Table S1. Primer sequences for qPCR analyses

Gene	Forward	Reverse
MUC 2	5’-CCTTAGCCAAGGGCTCGGAA-3’	5’-GGCCCGAGAGTAGACCTTGG-3’
Math1	5’-GCCTTGCCGGACTCGCTTCTC-3’	5’-TCTGTGCCATCATCGCTGTTAGGG-3’
Spedf	5’-CCGGTTGCCTGCTACTGTTC-3’	5’-GCCCATTGCTCCTGATGCT-3’
claudin1	5’-GATGTGGATGGCTGTCATTG-3’	5’-CCTGGCCAAATTCATACCTG-3’
claudin 3	5’-TCATCGTGGTGTCCATCCTGCT-3’	5’-AGAGCCGCCAACAGGAAAAGCA-3’
ZO 1	5’-CTTCTCTTGCTGGCCCTAAAC-3’	5’-TGGCTTCACTTGAGGTTTCTG-3’
occludin	5’-CACACTTGCTTGGGACAGAG-3’	5’-TAGCCATAGCCTCCATAGCC-3’
Klf4	5’-GTAGTGCCTGGTCAGTTCATC-3’	5’-AACCTATACCAAGAGTTCTCATCTC-3’
Reg3g	5’-TTCCTGTCCTCCATGATCAAA-3’	5’-CATCCACCTCTGTTGGGTTC-3’
β-actin	5’-GGCTGTATTCCCCTCCATCG-3’	5’-CCAGTTGGTAACAATGCCATGT-3’
A. muciniphila	5’-CAGCACGTGAAGGTGGGGAC-3’	5’- CCTTGCGGTTGGCTTCAGAT-3’

Table S2. Instrument conditions for the analysis of metabolomics samples

Instrument conditions			
Spectrum Column	ACQUITY UPLC HSS T3 (2.1×100 mm, 1.8μm)		
	Column temperature: 35 ℃		
Mobile Phase	For Positive		
	A: 0.1% Formic acid in water		
	B: 100% Methanol		
	For Negative		
	A: 100% Water		
	B: 100% Methanol		
Gradient Profile	Time (min)	Percentage B (%)	Flow rate (mL/min)
	0.00	2.0	0.30
	1.00	2.0	0.30
	10.00	98.0	0.30
	12.00	98.0	0.30
	12.10	2.0	0.30
	15.00	2.0	0.30
Injection Volume	2 μL		
Mass Parameters	Ion Source	Electrospray ionization	
	Ionspray voltage	3.8 kV	
	Capillary temperature	320 ℃	
	Sheath gas flow velocity	35 arb	
	Curtain gas flow velocity	15 arb	
	Curtain gas temperature	320 ℃	
	FramsScan	Full-scan MS/dd-MS2	
	Full MS		
	Resolution	70,000	
	AGC target	1e6	

Maximum IT	100 ms
Scan range	70 t0 1050 m/z
dd-MS2/dd-SIM	
Resolution	17,500
AGC target	5e4
Maximum IT	50 ms
Nnormalized collision energy	20、40、60 eV
Dynamic exclusion	10 s
TOP N	7

Table S3. All fecal metabolites in mums. The number is the normalized peak area of the metabolite; The first row is the compound name, and the second line is the sample name.

Table S4. All fecal metabolites in pups. The number is the normalized peak area of the metabolite; The first row is the compound name, and the second line is the sample name.

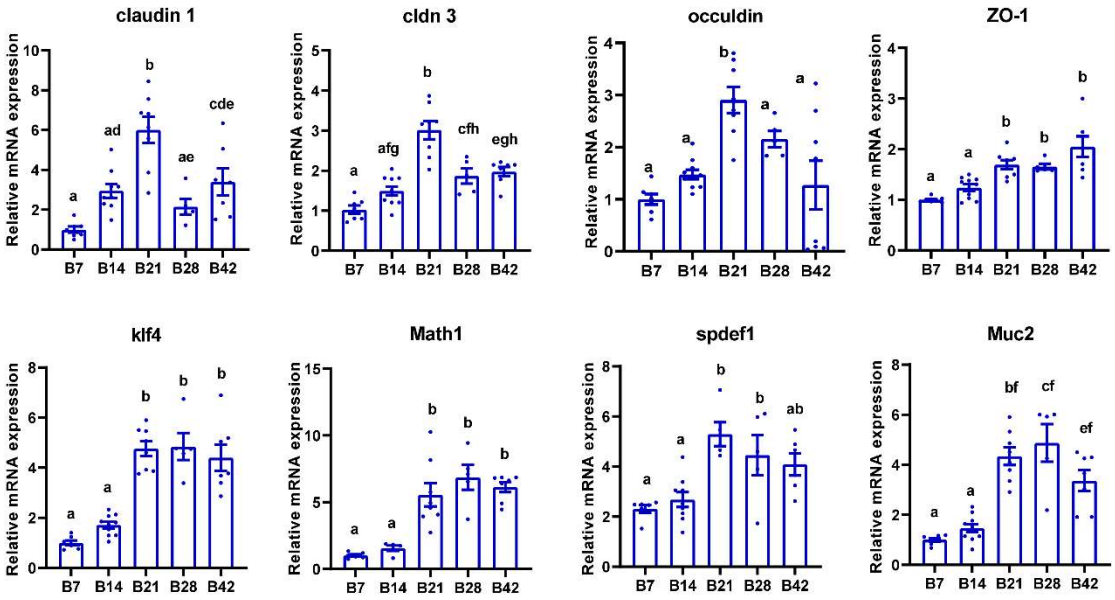

Figure S1. The mRNA expression of genes related to the intestinal barrier of mouse offspring in the CON group at B7, B14, B21, B28 and B42. The appearance of the same letter means that there is no marked difference among the groups under the condition of $p > 0.05$; otherwise, there is significant difference, $p < 0.05$.

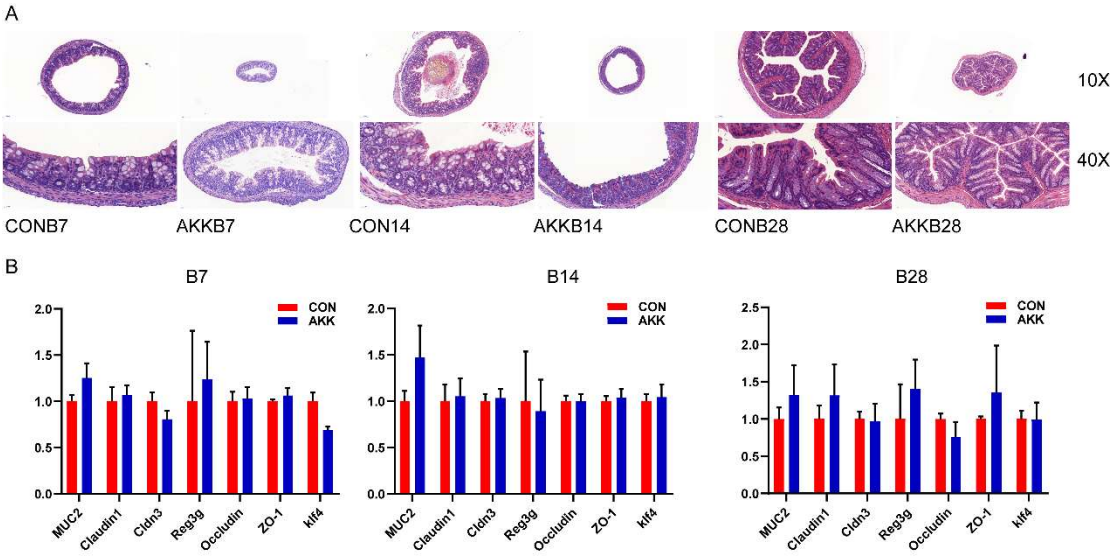

Figure S2. Effects of *A. muciniphila* supplementation during pregnancy and lactation on the intestinal barrier of mouse offspring. (A) Representative image of hematoxylin-eosin-stained colon tissue of offspring at different points after birth. (B) Comparison of mRNA expression of genes related to the intestinal barrier of mouse offspring.

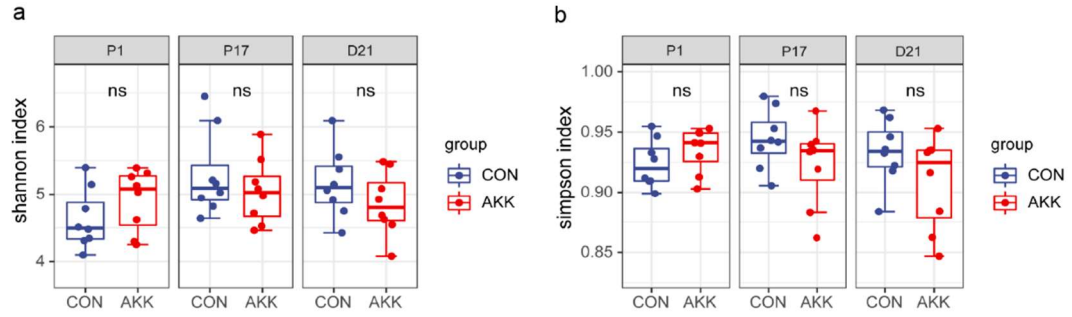

Figure S3. *A. muciniphila* supplementation results in favorable alterations in maternal gut microbiota. (a) The shannon index of mother mice. (b) The simpson index of mother mice.

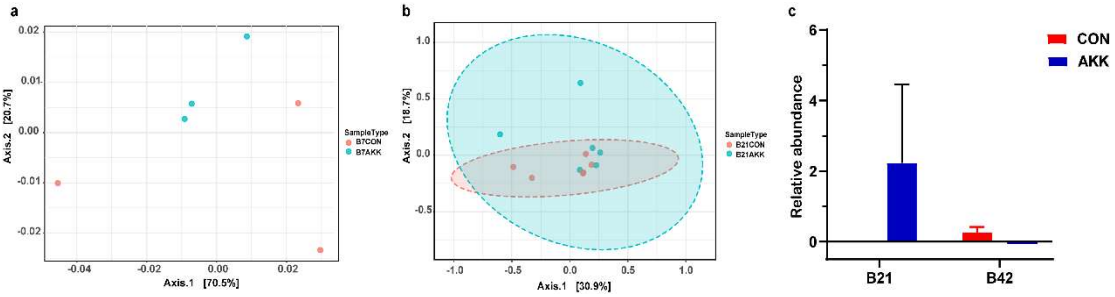

Figure S4. *A. muciniphila* supplementation results in favorable alterations in the gut microbiota of pups. PCoA describing the β-diversity clustering of the gut microbiota of pups at B7 (a) and B21 (b). (c) The relative abundance of *A. muciniphila* concentration in offspring feces.