

Table S

The sequencing reads for the fecal microbiota.

Sample	Reads	Number of bases (bp)	AvgLen (bp)	GC (%)
LFC_1	30577	13277966	450.06	54.25
LFC_2	38477	16538406	452.82	54.57
LFC_3	32577	14053022	452.47	54.53
LFC_4	35364	15501163	449.78	54.46
LFC_5	43191	18820745	443.57	54.59
HFC_1	41954	18561463	444.34	54.43
HFC_2	43067	19112743	449.23	54.77
HFC_3	42094	18574565	445.35	54.92
HFC_4	43833	19410261	446.27	54.99
HFC_5	31971	14234128	446.75	54.55
HFP_1	38827	17032556	443.46	54.52
HFP_2	32309	14143669	446.06	54.3
HFP_3	39230	17158152	448.89	54.94
HFP_4	34574	15176861	447.95	55.04
HFP_5	35575	15635500	449.33	55.52
HFR_1	40693	17800284	444.74	55.28
HFR_2	44546	19542073	478	54.55
HFR_3	43978	19321780	464	54.52
HFR_4	31460	13743720	477	54.3
HFR_5	40709	17846117	452	54.94
Total	765006			

A

Cladogram



B

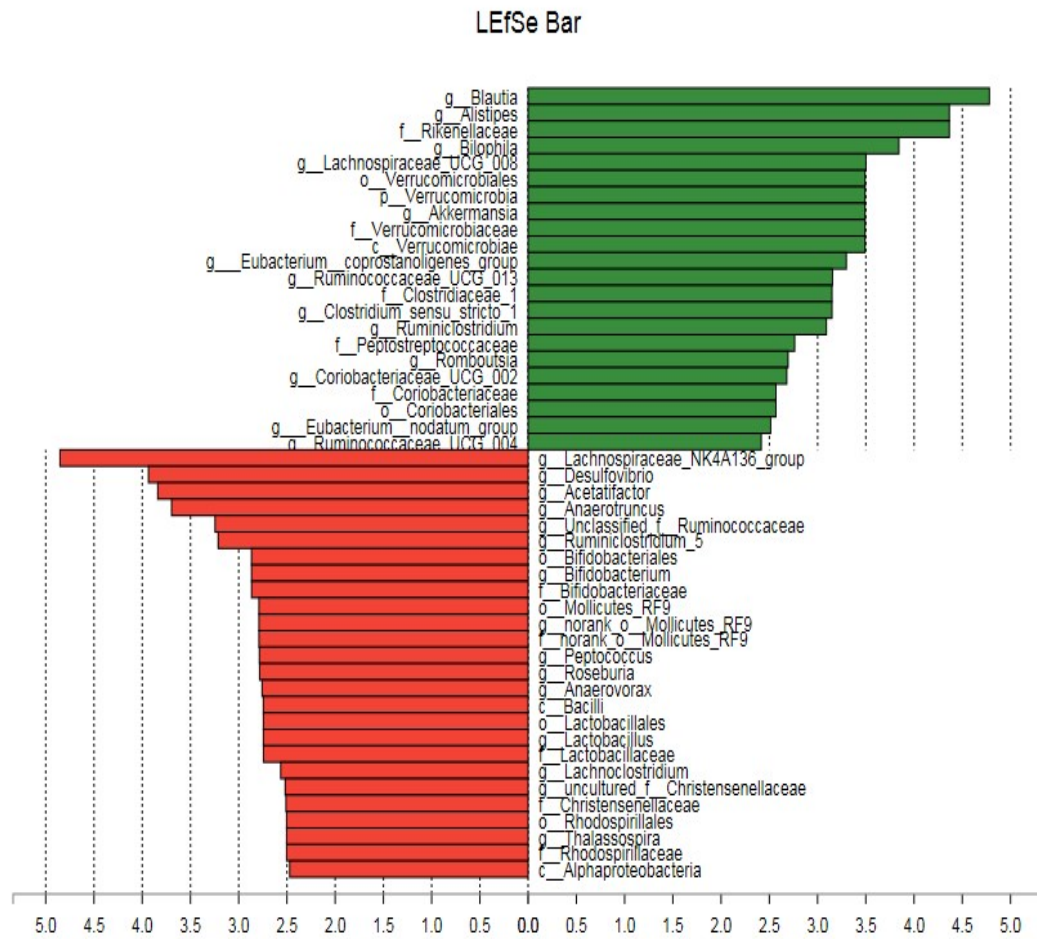


Fig. S. LEfSe analysis of key genera of gut microbiota in mice. (A) Taxonomic cladogram derived from LEfSe analysis of 16S rRNA sequences. (B) LDA score plot of bacterial taxa with LDA scores higher than 2.