

Supplemental figures and legends

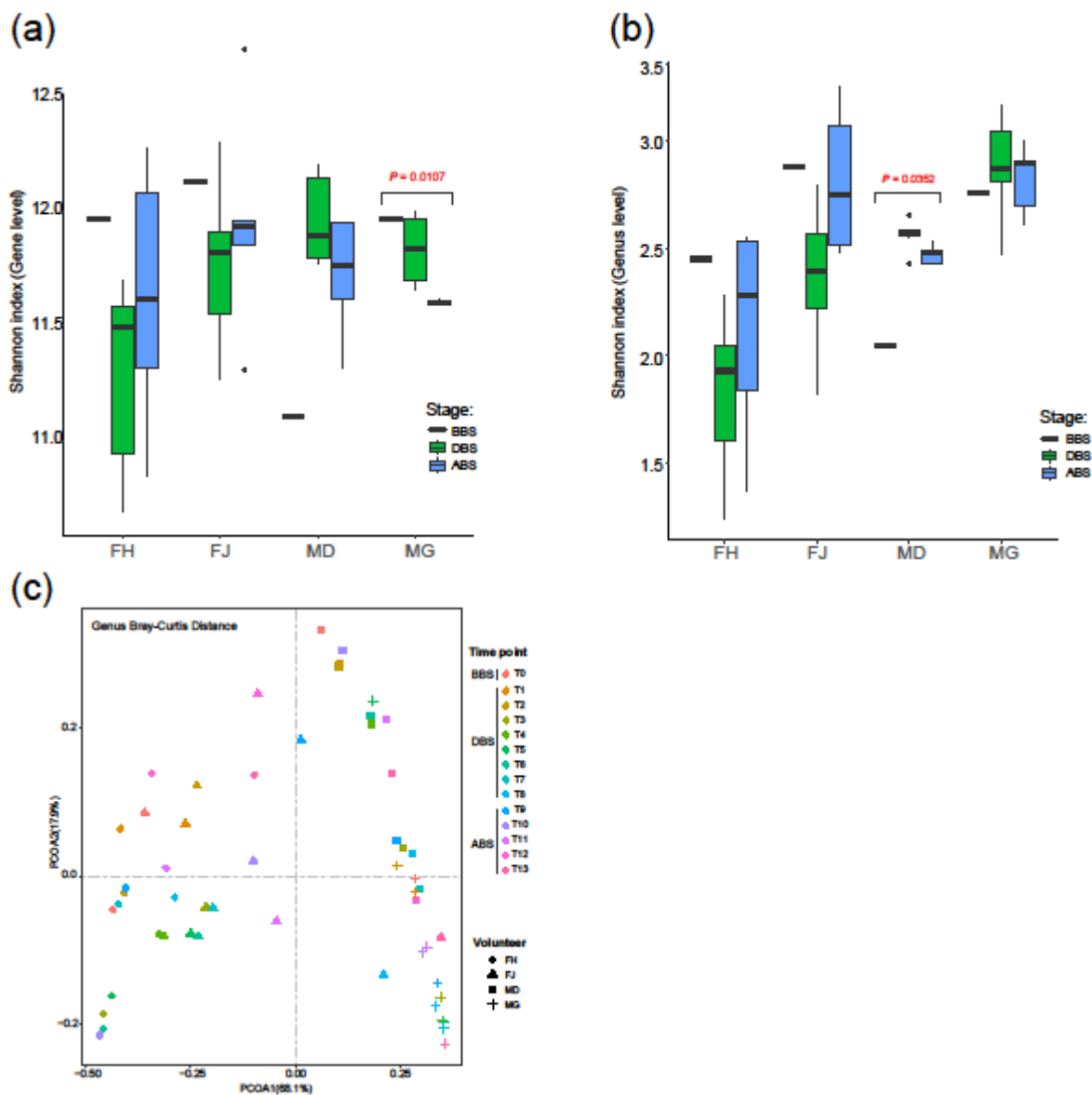


Figure S1. Changes in the gut microbiome tested by the Kruskal-Wallis rank sum test among different stages (BBS, DBS and ABS) at the gene (a) and genus (b) levels, as well as PCoA based on Bray-Curtis distance at the genus level (c).

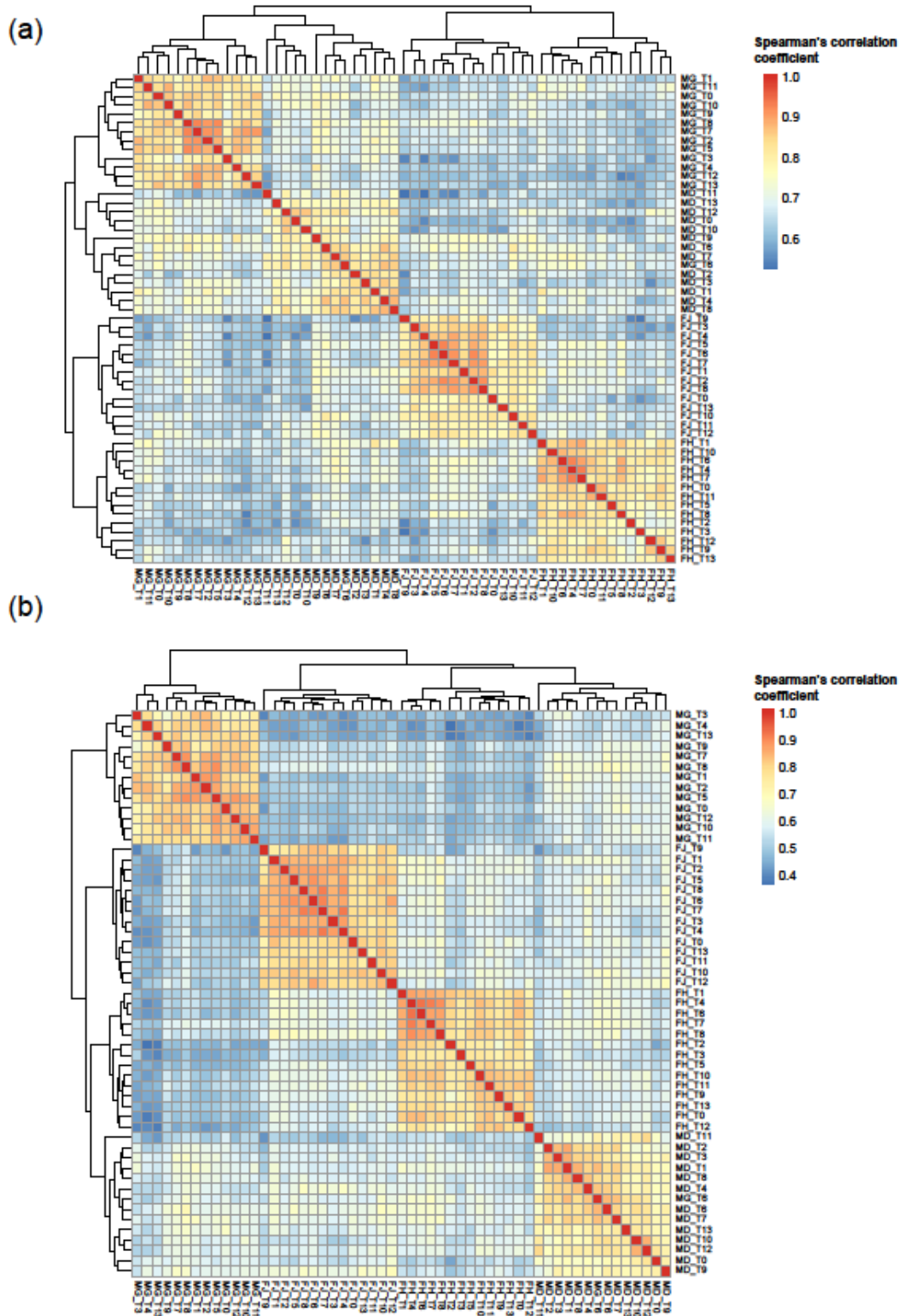


Figure S2. Trend of individual convergence of the gut microbiome at the species (a) and genus (b) levels by Spearman's rank correlation based on the species and genus profiling of the samples. Overall, the samples from each subject shared high similarity, and the DBS samples from each subject were clustered.

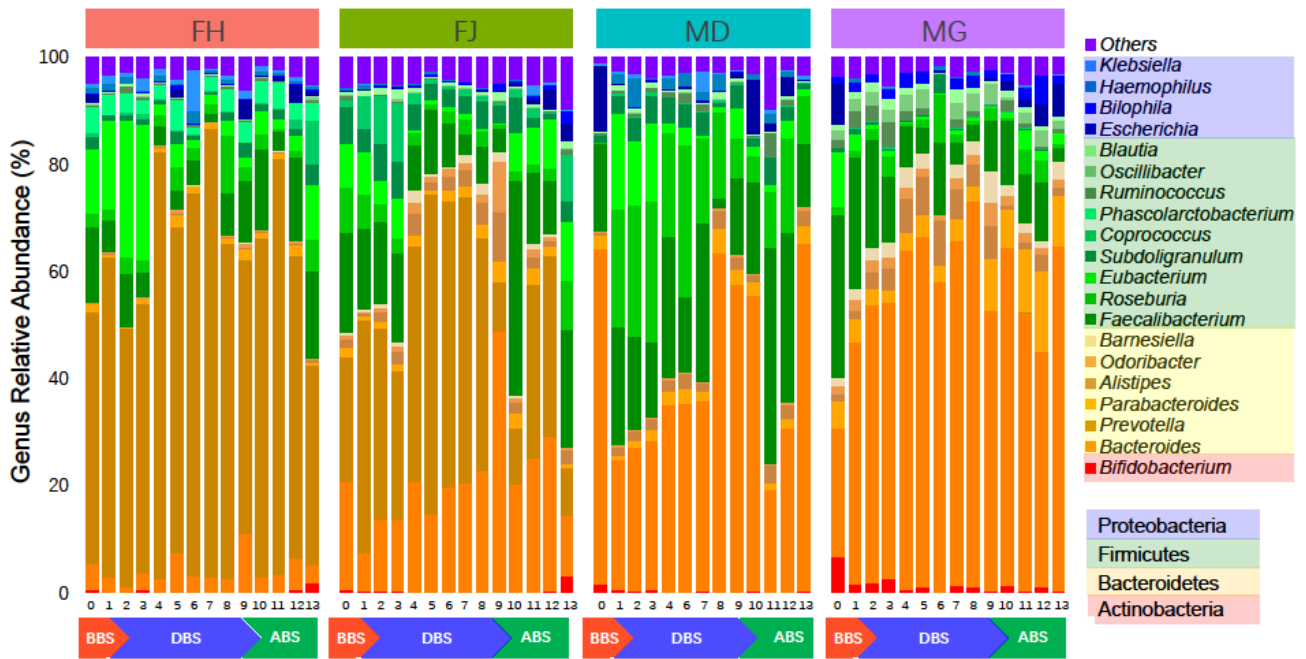


Figure S3. Top 20 genera of the gut microbiome based on mean relative abundance. BBS, DBS, and ABS represent the baseline, during the BLSS stat and after leaving the BLSS, respectively. The colors of the boxes below the figure key indicate the phylum that each genus belongs to.

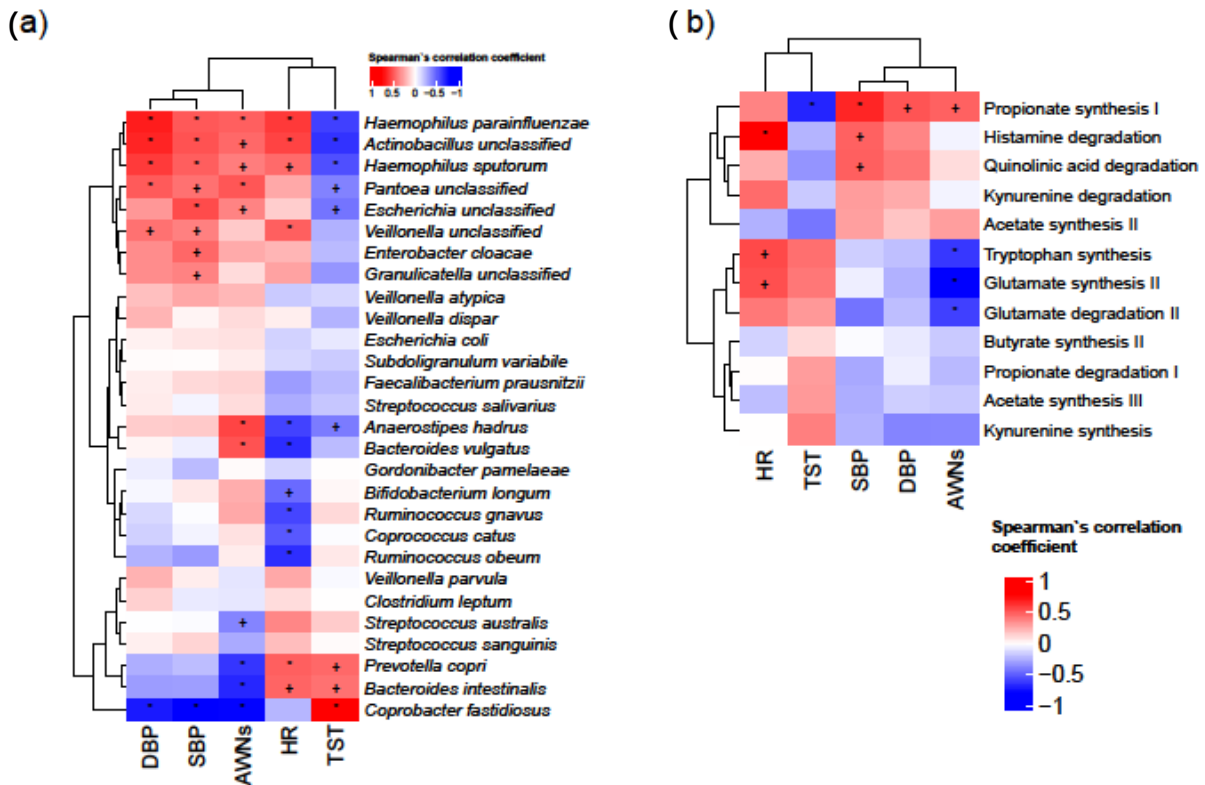


Figure S4. Heatmap of the Spearman's rank correlation between changed species **(a)** and GBMs **(b)** (Y-axis, by the Kruskal-Wallis rank sum test among stages and Wilcoxon rank sum test between stages, $p < 0.05$; the letters A, F, and M in brackets after the species name indicate whether the species was significantly changed in all subjects, female subjects and male subjects, respectively) among stages and host physiological parameters that might affect the gut microbiome (X-axis, assessed by PERMANOVA based on the gut microbial gene profile, $q < 0.01$). Red indicates positive associations, while blue indicates negative associations. The "+" and "*" in each grid indicate $p < 0.05$ and $p < 0.01$, respectively.

Legends for supplemental material (excel)

Table S1. Statistics for the shotgun metagenomic sequenced data (Tab S1a) and the taxonomic and functional module profiles (Table S1b, species profile; Table S1c, genus profile; Table S1d, phylum profile; Table S1e, GMM profile; Table S1f, GBM profile).

Table S2. Gut microbiome alterations among/between stages for subjects tested by the Kruskal-Wallis rank sum test (among BBS, DBS and ABS) and Wilcoxon rank sum test (between stages). (Tab S2a. Summary of changed species, genera and phyla; Tab S2b. Changes in phyla, genera and species for all subjects; Tab S2c. Changes in phyla, genera and species for female subjects; Tab S2d. Changes in phyla, genera and species for male subjects).

Table S3. GMM alterations among/between stages for subjects tested by the Kruskal-Wallis rank sum test (among BBS, DBS and ABS) and Wilcoxon rank sum test (between stages). (Tab S3a. Summary of changed GMMs; Tab S3b. GMM alteration for all subjects; Tab S3c. GMM alteration for female subjects; Tab S3d. GMM alteration for male subjects).

Table S4. GBM alterations among/between stages for subjects tested by the Kruskal-Wallis rank sum test (among BBS, DBS and ABS) and Wilcoxon rank sum test (between stages). (Tab S4a. Summary for changed GBMs; Tab S4b. GBM alteration for all subjects; Tab S4c. GBM alteration for female subjects; Tab S4d. GBM alteration for male subjects).

Table S5. Host physiological parameters, energy/nutrient intake record and analysis during the experiment. (TabS5a. Physical parameters recorded for subjects during the BLSS stay; TabS5b. Sleep record for each subject during the BLSS stay; Tab S5c. Comparison of the three major macronutrients (intake percentage), *Tenebrio molitor* (kcal/d) and edible fungi (kcal/d) between the inside and outside of the BLSS. Tab S5d. Phenotypes that might have an influence on the gut microbiome analyzed by PERMANOVA based on the gene profile. Tab S5e. Energy intake from foods during the BLSS; Tab S5f. Kinds of dietary nutrient intake during the BLSS; Tab S5g. Plant- and animal-sourced fat; Tab S5h. Plant- and animal-sourced protein).