

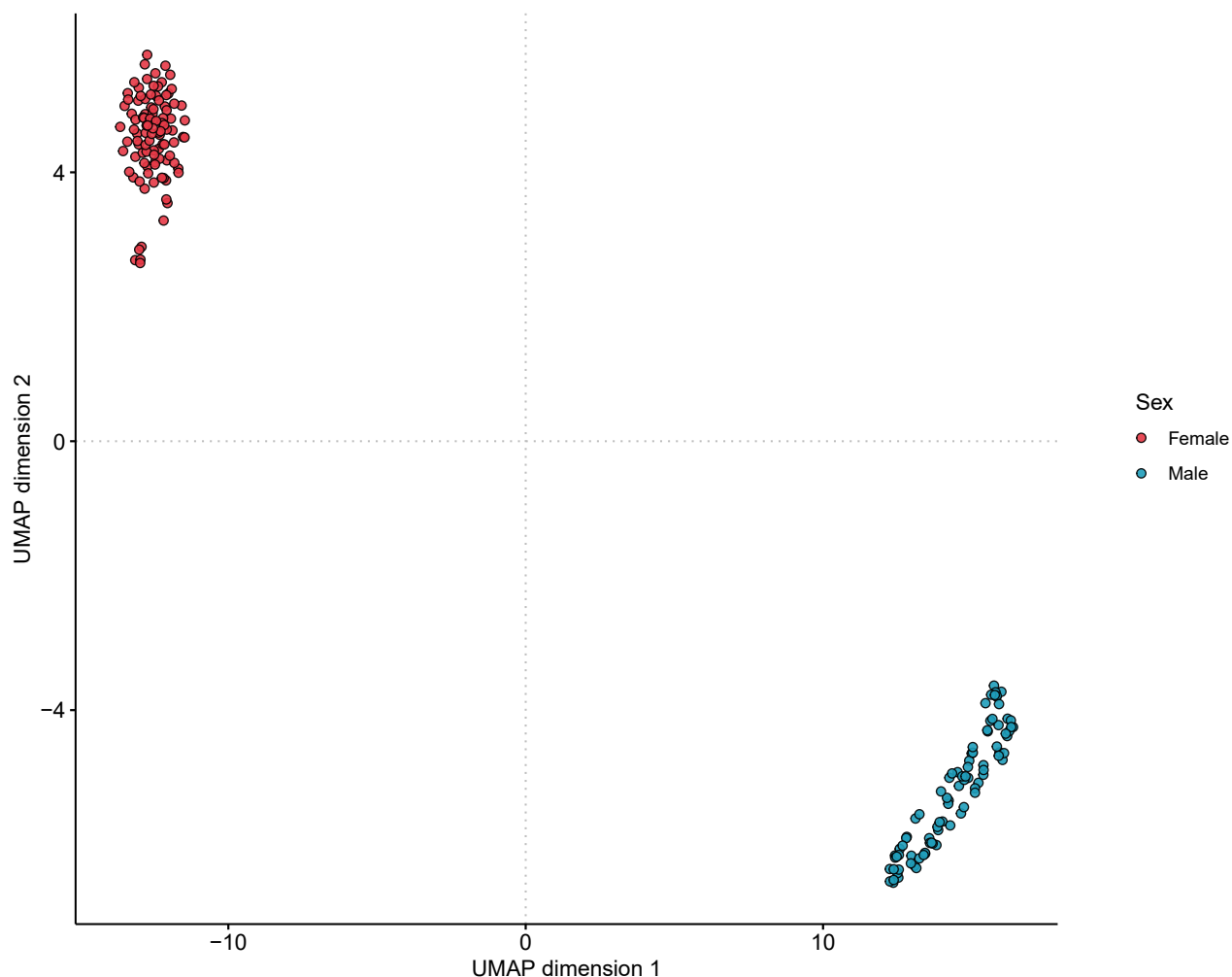
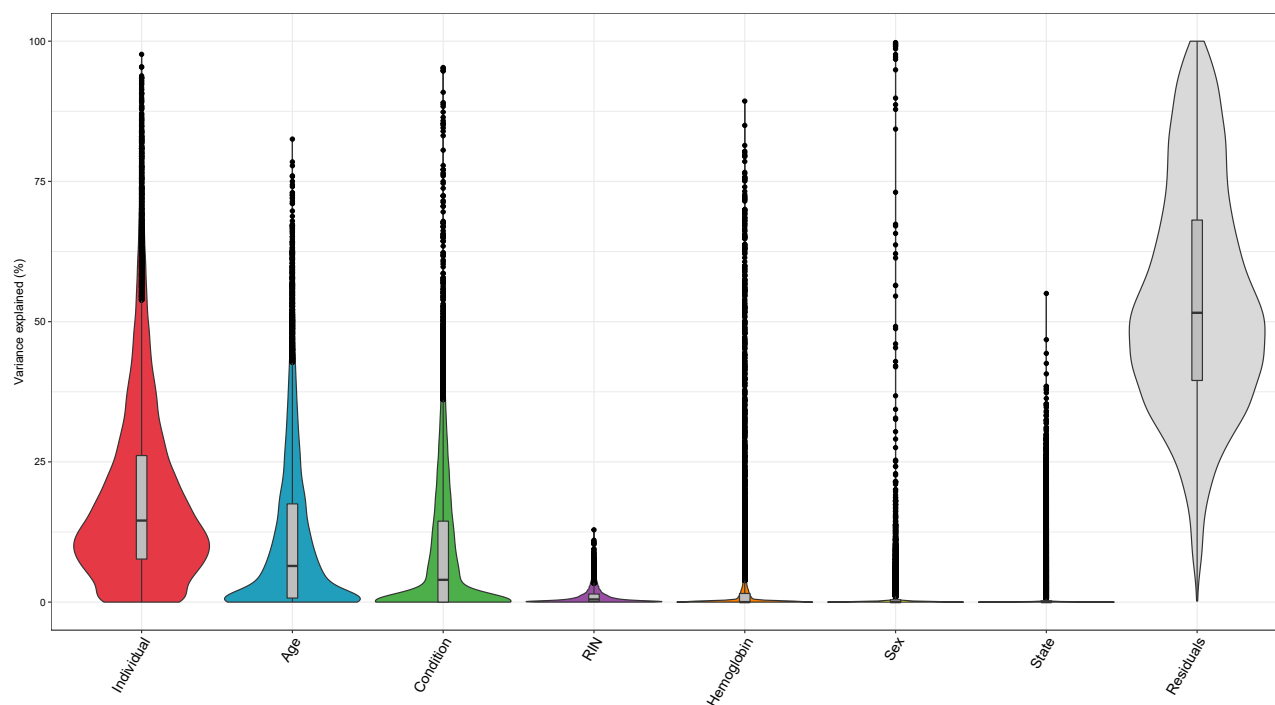
A**B**

Figure S1. A. UMAP plot demonstrates the sex incompatibility check between the genetically determined sex and the recorded morphologically determined sex of rhesus macaques. **B.** The variance partition analysis at the gene level of rhesus macaques. Primary sources of biological variation include age, individual, sex, condition, and health state. Primary sources of technical variation include RNA integrity, percentage of hemoglobin gene expression. Box in violin plot span the inter-quartile range (IQR), The line in the center of each box plot is the median value.

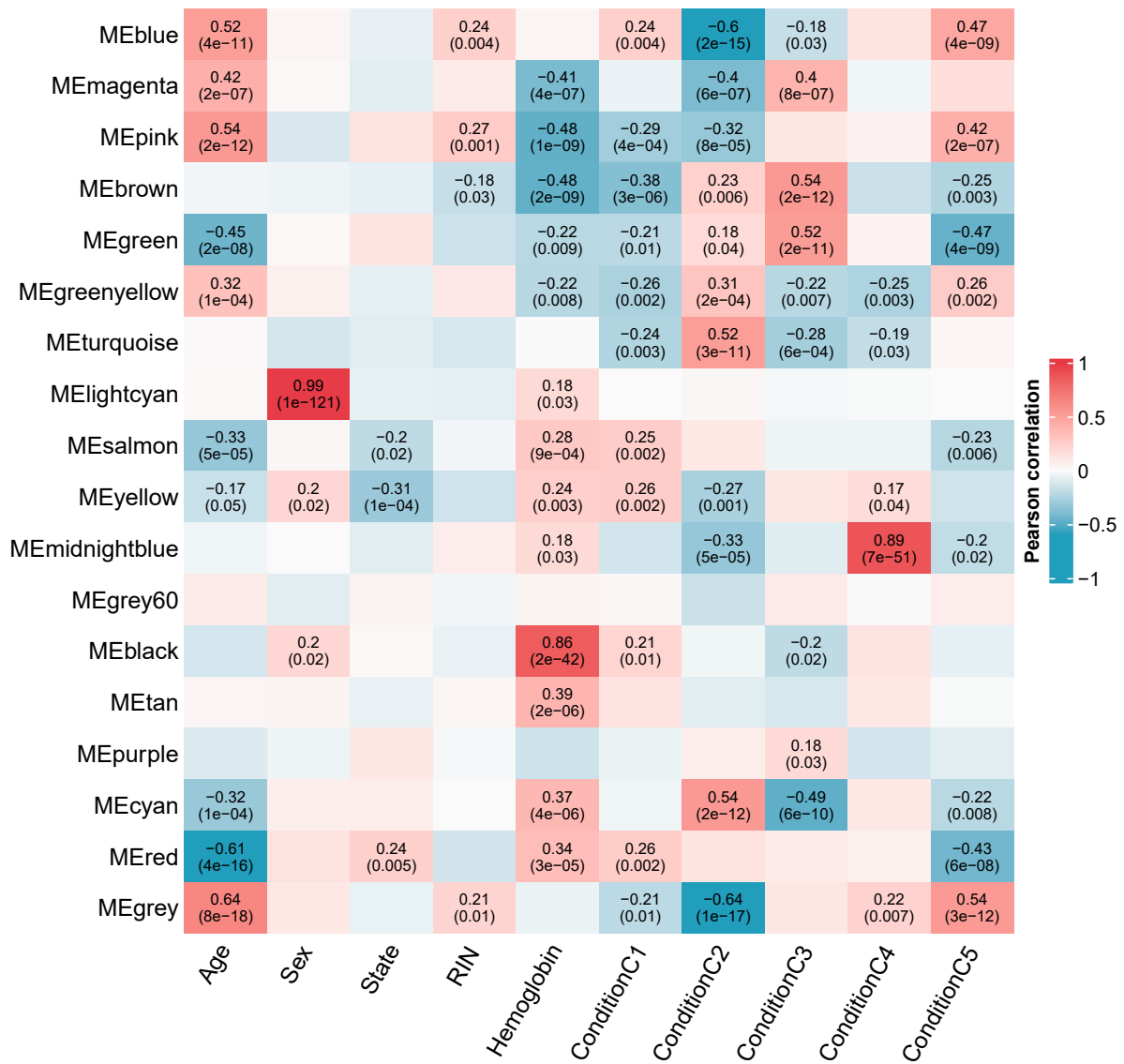
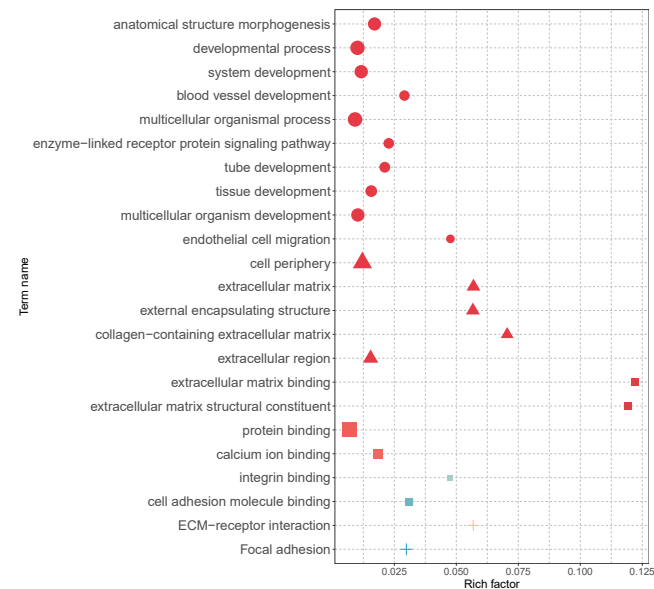
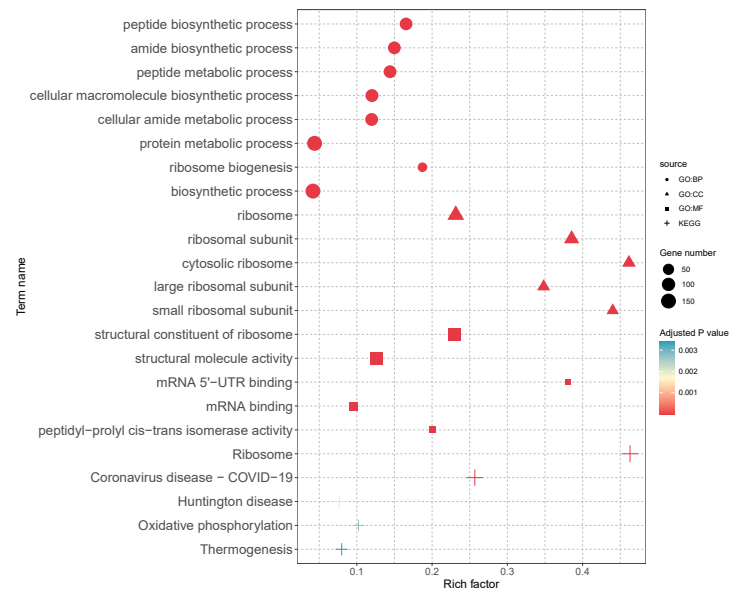
A**B****C**

Figure S2. A. Heatmap illustrates the correlation between traits and modules (using ME) based on the results of Weighted gene coexpression network analysis (WGCNA) in rhesus macaques. FDR less than 0.01 were not shown. **B.** The enrichment results of 83 hub genes of the module midnight-blue in WGCNA. **C.** The enrichment results of 500 hub genes of the module red in WGCNA.

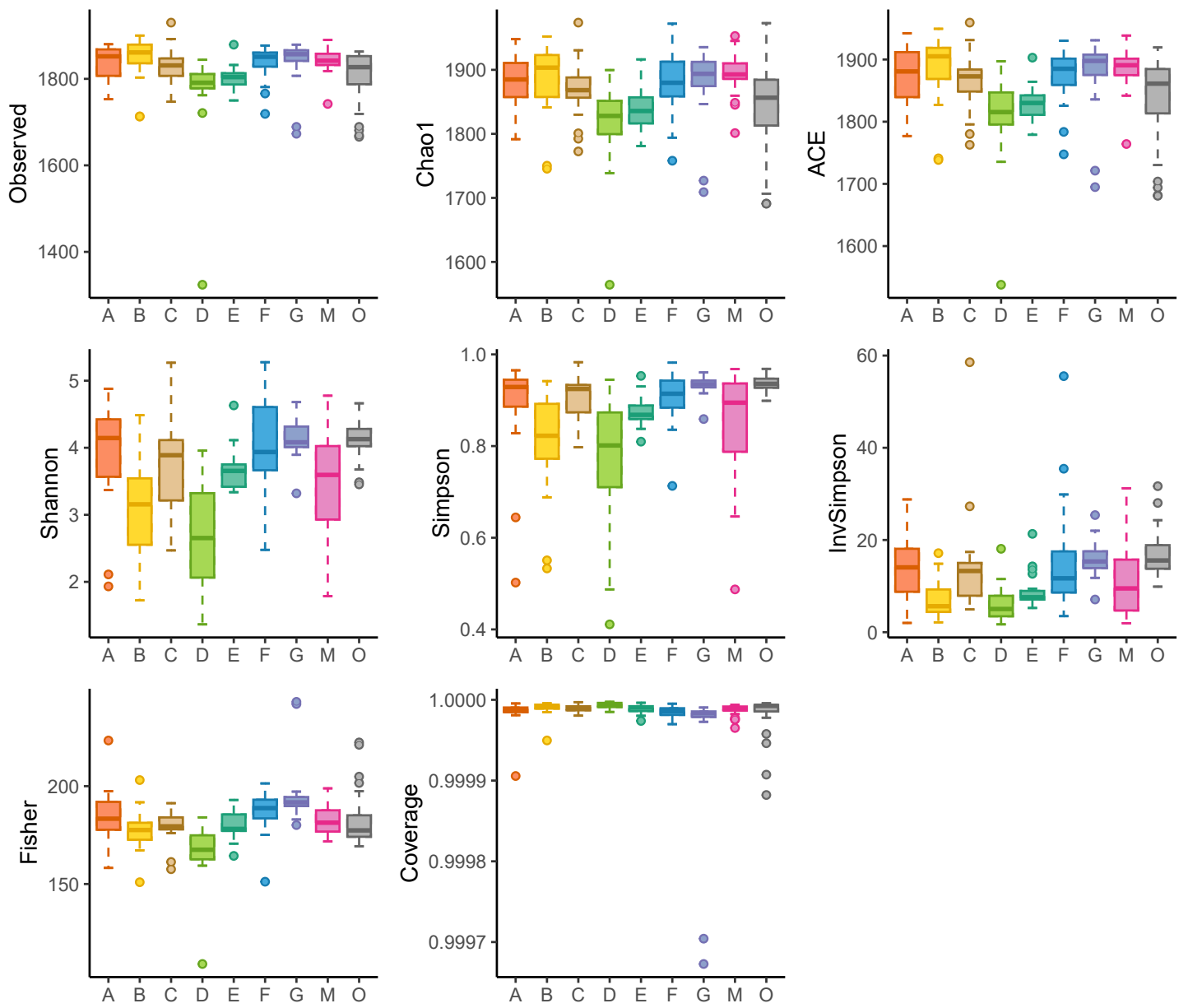


Figure S3. Box plots of different α -diversity indices of rhesus macaques. Infants: Satge A to G, M: mothers of infants, O: other unrelated healthy adults.

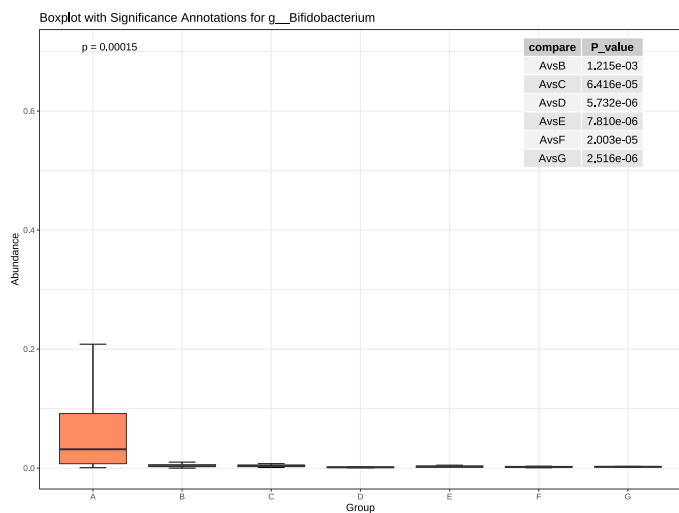
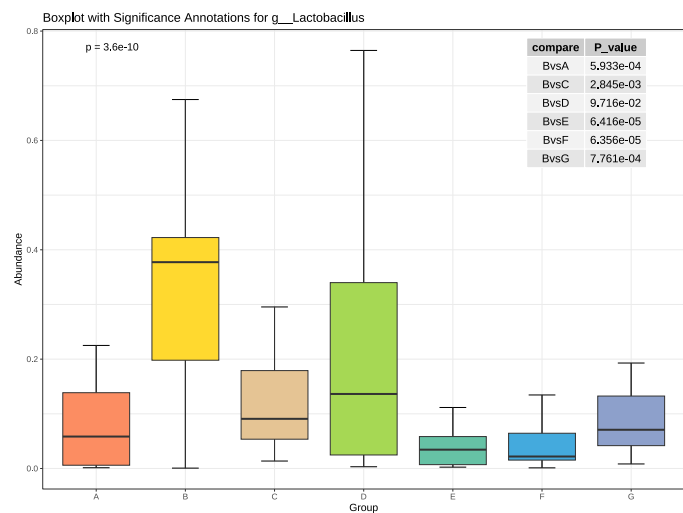
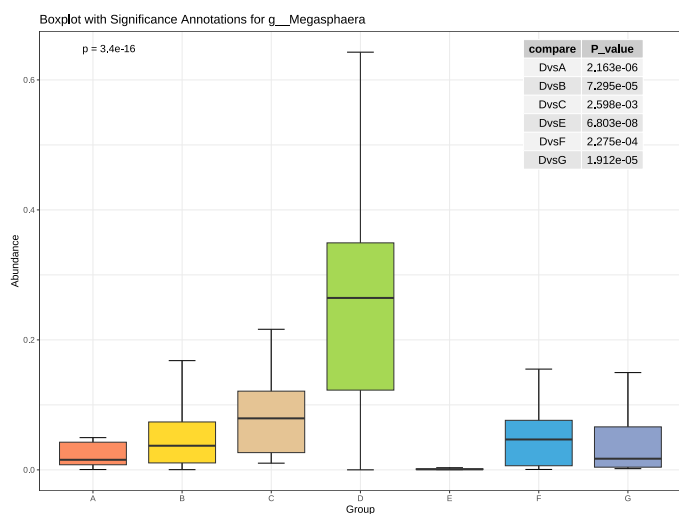
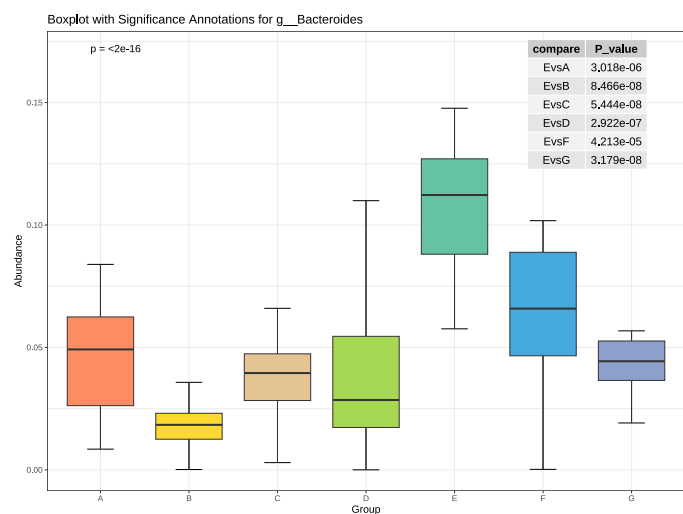
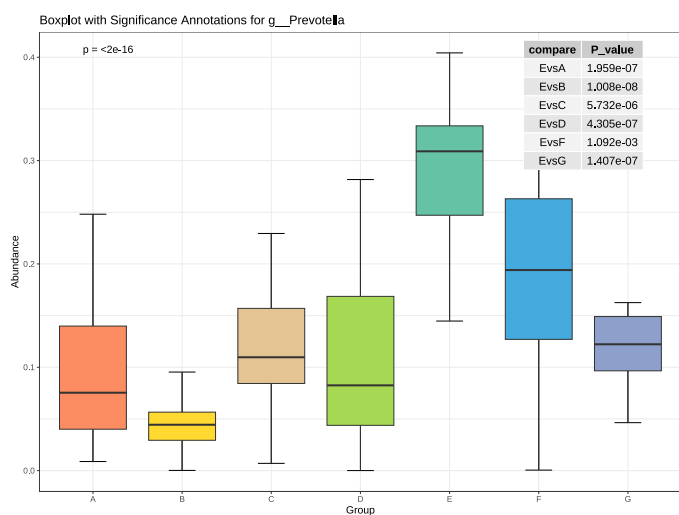
A**B****C****D****E**

Figure S4. Box plots illustrates the relative abundance of **A. Bifidobacterium**, **B. Lactobacillus**, **C. Megasphaera**, **D. Bacteroides** and **E. Prevotella** in infant macaques with the results of Wilcoxon's rank-sum test.

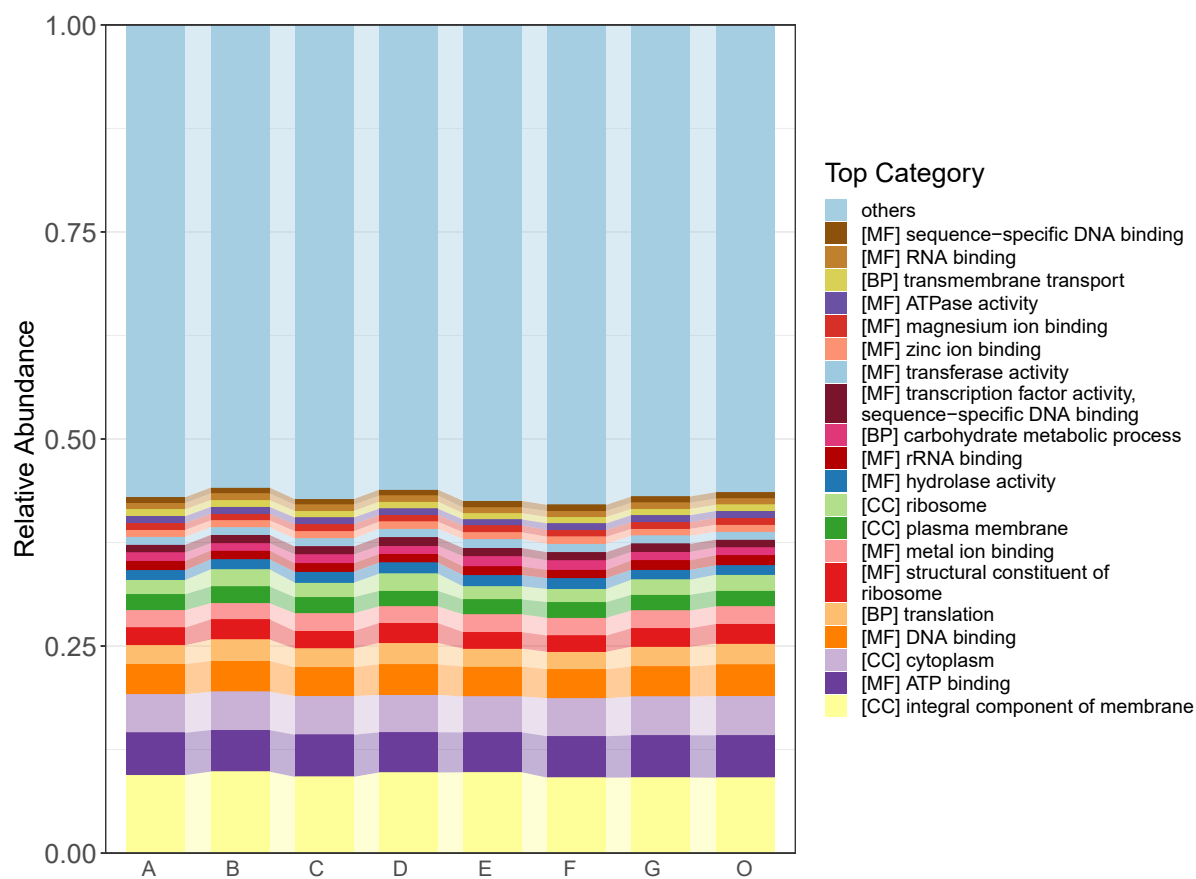
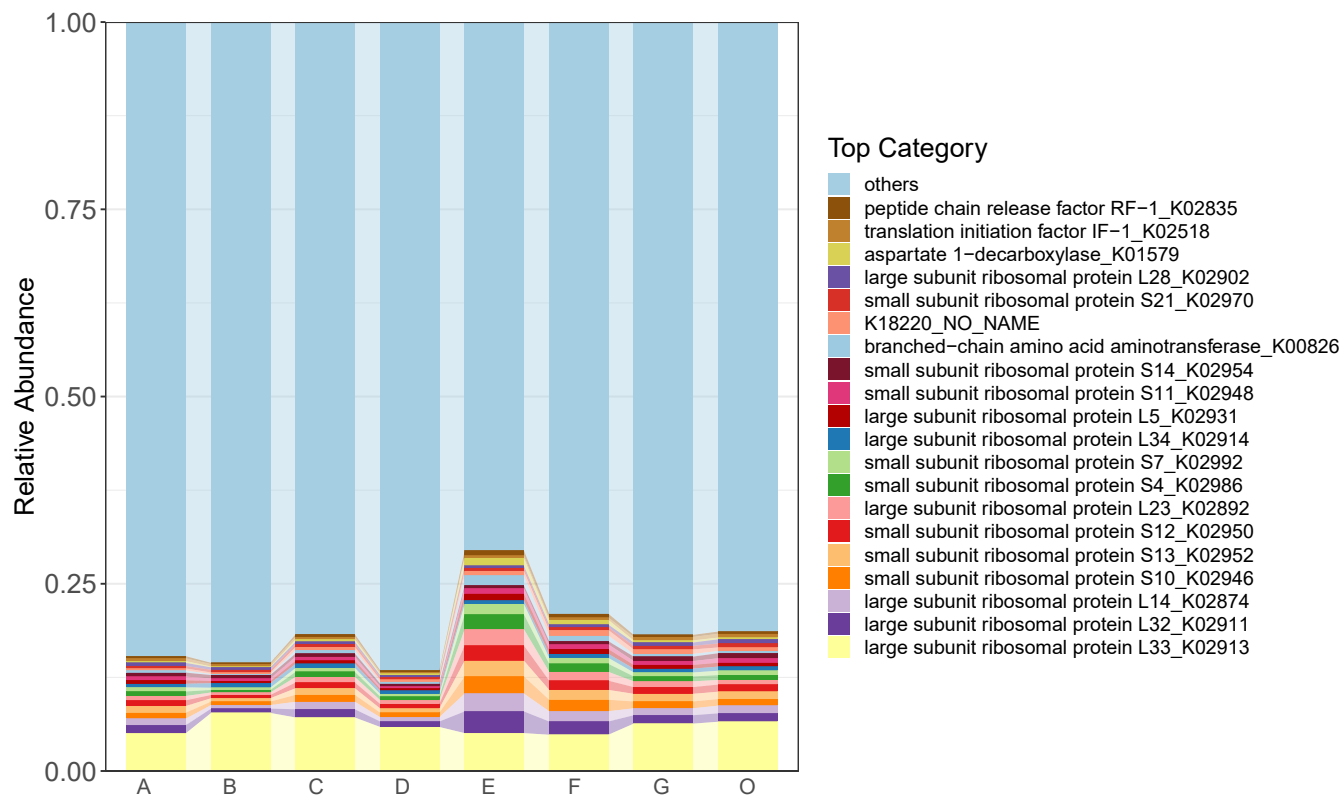
A**B**

Figure S5. The top 20 categories of **A.** Gene Orthology (GO) annotation and **B.** KEGG (Kyoto Encyclopedia of Genes and Genomes) Orthology (KO) annotation of rhesus macaques' gut microbiotas.

B

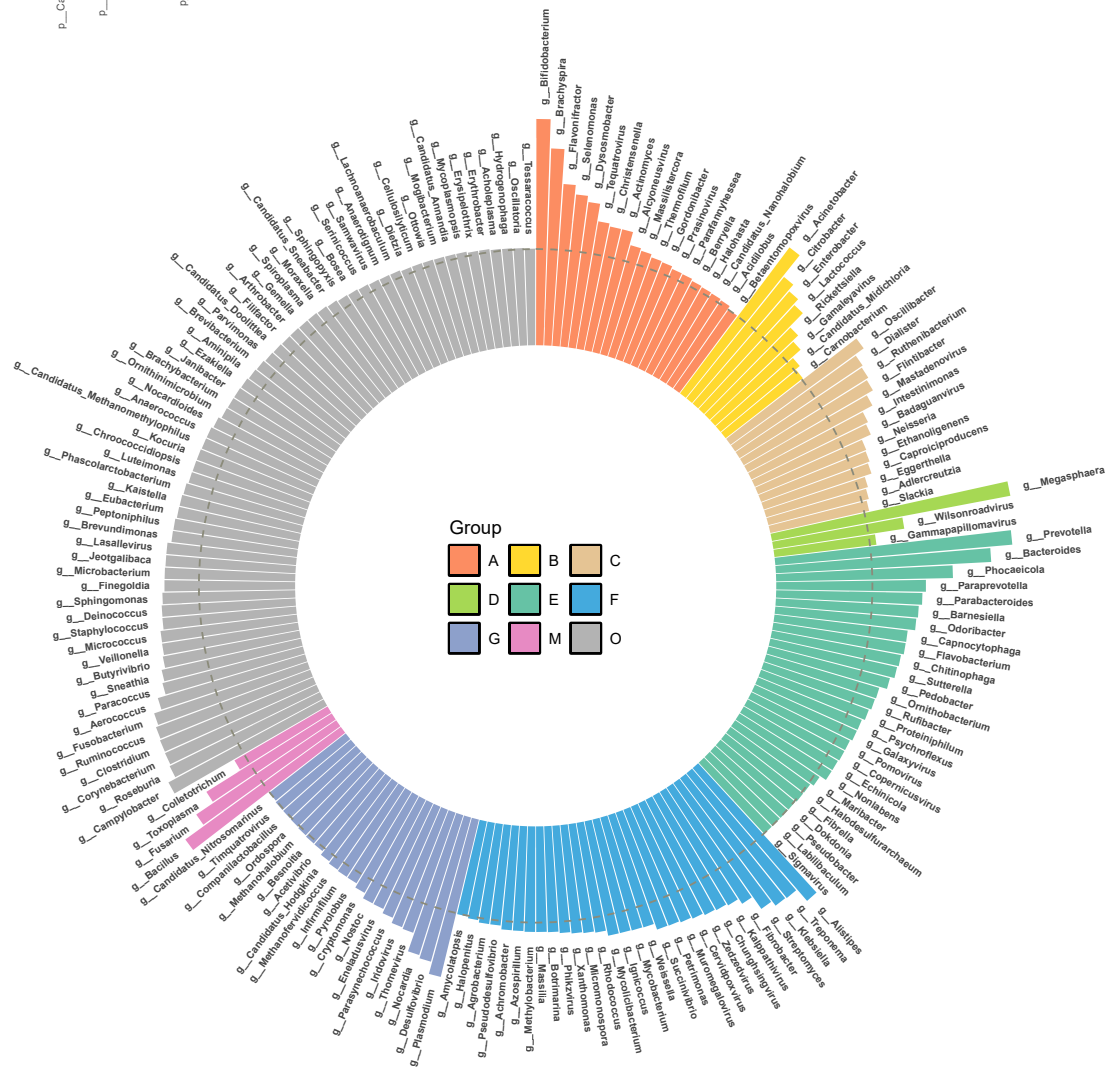


Figure S6. The microbial biomarkers at the **A.** phylum-level and **B.** genus-level in each age group of rhesus macaques were calculated using LEfSe, with significance determined by LDA > 2 and FDR < 0.05.

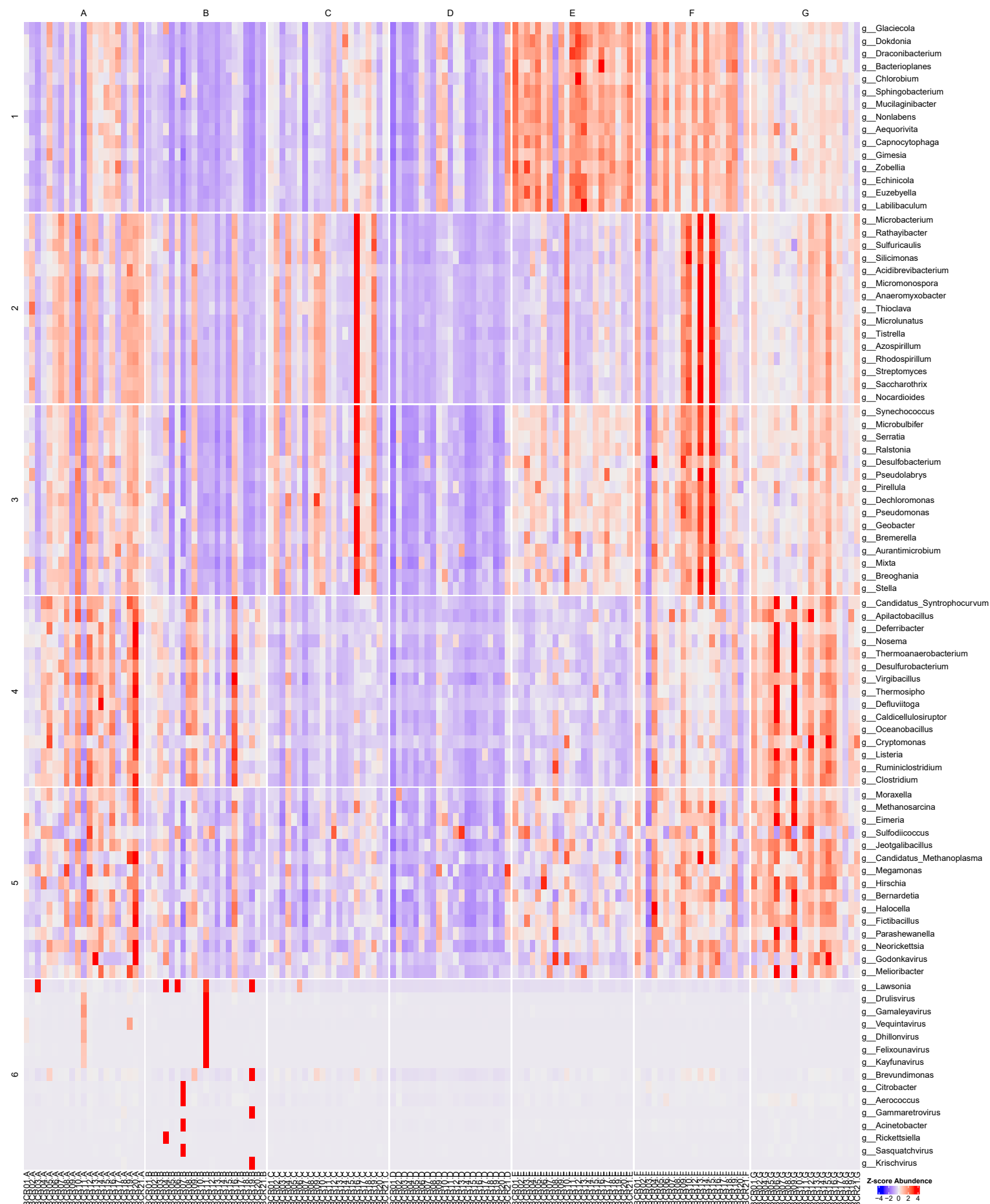


Figure S7. The heatmap displays the abundance of the top 10 genera in rhesus macaques with the highest membership within each Microbiota Cluster. The Microbiota Clusters were identified using the fuzzy c-means algorithm (FCMA). See the full list in Table S5.

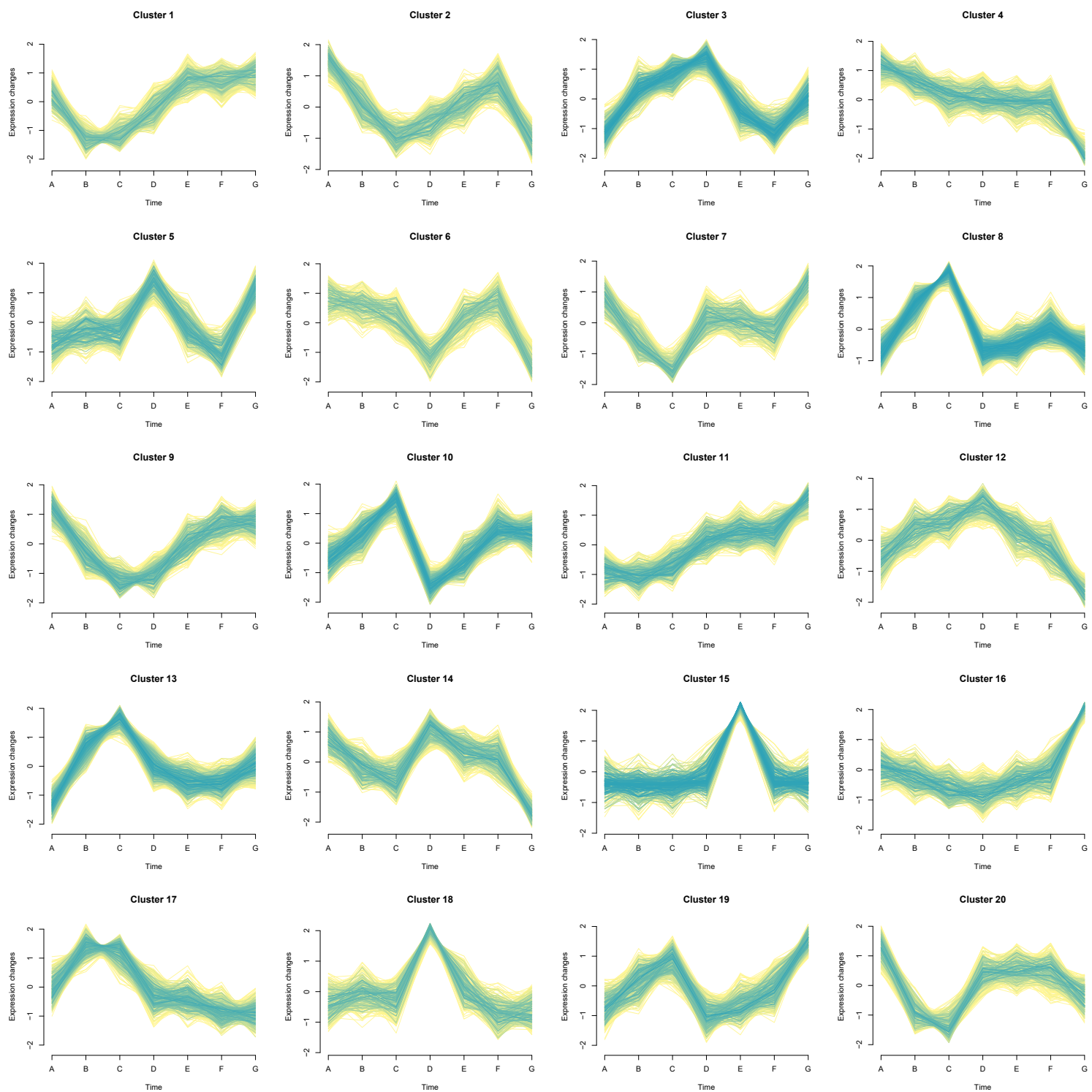


Figure S8. The 20 gene expression clusters of rhesus macaques were identified by the time-series analysis using fuzzy c-means algorithm (FCMA).

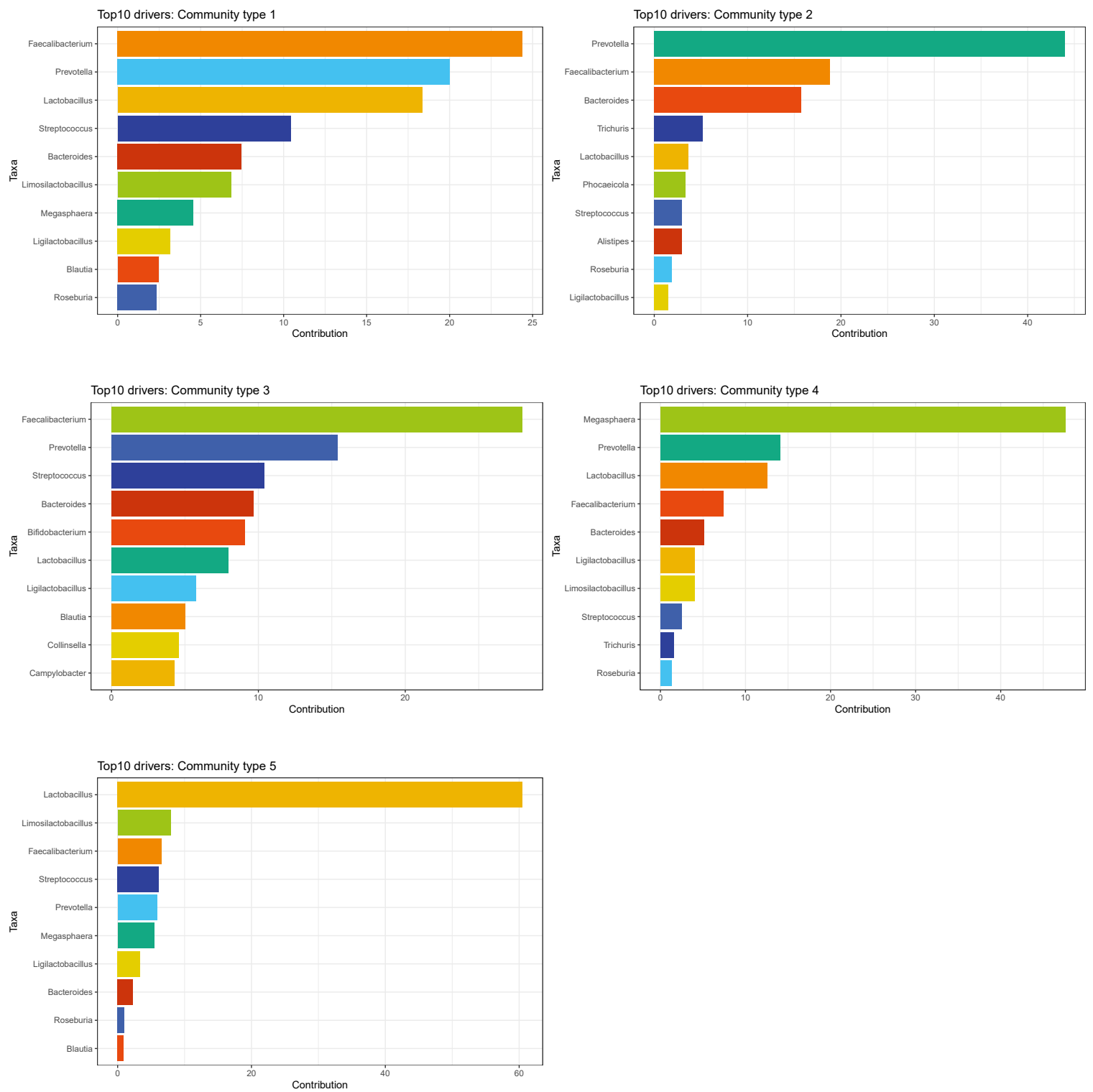


Figure S9. The box diagram illustrates the top 20 genera that contribute to each cluster (community type) identified by the Dirichlet multinomial mixtures (DMM). The bars arranged in descending order based on their contribution percentage from top to bottom.

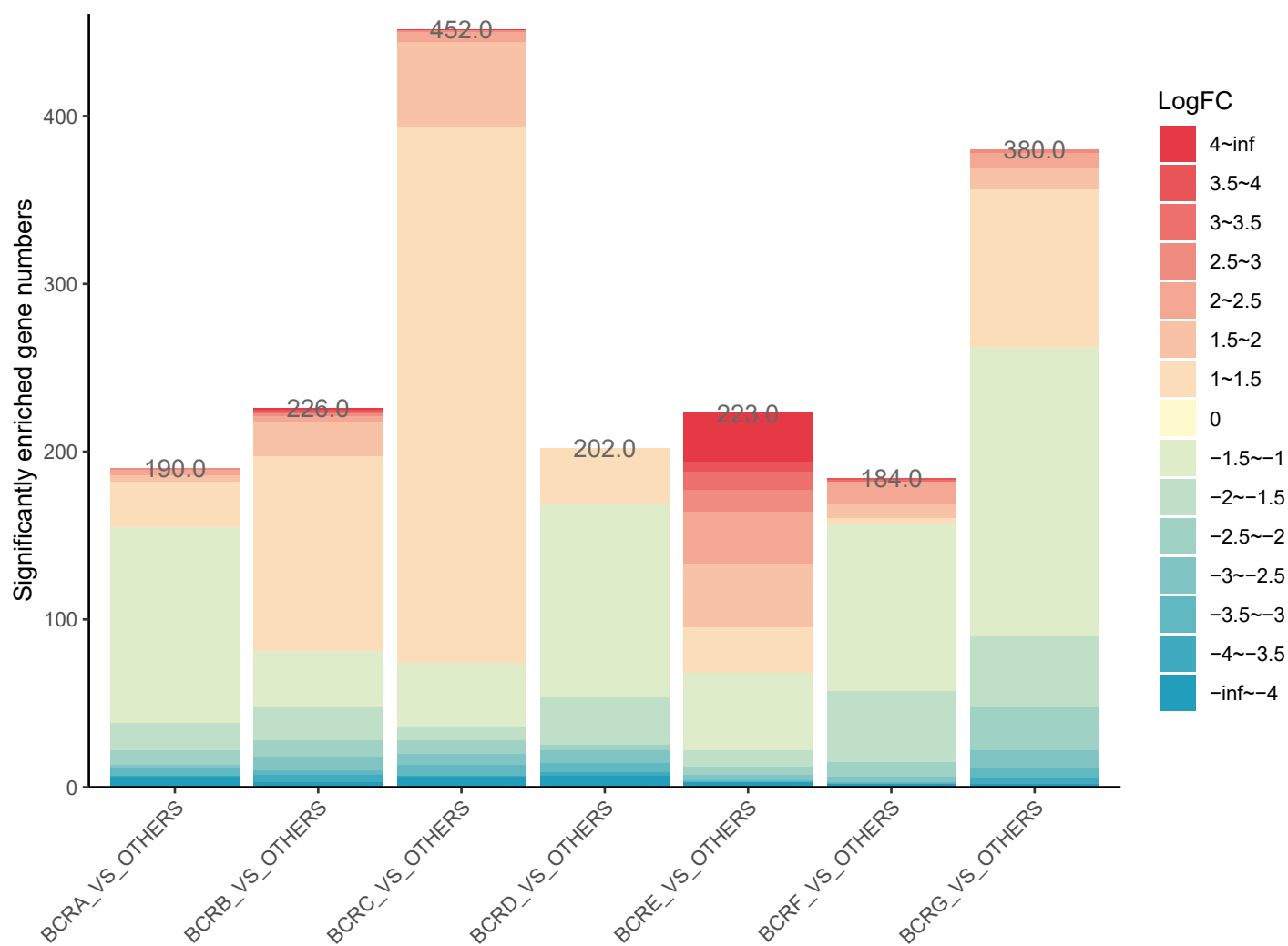


Figure S11. Statistics of logFC value for each stage-specific DEG (between one stage and the rest of the other six infant stages, e.g. AvsOthers).