

Cell Reports, Volume 27

Supplemental Information

**Dynamic and Asymmetric Changes of the Microbial
Communities after Cohousing in Laboratory Mice**

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SUPPLEMENTAL INFORMATION

Supplemental Information includes four figures and two tables.

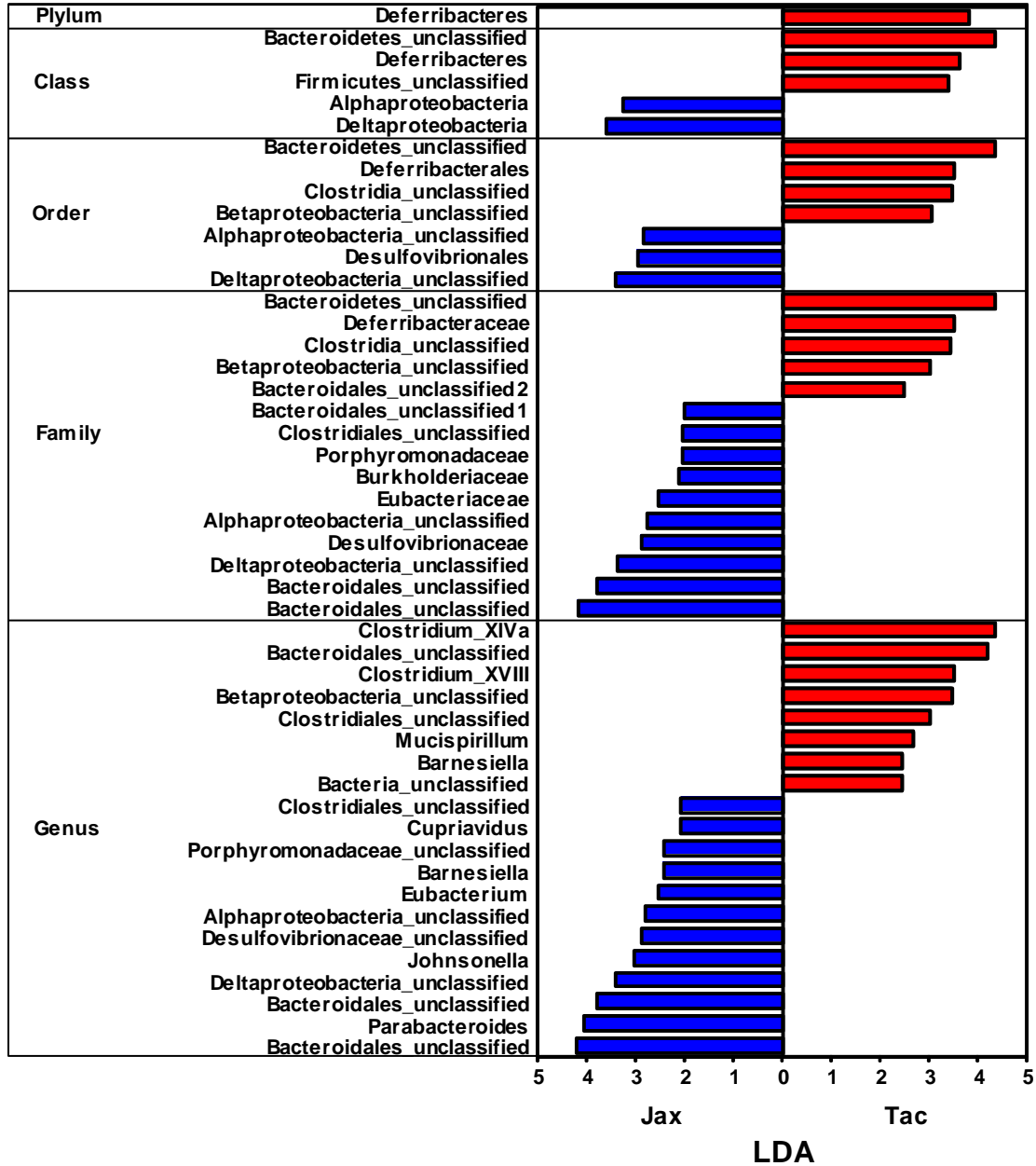


Figure S1: Distinct taxa in the fecal microbiotas of Jax and Tac mice. Related to Figure 1.

Taxons differentially abundant in Jax versus Tac mice detected by LefSe ($p < 0.05$) are shown with their LDA values.

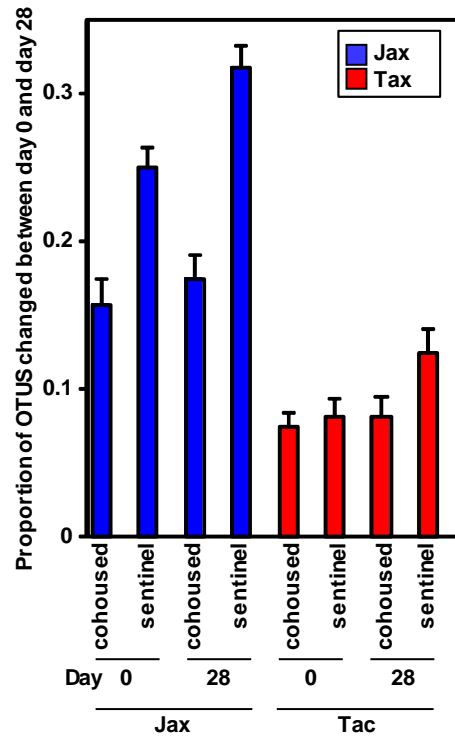
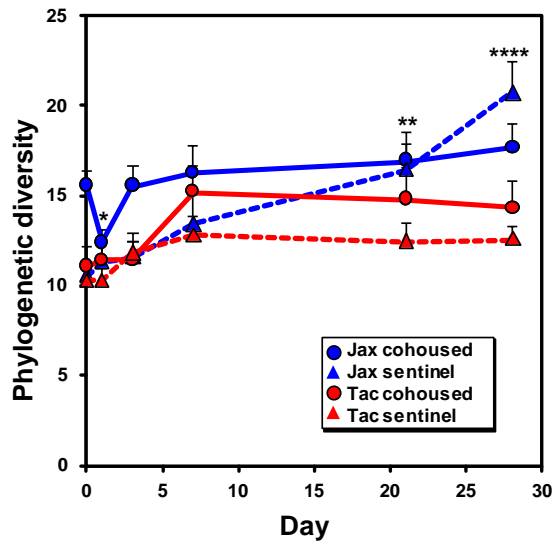


Figure S2: Proportion of OTUs changed between days 0 and 28 in cohoused and non-cohoused mice. Related to Figure 2. Average coverage of OTUs whose abundance is different in Jax versus Tac mice on day 0 and day 28 by LefSE is shown with SEM.

A



B

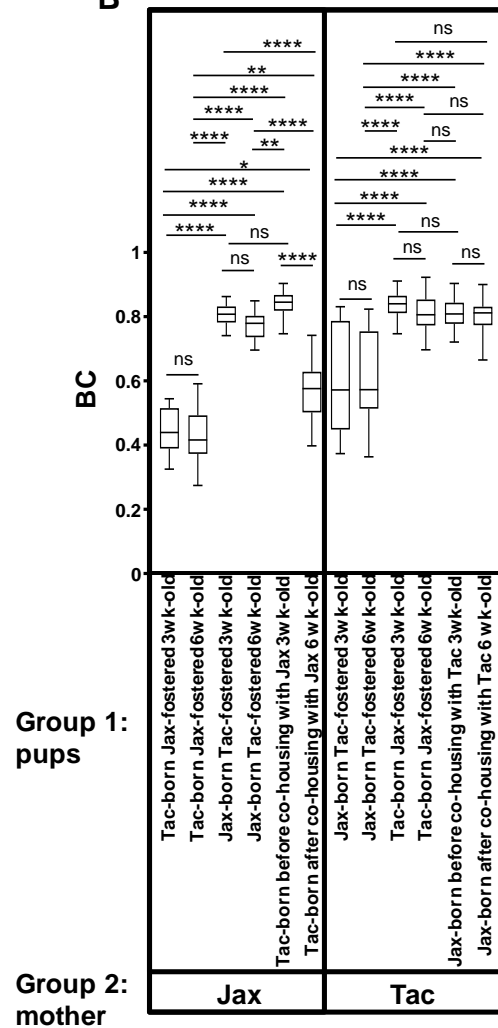


Figure S3: Changes of microbiota diversity during cohousing. Related to Figure 3.

(A) Phylogenetic diversity of fecal microbiotas of cohoused and sentinel mice during 4 weeks. Data are expressed as mean \pm SEM from 4 independent experiments in both panels A and B. All α -diversities of fecal microbiotas, except for Jax cohoused mice on day 0 vs day 1 (* $p < 0.05$) and for Jax sentinel mice on day 0 vs day 21 (** $p < 0.01$) and 28 (**** $p < 0.0001$), show no statistical difference over time (one-way ANOVA followed by Dunnett's multiple comparisons test). (B) Box plots showing Bray-Curtis (BC) indexes of mothers and pups in cohousing and cross-fostering experiments. Jax and Tac pups ($n = 7$ and 7 , respectively) were crossfostered within 2 days after birth. Data are pooled from two independent experiments. Box plots showing BC indexes between the microbiotas of mothers, that were used for both cross-fostering and cohousing experiments, and the microbiotas of crossfostered and cohoused

pups at weaning (3 wk-old) and 28 days after weaning (6 wk-old). Boxes represent the interquartile range between the first and third quartiles (25th and 75th percentiles, respectively), the horizontal line inside the box defines the median and whiskers represent the lowest and highest values. * $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$ and n.s., not significant (Kruskal-Wallis test followed by Dunn's multiple comparisons test).

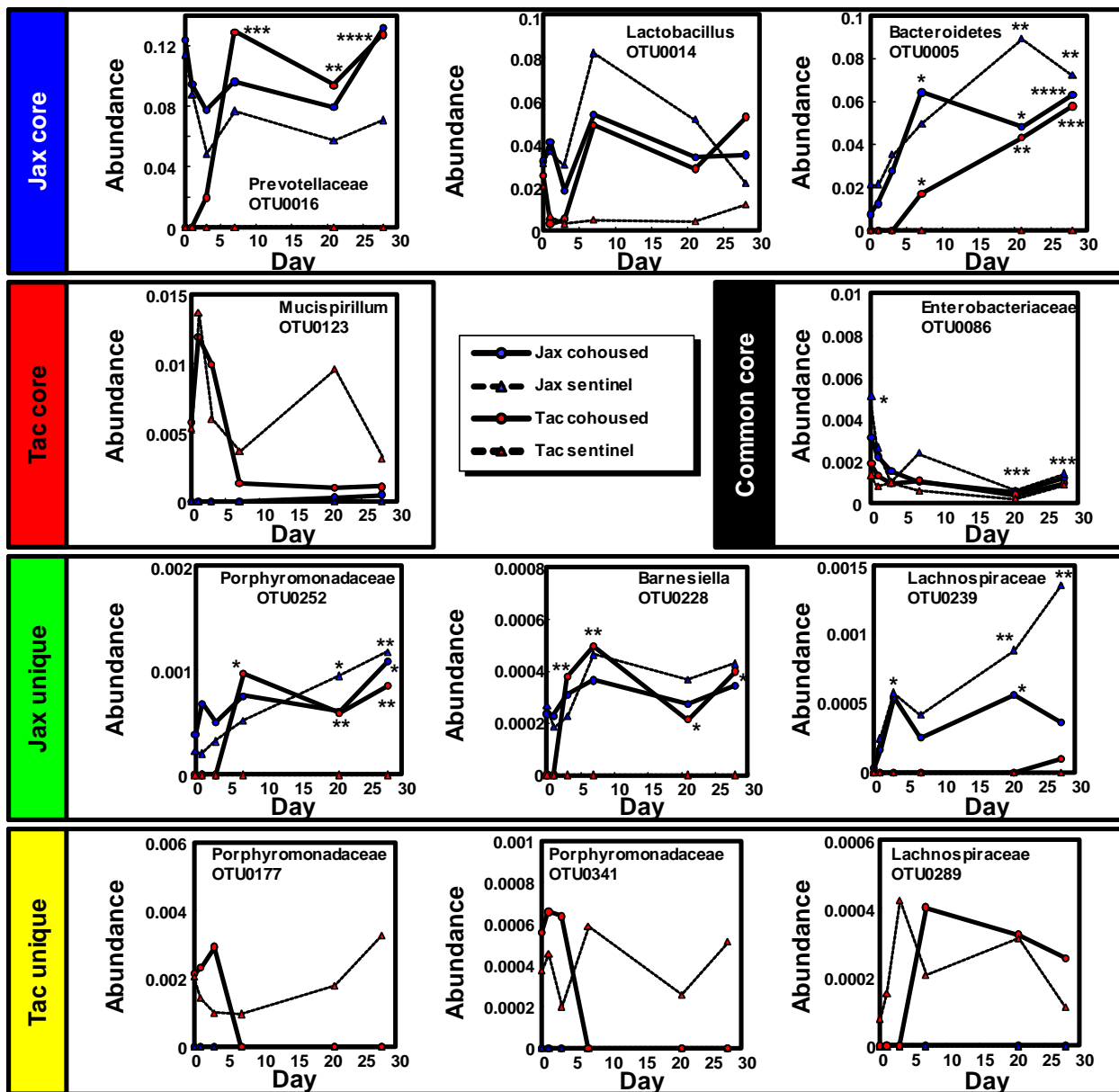


Figure S4. Kinetics of individual OTU during cohousing. Related to Figure 5.

The kinetics of top three OTUs (highest abundance levels in family members that were specific to indicated groups (as indicated in Figure 5)). Only one OTU (*Mucispirillum* and unclassified Enterobacteriaceae OTU0086) were found in family members that were specific to Tac and common core groups, respectively. The sequence of OTU0086 is identical to *E. coli*. Data are expressed as median. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$. (Friedman test followed by Dunn's multiple comparisons test).