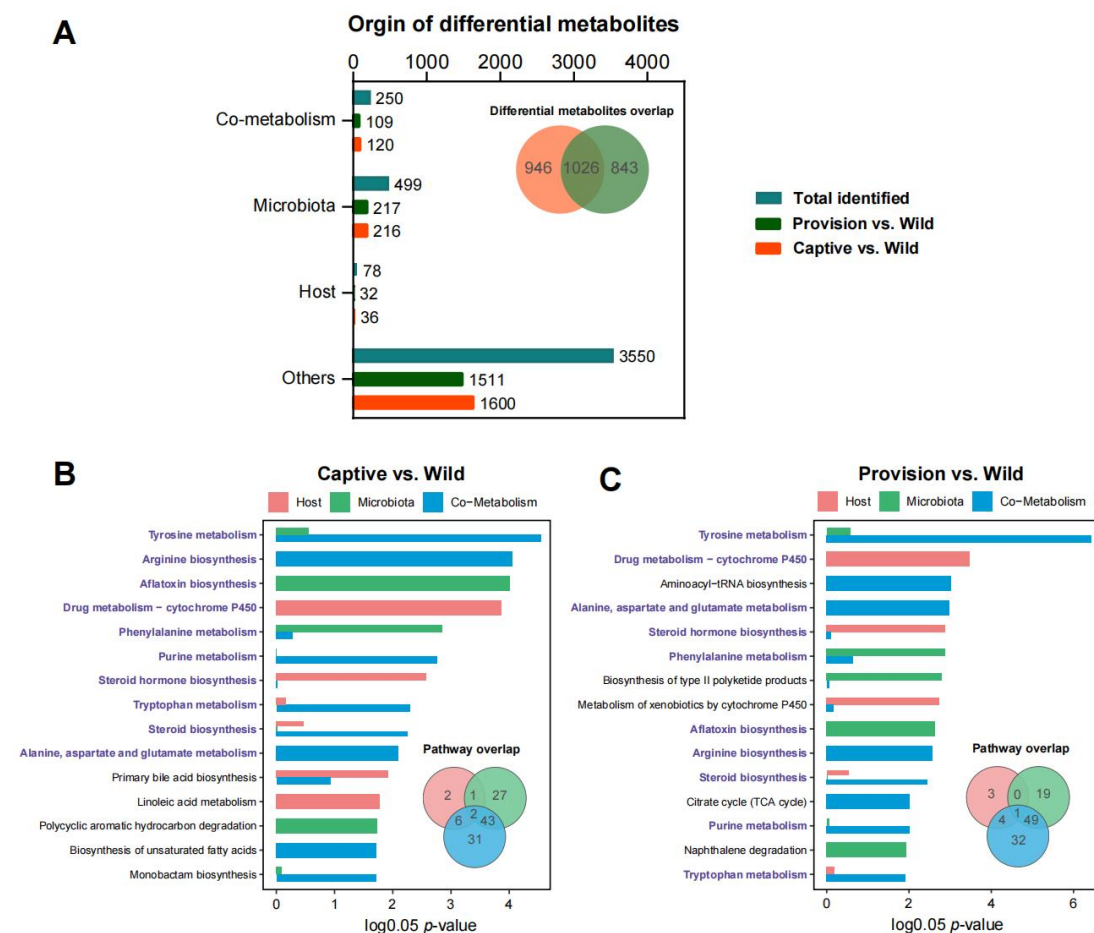


Figure S14. Origin-based differential metabolites analyses. (A) Origin statistic of differential metabolites. (B-C) Origin-based MPEA based on differential metabolites from Captive vs. Wild and Provisioned vs. Wild. MPEA, metabolic pathway enrichment analysis. The enrichment significance was assessed by Hypergeometric test. Pathways colored purple represents the shared pathways in (B) and (C).

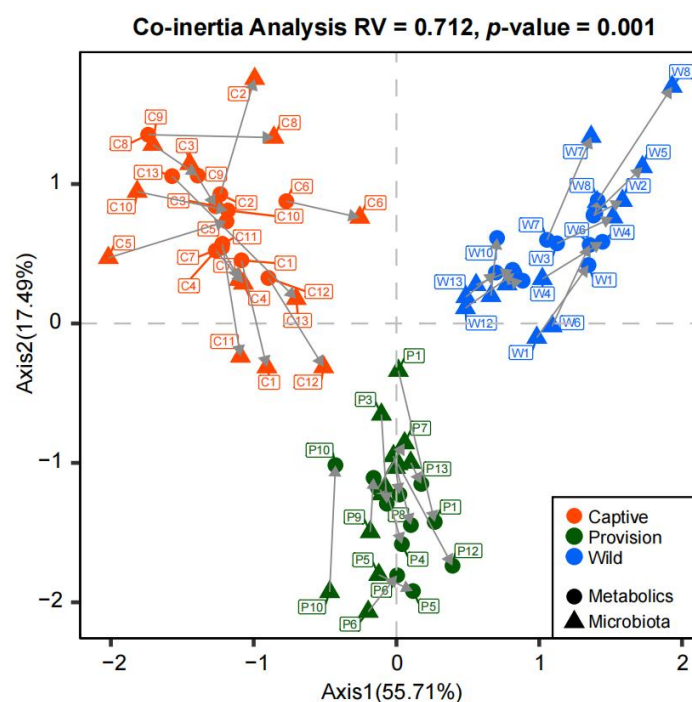


Figure S15. Co-inertia analysis illustrating the correlation between fecal metabolites and microbial species based on NMDS (Bray-Curtis) results of metabolites abundances and species abundances.

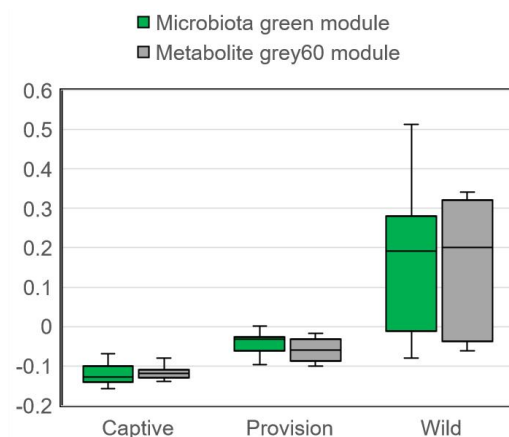


Figure S16. Eigengene value distribution of the correlated microbiota and metabolite module.

Supplementary Tables

Table S1. Summary of sequencing data and quality control for all samples.

Table S2. Relative abundance at phylum level.

Table S3. Relative abundance at genus level.

Table S4. Relative abundance at species level.

Table S5. Summary of assembly results for all samples.

Table S6. Function annotation statistics of golden snub-nosed monkey gut microbial gene catalog.

Table S7. The ion intensity and annotation of all the metabolites identified in golden snub-nosed

monkey fecal.

Table S8. Differential metabolites in Captive vs. Wild.

Table S9. Differential metabolites in Provisioned vs. Wild.

Table S10. Origin-based metabolic pathway enrichment analysis (MPEA) on differential metabolites from Captive vs. Wild

Table S11. Origin-based metabolic pathway enrichment analysis (MPEA) on differential metabolites from Provisioned vs. Wild

Table S12. Correlationship between microbial species from the green module and metabolites from the grey60 module.

Table S13. Origin-based metabolic pathway enrichment analysis (MPEA) on metabolites from WGCNA grey60 module.