

### Supplemental Material

**Supplemental Table S1.** Primer sequences used for Real-time PCR analysis, *A. muciniphila* quantification and 16S rRNA.

Gene	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
Gapdh	TGGTGAAGCAGGCATCTGAG	TGCTGTTGAAGTCGCAGGAG
β-actin	GGAGAGAAGGAAACCAAAGG	AGGGAAGCCAGTCATACCAG
ZO-1	ACCCGAAACTGATGCTGTGGATAG	AAATGGCCGGCAGAACTTGTGTA
Ocludin	GGAGGACTGGTCAGGAAATA	CGTCGTCTAGTTCTGCCTGT
MUC2	GAAGCCAGATCCCGAAACCA	GAATCGGTAGACATGCCGT
TLR2	ACCAAGATCCAGAACAGAGCCA	CATCACCGGTAGAAAACAA
TLR4	CACCAGGAAGCTTGAATCCCT	GGAATGTCATCAGGGACTTG
TLR5	GCAGGATCATGGCATGTCAAC	ATCTGGGTGAGGTTACAGCCT
MYD88	CCGCCTATCGCTGTTCTGA	GCCAGGCATCCAACAAACTG
NF-κB	CTGGGCACCAGTTCGATGG	TGACAGCATAAGGCACACACT

Quantification.	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
<i>Akkermansia muciniphila</i>	CAGCACGTGAAGGTGGGGAC	CCTTGCAGGTTGGCTTCAGAT

Lung 16S rRNA primer	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
Amplification primer	AGAGTTGATCCTGGCTCAG	GNTACCTTGTACGACTT
16S rRNA V3V4	CCTAYGGGRBGCASCAG	GGACTACNNGGTATCTAAT

Feces 16S rRNA primer	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
16S rRNA V3V4	TACGGRAGCAGAG	AAGGTATCTAATCCT

**Supplemental Table S2.** List of antibodies and ELISA kit we used

Antibody name	Catalog number	Manufacturer
<b>Anti-Myeloperoxidase antibody</b>	ab208670	Abcam, Cambridge, UK
<b>Anti-Ly6g antibody</b>	ab238132	Abcam
<b>F4/80 Rabbit mAb</b>	70076S	Cell Signaling Technology, MA, USA
<b>Anti-ZO1 tight junction protein antibody</b>	ab221547	Abcam
<b>Anti-Occludin antibody</b>	ab216327	Abcam

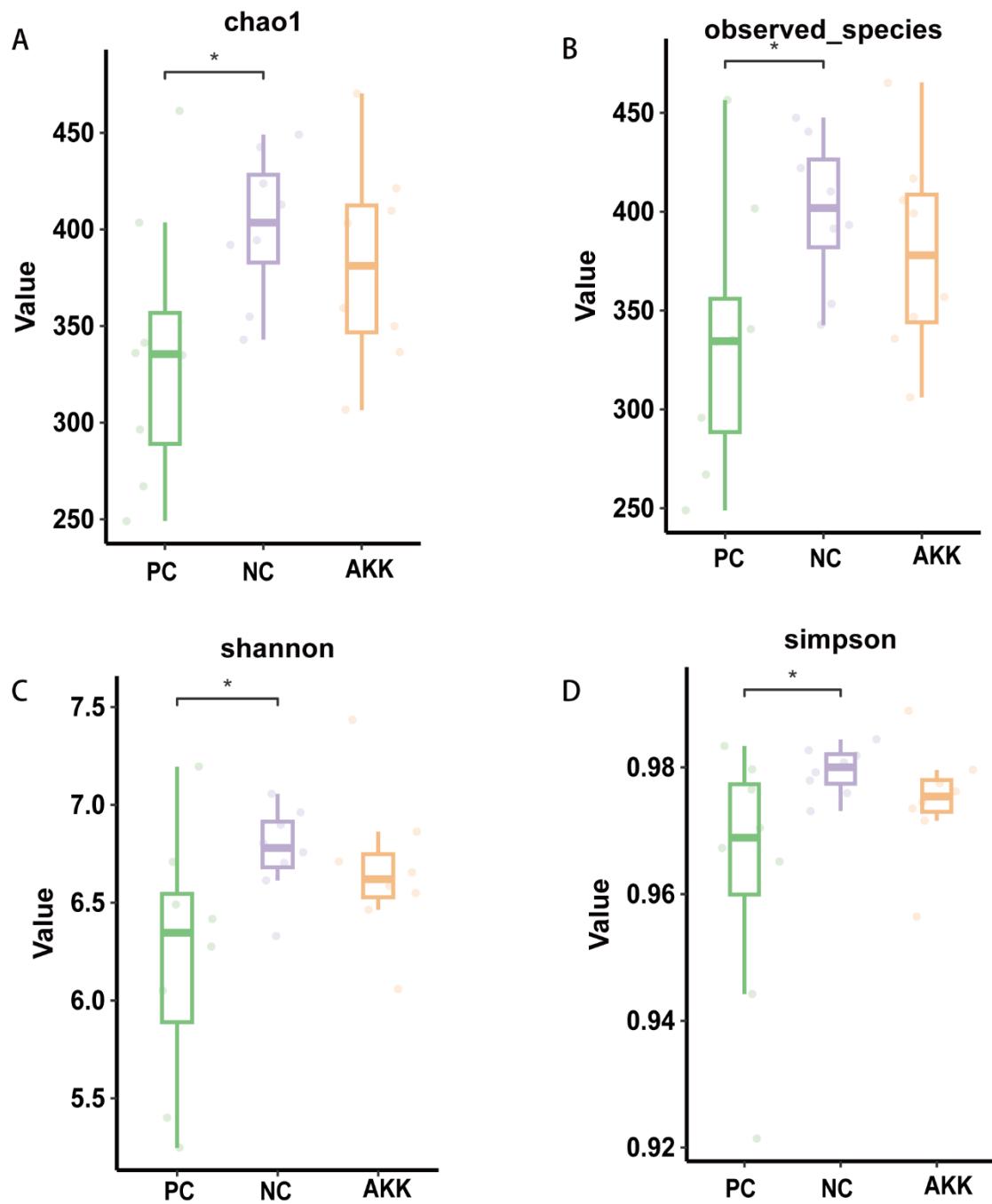
  

ELISA kit name	Catalog number	Manufacturer
<b>Mouse LBP ELISA Assay kit</b>	ab269542	Abcam, Cambridge, UK
<b>SOD Determination Kit</b>	19160	Sigma-Aldrich, PA, USA
<b>Lipid Peroxidation (MDA) Assay kit</b>	ab118970	Abcam
<b>Mouse IL-1 beta ELISA kit</b>	ab197742	Abcam
<b>Mouse IL-6 ELISA kit</b>	ab222503	Abcam
<b>Enhanced BCA Protein Assay Kit</b>	P0010	Beyotime, Nanjing, China
<b>Lactate Dehydrogenase Activity Assay Kit</b>	MAK066	Sigma-Aldrich

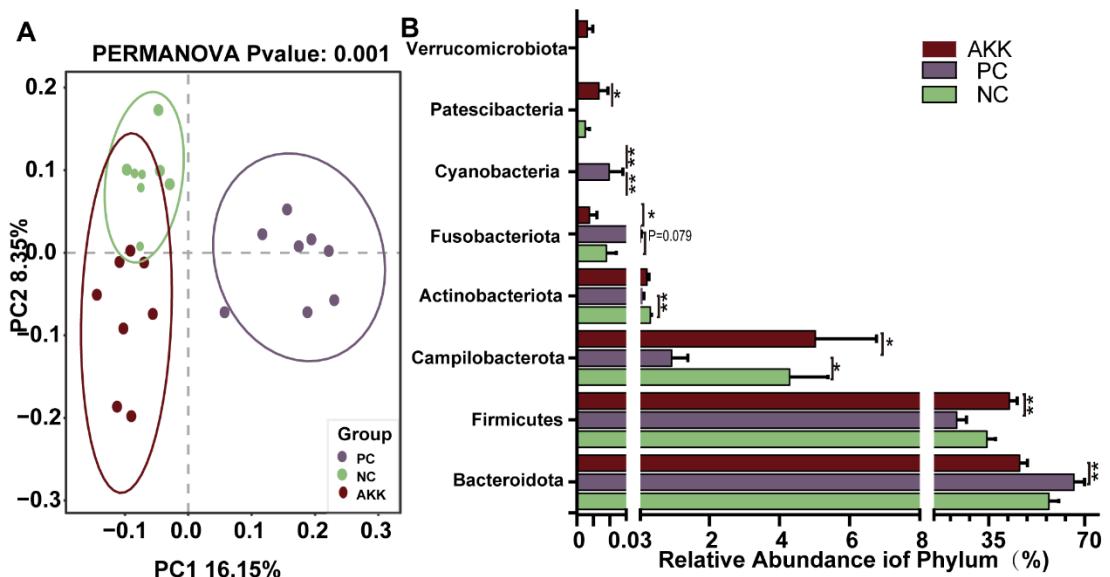
**Supplementary Table S3.** List of hub genes in PPI network of AKK vs PC.

Hub gene in cluster 1	Log2(fold change) in transcriptome (AKK vs PC)	P-value	Regulation
Tnf	-3.204178297	0.000437	downregulated
Lilr4b	-1.56858339	0.000758	downregulated
Bcl2a1b	-1.182020434	0.033646	downregulated
Bdkrb1	-1.368309161	0.005198	downregulated
C5ar1	-1.132436864	0.011974	downregulated
Casp1	-0.796837191	0.024685	downregulated
Ccl2	-2.755376319	0.00055	downregulated
Ccl20	-2.077085304	0.008089	downregulated
Ccl4	-2.9897643	0.000583	downregulated
Ccl9	-1.103842508	0.004593	downregulated
Ccr1	-1.605465072	0.001736	downregulated
Cd44	-0.489276361	0.042579	downregulated
Clec4n	-1.028954585	0.036211	downregulated
Csf1r	-0.889786024	0.033982	downregulated
Cxcl1	-3.446320805	9.54E-05	downregulated
Cxcl13	-2.072900146	0.012533	downregulated
Cxcl2	-4.762465368	1.63E-08	downregulated
Cxcl3	-3.287514873	0.012122	downregulated
Cxcl5	-3.166892054	0.019528	downregulated
Cxcl9	-3.062643588	0.035634	downregulated
Cxcr2	-1.218714173	5.04E-07	downregulated
Cyba	-0.934063339	0.022981	downregulated
Fcer1g	-1.22672505	0.002777	downregulated
Fcgr3	-1.513609542	0.020028	downregulated
Fcgr4	-1.526164474	0.000245	downregulated
Fpr1	-1.587359181	0.000137	downregulated
Fpr2	-2.431193418	8.19E-08	downregulated
Gbp2	-2.270570645	0.000259	downregulated
Gbp3	-1.653222049	0.00541	downregulated
Gbp7	-1.423049728	0.003462	downregulated
H2-T23	-0.948575564	0.001729	downregulated
Ifi204	-1.550758675	0.000341	downregulated
Ifi47	-1.574378091	0.006589	downregulated
Ifit1	-1.603991179	0.025082	downregulated
Igtp	-2.114969267	0.0013	downregulated
Il10	-2.242997239	0.0008	downregulated
Il10ra	-0.866464085	0.038821	downregulated
Il12b	-2.563852551	0.026182	downregulated
Il1b	-1.732200367	0.027157	downregulated
Irf7	-1.458434548	0.004253	downregulated

Irgm1	-1.725155188	0.000926	downregulated
Isg15	-1.771824711	0.00819	downregulated
Itgb2	-0.851837193	0.048566	downregulated
Jak2	-0.629473342	0.042668	downregulated
Ncf2	-1.028940823	7.23E-05	downregulated
Ncf4	-1.333298366	0.001234	downregulated
Nfkbia	-1.007011003	0.000208	downregulated
Oas1a	-1.060446107	0.042144	downregulated
Oas2	-1.253894038	0.008611	downregulated
Oas3	-1.678403454	0.001334	downregulated
Pilra	-0.915902476	0.023157	downregulated
Ptafr	-1.337969712	0.047313	downregulated
Samhd1	-0.963400283	0.000437	downregulated
Socs3	-1.311406039	0.000141	downregulated
Stat1	-1.167318807	0.040327	downregulated
Stat3	-0.441735523	0.003959	downregulated
Tap1	-1.357642406	0.001485	downregulated
Tlr2	-1.704103478	0.000516	downregulated
Tlr4	-0.456311223	0.02522	downregulated
Tyrobp	-0.877675879	0.033216	downregulated
Vav1	-1.062063524	0.029035	downregulated
Zbp1	-1.840291657	0.00375	downregulated

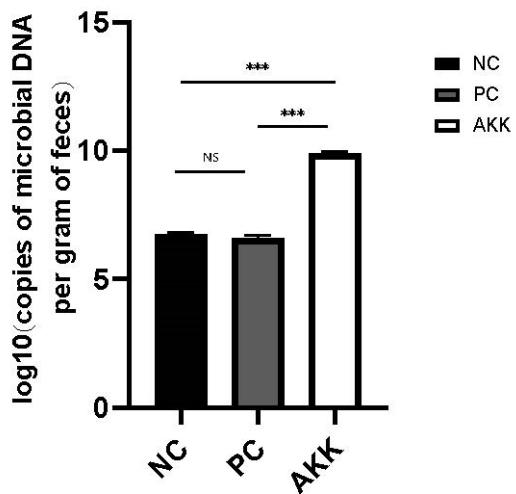


**Supplementary Figure 1** The alpha-diversity indexes including Chao1 index(A), observed species index(B), Shannon index(C), and Simpson index (D) of the gut microbiota among three groups were showed. Data are shown as the mean  $\pm$  SEM; Compared with the PC group, \*  $p < 0.05$ . NC, PBS + saline group; PC, PBS+LPS group; AKK, *A. muciniphila* + LPS group. n=8 each group.

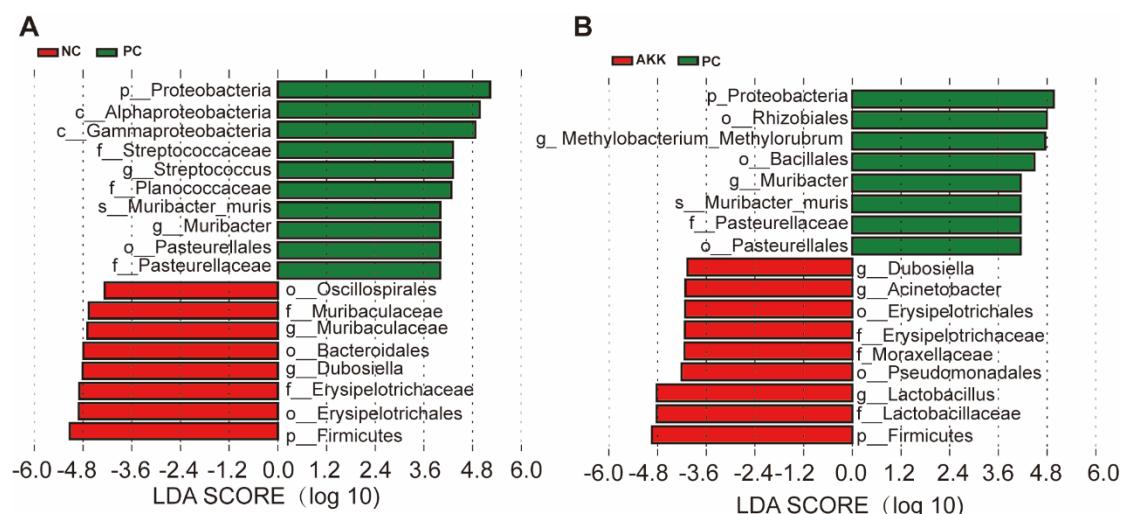


**Supplementary Figure 2 A. muciniphila reshaped the gut microbiota of mice.**

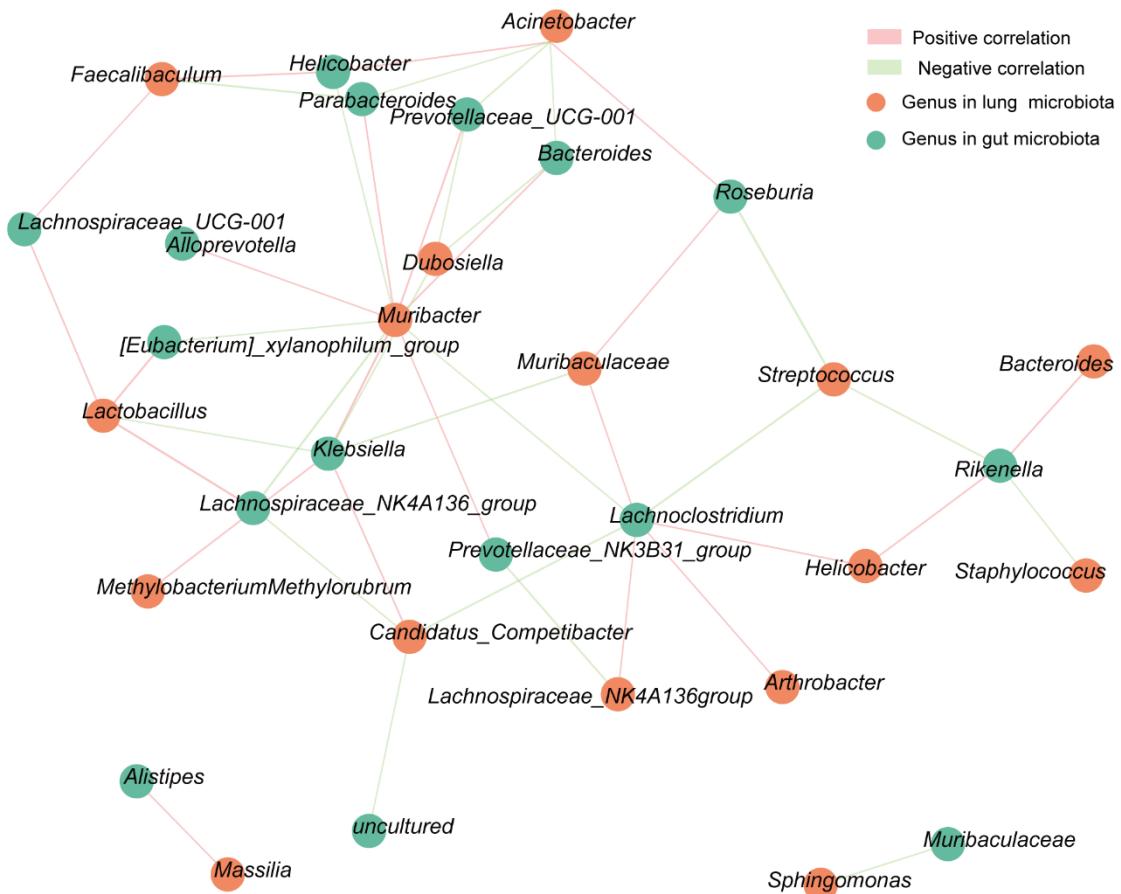
(A) A PCoA based on unweighted UniFrac distances showed that the microbial groups of AKK, NC, and LPS were significantly separated ( $p<0.01$ ). (B) Comparisons of the relative abundances of intestinal microbiota between the three groups were performed at the phylum levels. Data are shown as the mean  $\pm$  SEM; Compared with the PC group, \*  $p<0.05$ , \*\*  $p<0.01$ , and \*\*\*  $p<0.001$ . NC, PBS + saline group; PC, PBS+LPS group; AKK, *A. muciniphila* + LPS group. n=8 each group.



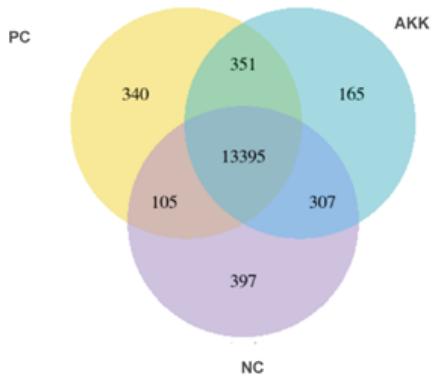
**Supplementary Figure 3** *A. muciniphila* load in the feces was measured 21 days of gavage. Data are presented as the mean  $\pm$  SEM; Compared with the PC group, \*  $p < 0.05$ . NC, PBS + saline group; PC, PBS+LPS group; AKK, *A. muciniphila* + LPS group. n=8 each group.



**Supplementary Figure 4** LEfSe analyses identified the differentially abundant taxa between the NC and PC groups (A) and the PC and AKK groups (B). NC, PBS + saline group; PC, PBS+LPS group; AKK, *A. muciniphila* + LPS group. n=4-5 per group. LEfSe, linear discriminant analysis effect size.



**Supplementary Figure 5** Correlation analysis between gut microbiota and lung microbiota. Spearman's rho non parametric correlation was performed and significant relationships with  $P < 0.05$  was showed. Dark green node: genus in gut microbiota. Orange node: genus in lung microbiota; The red line between nodes represents a positive relationship, while the green line represents a negative relationship.



**Supplementary Figure 6 Venn diagram of three groups.** 3-4 animals per group.  
NC, PBS + saline group; PC, PBS+LPS group; AKK, *A. muciniphila* + LPS group.