Electronic Supplementary Material (ESI) for Food & Function.

supplementary information

Fig. S1 Total energy intake per mice during 14 weeks.

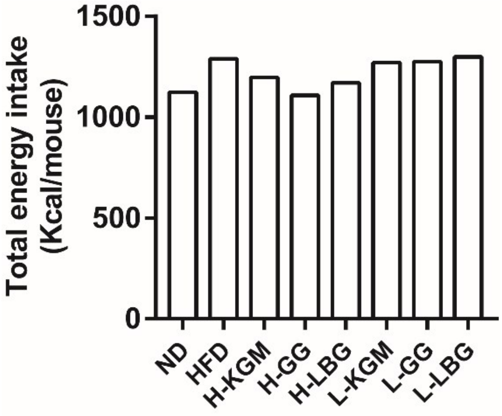


Fig. S2 Representative coat phenotype at different stages. **S2A&B**. At the 3th week and at the 10th week.

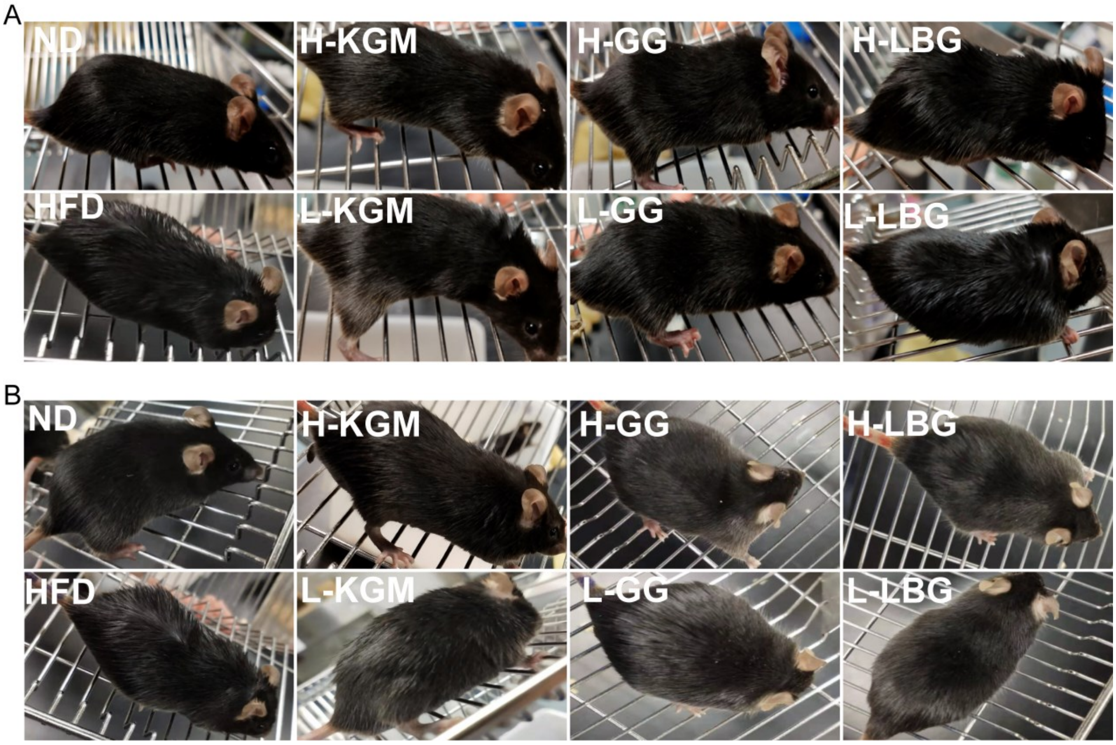


Fig. S3 Effects of mannan intervention on alpha diversity of gut microbiota. **A**. Observed OTUs. **B.** Ace index. **C**. Chao1 index. **D**. Simpson diversity index. **E**. Shannon diversity index. Data are shown as mean ± SD of mice (n=6) in each group. Statistical significances were assessed by Kruskal-Wallis test with Bonferroni correction. $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$.

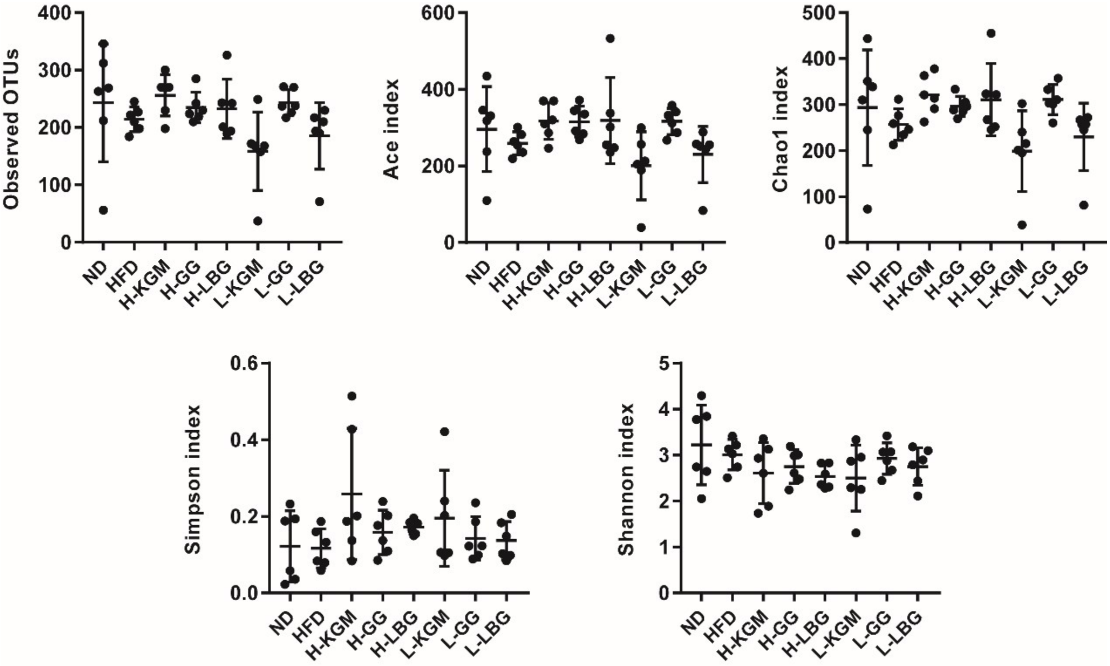
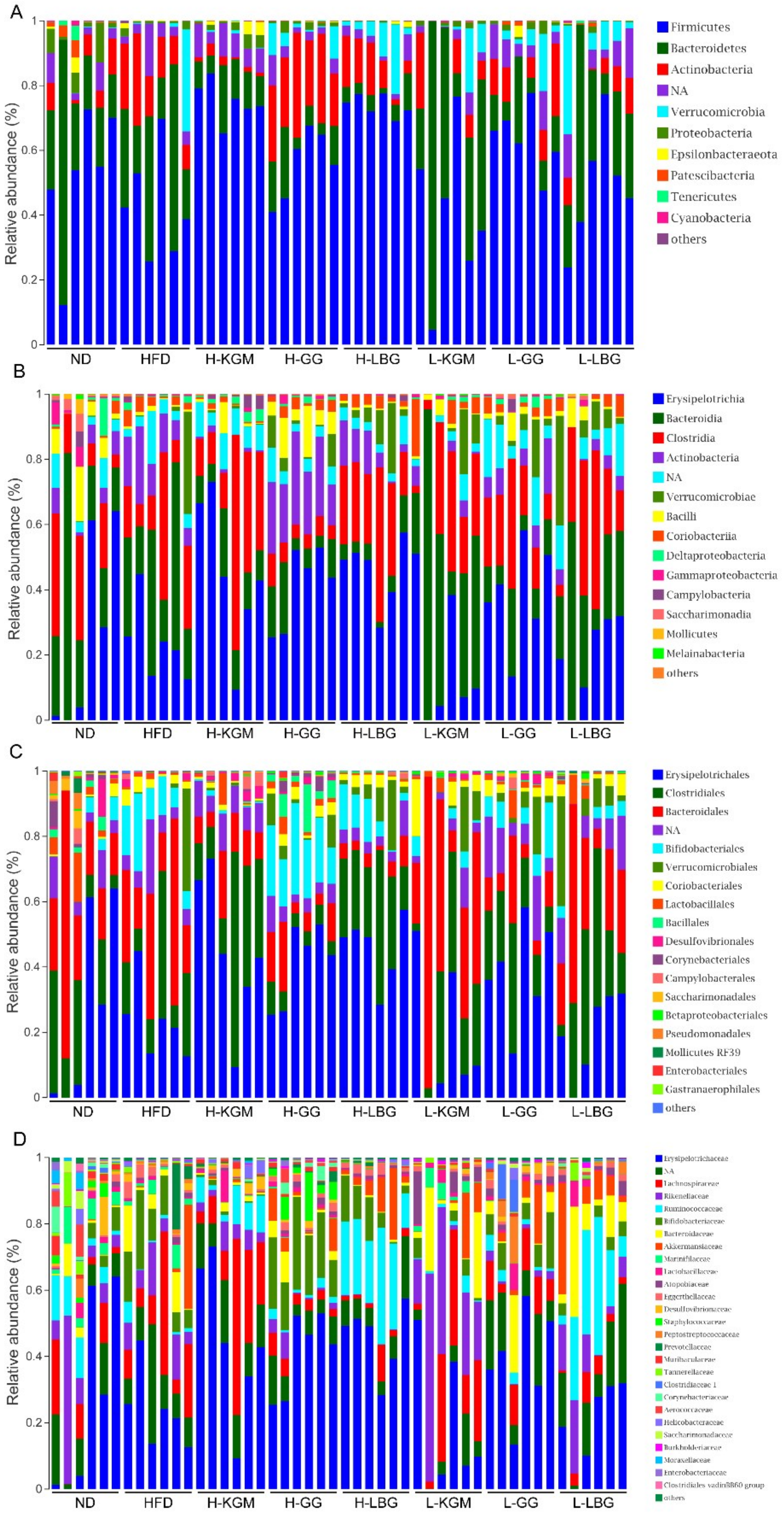


Fig. S4 Relative abundance of the gut microbiota in each of the mice at different taxonomic levels. **S4A-E**. At the phylum, class, order, family and genus level. Species with a relative abundance less than 1% in all samples were labeled as “others”.



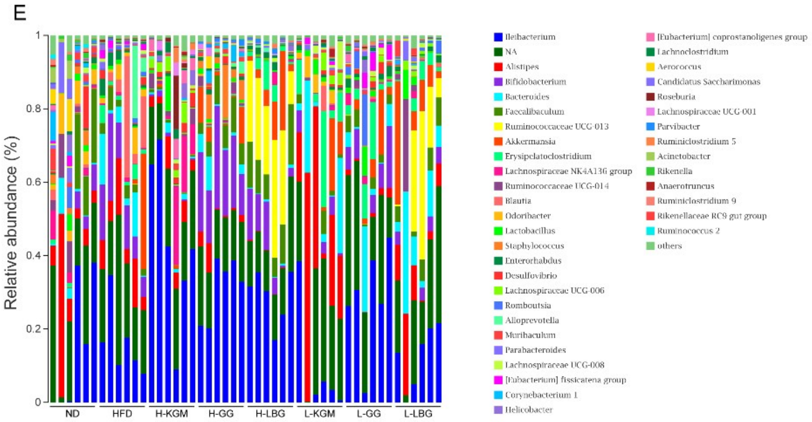

E
Relative abundance (%)
0
0.2
0.4
0.6
0.8
1
ND
HFD
H-KGM
H-GG
H-LBG
L-KGM
L-GG
L-LBG
Ileibacterium
NA
Alistipes
Bifidobacterium
Bacteroides
Faecalibaculum
Ruminococcaceae UCG-013
Akkermansia
Erysipelatoclostridium
Lachnospiraceae NK4A136 group
Ruminococcaceae UCG-014
Blautia
Odoribacter
Lactobacillus
Staphylococcus
Enterorhabdus
Desulfovibrio
Lachnospiraceae UCG-006
Romboutsia
Alloprevotella
Muribaculum
Parabacteroides
Lachnospiraceae UCG-008
[Eubacterium] fissicatena group
Corynebacterium 1
Helicobacter
[Eubacterium] coprostanoligenes group
Lachnoclostridium
Aerococcus
Candidatus Saccharimonas
Roseburia
Lachnospiraceae UCG-001
Parvibacter
Ruminiclostridium 5
Acinetobacter
Rikenella
Anaerotruncus
Ruminiclostridium 9
Rikenellaceae RC9 gut group
Ruminococcus 2
others

Table S1 Primers for real-time quantitative PCR

Genes	Forward primer (5' to 3')	Reverse primer (5' to 3')
β-actin	TCATCACTATTGGCAACGAGCG	CGGATGTCAACGTCACACTTCA
SREBP-2	GCGTTCTGGAGACCATGGA	ACAAAGTTGCTCTGAAAACAAATCA
HMGCR	TTCACGCTCATAGTCGC	AGGCTAAACTCAGGGTAAT
PPAR-γ	CAGGCTTGCTGAACGTGAAG	GGAGCACCTTGGCGAACA
CD11c	CTGGATAGCCTTTCTTCTGCTG	GCACACTGTGTCCGAACTC
leptin	CCTGTGGCTTTGGTCCTATCTG	AGGCAAGCTGGTGAGGATCTG
adiponectin	AGGTTGGATGGCAGGC	GTCTCACCCTTAGGACCAAGAA
TNF-α	ACGGCATGGATCTCAAAGAC	AGATAGCAAATCGGCTGACG
LBP	GTCCTGGGAATCTGTCCTTG	CCGGTAACCTTGCTGTTGTT
MCP-1	TTAAAAACCTGGATCGGAACCAA	GCATTAGCTTCAGATTTACGGGT

Table. S2 The taxonomic information and Spearman correlation coefficient between OTUs and obesity-related indexes of the 73 OTUs.

							Correlation				
	domain	Phylum	Class	Order	Family	Genus	body_weight	liver_weight	eAT_weight	Glucose	TC
OTU002	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium 1	-0.4146361				
OTU015	Bacteria	Tenericutes	Mollicutes	Mollicutes RF39	NA	NA	-0.5465852	-0.5486738	-0.520128	-0.39669	
OTU026	Bacteria	Firmicutes	Clostridia	Clostridiales	NA	NA	0.37078014	0.47286555	0.3888271		0.399297
OTU037	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Aerococcus	-0.4936704	-0.507139	-0.538039	-0.38741	-0.42947
OTU066	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	Saccharimonadaceae	Candidatus Saccharimonas	-0.4169563	-0.3993995	-0.516672	-0.41054	-0.39957
OTU080	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Muribaculaceae	Muribaculum	-0.5602326	-0.5074035	-0.502675		-0.36943
OTU098	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	Christensenella	0.43003064	0.55591781	0.4609432	0.388804	0.511944
OTU121	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Eisenbergiella	-0.3814462		-0.409256		
OTU147	Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	-0.4614115	-0.3709453	-0.495931		
OTU216	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA	0.41238618		0.3777211		
OTU220	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Ileibacterium	0.38476028				
OTU228	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA	0.39251339	0.53692806	0.5034939	0.386081	0.522424
OTU233	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae UCG-008	0.37148057	0.40947074			
OTU255	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA	0.39614412	0.51781447	0.4780112	0.452146	0.425651
OTU295	NA	NA	NA	NA	NA	NA	-0.3782393				
OTU308	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA	-0.4396395	-0.3899317	-0.376865		-0.42297
OTU452	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	NA	-0.3841244			-0.37655	
OTU459	Bacteria	Firmicutes	Clostridia	Clostridiales	Family XI_2	W5053	0.42942927	0.47223896			
OTU463	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelatoclostridium	0.42542336	0.46917004	0.4815307	0.385258	0.50749
OTU464	Bacteria	Firmicutes	Bacilli	Bacillales	Family XI	Gemella	0.36962508				
OTU468	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	[Eubacterium] fissicatena group	0.53393334	0.59700016	0.4649954	0.438415	0.584533
OTU530	Bacteria	Firmicutes	NA	NA	NA	NA	0.4440608	0.42192868	0.4356077		0.369609
OTU555	NA	NA	NA	NA	NA	NA	-0.4151072	-0.3845091			
OTU579	Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	-0.5335109	-0.4672753	-0.506396		
OTU590	Bacteria	Tenericutes	Mollicutes	Mollicutes RF39	NA	NA	-0.418132				
OTU594	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA	-0.389528	-0.3960786			
OTU596	Bacteria	Firmicutes	NA	NA	NA	NA	-0.480932	-0.4244523	-0.453801		-0.41778
OTU612	Bacteria	Firmicutes	NA	NA	NA	NA	-0.379569	-0.3927634	-0.384668		
OTU613	Bacteria	Firmicutes	NA	NA	NA	NA	-0.5334638	-0.4128459	-0.510486		
OTU652	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium 1	-0.4467618	-0.3698109	-0.416735		-0.36959
OTU699	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA	0.39174344				
OTU738	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA	0.37191603	0.48585851	0.4128282		
OTU803	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA	-0.5187117	-0.623712	-0.511872		-0.56219
OTU816	Bacteria	Firmicutes	Clostridia	Clostridiales	NA	NA	-0.4400323		-0.452161		
OTU025	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus 1		-0.4781344			
OTU055	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-014		-0.5146458			

OTU170	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia		0.4631096	0.4174938		
OTU176	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA		0.41023406			
OTU239	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-010		-0.3804855			
OTU256	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelatoclostridium		0.4107066			0.414312
OTU267	Bacteria	Firmicutes	Clostridia	Clostridiales	Family XI_2II	[Eubacterium] brachy group		0.40015537	0.4292542		
OTU282	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	NA		0.44936415			
OTU286	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae UCG-008		0.39228244			
OTU363	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Tyzzerella		0.38142687			
OTU477	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae UCG-001		0.44341764			
OTU490	Bacteria	Patescibacteria	WS6 (Dojkabacteria)	NA	NA	NA		0.37016614			
OTU552	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-014		-0.4176079			
OTU789	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter		0.39953658			
OTU171	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA			0.429176	0.474985	0.457019
OTU175	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA			0.3814708		
OTU258	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA			0.4586384		
OTU277	NA	NA	NA	NA	NA	NA			0.3884801		
OTU309	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Anaerotruncus			0.4223017	0.406805	
OTU354	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA			0.3796831	0.410148	0.388651
OTU446	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA			0.4776472	0.392338	0.450289
OTU493	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	NA			0.3816834		
OTU499	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	NA			0.3932691		
OTU618	Bacteria	Actinobacteria	Actinobacteria	NA	NA	NA			-0.381827		
OTU834	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA			-0.371946		
OTU542	NA	NA	NA	NA	NA	NA				0.410965	0.377365
OTU186	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA					0.386189
OTU231	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Ileibacterium					-0.37526
OTU238	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA					0.440849
OTU291	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	NA	NA					-0.46937
OTU347	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia					-0.38045
OTU373	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-010					-0.39155
OTU376	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA					0.398406
OTU388	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter					-0.48125
OTU421	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA					0.413501
OTU428	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes					0.386027
OTU481	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Herbaspirillum					0.409077
OTU522	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes					0.410812
OTU806	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA					-0.37381