

## *Supplementary Materials*

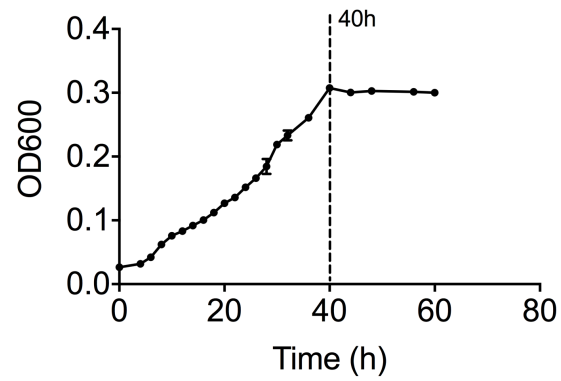
### Supplementary tables and Figures

**Supplementary Table S1. Sequences of primers used in research**

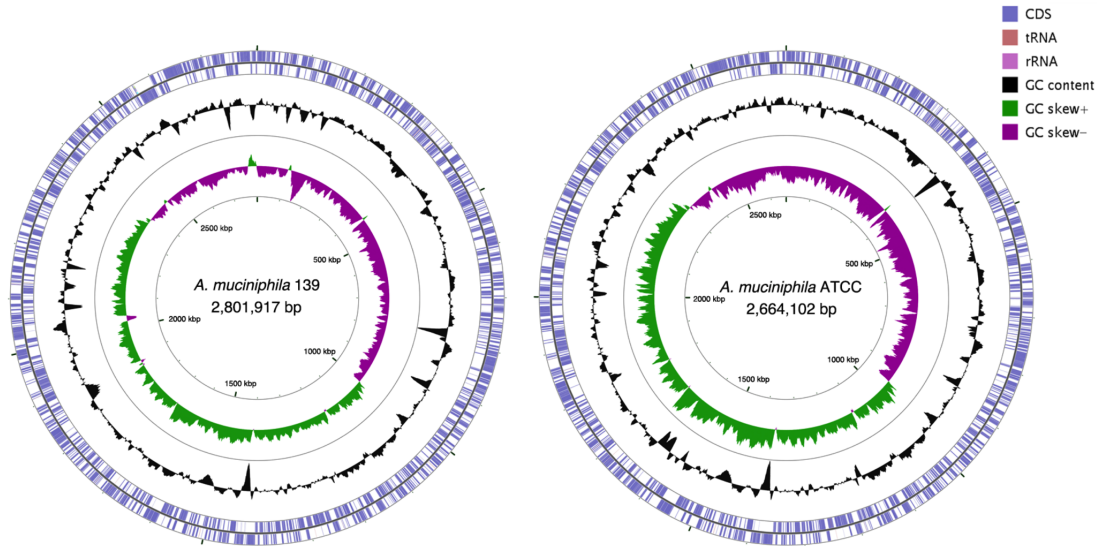
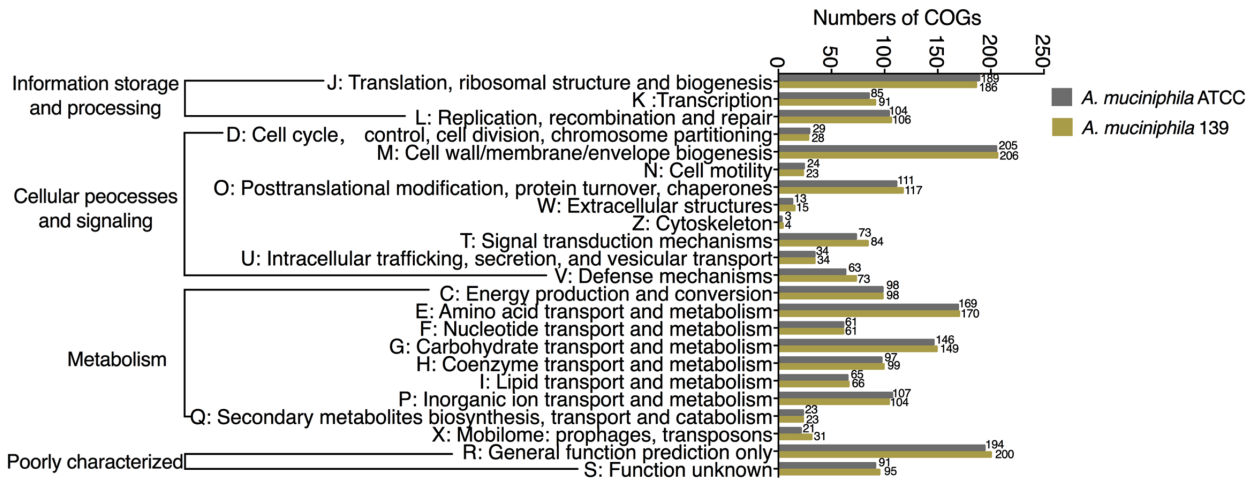
Name	Sequences
<i>IL-6</i>	F: 5' -TAGTCCTTCCTACCCCAATTTCC- 3' R: 5' -TTGGTCCTTAGCCACTCCTTC- 3'
<i>IL-1<math>\beta</math></i>	F: 5' -TCCATGAGCTTTGTACAAGGA- 3' R: 5' -AGCCCATACTTTAGGAAGACA- 3'
<i>TNF-<math>\alpha</math></i>	F: 5' -GTCCCCAAAGGGATGAGAAGTT- 3' R: 5' -GTCCCCAAAGGGATGAGAAGTT- 3'
<i>IFN-<math>\gamma</math></i>	F: 5' -GCCACGGCACAGTCATTGA- 3' R: 5' -TGCTGATGGCCTGATTGTCTT- 3'
<i>IL-22</i>	F: 5' -GTCAACCGCACCTTTATGCT- 3' R: 5' -GAACAGTTTCTCCCCGATGA- 3'
<i>GPR43</i>	F: 5' -CTTGATCCTCACGGCCTACAT- 3' R: 5' -CCAGGGTCAGATTAAGCAGGAG- 3'
<i>MUC2</i>	F: 5' -GCTGACGAGTGGTTGGTGAATG- 3' R: 5' -GATGAGGTGGCAGACAGGAGAC- 3'
<i>Occludin</i>	F: 5' -ATGTCCGGCCGATGCTCTC- 3' R: 5' -TTTGGCTGCTCTTGGGTCTGTAT- 3'
<i>Cldn3</i>	F: 5' -TCATCGGCAGCAGCATCATCAC- 3' R: 5' -ACGATGGTGATCTTGGCCTTGG- 3'
<i><math>\beta</math>-actin</i>	F: 5' -CCTTCTTGGGTATGGAATCCTGTG- 3' R: 5' -CAGCACTGTGTTGGCATAGAGG- 3'

**Supplementary Table S2. The genomic features of *A. muciniphila* 139 and *A. muciniphila* ATCC**

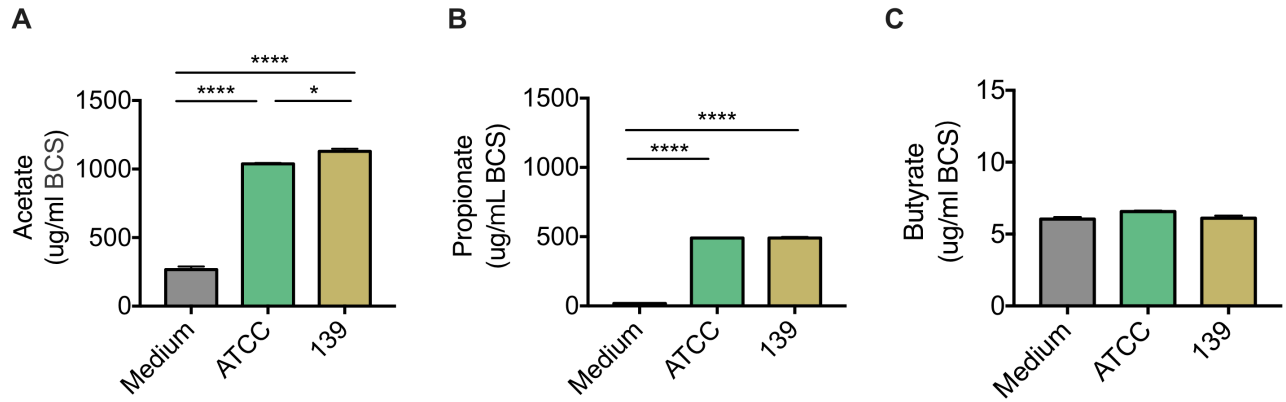
Feature	<i>A. muciniphila</i> ATCC	<i>A. muciniphila</i> 139
Genome size (bp)	2,664,100 bp	2,801,917 bp
G+C content	55.74%	55.80%
Number of tRNA genes	54	56
Number of 5S rRNA genes	3	3
Number of 16S rRNA genes	3	3
Number of 23S rRNA genes	3	3
Number of Coding Sequences	2182	2342
Protein-coding genes with assigned COG	2005 (91.89%)	2063 (88.09%)



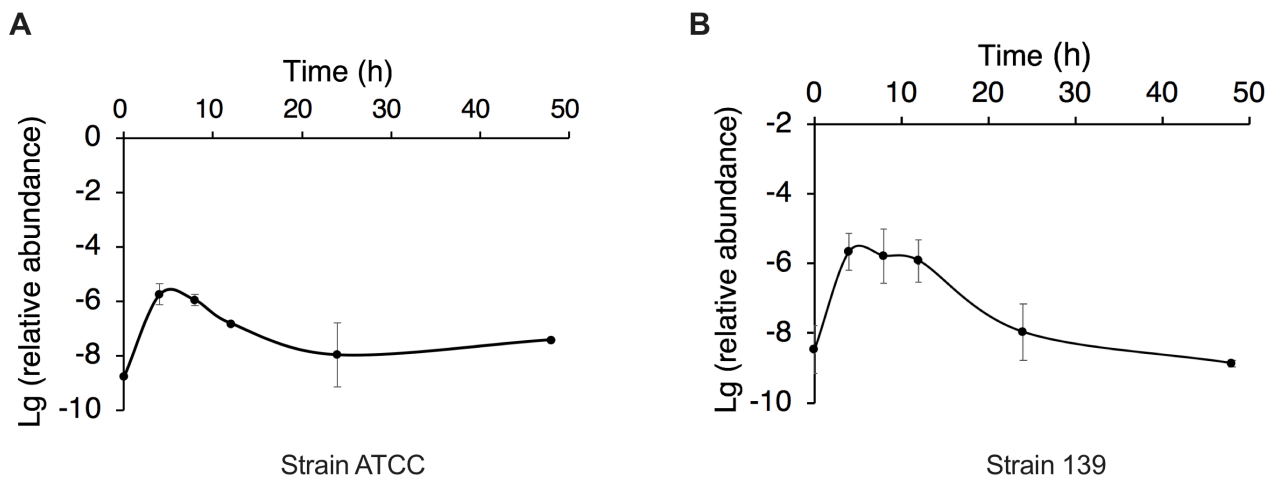
**Supplementary Figure S1. The growth curve of *A. muciniphila* 139 in synthetic medium.** Data are shown as mean  $\pm$  s.e.m,  $n = 3$  for each time point. The time for strain 139 growing to stationary phase are also labeled on the plot.

**A****B****Supplementary Figure S2. Visualization of genomic features of two strains of *A. muciniphila*.**

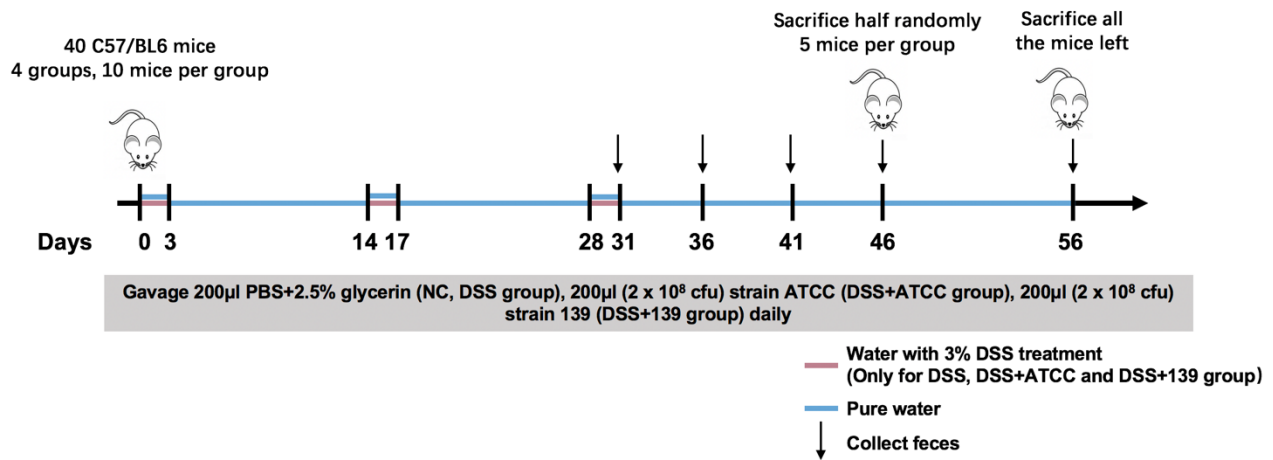
(A) Genome atlas of the two strains of *A. muciniphila*. From inner to outer: circle 1. GC skew  $(G - C) / (G + C)$ , circle 2. mean centered GC content, circle 3. tRNAs, rRNAs and CDS (reverse and forward strand). (B) Functional categories in the clusters of orthologous groups (COGs) analysis of *A. muciniphila* strain ATCC and 139.



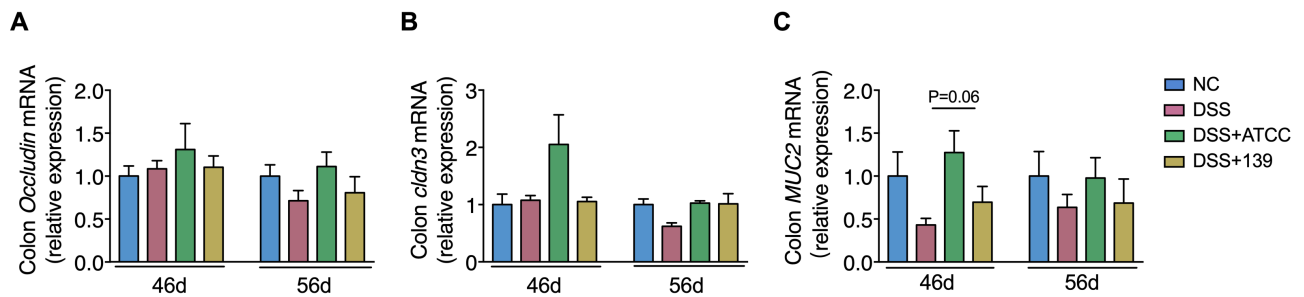
**Supplementary Figure S3. Both *A. muciniphila* strains produced acetate and propionate in vitro.** The content of acetate (A), propionate (B) and butyrate (C) in 200µl BCS of two strains. Data are shown as mean  $\pm$  s.e.m.  $n = 3$  for each group. Values of each group were calculated by one-way analysis of variance (ANOVA) followed by Tukey's post hoc test. \*  $P < 0.05$ , \*\*\*\*  $P < 0.0001$ .



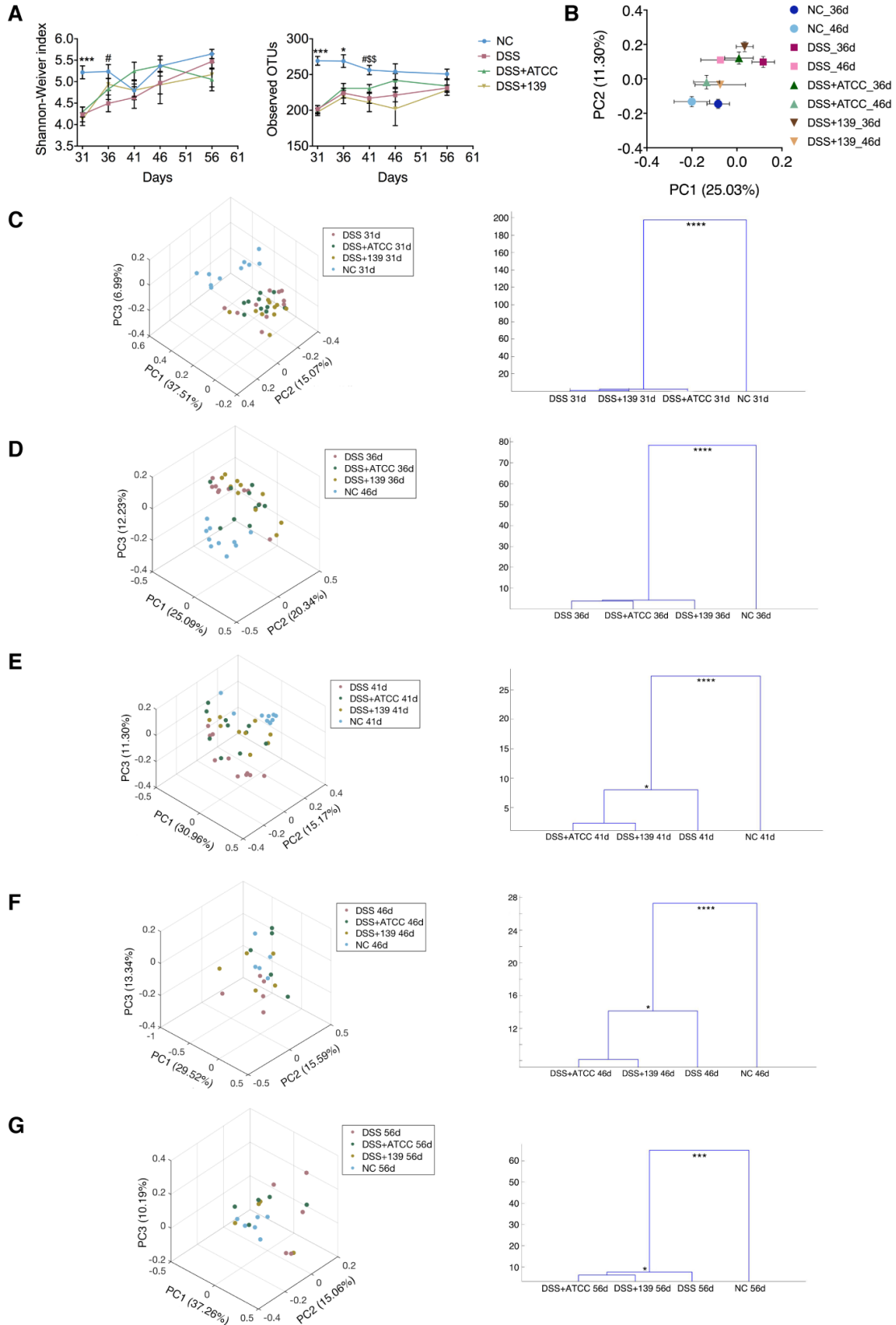
**Supplementary Figure S4. Change of relative abundance of fecal *A. muciniphila* after gavaging two strains.** (A) Lg (relative abundance) of *A. muciniphila* after gavaging strain ATCC, (B) Lg (relative abundance) of *A. muciniphila* after gavaging strain 139. Relative abundance means (copies of *A. muciniphila*) / (copies of total bacteria). All the data are shown as mean  $\pm$  s.e.m.  $n = 3$  for each group.



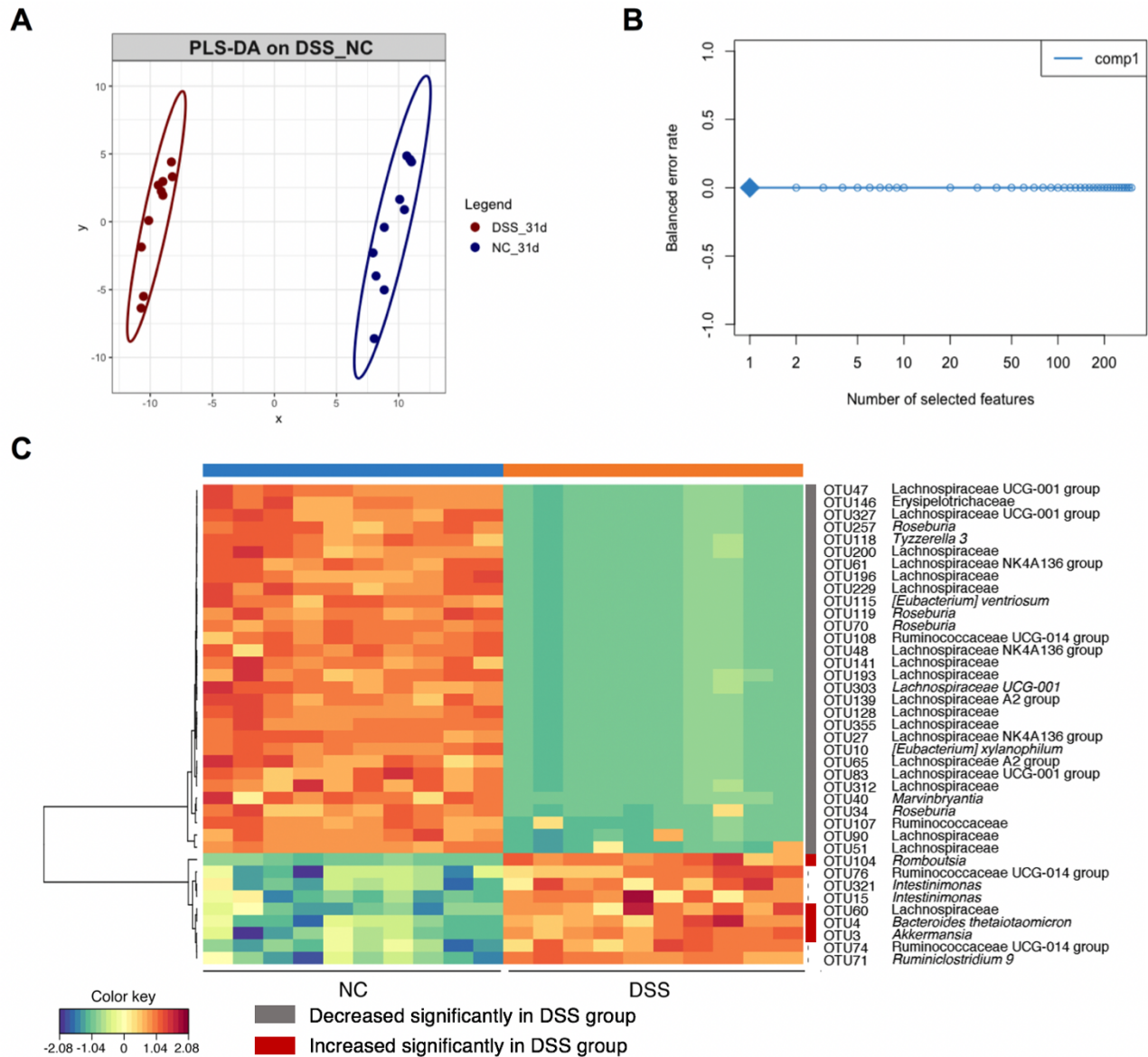
**Supplementary Figure S5. Animal experiment design.** 40 SPF mice were divided into 4 groups averagely, three groups of mice were treated with 3% DSS to induce chronic colitis, the other one group was healthy control group (NC).



**Supplementary Figure S6. *A. muciniphila* ATCC showed tendency to strength the gut permeability of mice.** mRNA expression of (A) *Occludin*, (B) *cldn3* and (C) *MUC2*. All the data are shown as mean ± s.e.m. n = 5 for each group. Values of each group were calculated by one-way analysis of variance (ANOVA) followed by Tukey's post hoc test.



**Supplementary Figure S7. Both *A. muciniphila* strains changed the diversity and structure of gut microbiota.** (A) Shannon index and observed OTUs in gut microbiota of mice. Data are shown as mean  $\pm$  s.e.m. Values of each group were calculated by one-way analysis of variance (ANOVA) followed by Tukey's post hoc test. \*\*\* $P < 0.001$  compared to all three groups treated with DSS, \* $P < 0.05$  compared to all three groups treated with DSS, #  $P < 0.05$  compared to DSS group, \$\$  $P < 0.01$  compared to DSS+139 group. (B) Bray-Curtis PCoA plot of Day 36 and 46 based on OTU abundance. (C-G) PCoA plot and MANOVA test of gut microbiota of mice based on the Bray-Curtis distance at each time point (Day 31, 36, 41, 46, 56).  $n=10$  for each group before 46d time point,  $n=5$  for each group from 46d time point.



**Supplementary Figure S8. 39 OTUs contributed to the form of chronic colitis of mice.** sPLS-DA model was used to pick up the OTUs responded to the DSS treatment after the establishment of chronic colitis mice model (Day 31). (A) PLS-DA plot of gut microbiota of mice in NC and DSS group. (B) Error rate of the sPLS-DA model. (C) Heat map of 39 OTUs at Day 31.