

Supplementary Materials for

Social behavior shapes the chimpanzee pan-microbiome

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Fig. S6. Sampling of chimpanzee maternal lines.

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(available at advances.sciencemag.org/cgi/content/full/2/1/e1500997/DC1)

Table S1. Fecal sample metadata.

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Table S3. Temporal shifts in bacterial frequencies.

Table S4. Among chimpanzee variance in fruit consumption across sampling seasons.

Table S5. Correlations between chimpanzee HWI and bacterial relative abundances.

Table S6. Consumption of food types by chimpanzees across seasons.

Supplemental Materials

Materials and Methods

Comparing mixed effects models. We employed linear mixed-effects modeling in the `lme4` package in **R** to test whether the seasonal mean number of microbial species recovered per chimpanzee gut microbiome was influenced by chimpanzee sociability independently of the composition of the chimpanzee diet. We compared two models, both of which included the individual chimpanzee from which each fecal sample was collected as a random effect. A likelihood-ratio test via `lrttest` in the package `lmttest` indicated that the seasonal mean number of microbial species recovered per chimpanzee gut microbiome was significantly better predicted by a model in which both mean HWI and dietary evenness were considered as fixed effects than by a model considering dietary diversity alone as a fixed effect (Chi-squared = 12.812; $p = 0.000344$).

In addition, we employed linear mixed-effects modeling in the `lme4` package in **R** to test whether the seasonal mean number of microbial species recovered per chimpanzee gut microbiome was influenced by the composition of the chimpanzee diet independently of chimpanzee sociability. We compared two models, both of which included the individual chimpanzee from which each fecal sample was collected as a random effect. A likelihood-ratio test via `lrttest` in the package `lmttest` indicated that the seasonal mean number of microbial species recovered per chimpanzee gut microbiome was significantly better predicted by a model in which both mean HWI and dietary diversity (as defined as the Shannon's evenness index of the proportions of food types listed in Table S6) were considered as fixed effects than by a model considering HWI alone as a fixed effect (Chi-squared = 10.848; $p = 0.000989$).

Supplementary Figures

Figure S1

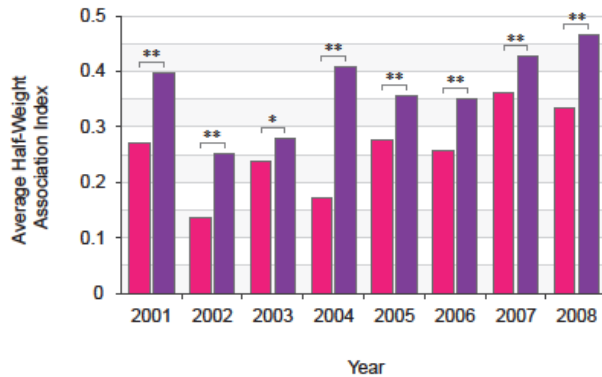


Fig. S1. Seasonal variation in chimpanzee sociability. Shown is the mean half-weight index of association across all unique dyads consisting of adult male and female chimpanzees for each season in which microbiomes were sampled. Red and blue bars denote dry and wet seasons, respectively. Significant differences between consecutive dry and wet seasons are indicated by asterisks (* $p < 0.01$; ** $p < 0.001$).

Figure S2

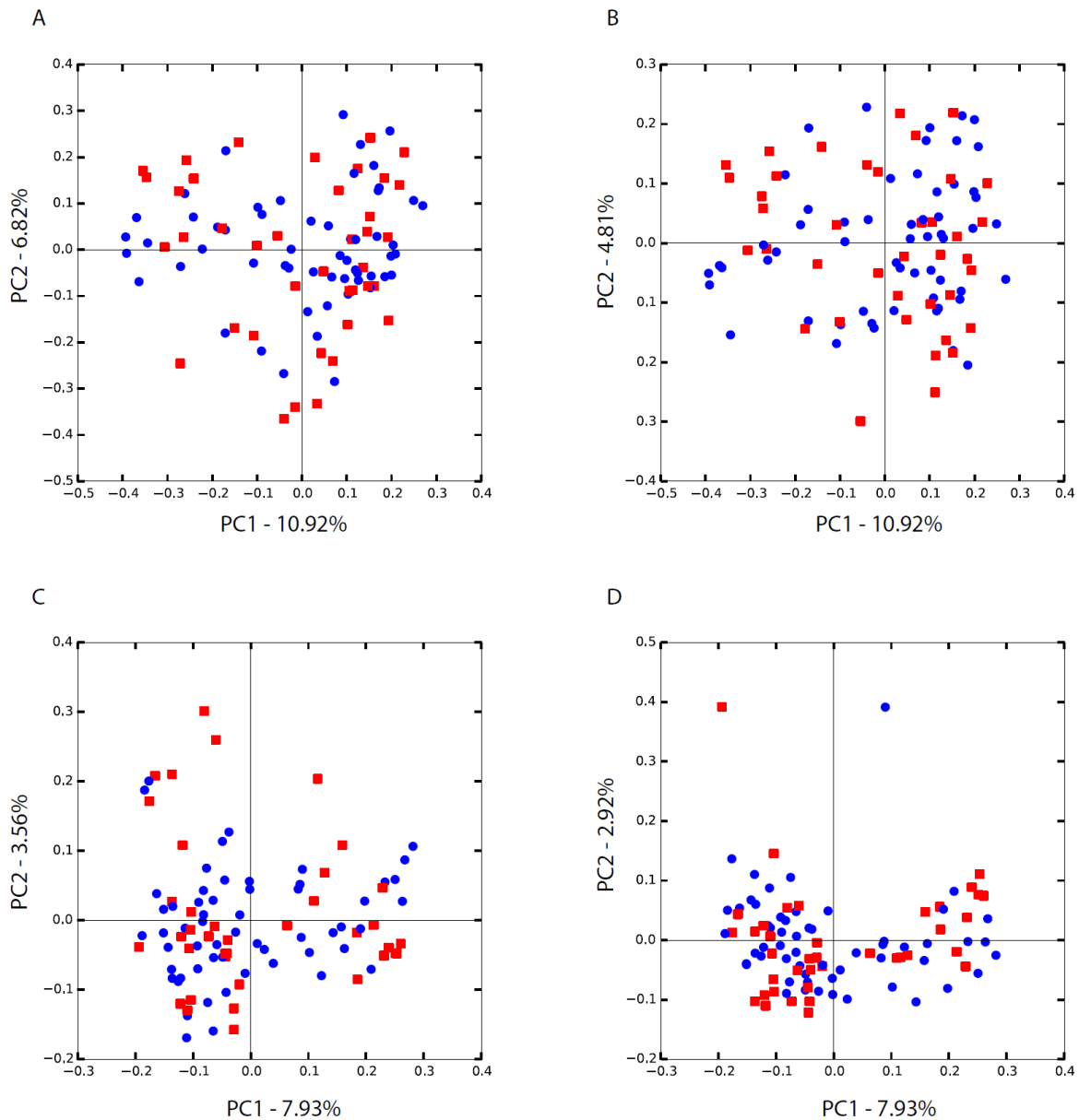


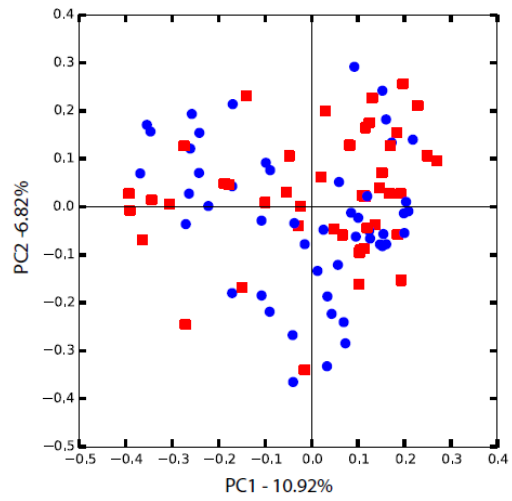
Fig. S2. Temporal shift in microbiome composition is not evident in PC2 of Bray-Curtis

dissimilarities or PC 1, PC2, or PC3 of Sorensen-Dice dissimilarities. (A) Microbiome samples from individual chimpanzees plotted against the first and second principal coordinates of pairwise Bray-Curtis dissimilarities. Blue triangles represent samples collected prior to May 1, 2005 and red circles represent samples collected after May 1, 2005. **(B)** Microbiome samples from individual chimpanzees plotted against the first and second principal coordinates of

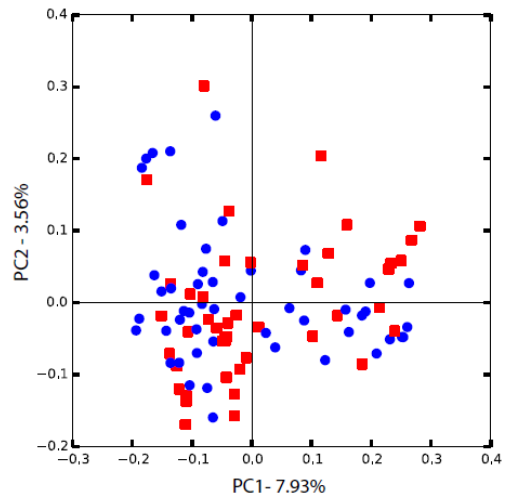
pairwise Sorensen-Dice dissimilarities. Blue triangles represent samples collected prior to May 1, 2005 and red circles represent samples collected after May 1, 2005 (C) Microbiome samples from individual chimpanzees plotted against the first and third principal coordinates of pairwise Sorensen-Dice dissimilarities. Blue triangles represent samples collected prior to May 1, 2005 and red circles represent samples collected after May 1, 2005.

Figure S3

A



B



C

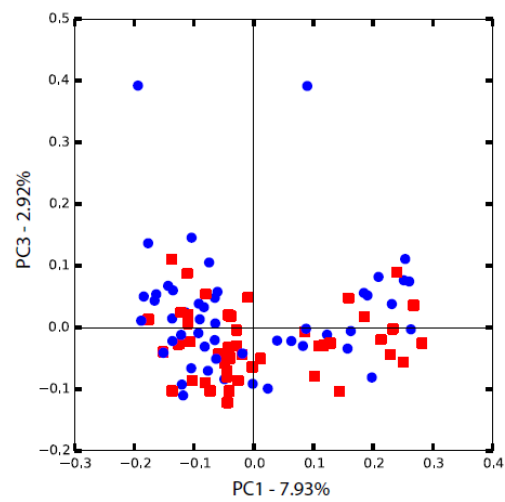


Fig. S3. Lack of differentiation between wet- and dry-season gut microbial communities.

(A) Microbiome samples from individual chimpanzees plotted against the first and second principal coordinates of pairwise Bray-Curtis dissimilarities. Blue triangles represent samples collected during wet seasons and red circles represent samples collected during dry seasons. (B) Microbiome samples from individual chimpanzees plotted against the first and third principal coordinates of pairwise Bray-Curtis dissimilarities. Blue triangles represent samples collected during wet seasons and red circles represent samples collected during dry seasons. (C) Microbiome samples from individual chimpanzees plotted against the first and second principal coordinates of pairwise Sorensen-Dice dissimilarities. Blue triangles represent samples collected during wet seasons and red circles represent samples collected during dry seasons (D) Microbiome samples from individual chimpanzees plotted against the first and third principal coordinates of pairwise Sorensen-Dice dissimilarities. Blue triangles represent samples collected during wet seasons and red circles represent samples collected during dry seasons.

Figure S4

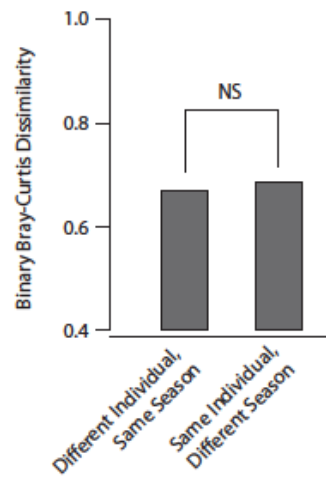


Fig. S4. Testing for signatures of host individual in chimpanzee gut microbiomes. Shown is the mean Sorensen-Dice dissimilarity between samples from different individuals during the same season versus the mean Sorensen-Dice dissimilarity between samples from the same individual in different seasons.

Figure S5

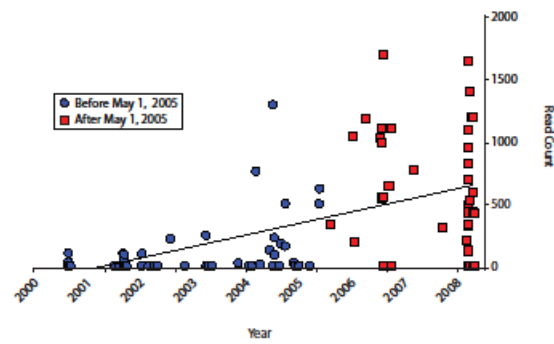


Fig. S5. Proliferation of an *Olsenella* phylotype over time. Colored shapes represent the number of reads corresponding to a specific *Olsenella* phylotype recovered from gut microbiome samples. Trend-line represents the regression between the time of sampling and the abundance of the *Olsenella* phylotype.

Figure S6

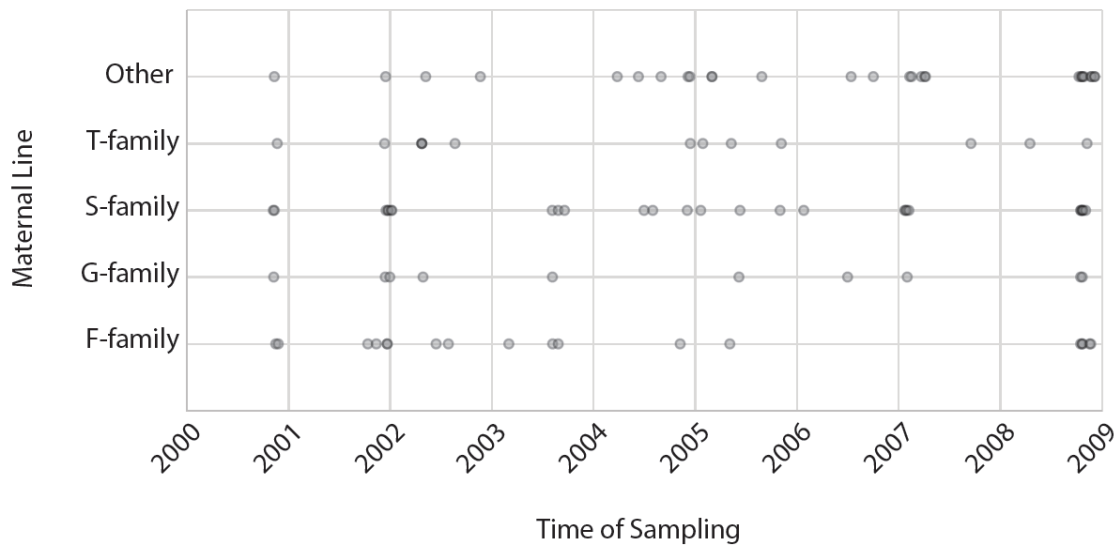


Fig. S6. Sampling of chimpanzee maternal lines. Shown is a timeline depicting when samples from each maternal line were collected. Each of the bottom four rows corresponds to a maternal line, and each point represents a sample. The top row depicts when chimpanzees from other maternal lines were sampled. Points are transparent such that dark clusters of points represent time points at which multiple samples from the same maternal line were collected. For a full list of samples and metadata, see Table S1.