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## Supplemental information

# The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping

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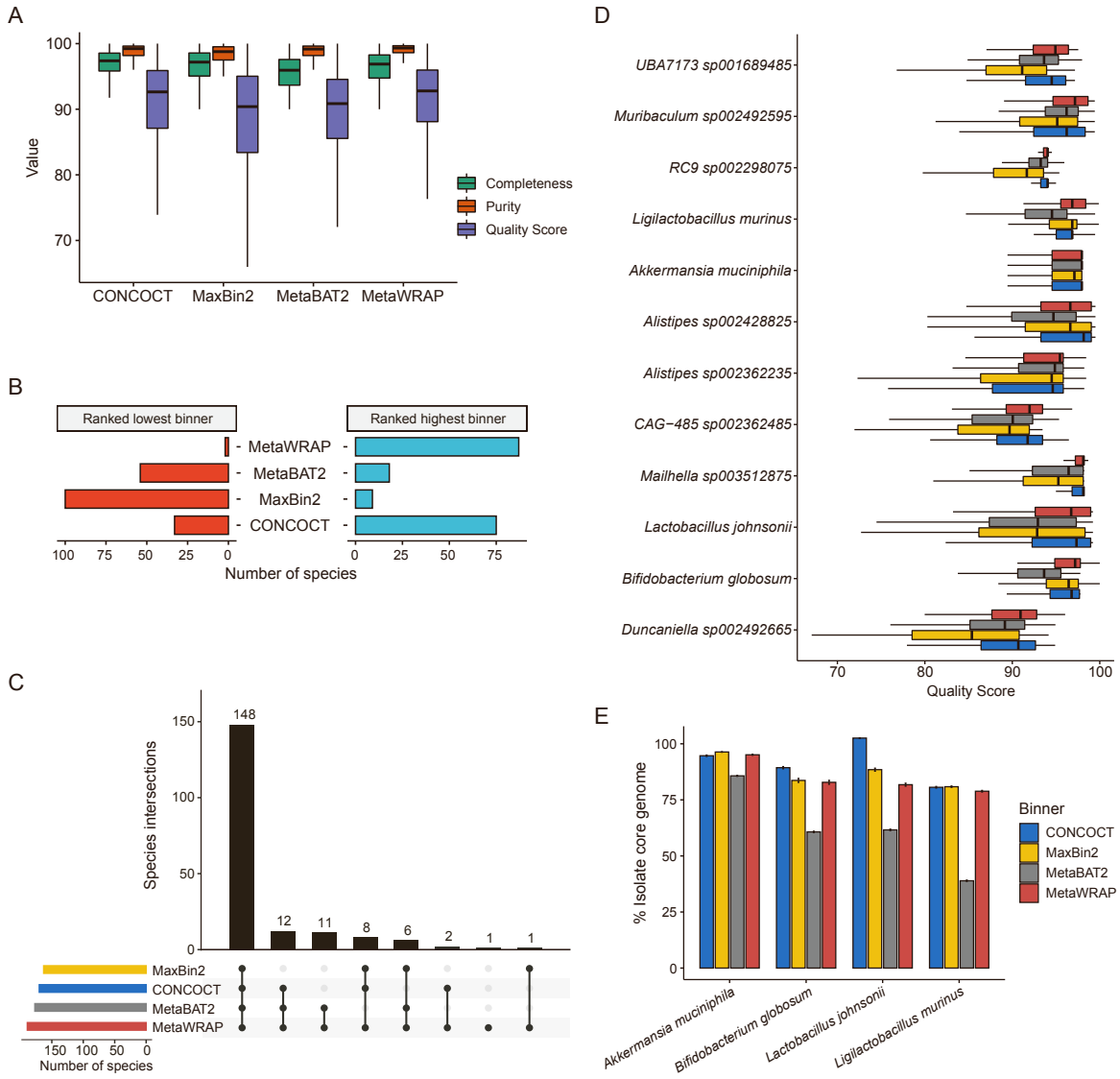
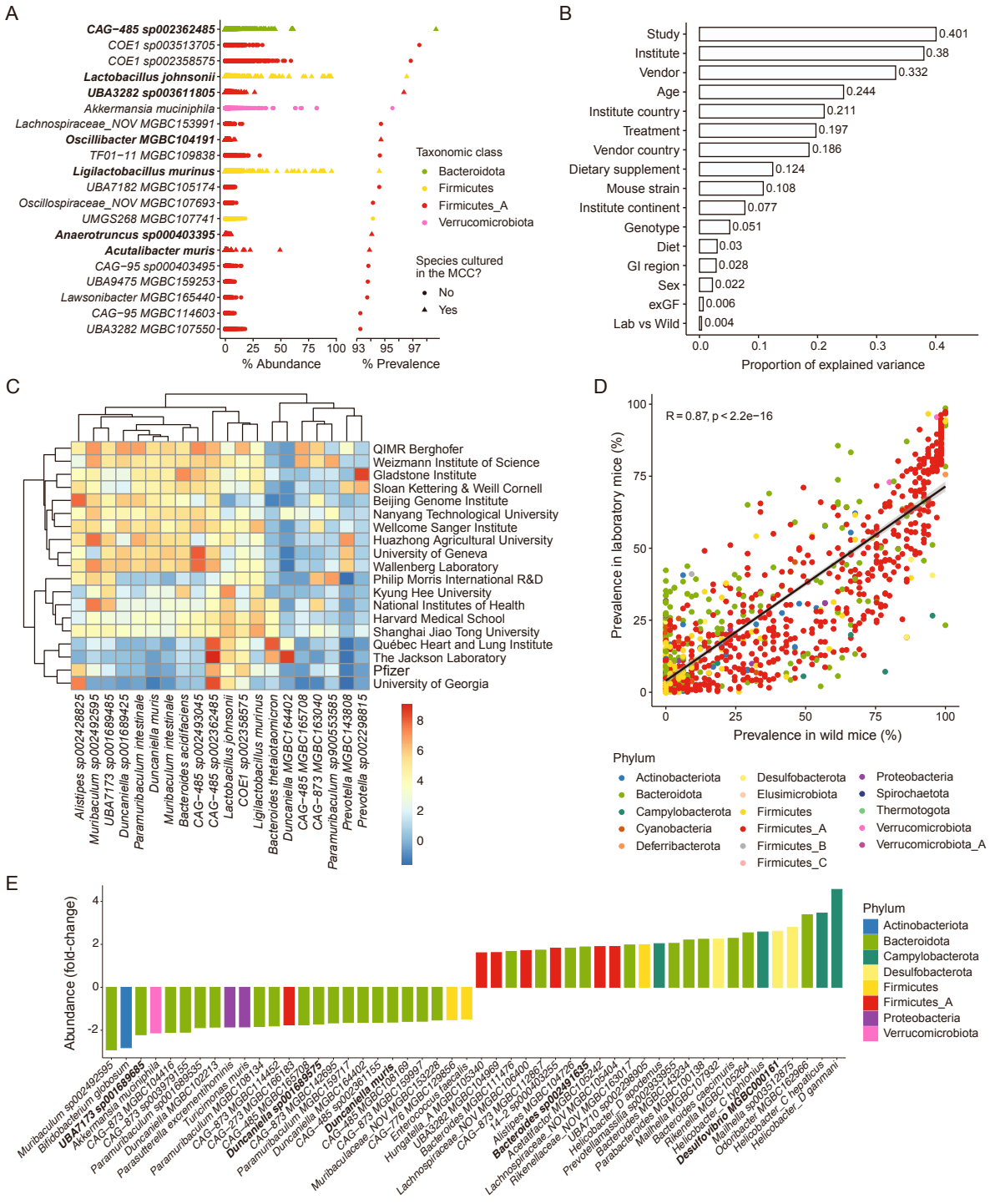
**Contents:**

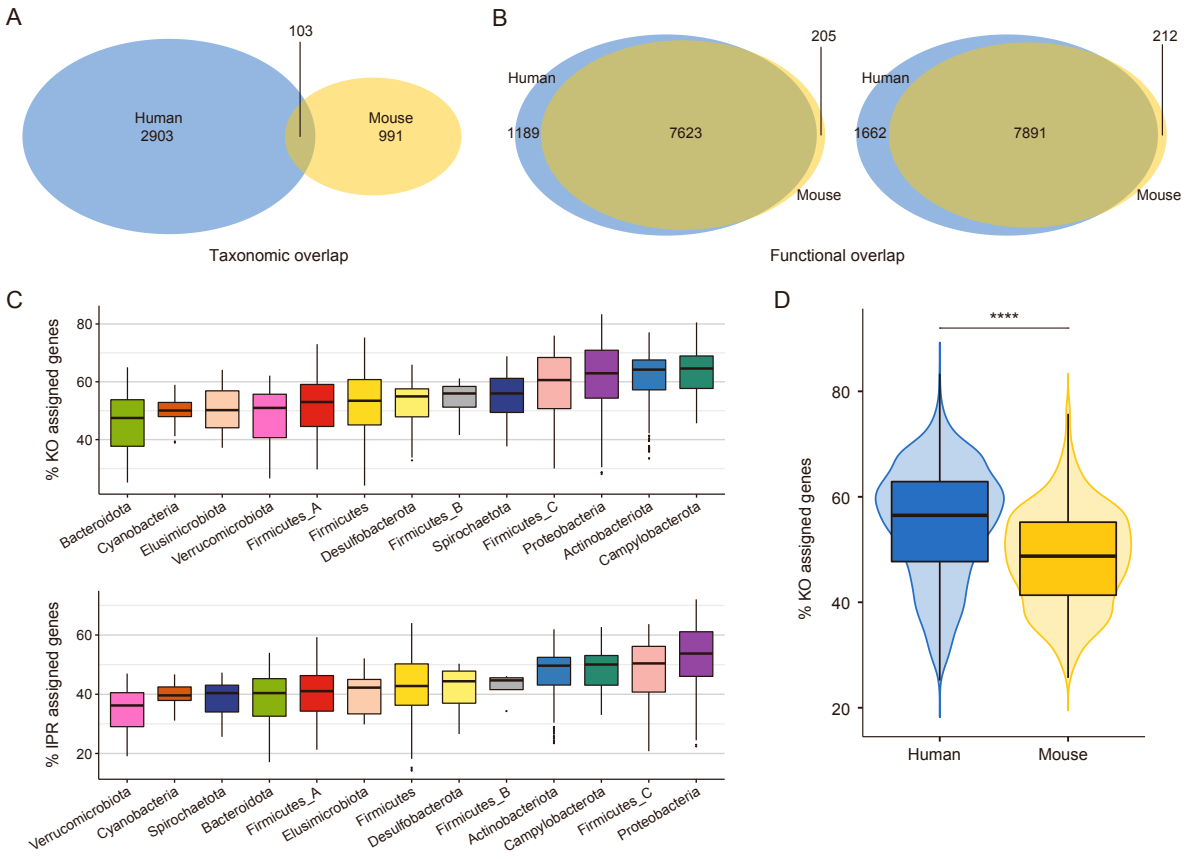



**Supplementary Figure 1: Comparison of common binners for MAG synthesis, related to STAR methods.** a) Quality scores of high-quality and medium-quality bins generated using the single binners MetaBAT2, MaxBin2, CONCOCT and hybrid bins from MetaWRAP (combined bins from all three single binners). b) Bars represent the number of species for which each binner generated the lowest quality bins ("Ranked lowest binner", red), and the highest quality ("Ranked highest binner", blue). c) UpSet plot illustrating the number of species represented by high-quality bins generated by each binner, and the species intersections between binners. d) MAG quality scores for the 12 most commonly binned species. e) Core genome size of commonly binned species when utilising different binners. Data represent the core genome size of MAG+isolate core genomes, compared to isolates alone. *A. muciniphila*, 100 iterations of 90 MAGs per binner and 136 isolate genomes; *B. globosum*, 100 iterations of 35 MAGs per binner and 62 isolate genomes; *L. johnsonii*, 100 iterations of 60 MAGs per binner and 54 isolate genomes; *L. murinus*, 100 iterations of 150 MAGs per binner and 58 isolate genomes. Aside from the medium quality MAG data in (a), only high-quality MAGs were used in these analyses.

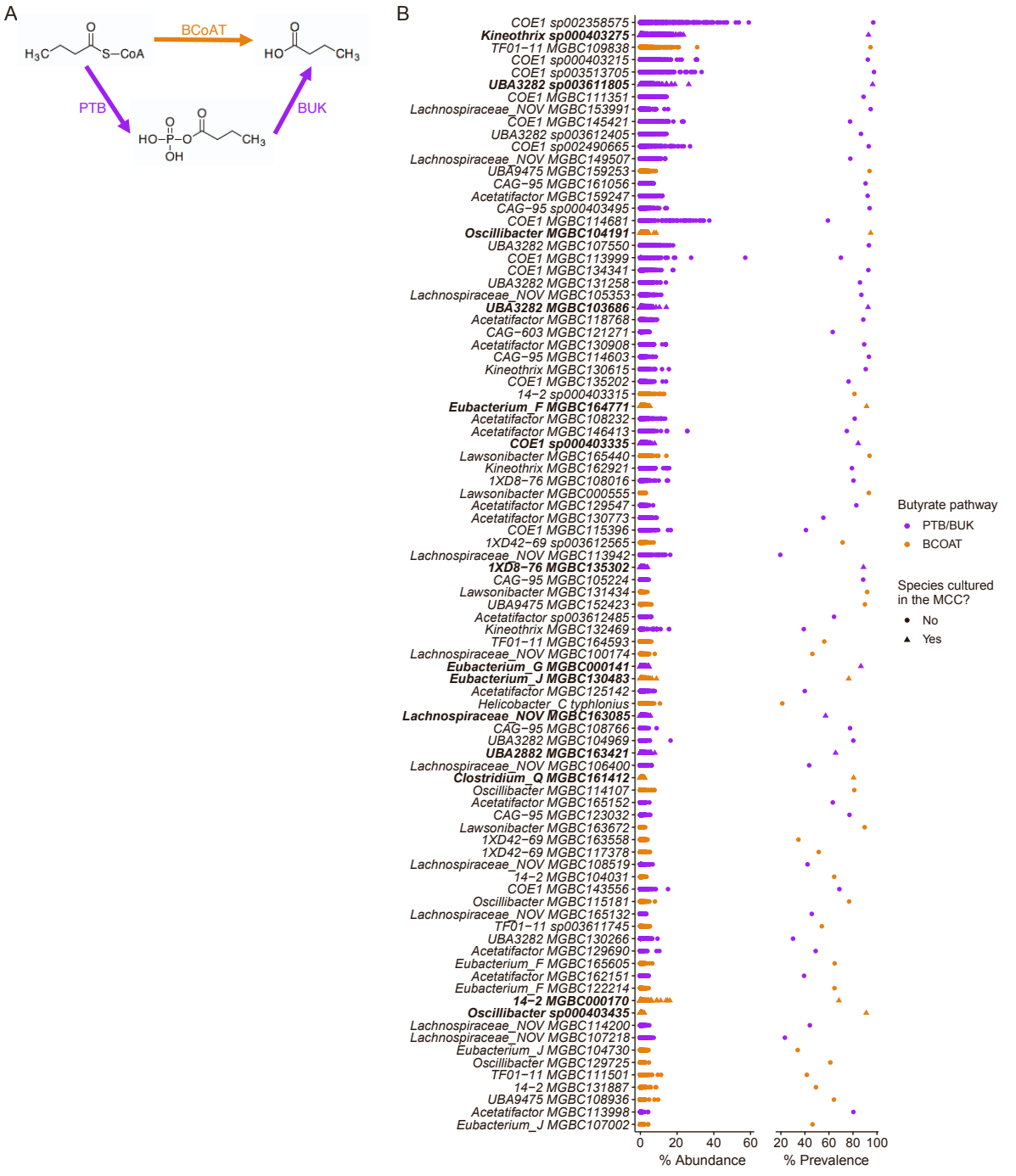



**Supplementary Figure 2: The mouse gut microbiota between institutes and wild mice, related to STAR methods.** a) Abundance and prevalence profiles of the 20 most prevalent species of the mouse gut microbiota across 2,446 samples. A species was determined as present in a sample if it was assigned ≥0.01% of classified reads. Point colour represents taxonomic phylum and point shapes and boldface labels indicate whether a species has been cultured as part of the MCC (triangles, bold) or not (circles). b) Proportion of variance explained (R2) by variables in the metadata using a permutational analysis of variance (PERMANOVA). All analyses were run with 999 permutations. Statistics for the PERMANOVA are provided in Table S7. c) Heatmap showing abundance of the top 20 most abundant species of the mouse microbiota across different institutes. Analyses include faecal samples from wildtype C57BL/6 “control” mice fed chow diets (n=432). Data are centre log-ratio

normalised read fractions, following Bayesian-multiplicative replacement of count zeros. d) Scatter plot comparing prevalence of species between untreated laboratory (n=1,065) and wild (n=65) mouse gut microbiotas. Each datapoint represents a mouse, and colour represents taxonomic phylum. Black line and shadow indicate linear regression line with 95% confidence interval ($r=0.87$, $p<2.2x10-16$). e) Fold-change in mean abundance of species in wild mice compared to untreated laboratory mice. Positive coefficient indicates enrichment in wild mice. Bar colour represents taxonomic phylum.




**Supplementary Figure 3: Taxonomic and functional analyses of the human and mouse gut microbiotas, related to Figure 4.** a) Venn diagram illustrating species sharing between human and mouse microbiotas. b) Venn diagrams illustrating the functional overlap of InterPro protein families (IPR; left) or KEGG Orthology (KO) groups (right) between all human (blue) and mouse (yellow) gut bacterial species. c) Functional annotation efficiency of bacterial pangenomes by taxonomic phylum for KO groups (top) and IPR families (bottom). Data represent the percentage of predicted protein-coding genes of each pangenome that could be assigned to an IPR or KO, coloured by phylum. d) Functional annotation efficiency of KO groups by host organism. A Wilcoxon signed-rank test was used to calculate statistical significance, ****P < 0.0001.




**Supplementary Figure 4: Butyrate metabolism by species of the mouse gut microbiota, related to Figure 6.** a) Schematic of the terminal pathways of butyrate synthesis by the gut microbiota. Butyrate CoA-transferase (BCoAT; orange); butyrate phosphotransferase/butyrate kinase (PTB/BUK; purple). b) Abundance and prevalence profiles of the 90 most abundant predicted butyrate producing species of the mouse gut microbiota. Point colour represents predicted encoded terminal butyrate pathway. Point shapes and boldface labels indicate whether a species has been cultured as part of the MCC (triangles, bold) or not (circles).

**Supplementary Table 5: PERMANOVA statistics, related to STAR methods.**
PERMANOVA comparing the extent to which factors in sample metadata explain variance between metagenomic samples.

| Metadata factor | DegreesFreedom | SumsOfSquares | MeanSquares | F.Model | R2 | P_value | Explanation of factor/variable: |
|---|---|---|---|---|---|---|---|
| Study | 74 | 2055298 | 27774.3 | 21.42 | 0.40067 | 0.001 | Study accession. |
| Institute | 62 | 1949409 | 31442.1 | 23.56 | 0.38002 | 0.001 | Experimental institute i.e., location of mice at time of sampling. |
| Vendor | 57 | 1688944 | 29630.6 | 20.646 | 0.33217 | 0.001 | Vendor's name with region if relevant e.g., Jackson, US vs Jackson, Denmark. |
| Age | 54 | 1084273 | 20079.1 | 12.347 | 0.24407 | 0.001 | Age at time of sampling. |
| Institute country | 16 | 1074085 | 67130 | 40.29 | 0.21124 | 0.001 | Country of the institute. |
| Treatment | 58 | 1010917 | 17429.6 | 10.102 | 0.19728 | 0.001 | What treatments did the mice receive e.g., control, high fat diet, specific drug treatment. |
| Vendor country | 14 | 932012 | 66572 | 38.714 | 0.18555 | 0.001 | Country of the vendor. |
| Dietary Supplement | 30 | 635939 | 21198 | 11.392 | 0.1241 | 0.001 | Dietary supplement, including in the drinking water e.g., glucose, NSAIDs, or DSS. |
| Mouse strain | 20 | 553619 | 27681 | 14.671 | 0.10806 | 0.001 | Strain of mice e.g., C57BL/6J vs C57BL/6NTac |
| Institute continent | 3 | 394842 | 131614 | 67.88 | 0.07697 | 0.001 | Continent of the institute. |
| Genotype | 17 | 263389 | 15493.5 | 7.7309 | 0.05141 | 0.001 | Genotype: wildtype, or specific knockout e.g., IL-10 deficient. |
| Diet | 10 | 152023 | 15202.3 | 7.437 | 0.03 | 0.001 | Diet: chow, high fat, low fibre, etc. |
| Sample source/GI location | 10 | 143611 | 14361.1 | 7.0171 | 0.02825 | 0.001 | Sampling location e.g., faeces, caecum, small intestine. |
| Sex | 1 | 94158 | 94158 | 45.948 | 0.02201 | 0.001 | Sex of mice. |
| exGF | 1 | 32620 | 32620 | 15.641 | 0.00636 | 0.001 | Endogenous (SPF) or reconstituted (ExGF) microbiota. |
| Lab vs Wild | 1 | 18098 | 18098.1 | 8.6532 | 0.00353 | 0.001 | Laboratory vs wild mice, reflecting their faecal origins e.g., in the case of ExGF mice |

| Technical features: | Permutation: | Free |
|---|---|---|
| | Number of permutations: | 999 |