Support Information

Table S1 The relative abundance of gut bacteria at the phylum level identified in intestinal digestion samples from mice with distinct induction groups.

Group	SF	CF	AX	AX.H.L	AX.H.M	AX.H.H	AX.L.L	AX.L.M	AX.L.H	AX.P.L	AX.P.M	AX.P.H
Others	3.62E-04	1.79E-03	7.90E-04	2.91E-03	2.27E-04	5.62E-04	5.89E-04	2.93E-03	8.33E-03	8.97E-04	3.88E-04	3.48E-04
Deferribacteres	2.60E-05	2.60E-05	0.00E+00	0.00E+00	0.00E+00	6.29E-04	3.08E-04	1.47E-04	6.60E-05	0.00E+00	3.48E-04	1.20E-04
Acidobacteriota	0.00E+00	3.08E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.60E-05	3.34E-03	4.15E-04	0.00E+00	0.00E+00
Cyanobacteria	8.84E-04	1.07E-03	4.95E-04	8.18E-03	2.41E-04	4.01E-04	1.87E-04	7.60E-03	7.09E-04	9.30E-05	4.28E-04	1.03E-03
Actinobacteria	5.65E-03	1.65E-03	3.42E-03	1.94E-03	4.68E-04	4.93E-03	2.00E-03	2.36E-03	8.56E-03	2.97E-03	9.77E-04	9.37E-04
Actinobacteriota	1.49E-03	1.90E-03	2.46E-03	1.98E-03	1.33E-03	8.18E-03	3.34E-03	6.16E-03	5.84E-03	7.17E-03	4.29E-03	3.82E-03
unidentified_Bacteria	7.30E-02	4.50E-02	3.22E-02	2.17E-02	1.49E-02	2.93E-02	1.22E-01	5.90E-02	4.05E-02	1.80E-02	5.54E-02	1.21E-02
Verrucomicrobiota	2.37E-02	4.44E-02	2.79E-02	8.34E-02	3.61E-02	1.08E-01	2.70E-02	1.91E-02	3.09E-02	1.40E-01	2.90E-02	2.05E-01
Proteobacteria	1.34E-01	1.58E-01	2.34E-01	1.81E-01	5.43E-01	8.70E-02	2.19E-02	4.34E-02	2.21E-01	2.33E-01	4.65E-02	2.28E-02
Firmicutes	2.04E-01	2.98E-01	1.80E-01	2.04E-01	8.77E-02	1.91E-01	2.76E-01	2.45E-01	1.74E-01	1.75E-01	2.44E-01	1.92E-01
Bacteroidota	5.56E-01	4.48E-01	5.19E-01	3.16E-01	5.71E-01	5.46E-01	5.46E-01	6.14E-01	5.07E-01	4.23E-01	6.18E-01	5.62E-01
F*：*B	2.73	1.50	2.88	1.55	6.51	2.86	1.98	2.51	2.91	2.42	2.53	2.93

Note: The results are expressed as mean values. n=10.

Table S2 The relative abundance heatmap of genes responsible for glycolysis and glycine metabolism identified in intestinal digestion samples from mice with distinct induction groups.

Entry	**EC**	**CF**	**SF**	**AX**	**AXH**	**AXL**	**AXP**
Glycolysis							
phosphoglucomutase [EC:5.4.2.2]	pgm	4.73E-04	4.52E-04	4.05E-04	4.46E-04	4.19E-04	4.08E-04
polyphosphate glucokinase [EC:2.7.1.1]	HK	2.19E-06	1.24E-06	7.97E-08	0.00E+00	5.62E-07	6.31E-07
glucose-6-phosphate isomerase [EC:5.3.1.9]	pgi	4.44E-04	4.38E-04	4.21E-04	4.82E-04	4.48E-04	3.98E-04
6-phosphofructokinase [EC:2.7.1.11]	PFK9	5.00E-04	4.79E-04	4.08E-04	4.81E-04	4.08E-04	4.52E-04
diphosphate-dependent phosphofructokinase [EC:2.7.1.90]	pfp	5.05E-04	4.64E-04	4.38E-04	4.82E-04	4.21E-04	4.51E-04
fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	ALDO	4.40E-04	4.09E-04	3.59E-04	4.18E-04	3.92E-04	3.40E-04
triosephosphate isomerase (TIM) [EC:5.3.1.1]	tpiA	3.48E-04	3.32E-04	3.11E-04	3.17E-04	3.06E-04	2.96E-04
glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	gapA	2.96E-04	3.19E-04	2.22E-04	3.05E-04	2.82E-04	2.28E-04
phosphoglycerate kinase [EC:2.7.2.3]	pgk	3.85E-04	3.90E-04	3.86E-04	4.11E-04	3.85E-04	3.54E-04
2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]	gpmI	6.26E-04	6.30E-04	7.32E-04	6.56E-04	6.44E-04	7.04E-04
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	gpmA	1.98E-04	2.18E-04	1.30E-04	3.33E-04	2.39E-04	1.87E-04
glyceraldehyde-3-phosphate dehydrogenase (NADP+) [EC:1.2.1.9]	gapN	1.91E-05	0.00E+00	2.34E-07	0.00E+00	0.00E+00	0.00E+00
enolase 1/2/3 [EC:4.2.1.11]	eno	3.68E-04	3.60E-04	3.60E-04	3.82E-04	3.53E-04	3.64E-04
pyruvate kinase [EC:2.7.1.40]	pyk	4.22E-04	4.00E-04	3.90E-04	3.53E-04	3.80E-04	2.77E-04
L-lactate dehydrogenase [EC:1.1.1.27]	ldh	1.69E-04	1.50E-04	1.16E-04	9.92E-05	5.77E-05	8.49E-05
choline dehydrogenase [EC:1.1.1.1]	gbsB	2.61E-04	2.45E-04	1.29E-04	2.13E-04	1.79E-04	1.22E-04
glycine betaine monooxygenase A [EC:1.14.13.251]	gbcA	9.58E-06	6.62E-06	1.15E-06	3.33E-06	4.02E-06	2.06E-06

glycine betaine-corrinoid protein Co-methyltransferase [EC:2.1.1.376]	mtgB	1.22E-06	3.47E-07	0.00E+00	0.00E+00	2.91E-07	4.66E-07
N,N-dimethylglycine/sarcosine dehydrogenase [EC:1.5.7.3]	dgcA	2.80E-06	1.23E-06	4.53E-07	1.37E-06	1.36E-06	5.60E-07
glycine hydroxymethyltransferase [EC:2.1.2.1]	glyA	3.96E-04	3.49E-04	3.57E-04	3.67E-04	3.64E-04	3.45E-04
L-serine/L-threonine ammonia-lyase [EC:4.3.1.17, 4.3.1.19]	SDS	2.70E-04	2.65E-04	2.51E-04	2.50E-04	2.46E-04	2.33E-04
		3.13E-04	2.64E-04	2.24E-04	2.72E-04	2.85E-04	2.43E-04
glycine C-acetyltransferase [EC:2.3.1.29]	kbl	1.31E-04	1.43E-04	1.43E-04	1.15E-04	1.26E-04	1.91E-04
threonine aldolase [EC:4.1.2.48]	ItaE	1.67E-04	1.78E-04	1.88E-04	1.67E-04	1.91E-04	1.88E-04
3-hydroxy acid dehydrogenase / malonic semialdehyde reductase [EC:1.1.1.381]	ydfG	1.75E-05	3.37E-05	2.11E-05	2.41E-05	4.10E-05	1.65E-05
monoamine oxidase [EC:1.4.3.4]	aofH	0.00E+00	3.64E-07	0.00E+00	1.55E-07	2.77E-06	1.18E-06
threonine 3-dehydrogenase [EC:1.1.1.103]	TDH	9.18E-05	9.16E-05	1.30E-04	6.51E-05	8.79E-05	1.33E-04
lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22]	aldA	4.02E-07	1.87E-07	8.70E-07	0.00E+00	2.70E-06	3.56E-06

Note: The results are expressed as mean values. n=10.

Table S3 CutC and CutD gene levels

Group	CutC	CutD
SF	1.73E-04±2.08E-07	2.93E-04±2.64E-07
CF	4.57E-04±1.20E-07	5.93E-04±1.73E-07
AX	2.11E-04±1.08E-07	4.70E-04±1.02E-07
AXH	2.22E-04±2.20E-07	3.80E-04±1.24E-07
AXL	2.69E-04±1.02E-07	3.37E-04±1.38E-07
AXP	2.11E-04±1.99E-07	3.15E-04±1.44E-07

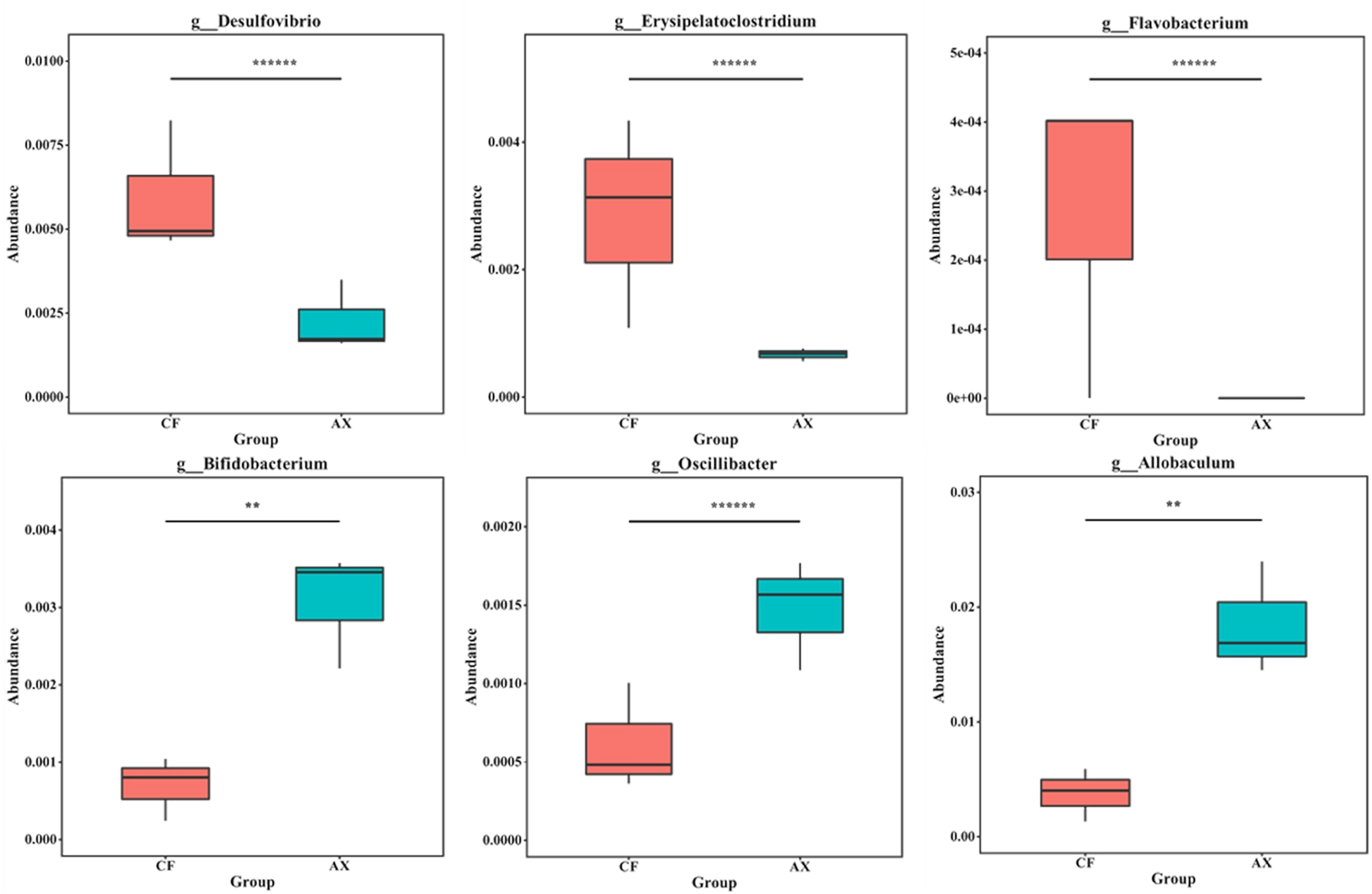

Figure S1 Differences in Mestase species analysis of intestinal digestion samples from mice in the CF and AX Groups. * indicate significant differences between groups at the level of $p<0.05$; ** indicate significant differences between groups at the level of $p<0.01$.

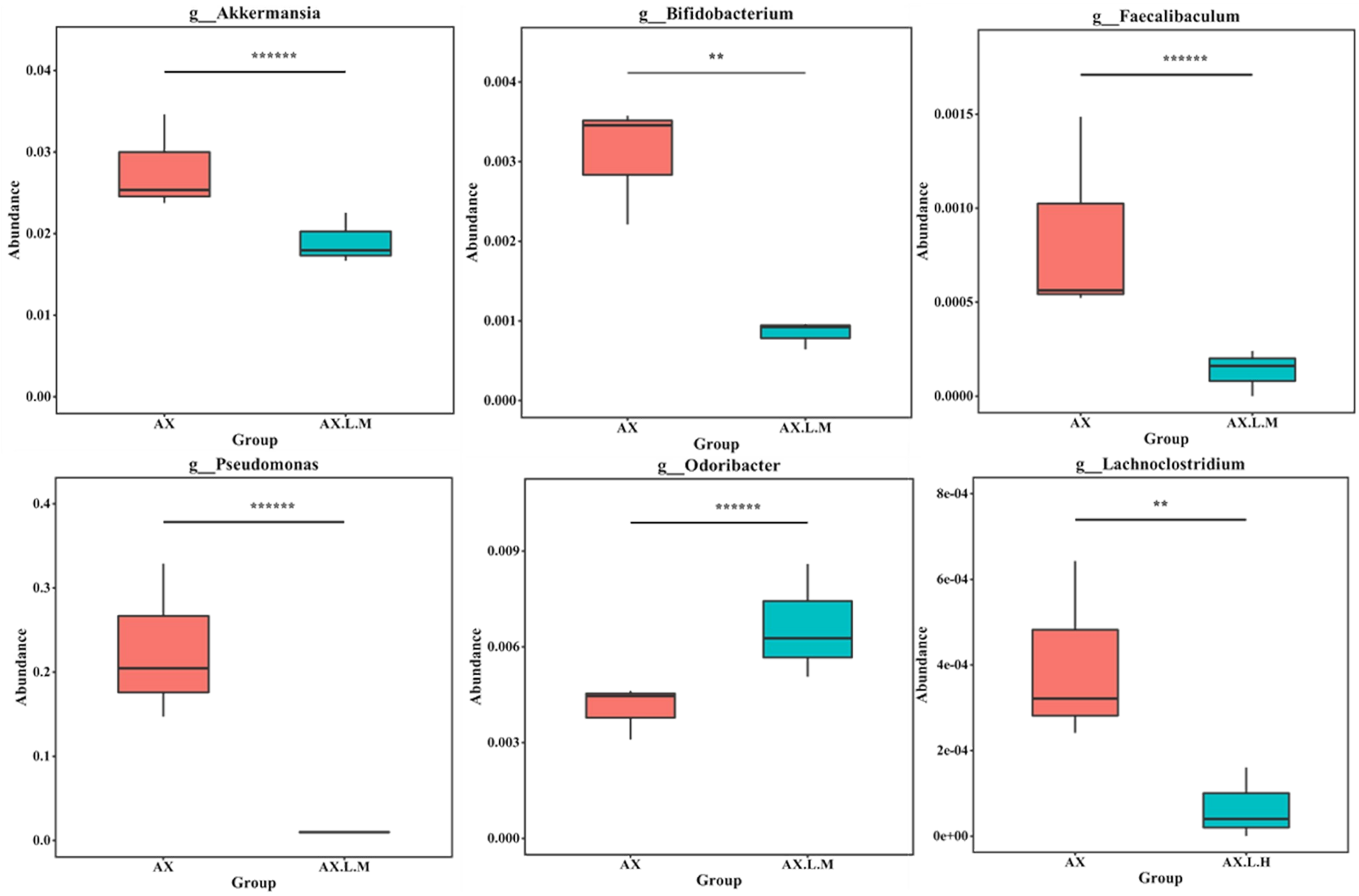

Figure S2 Differences in Mestase species analysis of intestinal digestion samples from mice in the AX and inhibitor I Groups. * indicate significant differences between groups at the level of $p<0.05$; ** indicate significant differences between groups at the level of $p<0.01$.

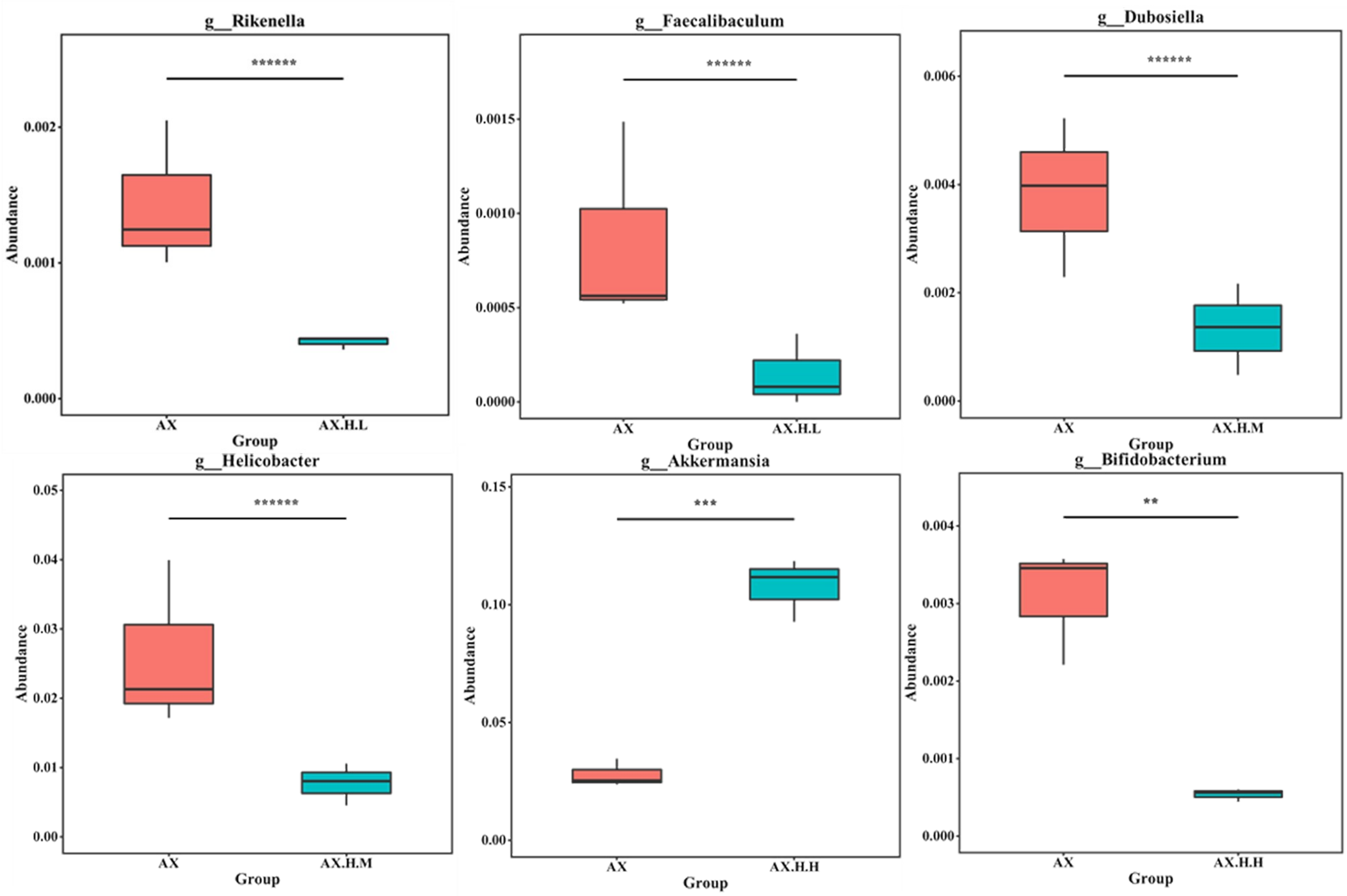

Figure S3 Differences in Mestase species analysis of intestinal digestion samples from mice in the AX and inhibitor II Groups. * indicate significant differences between groups at the level of $p<0.05$; ** indicate significant differences between groups at the level of $p<0.01$.

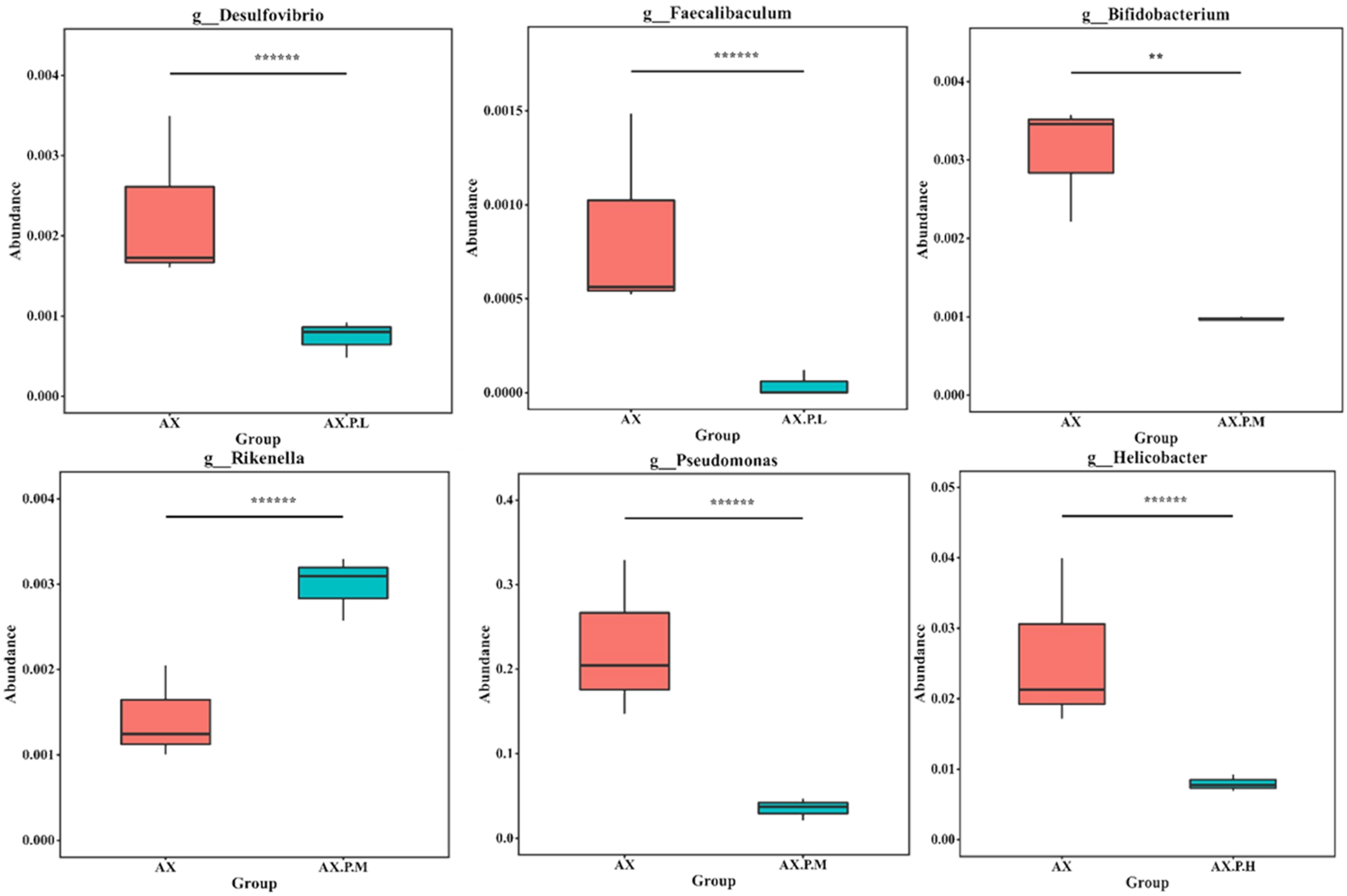

Figure S4 Differences in Mestase species analysis of intestinal digestion samples from mice in the AX and inhibitor III Groups. * indicate significant differences between groups at the level of $p<0.05$; ** indicate significant differences between groups at the level of $p<0.01$.