Table S1. Significantly enriched pathway following the intervention.

Pathway	DEGs with pathway annotation	All Genes with Pathway Annotation	P value	FDR	Pathway id
HF *vs* NC					
Metabolic pathways	103	1295	0.00000	0.00000	rno01100
Fatty acid metabolism	15	53	0.00000	0.00001	rno01212
PPAR signaling pathway	17	79	0.00000	0.00001	rno03320
Steroid biosynthesis	8	20	0.00001	0.00048	rno00100
Biosynthesis of unsaturated fatty acids	8	27	0.00005	0.00216	rno01040
Fatty acid degradation	9	47	0.00030	0.01002	rno00071
Carbon metabolism	14	121	0.00085	0.01982	rno01200
Steroid hormone biosynthesis	10	80	0.00271	0.03957	rno00140
Fatty acid elongation	5	27	0.00758	0.07716	rno00062
Citrate cycle (TCA cycle)	5	32	0.01399	0.13094	rno00020
Glycolysis / Gluconeogenesis	8	75	0.01586	0.13743	rno00010
alpha-Linolenic acid metabolism	4	25	0.02538	0.18560	rno00592
Glyoxylate and dicarboxylate metabolism	4	25	0.02538	0.18560	rno00630
Linoleic acid metabolism	5	40	0.03042	0.20935	rno00591
Bile secretion	7	72	0.03486	0.22180	rno04976
Propanoate metabolism	4	29	0.03871	0.22647	rno00640
Glycerophospholipid metabolism	8	92	0.04232	0.23577	rno00564
AMPK signaling pathway	10	130	0.04851	0.25924	rno04152
HF *vs* GB					
PPAR signaling pathway	4	79	0.00552	0.15730	rno03320
Bile secretion	3	27	0.02612	0.27447	rno04976
Steroid hormone biosynthesis	3	80	0.03384	0.27559	rno00140
GB *vs* NB					
Steroid hormone biosynthesis	10	80	0.00000	0.00040	rno00140
Biosynthesis of unsaturated fatty acids	6	27	0.00002	0.00130	rno01040
PPAR signaling pathway	8	79	0.00016	0.00695	rno03320
Fatty acid metabolism	5	53	0.00363	0.06393	rno01212
Linoleic acid metabolism	4	40	0.00757	0.12107	rno00591
Bile secretion	5	72	0.01193	0.13998	rno04976
Metabolic pathways	35	1295	0.01330	0.14632	rno01100
Arachidonic acid metabolism	5	78	0.01610	0.14910	rno00590
Primary bile acid biosynthesis	2	16	0.03980	0.28664	rno00120

NC: normal diet group; HF: high-fat diet group; NB: high-fat diet containing untreated bran; GB: high-fat diet containing GABA-enrich wheat bran.