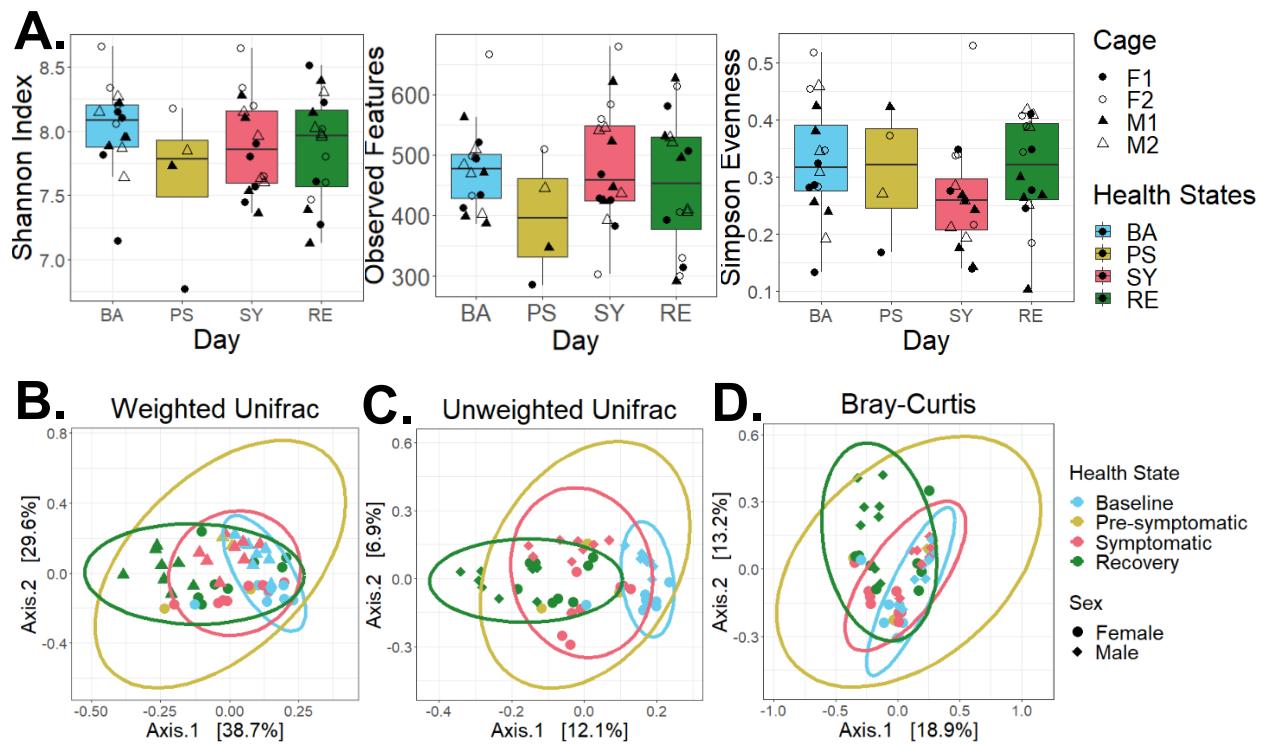
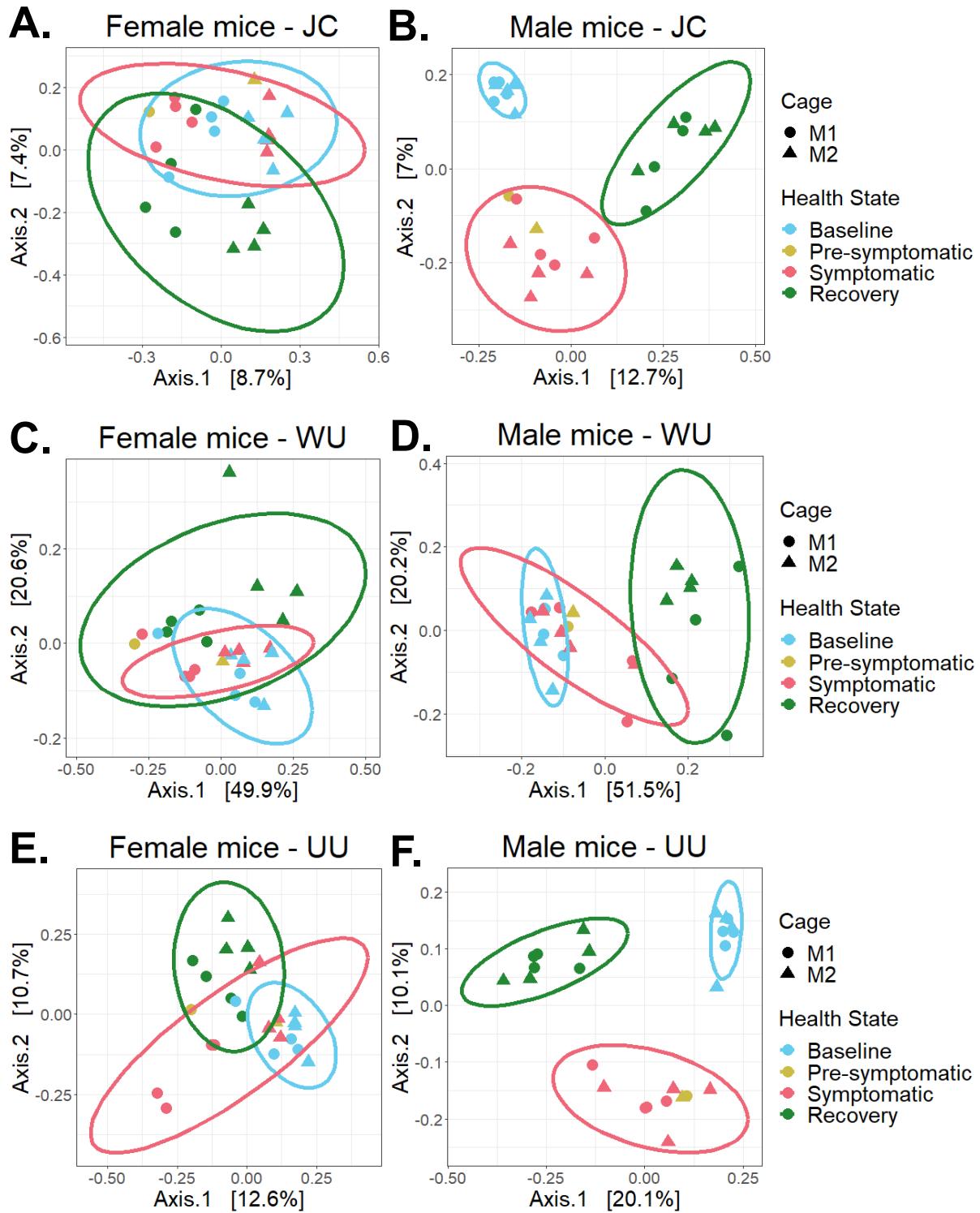
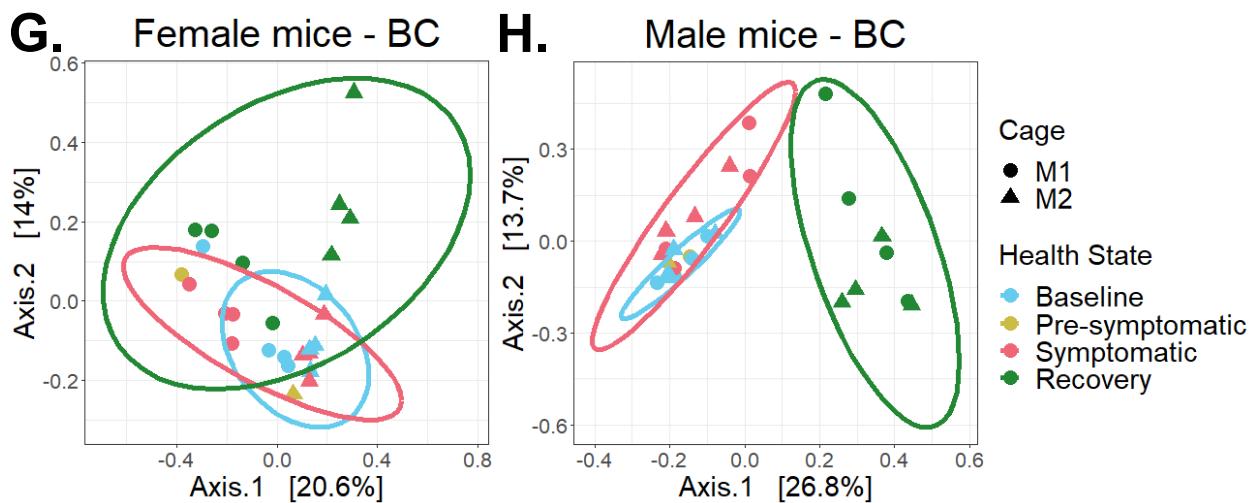


**Supplementary Figure 1.** Mouse health parameters during first DSS colitis experiment. Three main indicators of colitis were followed in four cages of mice before, during, and after the administration of DSS. (A) Relative change in mouse weight, relative to their starting weight at the beginning of the experiment. (B) Levels of lipocalin-2 (LCN-2) reported as nanograms per gram of feces (ng/g). (C) Presence (+) or absence (-) of blood in the feces of mice in each cage, as determined by hemoccult analysis

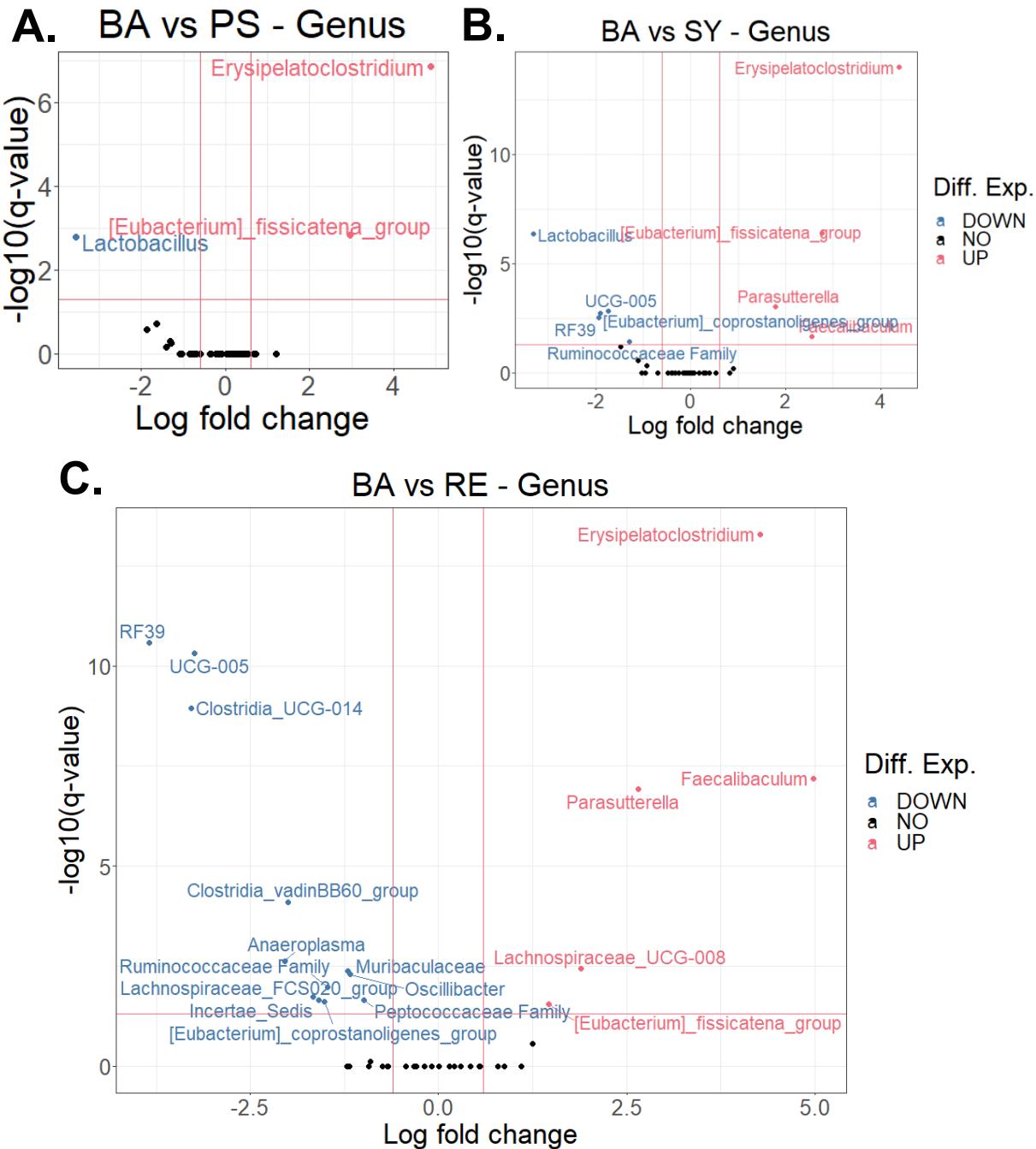


**Supplementary Figure 2.** Alpha and beta diversity statistics for first DSS mouse experiment. (A) Alpha diversity for all cages combined – Shannon index (left), observed features (middle), and Simpson evenness (right). (B-D) Beta diversity for all cages combined. Colors of dots and ellipses/grouping determined by health state. (B) Weighted Unifrac distance (WU), (C) Unweighted Unifrac distance (UU), and (D) Bray-Curtis dissimilarity (BC).

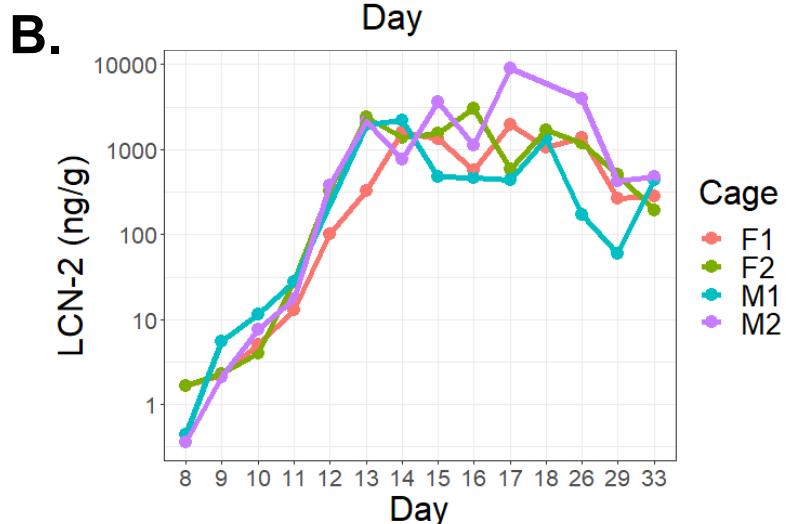
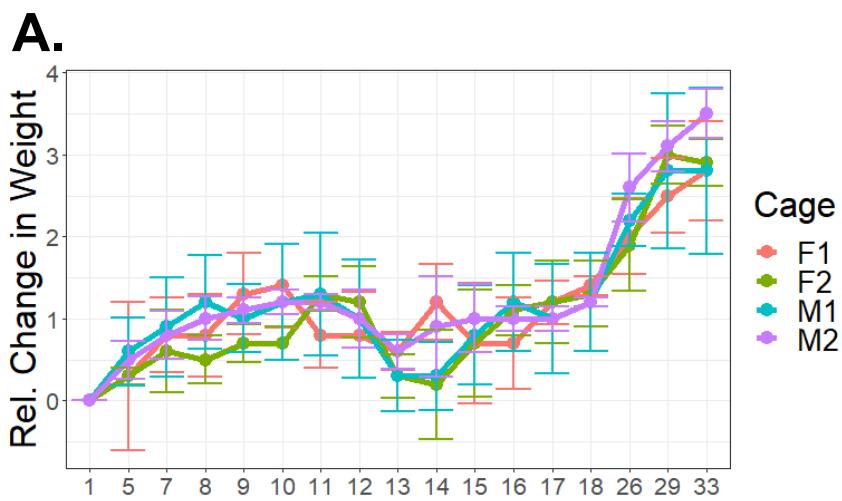




**Supplementary Figure 3.** Beta diversity statistics per sex, grouped by health state. Beta diversity statistics per sex, grouped by health state, for the first DSS experiment. (A-B) Jaccard index (JC) (C-D) Weighted Unifrac distance (WU). (E-F) Unweighted Unifrac distance (UU) (G-H) Bray-Curtis dissimilarity (BC)



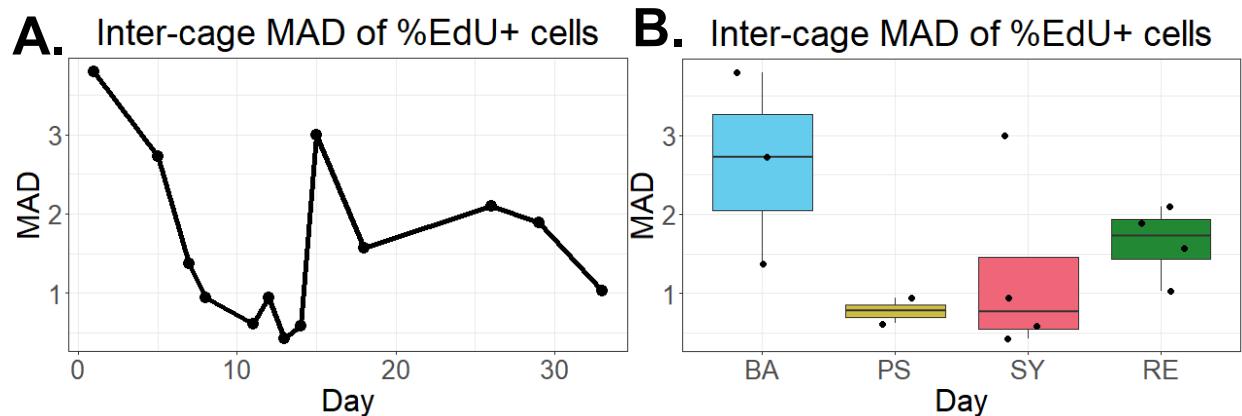
**Supplementary Figure 4.** Taxa marked as differentially abundant as compared to the baseline state during DSS colitis. Taxa marked as differentially abundant as compared to the baseline state, during the first DSS colitis experiment. (A-C) Volcano plots showing the differentially abundant taxa at the genus level, when comparing from the baseline state (BA) to the (A) pre-symptomatic (PS), (B) symptomatic (SY), and (C) recovery (RE) state. Taxa with increased abundances (Diff Exp = UP) during the health state of interest (pre-symptomatic, symptomatic, recovery) versus baseline are in red/pink on the upper right of each plot, whereas taxa with increased abundances in the baseline state (Diff Exp = DOWN) as compared to the health state of interest are in blue, on the upper left of each plot. Note that the taxa labelled as Clostridia\_vadinBB60\_group here is the same as the undefined Clostridia in Figure 1D.



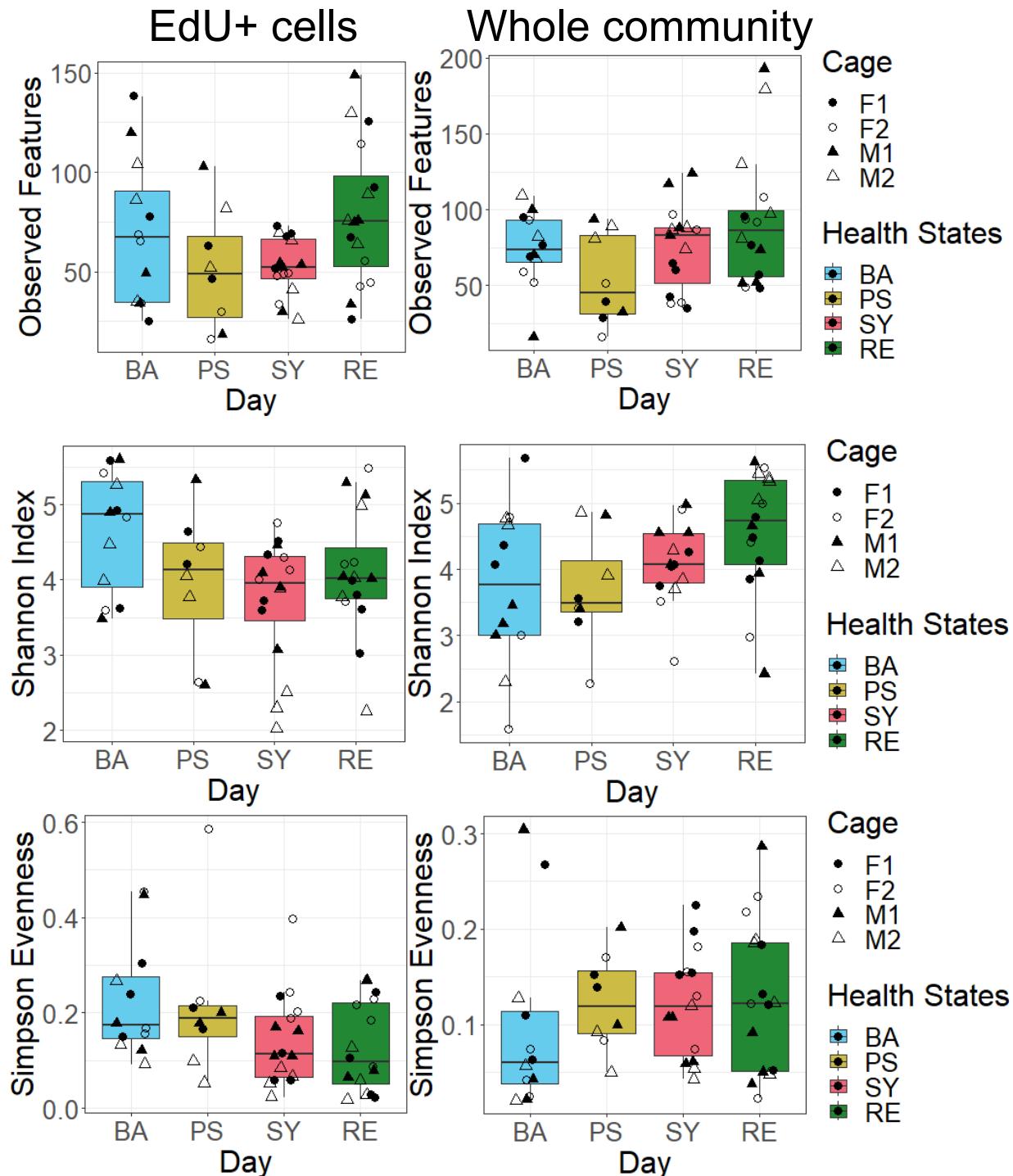
**C.**

Date	Cage				Day	Health State
	F1	F2	M1	M2		
22 April 2021	-	-	-	-	8	Pre-symptomatic
23 April 2021	-	-	-/+	-	9	Pre-symptomatic
24 April 2021	-	-	-	-	10	Pre-symptomatic
25 April 2021	-	~	-	~	11	Pre-symptomatic
26 April 2021	-	+/-	+/-	+	12	Symptomatic
27 April 2021	~	-	+	+	13	Symptomatic
28 April 2021	-	-	-	-	14	Symptomatic
29 April 2021	-	-	-	-	15	Symptomatic
30 April 2021	-	-	-	-	16	Recovery

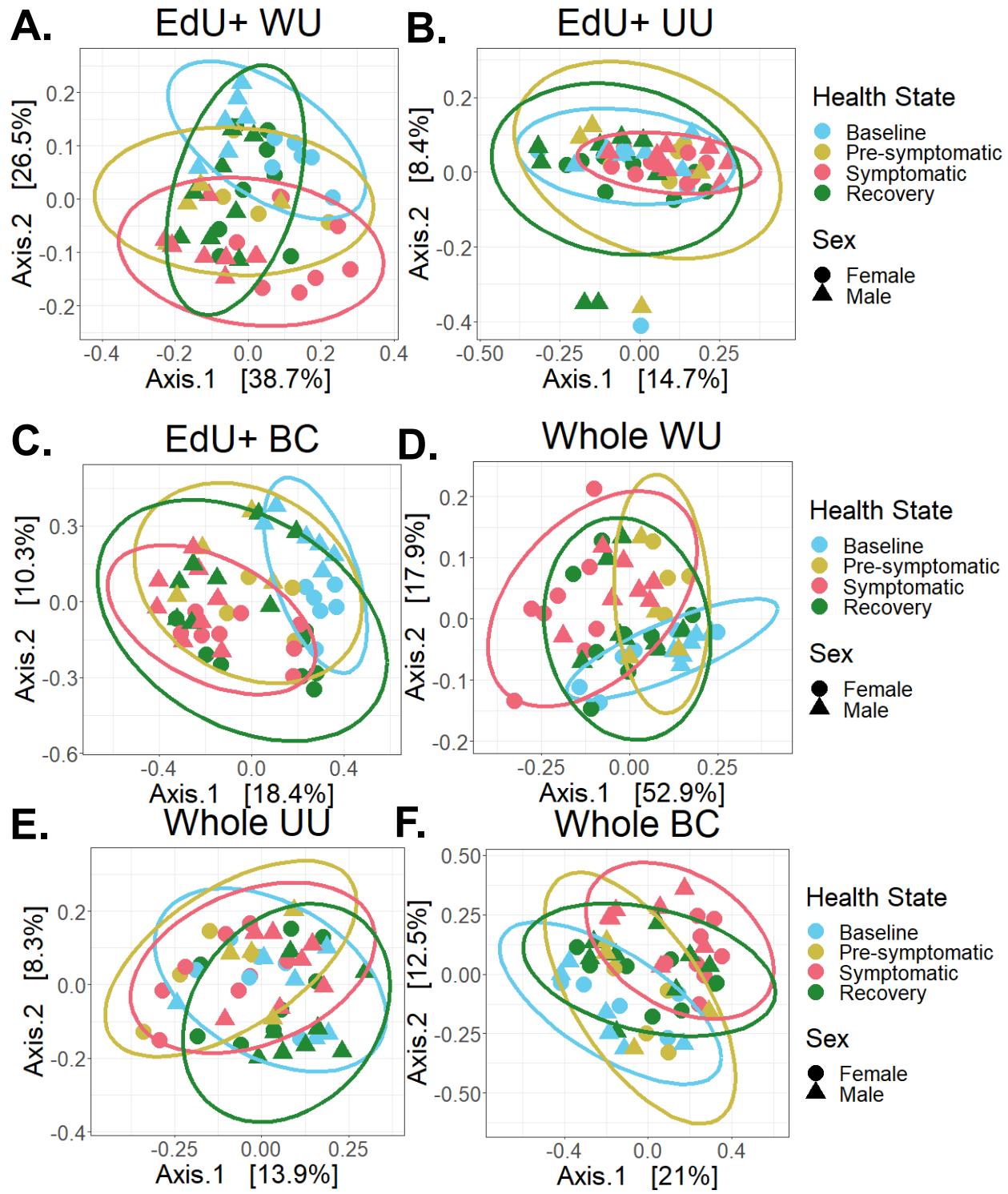
**Supplementary Figure 5.** Mouse health parameters during second DSS colitis experiment. Three main indicators of colitis were followed in four cages of mice before, during, and after the administration of DSS. (A) Relative change in mouse weight, relative to their starting weight at the beginning of the experiment. (B) Levels of lipocalin-2 (LCN-2) reported as nanograms per gram of feces (ng/g). (C) Presence (+) or absence (-) of blood in the feces of mice in each cage, as determined by hemoccult analysis. When some fecal samples had a positive signal and others had a negative signal for presence of blood in stool, the symbol “-/+” or “+/-” is used. For indeterminate results, the tilde symbol “~” is used.



**Supplementary Figure 6.** Median absolute deviation (MAD) of replicating ( $\text{EdU}^+$ ) cells. (A-B) MAD of the proportion of replicating ( $\text{EdU}^+$ ) cells between cages over time in each health state, visualized as a line plot (A) and as boxplots with per-cage MAD values grouped per health state. BA = baseline, PS = pre-symptomatic, SY = symptomatic, RE = recovery.

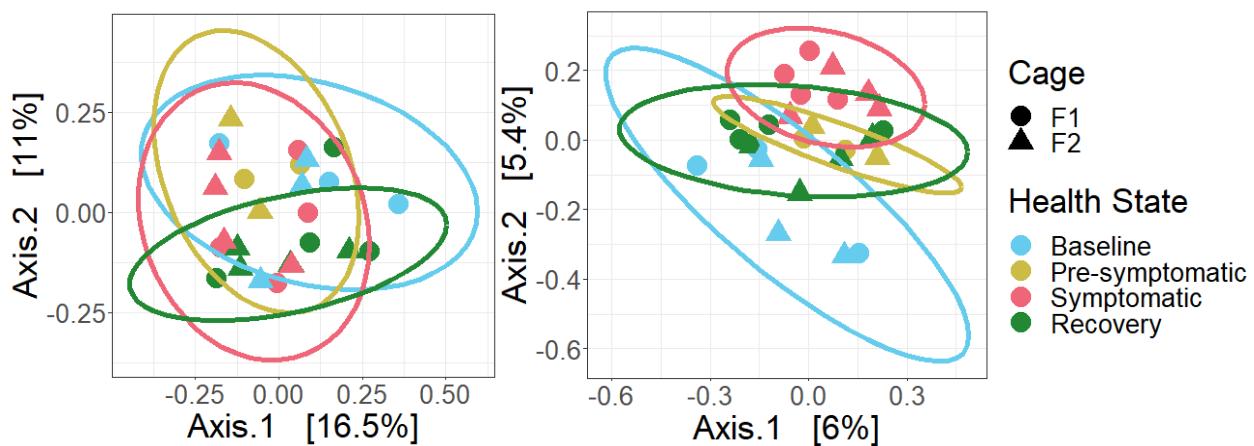


**Supplementary Figure 7.** Alpha diversity metrics during DSS colitis. Observed features, Shannon index, and Simpson evenness for data from all cages combined during the second DSS mouse experiment, for both the replicating ( $\text{EdU}^+$ ) cells and the whole community (Whole) of bacterial cells. BA = baseline, PS = pre-symptomatic, SY = symptomatic, RE = recovery.

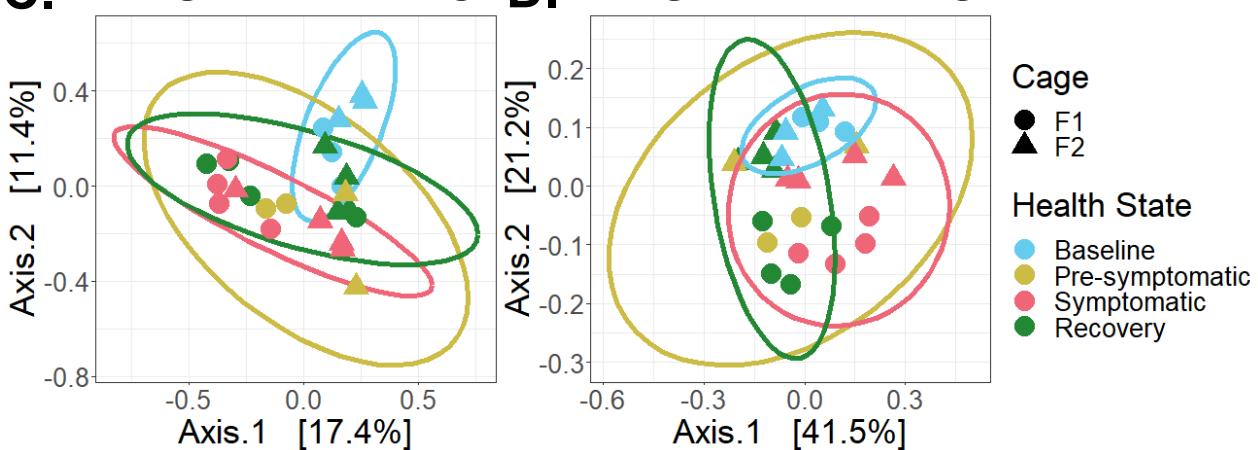


**Supplementary Figure 8.** Beta diversity of the replicating ( $EdU^+$ ) and whole community (Whole) of bacterial cells. (A-C) Beta diversity for the replicating bacterial cells, grouped by health state. (A) Weighted Unifrac distance (WU) (B) Unweighted Unifrac distance (UU) (C) Bray-Curtis dissimilarity (BC). (D-F) Beta diversity for the whole community of bacterial cells, grouped by health state. (D) Weighted Unifrac distance (WU) (E) Unweighted Unifrac distance (UU) (F) Bray-Curtis dissimilarity (BC).

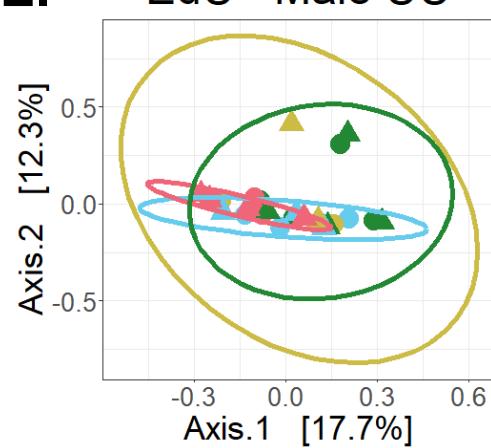
**A. EdU+ Female UU    B. EdU+ Female JC**



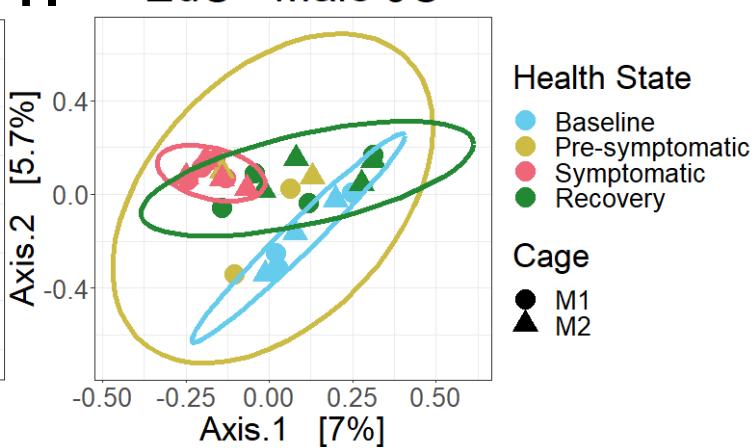
**C. EdU+ Female BC    D. EdU+ Female WU**

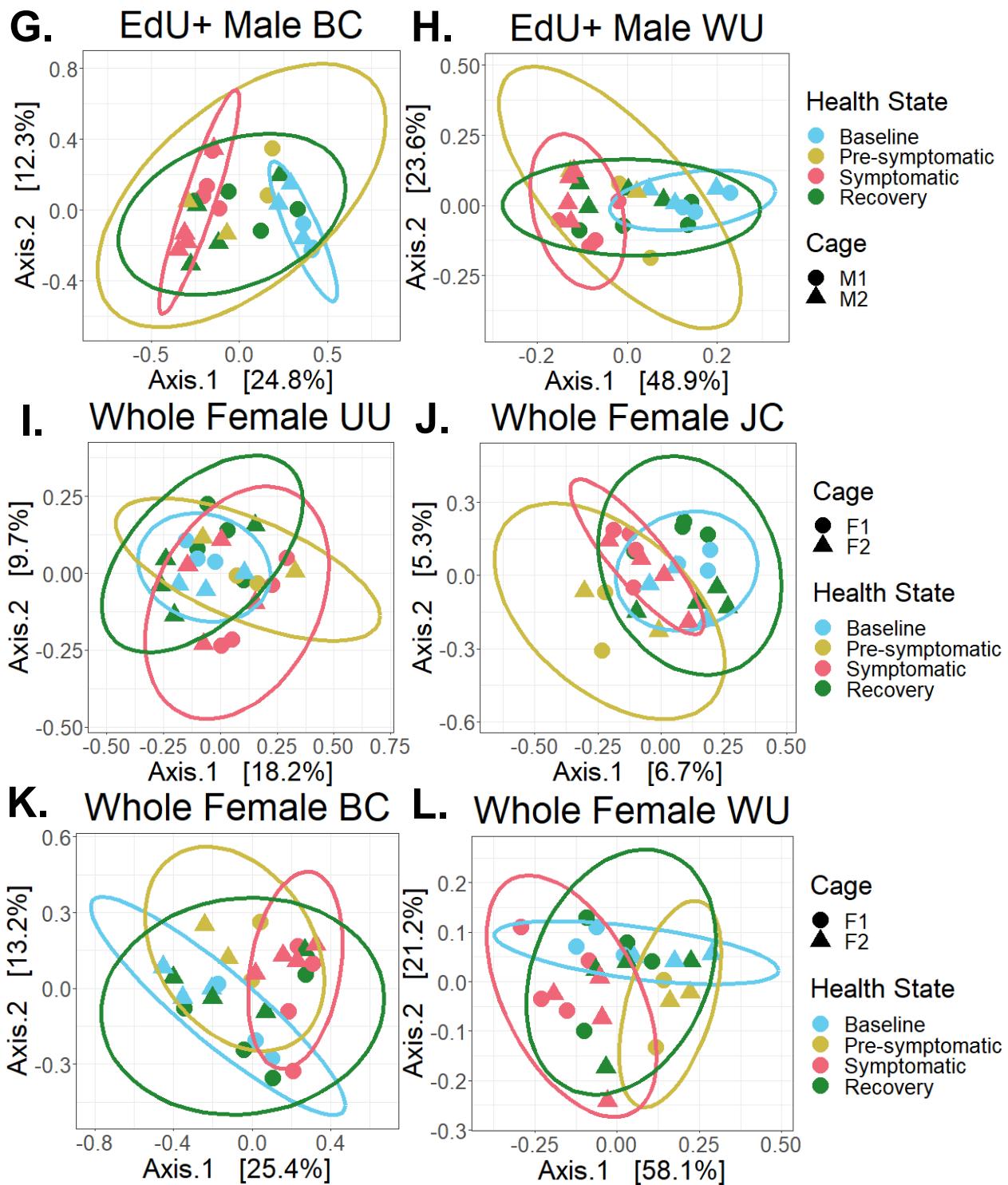


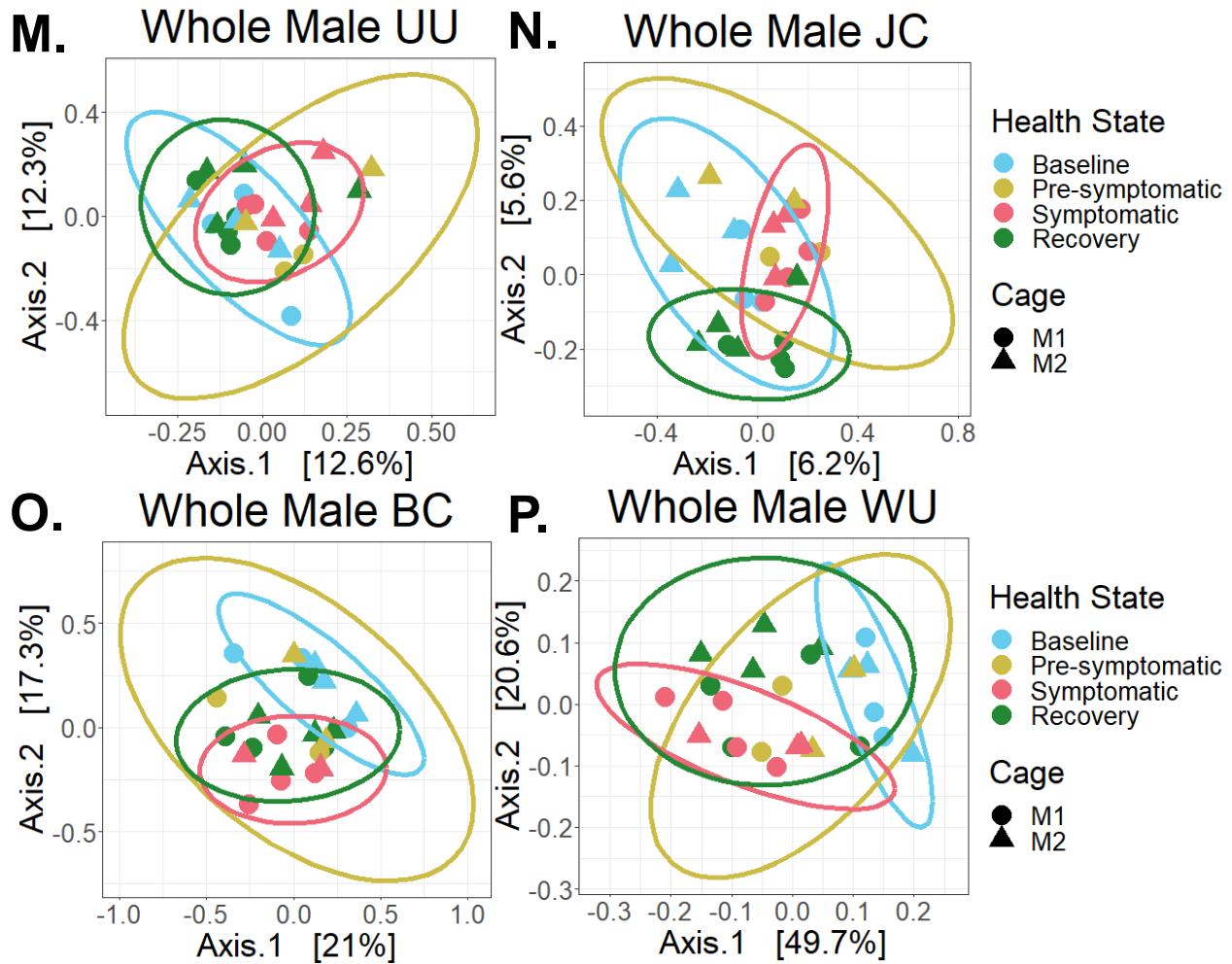
**E. EdU+ Male UU**



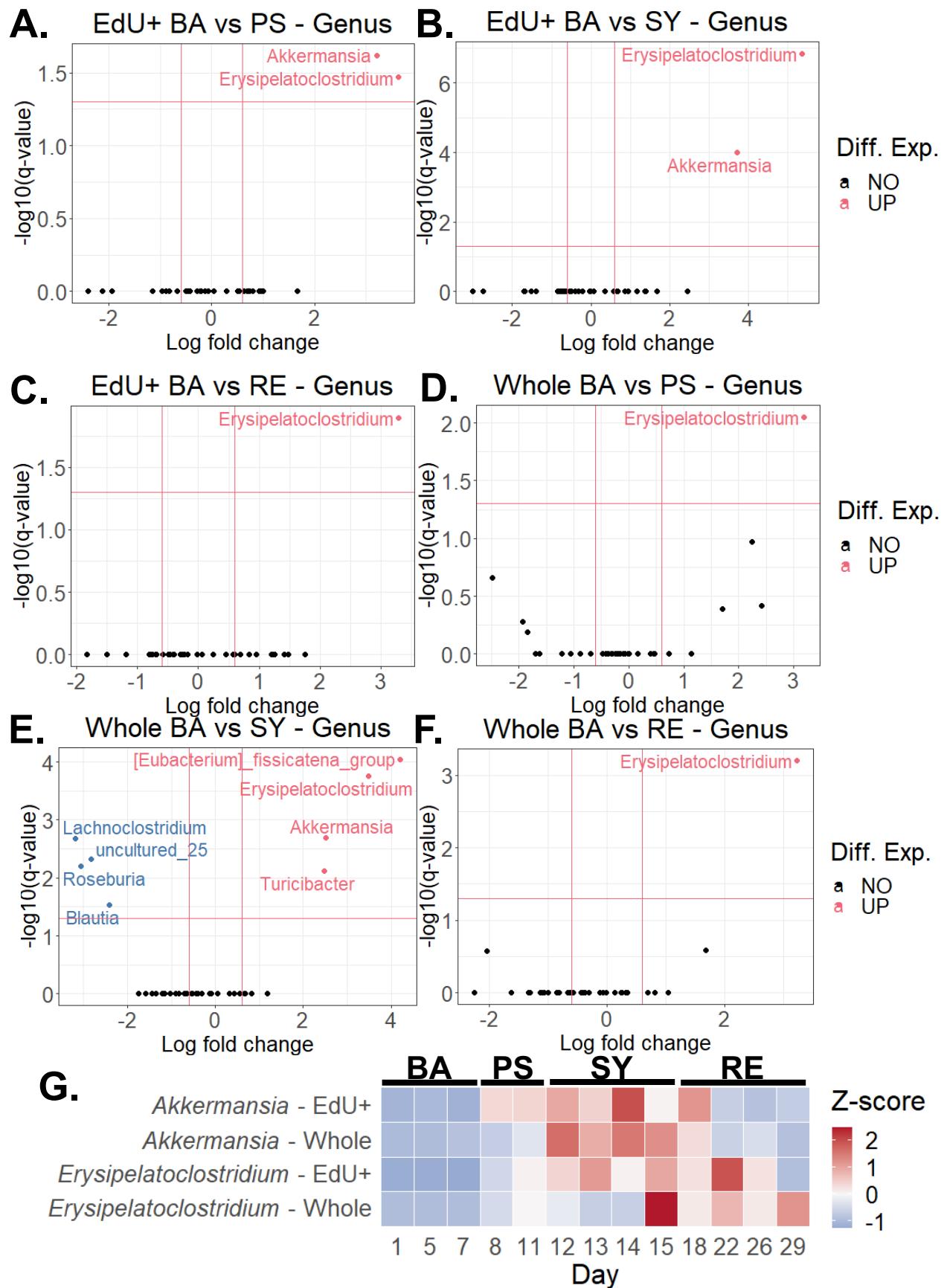
**F. EdU+ Male JC**



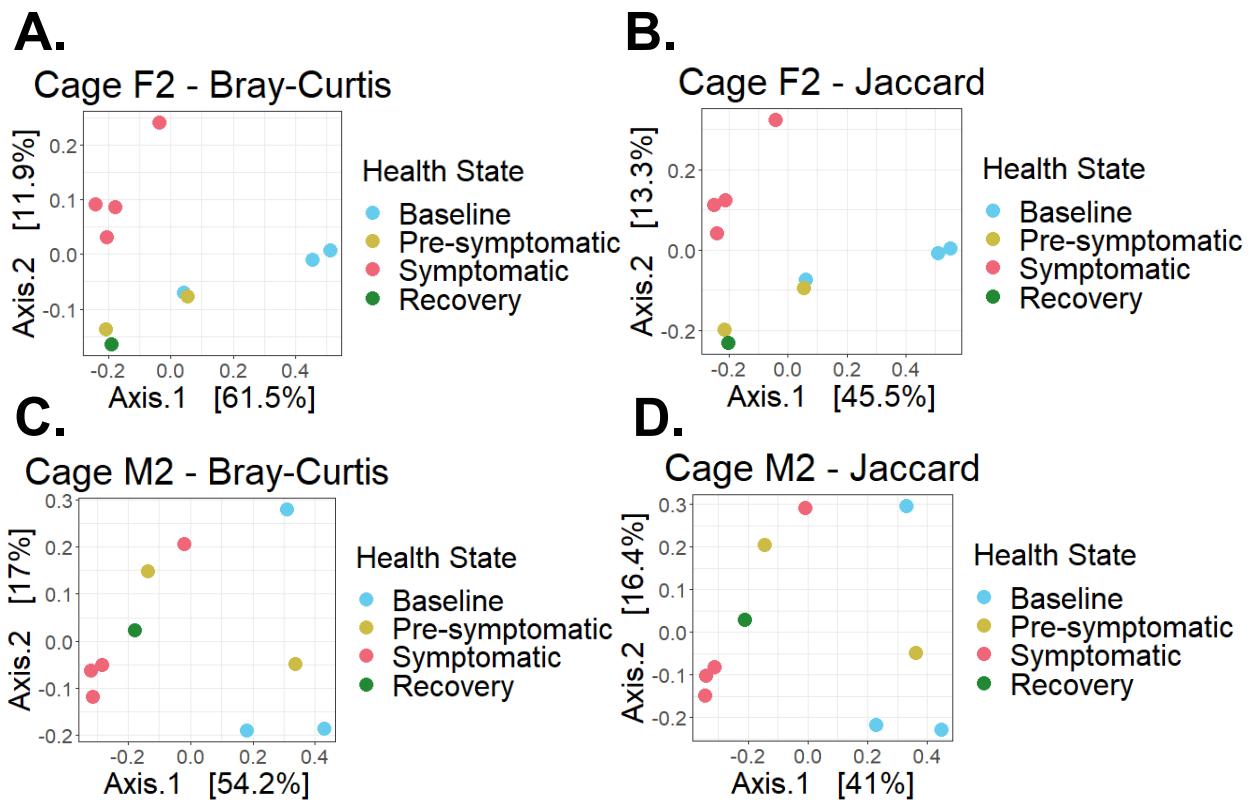




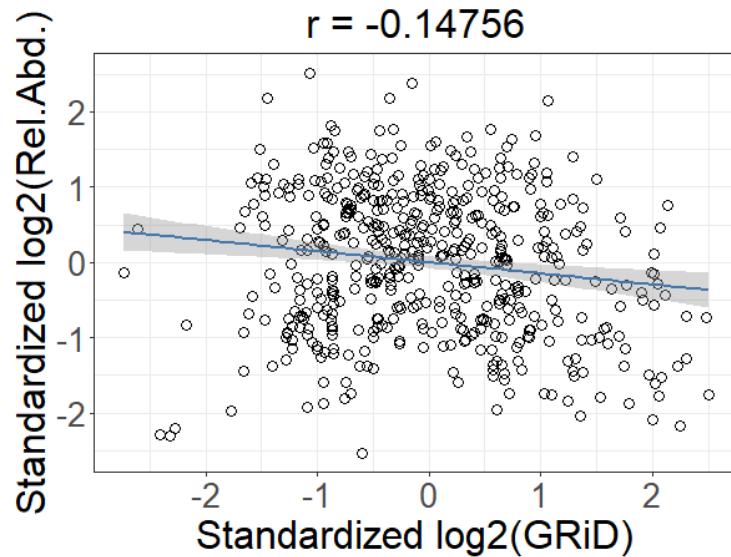
**Supplementary Figure 9.** Beta diversity statistics grouped per sex for each sorted fraction. (A-D) Beta diversity statistics for the replicating ( $EdU^+$ ) bacteria of both cages of Female mice. (A) Unweighted Unifrac distance (UU) (B) Jaccard index (JC) (C) Bray-Curtis dissimilarity (BC) (D) Weighted Unifrac distance (WU). (E-H) Beta diversity statistics for the replicating ( $EdU^+$ ) bacteria of both cages of Male mice. (E) Unweighted Unifrac distance (UU) (F) Jaccard index (JC) (G) Bray-Curtis dissimilarity (BC) (H) Weighted Unifrac distance (WU). (I-L) Beta diversity statistics for the whole community of bacteria of both cages of Female mice. (I) Unweighted Unifrac distance (UU) (J) Jaccard index (JC) (K) Bray-Curtis dissimilarity (BC) (L) Weighted Unifrac distance (WU). (M-P) Beta diversity statistics for the whole community of bacteria of both cages of Male mice. (M) Unweighted Unifrac distance (UU) (N) Jaccard index (JC) (O) Bray-Curtis dissimilarity (BC) (P) Weighted Unifrac distance (WU).



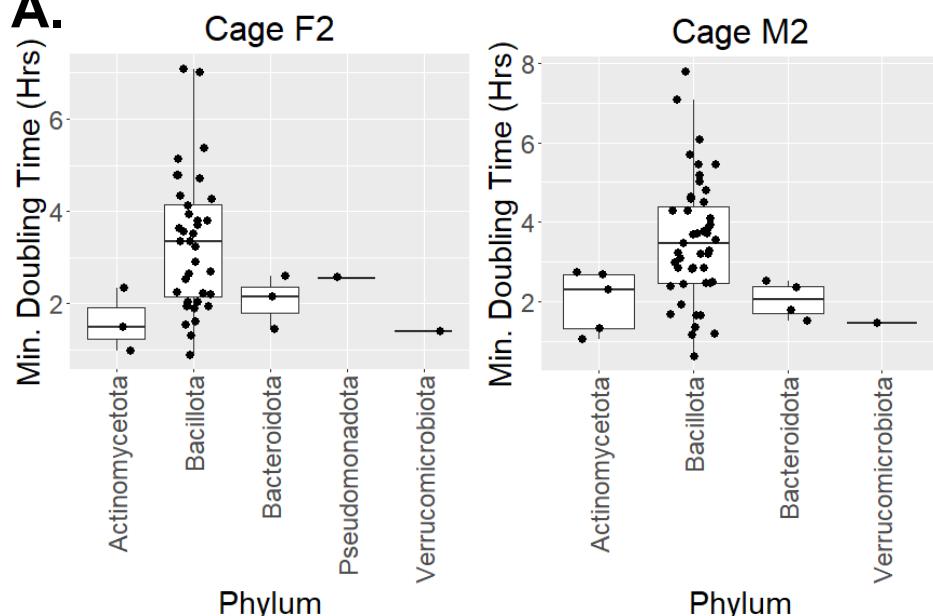
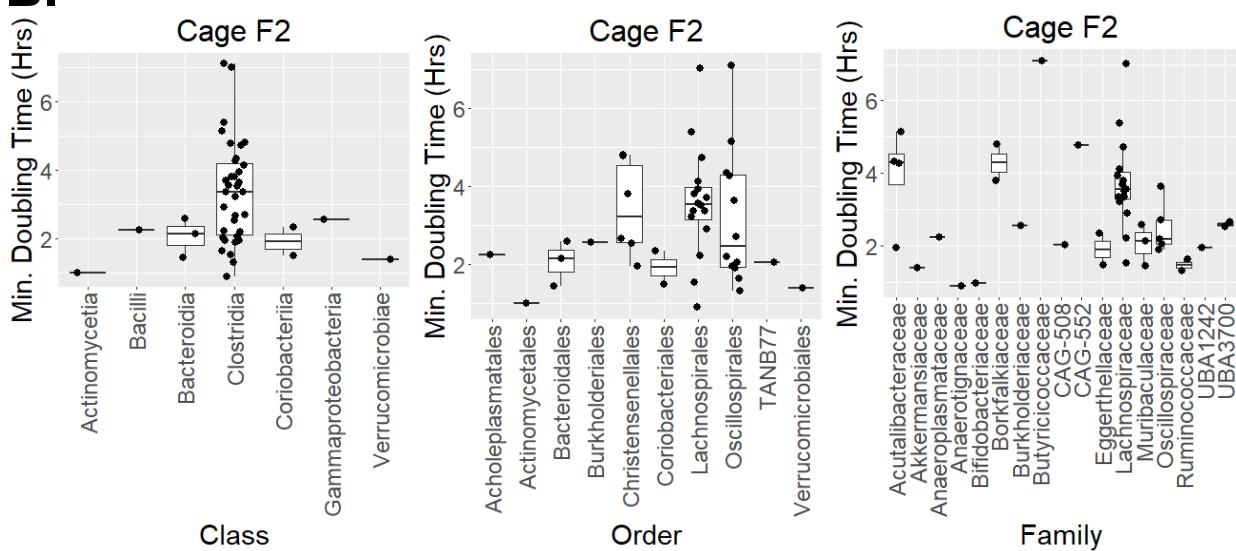
**Supplementary Figure 10.** Differentially abundant taxa for replicating ( $\text{EdU}^+$ ) and whole community of bacteria. (A-C) Differentially abundant taxa as compared to the baseline state for replicating ( $\text{EdU}^+$ ) cells in the second DSS experiment during the (A) pre-symptomatic (PS) (B) symptomatic (SY) and (C) recovery (RE) state. (D-F) Differentially abundant taxa as compared to the baseline state for the whole community of bacterial cells during the (D) pre-symptomatic (PS) (E) symptomatic (SY) (F) recovery (RE) state. Taxa with increased abundances during the health state of interest (pre-symptomatic, symptomatic, recovery) versus baseline are in red/pink on the upper right of each plot, whereas taxa with increased abundances in the baseline state as compared to the health state of interest are in blue, on the upper left of each plot. (G) Heat map of standardized abundances of Akkermansia and Erysipelatoclostridium in both the replicating ( $\text{EdU}^+$ ) and whole community (Whole) fractions during each health state. BA = baseline; PS = pre-symptomatic; SY = symptomatic; RE = recovery.

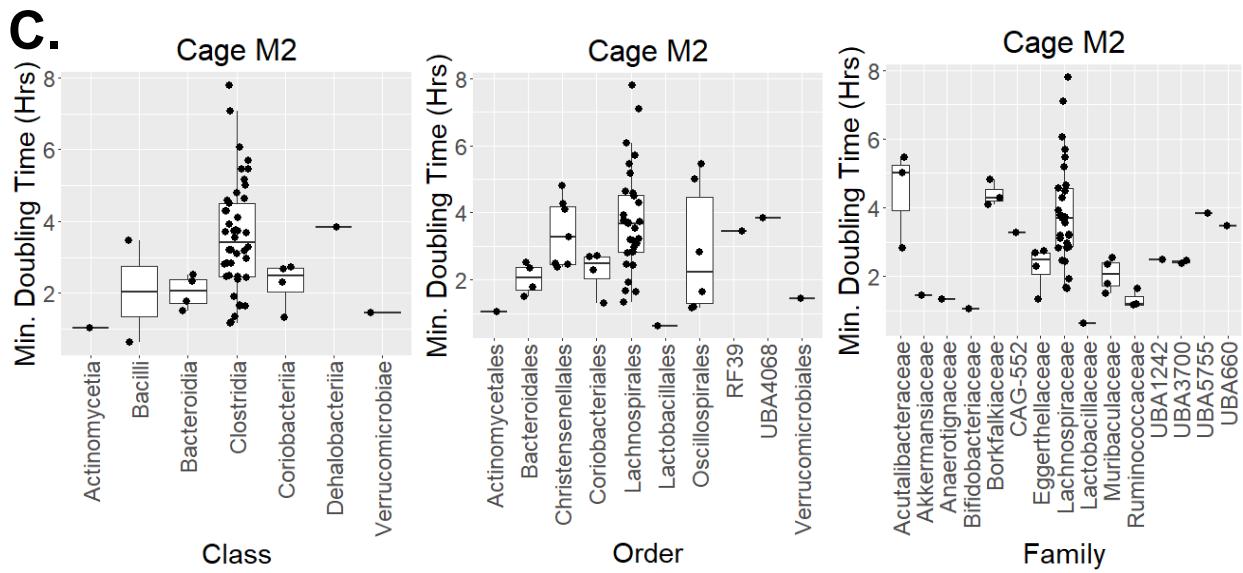


**Supplementary Figure 11.** Beta diversity of metagenome assembled genomes (MAGs). (A-B) Beta diversity for the community of MAGs from cage F2 for Bray-Curtis dissimilarity (A) and Jaccard index (B). (C-D) Beta diversity for the community of MAGs from cage M2 for Bray-Curtis dissimilarity (C) and Jaccard index (D).

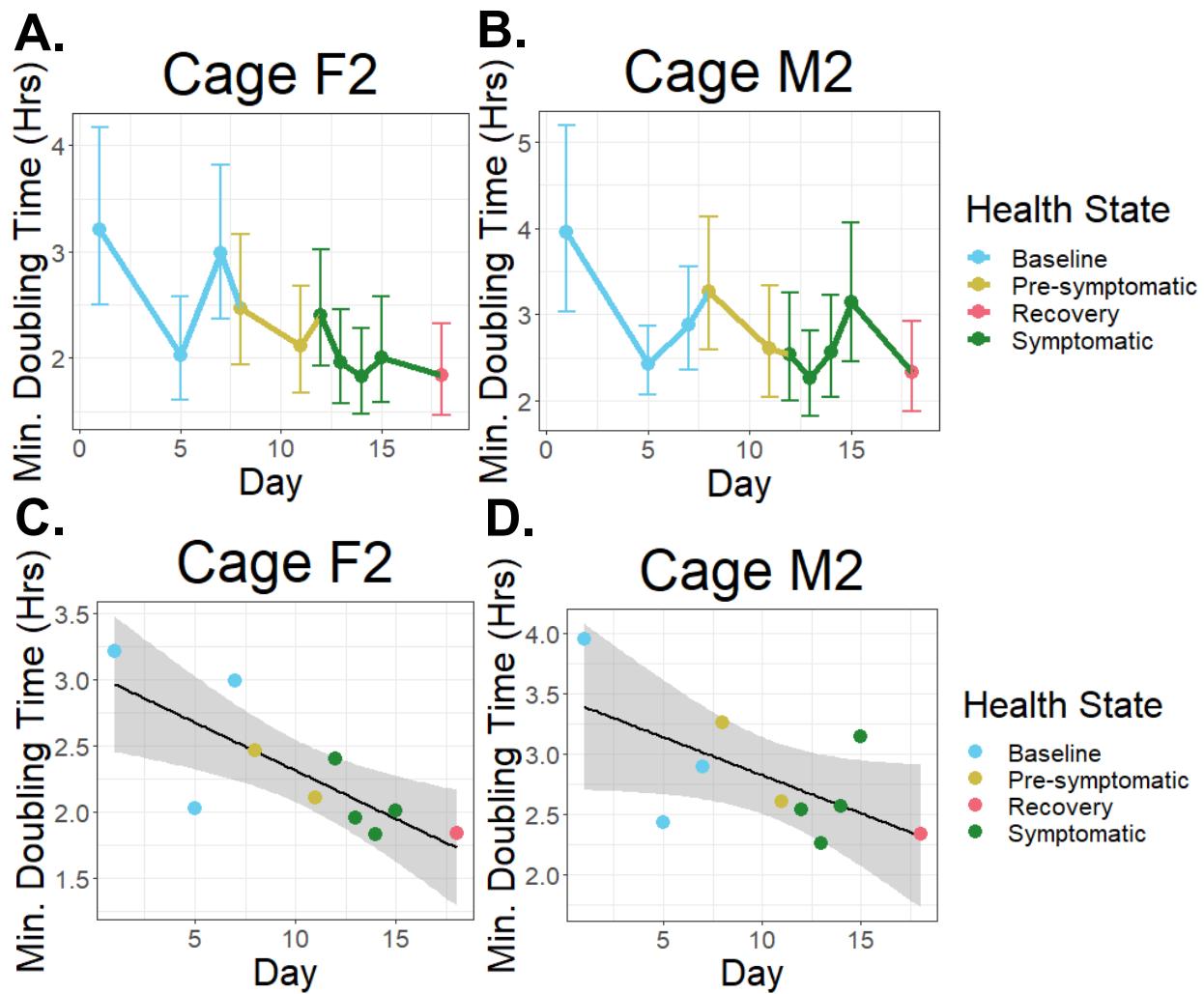


**Supplementary Figure 12.** Correlation between replication rates and relative abundances. Standardized, log<sub>2</sub>-transformed values of GRiD-calculated replication rates were correlated using Pearson correlation with standardized log<sub>2</sub>-transformed values of corresponding metagenome assembled genomes.

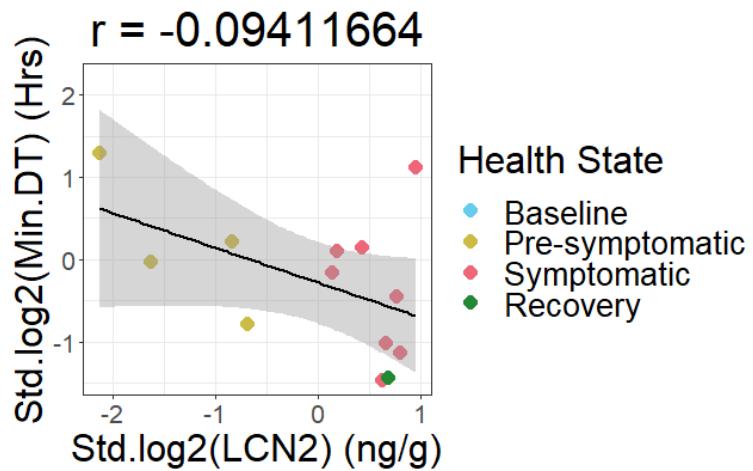
**A.****B.**



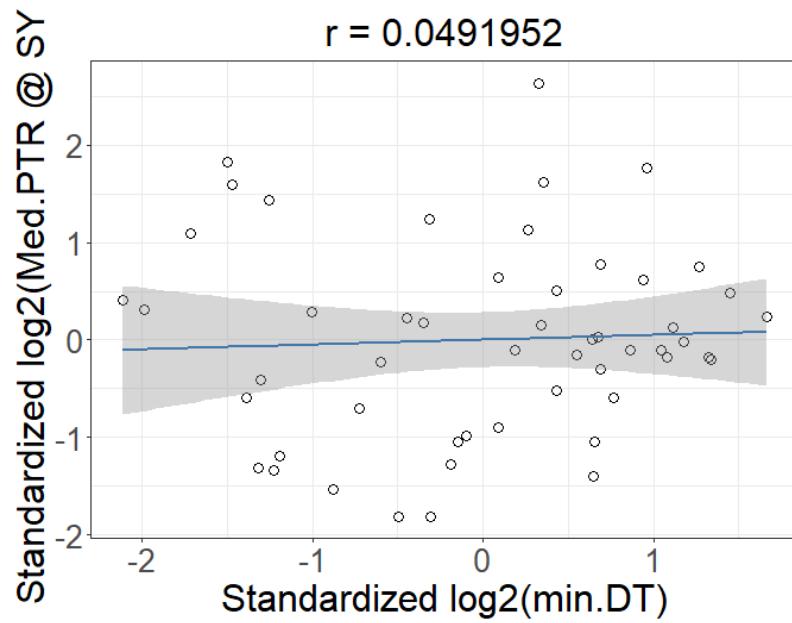
**Supplementary Figure 13.** Minimal doubling times for metagenome-assembled genomes (MAGs) at various taxonomic levels. (A) Estimated minimal doubling times for each MAG, as calculated by gRodon, at the phylum level for cages F2 (left) and M2 (right). (B) Estimated minimal doubling times for each MAG, as calculated by gRodon, at the class (left), order (middle), and family (right) level for cage F2. (C) Estimated minimal doubling times for each MAG, as calculated by gRodon, at the class (left), order (middle), and family (right) level for cage M2.



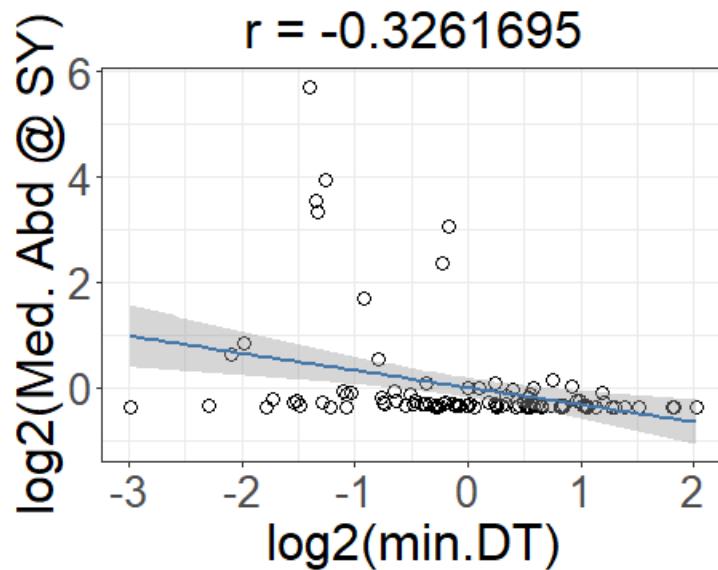
**Supplementary Figure 14.** Minimal doubling time for all bacterial reads from whole genome shotgun (WGS) sequencing data. Line plots (A-B) and linear regressions (C-D) of the estimated minimal doubling time for the whole bacterial community from the baseline state to the beginning of the recovery state for cage F2 (A, C) and cage M2 (B, D).



**Supplementary Figure 15.** Correlation between lipocalin-2 and minimal doubling times Linear mixed effects model for the standardized,  $\log_2$ -transformed values of lipocalin-2 (LCN2) versus minimal doubling time (DT) as calculated with gRodon. Random intercept effects included Day (time effect) and cage (host origin of bacteria). Fixed effects included levels of LCN2.



**Supplementary Figure 16.** Correlation between minimal doubling times and replication rates Pearson correlation between the standardized, log<sub>2</sub>-transformed estimations of minimum doubling time (calculated from gRodon) and median replication rate (calculated from GRiD) of all recoverable metagnome-assembled genomes (MAGs) during the symptomatic phase.



**Supplementary Figure 17.** Correlation between minimal doubling time and relative abundance Pearson correlation between the standardized, log2-transformed estimated minimal doubling time (calculated from gRodon) and standardized, log2-transformed median relative abundance during the symptomatic state.

<b>Score</b>	<b>Weight loss (%)</b>	<b>Blood in stool</b>	<b>Lipocalin-2 levels (ng/g)</b>
0	0-1	None	0-10
1	1-5	Mildly hemoccult positive	10-10 <sup>2</sup>
2	5-10	Hemoccult positive	10 <sup>2</sup> -10 <sup>3</sup>
3	10-15	-	10 <sup>3</sup> -10 <sup>4</sup>
4	>15	-	>10 <sup>4</sup>

**Supplementary Table 1.** Colitis scoring method. Scores for weight loss and blood in stool are based on those used by Kim JJ et al. (2012).<sup>14</sup> Lipocalin-2 levels are expressed as nanograms per gram of feces (ng/g).

Cage	Day									
	8	11	12	13	14	15	18	26	29	33
F1	0	0	1	4	5	4	2	2	0	3
F2	0	0	1	4	6	4	3	2	1	1
M1	0	0	4	5	7	8	4	3	3	3
M2	0	0	3	4	4	4	3	3	3	3

**Supplementary Table 2.** Colitis scores during first DSS experiment. Colitis scores for each cage of mice during the first DSS experiment, starting one day before DSS administration (day 8) and ending 21 days (3 weeks) after termination of DSS administration (day 33).

## Friedman test

Alpha diversity metric	Number of Samples	Friedman statistic	Degrees of Freedom	P-value
Observed Features	4	3.9	3	0.272
Shannon Index	4	8.1	3	0.044
Simpson Evenness	4	5.7	3	0.127

## Wilcoxon signed-rank test: Shannon Index

Health state (vs Baseline)	Number of Samples	Wilcoxon signed-rank statistic	Adjusted p-value
Pre-symptomatic	4	10	0.375
Symptomatic	4	10	0.375
Recovery	4	10	0.375

**Supplementary Table 3.** Alpha diversity metric statistics for first DSS mouse experiment. The Friedman test was conducted by comparing the median alpha diversity values of each cage per health state to the baseline state, to determine whether alpha diversity significantly changed from the baseline state. The post-hoc Wilcoxon signed-rank test was performed using default settings on the Shannon index to determine which health state was responsible for the significant difference.

i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.045841	0.938
Baseline vs Symptomatic	0.04198	<b>0.039</b>
Baseline vs Recovery	0.043321	<b>0.039</b>
Pre-symptomatic vs Symptomatic	0.047069	0.938
Pre-symptomatic vs Recovery	0.054856	0.4545
Symptomatic vs Recovery	0.035455	0.38

ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.02825	0.96
Baseline vs Symptomatic	0.041504	0.514
Baseline vs Recovery	0.057312	0.18
Pre-symptomatic vs Symptomatic	0.039094	0.9024
Pre-symptomatic vs Recovery	0.060693	0.514
Symptomatic vs Recovery	0.033323	0.576

iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.013401	0.91
Baseline vs Symptomatic	0.031468	0.824
Baseline vs Recovery	0.053339	0.786
Pre-symptomatic vs Symptomatic	0.019456	0.91
Pre-symptomatic vs Recovery	0.05361	0.824
Symptomatic vs Recovery	0.021468	0.91

iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.045931	0.775
Baseline vs Symptomatic	0.047178	0.142
Baseline vs Recovery	0.041644	0.142
Pre-symptomatic vs Symptomatic	0.045238	0.775
Pre-symptomatic vs Recovery	0.064268	0.2055
Symptomatic vs Recovery	0.045713	0.142

**Supplementary Table 4.** PERMANOVA for all cages during first DSS mouse experiment.

Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv) Green Q-values indicate statistically significant results. .

i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.121378	0.2184
Baseline vs Symptomatic	0.078724	0.114
Baseline vs Recovery	0.084679	<b>0.081</b>
Pre-symptomatic vs Symptomatic	0.123074	0.269
Pre-symptomatic vs Recovery	0.136845	<b>0.092</b>
Symptomatic vs Recovery	0.087587	<b>0.081</b>

ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.123265	0.3735
Baseline vs Symptomatic	0.068066	0.463
Baseline vs Recovery	0.081079	0.3735
Pre-symptomatic vs Symptomatic	0.111157	0.463
Pre-symptomatic vs Recovery	0.172005	0.3735
Symptomatic vs Recovery	0.118392	0.174

iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.098328	0.468
Baseline vs Symptomatic	0.073319	0.468
Baseline vs Recovery	0.062572	0.468
Pre-symptomatic vs Symptomatic	0.118831	0.468
Pre-symptomatic vs Recovery	0.216362	0.468
Symptomatic vs Recovery	0.101067	0.468

iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.116368	0.355
Baseline vs Symptomatic	0.082875	0.1212
Baseline vs Recovery	0.106668	<b>0.027</b>
Pre-symptomatic vs Symptomatic	0.152435	<b>0.066</b>
Pre-symptomatic vs Recovery	0.18919	<b>0.042</b>
Symptomatic vs Recovery	0.109524	<b>0.027</b>

**Supplementary Table 5.** PERMANOVA for all female mice during first DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv). Green Q-values indicate statistically significant results. Red Q-values indicate near statistically significant results (q >0.05 but <0.1)

i. Jaccard			ii. Bray-Curtis		
Pairs	R^2	Q-value	Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.121967	0.1764	Baseline vs Pre-symptomatic	0.128579	0.342
Baseline vs Symptomatic	0.091558	<b>0.036</b>	Baseline vs Symptomatic	0.132294	<b>0.039</b>
Baseline vs Recovery	0.094574	<b>0.012</b>	Baseline vs Recovery	0.116901	<b>0.033</b>
Pre-symptomatic vs Symptomatic	0.10514	0.67	Pre-symptomatic vs Symptomatic	0.091317	0.713
Pre-symptomatic vs Recovery	0.1712	<b>0.036</b>	Pre-symptomatic vs Recovery	0.246801	<b>0.039</b>
Symptomatic vs Recovery	0.114526	<b>0.015</b>	Symptomatic vs Recovery	0.189357	<b>0.033</b>

iii. Weighted Unifrac			iv. Unweighted Unifrac		
Pairs	R^2	Q-value	Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.132813	0.3672	Baseline vs Pre-symptomatic	0.112771	0.4164
Baseline vs Symptomatic	0.163692	0.092	Baseline vs Symptomatic	0.119806	<b>0.02</b>
Baseline vs Recovery	0.127476	0.126	Baseline vs Recovery	0.147942	<b>0.018</b>
Pre-symptomatic vs Symptomatic	0.041701	0.92	Pre-symptomatic vs Symptomatic	0.091906	0.749
Pre-symptomatic vs Recovery	0.416558	<b>0.063</b>	Pre-symptomatic vs Recovery	0.222486	<b>0.0315</b>
Symptomatic vs Recovery	0.291288	<b>0.06</b>	Symptomatic vs Recovery	0.152949	<b>0.02</b>

**Supplementary Table 6.** PERMANOVA for all male mice during first DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv). Green Q-values indicate statistically significant results. Red Q-values indicate near statistically significant results (q >0.05 but <0.1)

Cage	Day									
	8	11	12	13	14	15	18	26	29	33
F1	0	2	2	5	3	3	3	3	2	2
F2	1	2	4	4	4	3	3	3	2	2
M1	0	1	2	8	4	3	3	2	1	2
M2	0	2	4	8	3	4	NA	3	2	2

**Supplementary Table 7.** Colitis scores during second DSS experiment. Colitis scores for each cage of mice during the second DSS experiment, starting one day before DSS administration (day 8) and ending 21 days (3 weeks) after termination of DSS administration (day 33). The NA is because there was not enough stool from this cage at this time point to perform a lipocalin-2 test.

## Friedman test: EdU+ cells

Alpha diversity metric	Number of Samples	Friedman statistic	Degrees of Freedom	P-value
Observed Features	4	5.7	3	0.127
Shannon Index	4	7.5	3	0.0576
Simpson Evenness	4	6	3	0.112

## Friedman test: Whole community

Alpha diversity metric	Number of Samples	Friedman statistic	Degrees of Freedom	P-value
Observed Features	4	3.6	3	0.308
Shannon Index	4	4.8	3	0.187
Simpson Evenness	4	5.1	3	0.165

## Wilcoxon signed-rank test: Shannon index – EdU+ cells

Health state (vs Baseline)	Number of Samples	Wilcoxon signed-rank statistic	Adjusted p-value
Pre-symptomatic	4	10	0.375
Symptomatic	4	10	0.375
Recovery	4	10	0.375

**Supplementary Table 8.** Alpha diversity metric statistics for second DSS mouse experiment. Alpha diversity metric statistics for the second DSS mouse experiment, for both the replicating (EdU+) and whole community (Whole) of bacteria. The Friedman test was conducted by comparing the median alpha diversity values of each cage per health state and per sorted fraction to the baseline state, to determine whether alpha diversity significantly changed from baseline. The post-hoc Wilcoxon signed-rank test was performed using default settings on each alpha diversity metric (observed features, Shannon index, Simpson evenness) to determine which health state was responsible for the significant difference, where relevant.

### i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.051963	0.6396
Baseline vs Symptomatic	0.044917	<b>0.012</b>
Baseline vs Recovery	0.035873	0.705
Pre-symptomatic vs Symptomatic	0.052912	<b>0.012</b>
Pre-symptomatic vs Recovery	0.046254	0.177
Symptomatic vs Recovery	0.034857	0.156

### ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.05661	0.507
Baseline vs Symptomatic	0.055474	0.136
Baseline vs Recovery	0.032264	0.7224
Pre-symptomatic vs Symptomatic	0.082471	<b>0.078</b>
Pre-symptomatic vs Recovery	0.065121	0.136
Symptomatic vs Recovery	0.025727	0.734

### iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.025918	0.786
Baseline vs Symptomatic	0.054666	0.567
Baseline vs Recovery	0.028244	0.786
Pre-symptomatic vs Symptomatic	0.068003	0.567
Pre-symptomatic vs Recovery	0.026719	0.786
Symptomatic vs Recovery	0.020692	0.786

### iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.038486	0.964
Baseline vs Symptomatic	0.049249	0.672
Baseline vs Recovery	0.034419	0.951
Pre-symptomatic vs Symptomatic	0.038552	0.951
Pre-symptomatic vs Recovery	0.025083	0.964
Symptomatic vs Recovery	0.037809	0.708

**Supplementary Table 9.** PERMANOVA for replicating ( $EdU^+$ ) bacteria. PERMANOVA analyses for replicating ( $EdU^+$ ) bacterial cells from all cages combined during the second DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv). Green Q-values indicate statistically significant results. Red Q-values indicate near statistically significant results (q >0.05 but <0.1)

i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.052602	0.6885
Baseline vs Recovery	0.03725	0.6885
Baseline vs Symptomatic	0.039152	0.6885
Symptomatic vs Pre-symptomatic	0.043786	0.782
Symptomatic vs Recovery	0.031947	0.782
Recovery vs Pre-symptomatic	0.044272	0.6885

ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.044454	0.941
Baseline vs Recovery	0.043382	0.675
Baseline vs Symptomatic	0.021576	0.941
Symptomatic vs Pre-symptomatic	0.031444	0.941
Symptomatic vs Recovery	0.034494	0.788
Recovery vs Pre-symptomatic	0.050144	0.675

iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.049441	0.938
Baseline vs Recovery	0.012387	0.938
Baseline vs Symptomatic	0.020775	0.938
Symptomatic vs Pre-symptomatic	0.018218	0.938
Symptomatic vs Recovery	0.007684	0.938
Recovery vs Pre-symptomatic	0.036625	0.938

iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.050435	0.99
Baseline vs Recovery	0.04223	0.666
Baseline vs Symptomatic	0.046529	0.666
Symptomatic vs Pre-symptomatic	0.024843	0.99
Symptomatic vs Recovery	0.020302	0.99
Recovery vs Pre-symptomatic	0.030223	0.99

**Supplementary Table 10.** PERMANOVA for whole bacterial communityResults from PERMANOVA analysis for the whole community of bacterial cells from all cages combined during the second DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv).

### i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.110608	0.744
Baseline vs Symptomatic	0.080674	0.444
Baseline vs Recovery	0.083767	0.27
Pre-symptomatic vs Symptomatic	0.088671	0.7728
Pre-symptomatic vs Recovery	0.094208	0.444
Symptomatic vs Recovery	0.063064	0.895

### ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.12225	0.5745
Baseline vs Symptomatic	0.081631	0.5745
Baseline vs Recovery	0.115719	0.402
Pre-symptomatic vs Symptomatic	0.074158	0.708
Pre-symptomatic vs Recovery	0.091492	0.5745
Symptomatic vs Recovery	0.056301	0.708

### iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.140462	0.52
Baseline vs Symptomatic	0.106459	0.52
Baseline vs Recovery	0.107665	0.52
Pre-symptomatic vs Symptomatic	0.065437	0.8088
Pre-symptomatic vs Recovery	0.034348	0.874
Symptomatic vs Recovery	0.038775	0.8088

### iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.09008	0.973
Baseline vs Symptomatic	0.068093	0.973
Baseline vs Recovery	0.098711	0.357
Pre-symptomatic vs Symptomatic	0.099308	0.578
Pre-symptomatic vs Recovery	0.1299	0.348
Symptomatic vs Recovery	0.040854	0.973

**Supplementary Table 11.** PERMANOVA for replicating ( $EdU^+$ ) bacteria from female miceResults from PERMANOVA analysis for the replicating ( $EdU^+$ ) bacterial cells from cages of female mice during the second DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv).

i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.113364	0.501
Baseline vs Symptomatic	0.079195	0.501
Baseline vs Recovery	0.076731	0.528
Pre-symptomatic vs Symptomatic	0.095047	0.501
Pre-symptomatic vs Recovery	0.093682	0.501
Symptomatic vs Recovery	0.064991	0.679

ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.104188	0.9012
Baseline vs Symptomatic	0.110056	0.33
Baseline vs Recovery	0.126303	0.33
Pre-symptomatic vs Symptomatic	0.065456	0.9012
Pre-symptomatic vs Recovery	0.076705	0.9012
Symptomatic vs Recovery	0.04294	0.926

iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.04747	0.9
Baseline vs Symptomatic	0.111795	0.684
Baseline vs Recovery	0.10844	0.684
Pre-symptomatic vs Symptomatic	0.056778	0.9
Pre-symptomatic vs Recovery	0.033083	0.9
Symptomatic vs Recovery	0.018963	0.9

iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.093585	0.7716
Baseline vs Symptomatic	0.0891	0.7716
Baseline vs Recovery	0.073986	0.7716
Pre-symptomatic vs Symptomatic	0.085634	0.7716
Pre-symptomatic vs Recovery	0.090913	0.7716
Symptomatic vs Recovery	0.053469	0.777

**Supplementary Table 12.** PERMANOVA for whole community of bacteria from female miceResults from PERMANOVA analysis for the whole community of bacterial cells from cages of female mice during the second DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv).

i. Jaccard			ii. Bray-Curtis		
Pairs	R^2	Q-value	Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.108495	0.671	Baseline vs Pre-Symptomatic	0.138634	0.36
Baseline vs Symptomatic	0.077584	0.671	Baseline vs Symptomatic	0.097091	0.36
Baseline vs Recovery	0.077762	0.671	Baseline vs Recovery	0.12935	0.222
Pre-symptomatic vs Symptomatic	0.093686	0.671	Pre-symptomatic vs Symptomatic	0.073541	0.773
Pre-symptomatic vs Recovery	0.087462	0.671	Pre-symptomatic vs Recovery	0.082144	0.773
Symptomatic vs Recovery	0.065421	0.671	Symptomatic vs Recovery	0.046685	0.773

iii. Weighted Unifrac			iv. Unweighted Unifrac		
Pairs	R^2	Q-value	Pairs	R^2	Q-value
Baseline vs Pre-Symptomatic	0.106604	0.792	Baseline vs Pre-Symptomatic	0.086912	0.865
Baseline vs Symptomatic	0.153442	0.267	Baseline vs Symptomatic	0.074004	0.865
Baseline vs Recovery	0.239845	0.12	Baseline vs Recovery	0.057206	0.865
Pre-symptomatic vs Symptomatic	0.016009	0.973	Pre-symptomatic vs Symptomatic	0.099079	0.865
Pre-symptomatic vs Recovery	0.061917	0.792	Pre-symptomatic vs Recovery	0.081139	0.865
Symptomatic vs Recovery	0.04592	0.792	Symptomatic vs Recovery	0.054144	0.865

**Supplementary Table 13.** PERMANOVA for replicating ( $EdU^+$ ) bacteria from male miceResults from PERMANOVA analysis for the replicating ( $EdU^+$ ) bacterial cells from cages of male mice during the second DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv).

### i. Jaccard

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.106514	0.806
Baseline vs Symptomatic	0.086684	0.3
Baseline vs Recovery	0.084718	0.12
Pre-symptomatic vs Symptomatic	0.104199	0.28
Pre-symptomatic vs Recovery	0.101511	0.108
Symptomatic vs Recovery	0.072846	0.366

### ii. Bray-Curtis

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.121553	0.354
Baseline vs Symptomatic	0.099769	0.3315
Baseline vs Recovery	0.073155	0.485
Pre-symptomatic vs Symptomatic	0.124618	0.3315
Pre-symptomatic vs Recovery	0.149152	0.207
Symptomatic vs Recovery	0.136762	0.114

### iii. Weighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.158211	0.254
Baseline vs Symptomatic	0.10374	0.254
Baseline vs Recovery	0.097815	0.254
Pre-symptomatic vs Symptomatic	0.156481	0.254
Pre-symptomatic vs Recovery	0.358568	0.042
Symptomatic vs Recovery	0.217918	0.078

### iv. Unweighted Unifrac

Pairs	R^2	Q-value
Baseline vs Pre-symptomatic	0.109378	0.6816
Baseline vs Symptomatic	0.079092	0.6816
Baseline vs Recovery	0.097012	0.402
Pre-symptomatic vs Symptomatic	0.095173	0.6816
Pre-symptomatic vs Recovery	0.138001	0.066
Symptomatic vs Recovery	0.063894	0.684

**Supplementary Table 14.** PERMANOVA for whole bacterial community from male miceResults from PERMANOVA analysis for the whole community of bacterial cells from cages of male mice during the second DSS mouse experiment. Jaccard (i), Bray-Curtis (ii), Weighted Unifrac (iii), and Unweighted Unifrac (iv). Green Q-values indicate statistically significant results. Red Q-values indicate near statistically significant results (q >0.05 but <0.1)

Cage	% alignment	Total # of MAGs	# HQ	# MQ	# LQ	# unusable	# gRodon	# GRiD
F2	36.74%	60	18/60 (30%)	26/60 (43%)	12/60 (20%)	4/60 (7%)	44/60 (73%)	32/60 (53%)
M2	35.07%	68	22/68 (32%)	35/68 (52%)	7/68 (10%)	4/68 (6%)	57/68 (84%)	44/68 (65%)

**Supplementary Table 15.** Metagenome-assembled genomes (MAGs) statistics from second DSS experiment. Percent (%) alignment denotes the percent of all the DNA sequences from the experiment which were captured by assembling these bacterial genomes. HQ = high quality, MQ = medium quality, LQ = low quality, according to the MIMAGS definition of MAG quality (Bowers R.M. et al. 2017).<sup>148</sup> The quantity and percentage of the MAGs which could be used for gRodon (# gRodon) and GRiD (# GRiD) are additionally quantified.

Bin	Taxonomy	Day 1	Day 5	Day 7	Day 8	Day 11	Day 12	Day 13	Day 14	Day 15	Day 18
bin.1	<i>Scatovivens</i>	1.24	1.18	1.11	1.11	1.21	1.41	1.25	1.19	1.3	1.16
bin.109	<i>Lachnospiraceae</i> CAG-95 sp910587295	1.48	1.44	1.22	1.39	1.4	1.36	1.25	1.55	1.28	1.56
bin.114	<i>Acutalibacter</i> sp009917525	1.13	1.46	1.48	1	1.53	1.26	1.19	1.31	1.41	1.43
bin.118	<i>Sporofaciens</i> sp910585725	1.34	1.28	1.33	1.3	1.34	1.31	1.29	1.39	1.28	1.33
bin.122	<i>Duncaniella</i> sp910589485	1.13	1.03	1.06	1.14	1.02	1.04	1.23	1.11	1.05	1.07
bin.127	<i>Coproplasma</i> sp910578765	1.18	1.45	1.21	1.14	1.28	1.3	1.33	1.3	1.37	1.45
bin.14	<i>Lachnospiraceae</i> UBA3282 sp910575775	1.24	1.38	1.29	1.26	1	2.38	1.68	1.55	1.7	1
bin.145	<i>Lachnospiraceace</i> 1XD8-76 sp	1.19	1.33	1.18	1.15	1.25	1.22	1.19	1.25	1.18	1.38
bin.32	<i>Lachnospiraceace</i> COE1 sp009774345	1.31	1.44	1.41	1	1	1	1.63	1	1.2	1
bin.35	<i>Sporofaciens</i> sp910574885	1.36	1.61	1.42	1.4	1.57	1.4	1.26	1.45	1.52	1.37
bin.38	<i>Acetatifactor</i> sp003612485	1.09	1.08	1.04	1.14	1.22	1.24	1.24	1.28	1.35	1.29
bin.45	<i>Eggerthellaceae</i> D16-63 sp910588095	2.02	1.53	2.22	1.65	1.66	1.73	1.46	1.44	1.76	1.51
bin.5	<i>Acutalibacter</i> sp009936035	2.01	1.53	1.44	1.72	1.77	1.86	1.77	1.55	1.69	1.42
bin.52	<i>Adlercreutzia muris</i>	2.15	1.74	2.39	1.78	1.8	1.97	1.57	1.6	1.69	1.65
bin.55	<i>Duncaniella</i> sp910576785	1.12	1.06	1.07	1.11	1	1	1	1	1	1
bin.7	<i>Acutalibacter</i> sp910587995	1.35	1	1	1.3	1.45	1.68	1.69	1.22	1	1.42
bin.71	<i>Gallimonas</i> sp910585595	1	2.8	1.46	2.18	1.49	1.43	1.4	1.8	1.54	1.32
bin.8	<i>Lawsonibacter</i> sp910588635	1.24	1.41	1.38	1.18	1.52	1.53	1.17	1.41	1.32	1.55
bin.9	UBA3282 sp009774585	1.07	1.38	1.24	1.24	1.28	1.22	1.22	1.2	1.27	1.4
bin.94	<i>Muribaculaceae</i> CAG-485 sp002362485	1.19	1.11	1.18	1.06	1.08	1.12	1.15	1.15	1.09	1.1
maxbin.006_sub	<i>Akkermansia muciniphila</i>	1.18	1.19	1.24	1.29	1.18	1.26	1.22	1.14	1.19	1.22
maxbin.016_sub	<i>Bifidobacterium globosum</i>	1.42	1.46	1.45	1.27	1.42	1.4	1.41	1.39	1.43	1.45

**Supplementary Table 16.** GRiD replication rates – cage F2. Replication rate values from GRiD for all recoverable metagenome-assembled genomes (MAGs) at all measured time points from cage F2

Bin	Taxonomy	Day 1	Day 5	Day 7	Day 8	Day 11	Day 12	Day 13	Day 14	Day 15	Day 18
bin.101	<i>Acutalibacter</i> sp910587995	1.03	1.1	1.11	1.09	1.1	1.11	1.13	1.17	1.22	1.08
bin.110	<i>Lachnospiraceae</i> MD308 sp010206225	1.03	1.34	1.36	1.24	1	1.25	1.65	1.49	1.19	1.95
bin.126_sub	<i>Duncaniella</i> sp910589485	1.16	1.19	1.07	1.14	1.02	1.09	1.04	1.09	1.06	1.05
bin.129	<i>Acutalibacter</i> sp009936035	1.31	1.38	1.27	1.24	1.23	1.8	1.21	1.58	1.38	1.36
bin.13	<i>Choladocola</i> sp009774135	1.39	1.29	1.41	1.41	1.31	1.27	1.38	1.25	1.31	1.3
bin.135	<i>Muribaculaceae</i> CAG-485 sp002362485	1.13	1.21	1.16	1.09	1.09	1.12	1.07	1.13	1.13	1.08
bin.137	<i>Paramuribaculum</i> sp910579675	1.03	1.09	1.06	1.03	1.05	1.05	1.03	1.04	1.06	1.04
bin.140	<i>Lachnospiraceae</i> 1XD8-76 sp	1.14	1	1.06	1	1.18	1	1	1.34	1.13	1.22
bin.152	<i>Kineothrix</i> sp000403275	1.23	1.61	1.8	1.33	1.29	1.36	2	1.33	1.25	1.33
bin.155	<i>Lachnospiraceae</i> RGIG7193 sp910586125	1.12	1.05	1.08	1	1.03	1.06	1.19	1.25	1.18	1.13
bin.166	<i>Acetatifactor</i> sp910584235	1.3	1.39	1.55	1.21	1.33	1.58	1.88	1.56	1.41	1.3
bin.20	<i>Lachnospiraceae</i> UBA3282 sp910579735	1.23	1	1	1	1.16	1	1	1.34	1.25	1.09
bin.21	<i>Lachnospiraceae</i> VSOB01 sp910587635	1.17	1.14	1.28	1.08	1.13	1.3	1.35	1.26	1.15	1.25
bin.25	<i>Lachnospiraceae</i> UBA3282 sp009774585	1	1	1	1	1.34	1	1.6	1.38	1.32	1.19
bin.3	<i>Akkermansia muciniphila</i>	1.2	1.08	1.13	1.37	1.27	1.23	1.17	1.31	1.25	1.24
bin.30	<i>Acetatifactor</i> sp910579755	1.28	1.16	1.32	1.37	1.13	1.3	1.3	1.34	1.21	1
bin.35_sub	<i>Adlercreutzia muris</i>	1.85	1.97	1.69	1.86	1.74	1.74	1.68	1.75	1.81	1.74
bin.40	<i>Ruminiclostridium</i> sp910585505	1	2.06	1.57	1.52	1.48	1.5	1.62	1.62	1.48	1.42
bin.46	<i>Caccovivens</i> sp	1.23	1	1.31	1.25	1.15	1.16	1.13	1.04	1	1.57
bin.56_sub	<i>Eggerthellaceae</i> D16-63 sp910588095	1.49	1.6	1.39	1.5	1.39	1.42	1.28	1.29	1.52	1.51
bin.60	<i>Lachnospiraceae</i> UBA3282 sp910577735	1	1	1.36	1.13	1.26	1.33	1.24	1.71	1.18	1.16

bin.71	<i>Lachnospiraceae</i> UBA3282 sp009774655	1.26	1.33	1.33	1.24	1.23	1.46	1.45	1.57	1.29	1.49
bin.76	<i>Lachnospiraceae</i> COE1 sp009774375	1.16	1	1	1	1.38	1	1.3	1.39	1.3	1.31
bin.79	<i>Lachnospiraceae</i> CAG-95 sp910587295	1.27	1	1.29	1.33	1.32	1.27	1.3	1.37	1.35	1.3
bin.81	<i>Lachnospiraceae</i> An181 sp910585545	1	1	1.18	1.46	1.4	1.3	1.34	1.54	1.42	1.31
bin.82	<i>Anaerotignum</i> sp910576545	1.3	1.39	1.47	1.25	1.48	1.8	1.77	1.6	1.45	1.48
bin.89	<i>Acutalibacter muris</i>	1.35	1.34	1.33	1.26	1.27	1.62	1.44	1.32	1.4	2.3
bin.95	<i>Lachnospiraceae</i> CAG-95 sp910579425	1.62	2.16	1.75	1.49	2	1.86	2.11	2.09	1.55	1.7
maxbin.003	<i>Muribaculaceae</i> CAG-873 sp910577315	1	1.12	1.06	1	1	1	1.02	1	1	1
maxbin.010	<i>Bifidobacterium</i> <i>globosum</i>	1.74	1.37	1.49	1.5	1.41	1.32	1.51	1.35	1.42	1.35

**Supplementary Table 17.** GRiD replication rates – cage M2. Replication rate values from GRiD for all recoverable metagenome-assembled genomes (MAGs) at all measured time points from cage M2

Taxonomic Level	Classification	# Genomes	Median DT (hrs)	MAD DT (hrs)	Range DT (min-max) (hrs)
Phylum	Actinomycetota	3	1.479889	0.7392811	0.9812507 - 2.331694
	Bacteroidota	3	2.138517	0.6635747	1.4394080 - 2.586092
	Bacillota	36	3.348365	1.6693594	0.8907596 - 7.091410
	Pseudomonadota	1	2.559108	0	NA
	Verrucomicrobiota	1	1.390831	0	NA
Class	Actinomycetia	1	0.9812507	0	NA
	Bacilli	1	2.2365960	0	NA
	Bacteroidia	3	2.1385170	0.6635747	1.4394080 - 2.5860920
	Clostridia	35	3.3489730	1.6913115	0.8907596 - 7.0914100
	Coriobacteria	2	1.9057915	0.6314430	1.4798890 - 2.3316940
	Gammaproteobacteria	1	2.5591080	0	NA
	Verrucomicrobiae	1	1.3908310	0	NA
Family	<i>Acutalibacteraceae</i>	4	4.2957880	0.64629944	1.9423370 - 5.1388040
	<i>Akkermansiaceae</i>	1	1.3908310	0	NA
	<i>Anaeroplasmataceae</i>	1	2.2365960	0	NA
	<i>Anaerotignaceae</i>	1	0.8907596	0	NA
	<i>Bifidobacteriaceae</i>	1	0.9812507	0	NA
	<i>Borkfalkiaceae</i>	2	4.2903810	0.74010651	3.7911860 - 4.7895760
	<i>Burkholderiaceae</i>	1	2.5591080	0	NA
	<i>Butyricicoccaceae</i>	1	7.0914100	0	NA
	CAG-508	1	2.0313190	0	NA
	CAG-552	1	4.7833250	0	NA
	<i>Eggerthellaceae</i>	2	1.9057915	0.63144305	1.4798890 - 2.3316940
	<i>Lachnospiraceae</i>	15	3.5469460	0.56908563	1.5265180 - 7.0079730

<i>Muribaculaceae</i>	3	2.1385170	0.66357469	1.4394080 - 2.5860920
<i>Oscillospiraceae</i>	5	2.1885110	0.44335819	1.8894700 - 3.6329120
<i>Ruminococcaceae</i>	2	1.4592180	0.23618263	1.2999150 - 1.6185210
UBA1242	1	1.9398740	0	NA
UBA3700	2	2.5918305	0.08896712	2.5318230 - 2.6518380

**Supplementary Table 18.** gRodon minimal doubling times – cage F2. Statistics on metagenome-assembled genomes (MAGs) with calculated minimal doubling times for cage F2. Number of metagenome-assembled genomes (MAGs) (# Genomes) at a certain taxonomic level, median doubling time (DT) and median absolute deviation (MAD) of minimal DTs calculated by gRodon at that taxonomic level, and range of minimal DT values at that taxonomic level.

Taxonomic Level	Classification	# Genomes	Median DT (hrs)	MAD DT (hrs)	Range DT (min-max) (hrs)
Phylum	Actinomycetota	5	2.293357	0.6353208	1.0420970 - 2.721875
	Bacteroidota	4	2.059424	0.5533160	1.4997510 - 2.526055
	Bacillota	47	3.462887	1.4758512	0.6271748 - 7.791964
	Verrucomicrobiota	1	1.448462	0	NA
Class	Actinomycetia	1	1.042097	0	NA
	Bacilli	2	2.045031	2.1021135	0.6271748 - 3.462887
	Bacteroidia	4	2.059424	0.5533160	1.4997510 - 2.526055
	Clostridia	44	3.407229	1.3954365	1.1502340 - 7.791964
	Coriobacteria	4	2.485785	0.3176604	1.3169100 - 2.721875
	Dehalobacteriia	1	3.842034	0	NA
	Verrucomicrobiae	1	1.448462	0	NA
Family	<i>Acutalibacteraceae</i>	3	5.0057120	0.66772746	2.8320540 - 5.4560880
	<i>Akkermansiaceae</i>	1	1.4484620	0	NA
	<i>Anaerotignaceae</i>	1	1.3373510	0	NA
	<i>Bifidobacteriaceae</i>	1	1.0420970	0	NA
	<i>Borkfalkiaceae</i>	3	4.2780510	0.27305341	4.0938790 - 4.8033180
	CAG-552	1	3.2732290	0	NA
	<i>Eggerthellaceae</i>	4	2.4857850	0.31766039	1.3169100 - 2.7218750
	<i>Lachnospiraceae</i>	30	3.6981240	1.27655122	1.6382450 - 7.7919640
	<i>Lactobacillaceae</i>	1	0.6271748	0	NA
	<i>Muribaculaceae</i>	4	2.0594245	0.55331596	1.4997510 - 2.5260550
	<i>Ruminococcaceae</i>	3	1.1852620	0.05193251	1.1502340 - 1.6437540

	UBA1242	1	2.4768930	0	NA
	UBA3700	2	2.4242430	0.06404239	2.3810470 - 2.4674390
	UBA5755	1	3.8420340	0	NA
	UBA660	1	3.4628870	0	NA

**Supplementary Table 19.** gRodon minimal doubling times – cage M2. Statistics on metagenome-assembled genomes (MAGs) with calculated minimal doubling times for cage M2. Number of metagenome-assembled genomes (MAGs) (# Genomes) at a certain taxonomic level, median doubling time (DT) and median absolute deviation (MAD) of minimal DTs calculated by gRodon at that taxonomic level, and range of minimal DT values at that taxonomic level.

## Random Effects

Groups	Name	Variance	Std.Dev
Day	(Intercept)	0.16693	0.4086
Cage	(Intercept)	0.12583	0.3547
Residual		0.06365	0.2523

## Fixed Effects

Term	Estimate	Std.Err	Df	T-value	P-value
(Intercept)	2.9154	0.3594	3.2704	8.112	0.00283
Pre-symptomatic	-0.3044	0.4070	6	-0.748	0.48279
Symptomatic	-0.5774	0.3405	6	-1.696	0.14087
Recovery	-0.8277	0.5148	6	-1.608	0.15899

**Supplementary Table 20.** Linear regression statistics –Figure 3.5E. Statistics on the random effects and fixed effects for the linear regression performed in Figure 3.5E

## Random Effects

Groups	Name	Variance	Std.Dev
Day	(Intercept)	0.04209	0.2052
Cage	(Intercept)	0.66695	0.8167
Residual		0.22713	0.4766

## Fixed Effects

Term	Estimate	Std.Err	Df	T-value	P-value
(Intercept)	-0.2399	0.5977	1.0333	-0.401	0.7553
LCN2	-0.3637	0.1610	4.9130	-2.260	0.0743

**Supplementary Table 21.** Linear regression statistics – Supplementary Figure 15. Statistics on the random effects and fixed effects for the linear regression performed in Supplementary Figure 15.