

**S11 Table.** Significantly different OTUs in the colon microbiota of healthy mice fed the control diet vs. 5<sup>th</sup> cutting chloroform extract at 21dpi.

OTU	LDA effect size score	Treatment in which OTU is more abundant	p-value	Taxonomy
OTU 3	4.26	5 <sup>th</sup> cutting chloroform extract	0.043	<i>Bacteroides</i>
OTU 8	4.45	5 <sup>th</sup> cutting chloroform extract	0.021	<i>Akkermansia</i>
OTU 10	3.51	Control	0.020	<i>Muribaculaceae ge</i>
OTU 15	3.85	Control	0.018	<i>Lachnospiraceae NK4A136 group</i>
OTU 18	3.37	Control	0.042	<i>Anaeroplasma</i>
OTU 27	3.03	5 <sup>th</sup> cutting chloroform extract	0.043	<i>Bacteroides</i>
OTU 32	3.47	Control	0.018	<i>Lachnospiraceae unclassified</i>
OTU 35	3.41	Control	0.042	<i>Lachnospiraceae NK4A136 group</i>
OTU 36	2.80	Control	0.021	<i>Oscillibacter</i>
OTU 38	2.87	Control	0.021	<i>Lachnospiraceae NK4A136 group</i>
OTU 40	3.03	Control	0.020	<i>Ruminiclostridium 5</i>
OTU 42	3.40	Control	0.021	<i>Lachnospiraceae NK4A136 group</i>
OTU 48	3.12	Control	0.018	<i>Lachnoclostridium</i>
OTU 53	2.96	Control	0.043	<i>Ruminococcaceae unclassified</i>
OTU 55	2.88	Control	0.042	<i>Ruminiclostridium</i>
OTU 59	2.88	Control	0.021	<i>Lachnospiraceae NK4A136 group</i>
OTU 63	2.78	Control	0.021	<i>Lachnospiraceae unclassified</i>
OTU 64	2.98	Control	0.042	<i>Lachnoclostridium</i>
OTU 65	3.62	Control	0.038	<i>Lachnospiraceae UCG-001</i>
OTU 71	3.16	Control	0.047	<i>Lachnospiraceae unclassified</i>
OTU 73	2.64	Control	0.021	<i>Lachnospiraceae uncultured</i>
OTU 76	2.71	Control	0.043	<i>Muribaculaceae ge</i>
OTU 78	2.65	Control	0.043	<i>Muribaculaceae ge</i>
OTU 83	2.18	Control	0.014	<i>Muribaculaceae ge</i>
OTU 84	2.40	Control	0.038	<i>Lachnospiraceae A2</i>
OTU 86	2.49	Control	0.020	<i>Lachnoclostridium</i>
OTU 87	2.13	Control	0.014	<i>Muribaculaceae ge</i>
OTU 89	2.25	Control	0.021	<i>Lachnospiraceae UCG-006</i>
OTU 98	2.61	Control	0.021	<i>Lachnospiraceae unclassified</i>