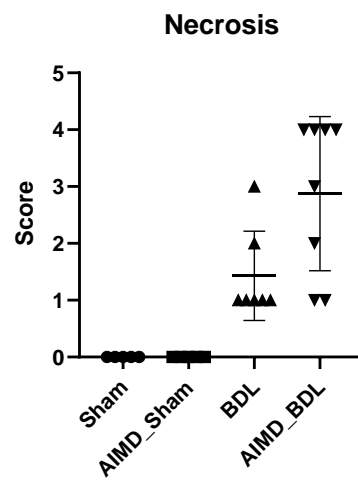
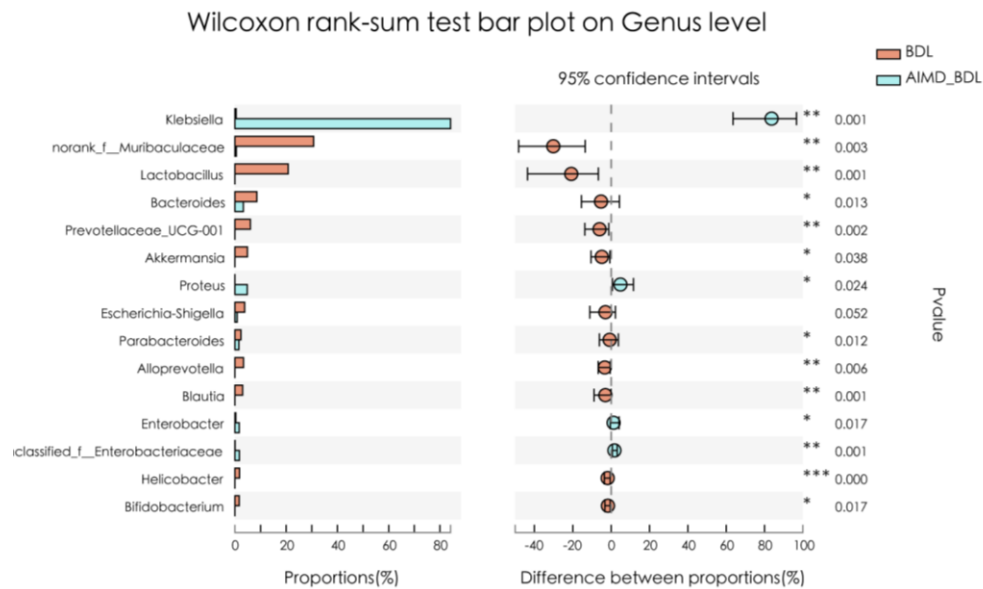


**Figure S1.**



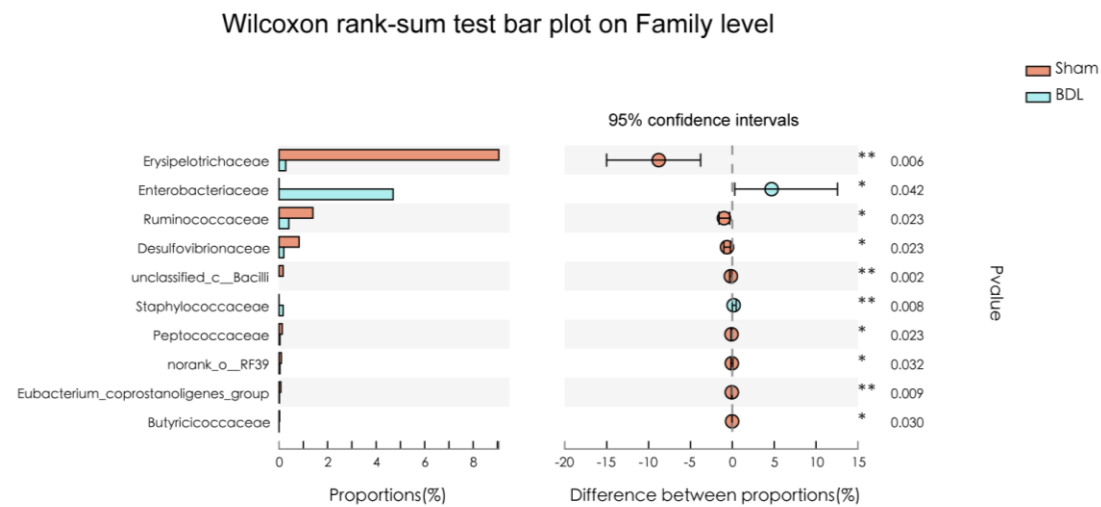
HE staining of liver tissues showed a significant higher scores for necrosis in the AIMD\_BDL mice compared with the BDL mice.

Figure S2.



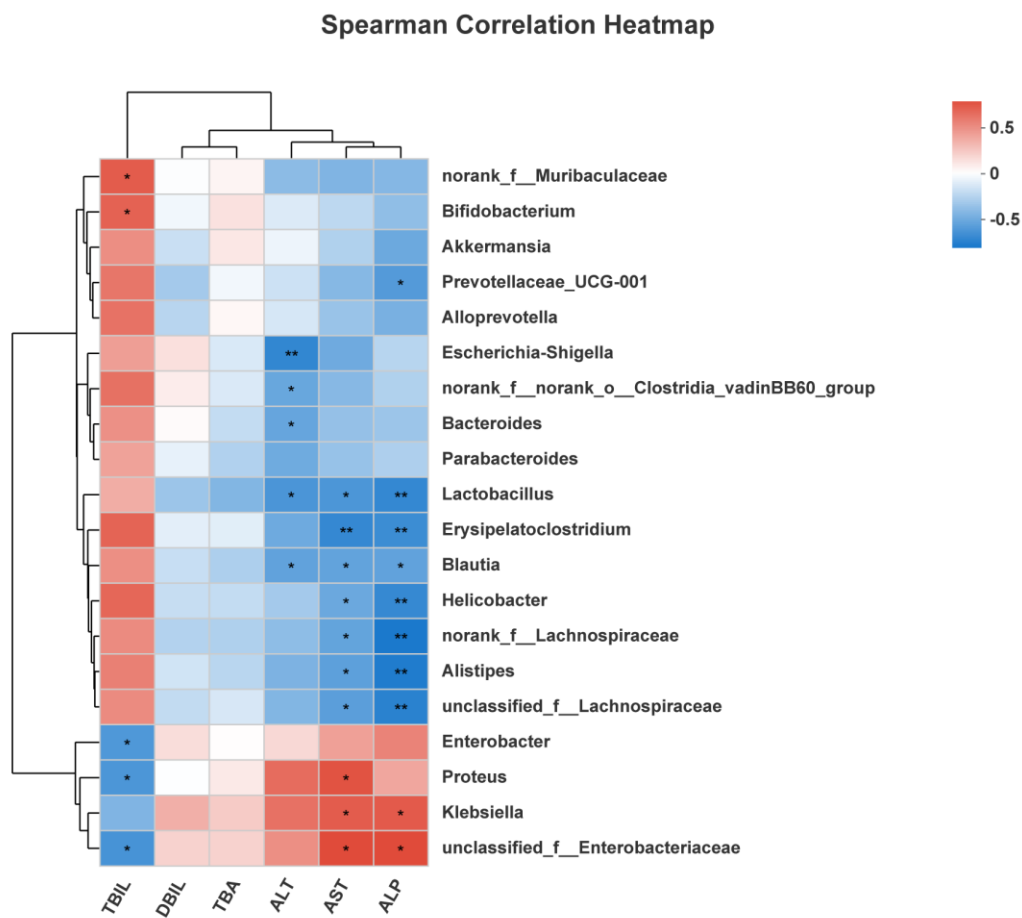
Relative abundances of top 15 genera responsible for discriminating the BDL and AIMD\_BDL groups. BDL, n = 7; AIMD\_BDL groups, n = 8. \* P < 0.05 vs control; \*\* P < 0. 01; \*\*\* P < 0. 001.

Figure S3.



Relative abundances of top 10 families responsible for discriminating the BDL and Sham groups. BDL group, n = 7; Sham groups, n = 5. \*  $P < 0.05$  vs control; \*\*  $P < 0.01$ .

**Figure S4.**



The association between gut microbiota and serum markers of liver injury in AIMD\_BDL group and BDL group at genus level. Red represents positive correlation, and blue represents negative correlation. \*  $P < 0.05$ ; \*\*  $P < 0.01$ ; \*\*\*  $P < 0.001$ .

**Table S1.** 16S RNA sequencing details for each sample.

ID	Group name	Seq_num	Base_num	Mean_length	Min_length	Max_length
Sh1	Sham	55649	23486983	422.055796	332	511
Sh2	Sham	51971	21897431	421.33942	277	494
Sh3	Sham	47703	20095016	421.252668	248	496
Sh4	Sham	53288	22569785	423.543481	262	438
Sh5	Sham	64638	27091437	419.125545	280	483
ASh1	AIMD_sham	36566	15684610	428.939725	403	430
ASh2	AIMD_sham	40671	17447275	428.985641	404	454
ASh3	AIMD_sham	45508	19522319	428.98653	404	472
ASh4	AIMD_sham	40207	17248339	428.98846	404	478
ASh5	AIMD_sham	41546	17820449	428.932966	308	431
B1	BDL	38171	16096295	421.68911	345	444
B2	BDL	61252	25863295	422.24409	265	430
B3	BDL	52977	22242598	419.853861	252	444
B4	BDL	37707	16146914	428.220596	277	477
B5	BDL	56101	23632010	421.240441	258	473
B6	BDL	46688	19725582	422.497901	277	444
B7	BDL	56287	23768281	422.269458	325	445
AB1	AIMD_BDL	61044	26187085	428.987042	404	430
AB2	AIMD_BDL	36575	15573043	425.783814	333	444
AB3	AIMD_BDL	37909	16262252	428.981297	371	503
AB4	AIMD_BDL	38416	16479933	428.986178	404	430
AB5	AIMD_BDL	44843	19237073	428.9872	404	431
AB6	AIMD_BDL	38497	16514273	428.975583	282	430
AB7	AIMD_BDL	41269	17701606	428.932274	403	517
AB8	AIMD_BDL	38054	16317937	428.810033	251	431

Sham, sham surgery; BDL, bile duct-ligated surgery; AIMD, Antibiotic-induced microbiome depletion.

**Table S2.** Alpha diversity for each sample.

ID	Group	sobs	shannon	simpson	ace	chao	invsimpson	coverage
Sh1	Sham	392	4.0801	0.0364	442.5732	447.5610	27.4894	0.9977
Sh2	Sham	377	4.0832	0.0336	416.7544	420.8718	29.7997	0.9980
Sh3	Sham	346	3.7978	0.0665	392.6966	427.3750	15.0372	0.9979
Sh4	Sham	336	3.7310	0.0521	388.6073	407.5000	19.2063	0.9978
Sh5	Sham	285	2.6387	0.2256	331.2086	342.0000	4.4318	0.9981
ASh1	AIMD_sham	32	0.1455	0.9565	85.1375	67.0000	1.0455	0.9995
ASh2	AIMD_sham	17	0.1725	0.9415	177.9428	72.0000	1.0622	0.9996
ASh3	AIMD_sham	19	0.1027	0.9697	117.3406	74.0000	1.0313	0.9996
ASh4	AIMD_sham	14	0.3542	0.8466	22.7500	17.3333	1.1812	0.9998
ASh5	AIMD_sham	19	0.1580	0.9527	25.7552	21.0000	1.0497	0.9999
B1	BDL	154	2.6791	0.1328	188.8539	217.0000	7.5321	0.9988
B2	BDL	148	3.1352	0.0786	169.3606	180.5000	12.7250	0.9991
B3	BDL	277	3.3344	0.0791	307.3671	304.9730	12.6369	0.9985
B4	BDL	208	1.6315	0.3578	244.2514	237.2162	2.7945	0.9984
B5	BDL	240	3.0548	0.1178	281.5917	274.8710	8.4902	0.9984
B6	BDL	268	3.0984	0.1138	301.2110	322.0500	8.7890	0.9984
B7	BDL	263	3.1818	0.1169	282.5387	281.3704	8.5568	0.9989
AB1	AIMD_BDL	10	0.1441	0.9529	13.6857	11.5000	1.0495	0.9999
AB2	AIMD_BDL	61	2.0114	0.1847	63.8895	62.6667	5.4132	0.9998
AB3	AIMD_BDL	17	0.0673	0.9799	302.4341	50.0000	1.0205	0.9996
AB4	AIMD_BDL	8	0.0837	0.9750	11.6667	9.0000	1.0256	0.9999
AB5	AIMD_BDL	13	0.2396	0.9146	34.2342	23.0000	1.0933	0.9998
AB6	AIMD_BDL	18	0.2000	0.9301	23.5000	21.7500	1.0752	0.9998
AB7	AIMD_BDL	57	0.8857	0.5104	124.1668	114.2727	1.9591	0.9988
AB8	AIMD_BDL	94	0.4515	0.8324	140.9383	131.0500	1.2013	0.9987

Sham, sham surgery; BDL, bile duct-ligated surgery; AIMD, Antibiotic-induced microbiome depletion.