

1 **Supplementary Materials**

2 **Table S1. Analysis of 16S rRNA gene sequences.**

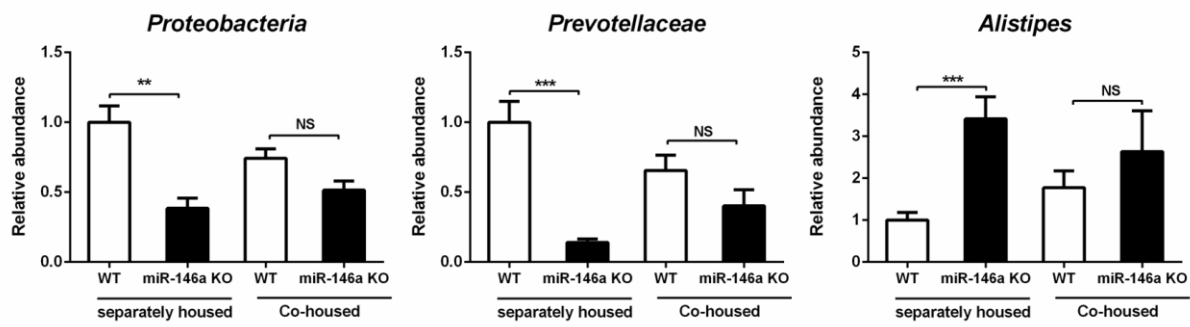
Sample Name	No.reads	Observed -species	Shannon	Simpson	Chao1	ACE	Good's coverage
WT 1	59,243	353	5.933	0.961	419.300	387.581	0.998
WT 2	50,362	355	6.218	0.972	366.447	372.208	0.999
WT 3	59,288	362	5.860	0.957	417.000	403.746	0.998
WT 4	67,117	360	5.905	0.964	465.286	412.770	0.998
WT 5	62,160	352	5.917	0.964	422.714	394.597	0.998
WT 6	48,838	353	6.137	0.967	373.517	375.591	0.999
WT 7	63,900	370	5.969	0.959	403.176	403.059	0.999
WT 8	61,243	362	6.189	0.969	397.037	392.522	0.999
miR146a KO 1	55,575	383	6.093	0.961	414.364	409.697	0.999
miR-146a KO 2	52,511	394	6.248	0.964	404.568	408.526	0.999
miR-146a KO 3	63,629	412	6.147	0.965	455.872	448.665	0.998
miR-146a KO 4	64,696	392	6.386	0.97	420.447	420.744	0.999
miR-146a KO 5	67,937	410	6.552	0.975	455.370	440.006	0.999
miR-146a KO 6	60,355	405	6.356	0.971	433.286	429.992	0.999
miR-146a KO 7	50,537	374	6.055	0.965	398.118	398.281	0.999
miR-146a KO 8	56,328	370	5.819	0.953	416.406	406.935	0.998

3 Number of sequences, observed-species, Shannon index, simpson index, Chao1 index, ACE index and Good's coverage
4 calculated for the microbial communities of lamb packaged in the VP and MAP environments for each storage period for
5 high-throughput sequence reads determined at a 97% similarity.

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7 **Table S2. Sequences of 16S rRNA V4 primer.**

16S rRNA V4 primers	Sequence (5' to 3')
515F	GTGCCAGCMGCCGCGGTAA
806R	GGACTACH-VGGGTWTCTAAT



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9 **Figure S1. Relative abundance of bacterial populations in separately housed and co-housed mice.** The
 10 results are means \pm SEM of 8 mice/group; significance of differences: *P < 0.05; **P < 0.01; ***P < 0.001; NS, no
 11 significance.

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