Supplementary Figure

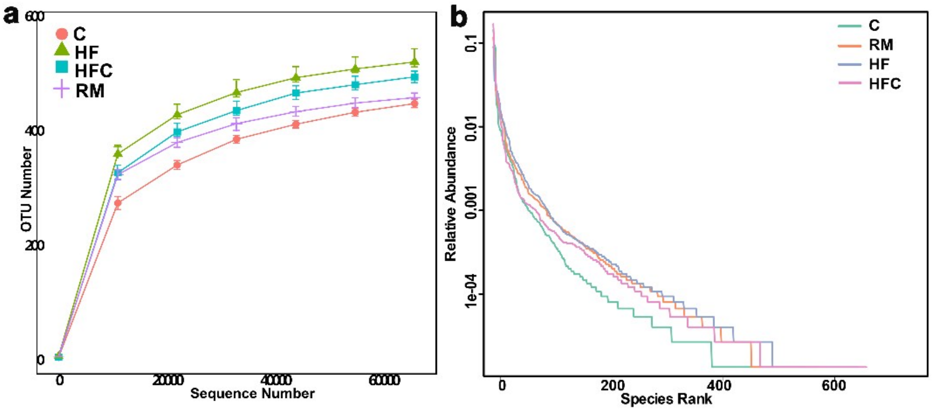

Figure 1. The biodiversity curves of gut microbiota. a, The rarefaction curve of gut microbiota based on random extraction of sequencing data from samples. b, Rank abundance based on the relative abundance of OTUs.

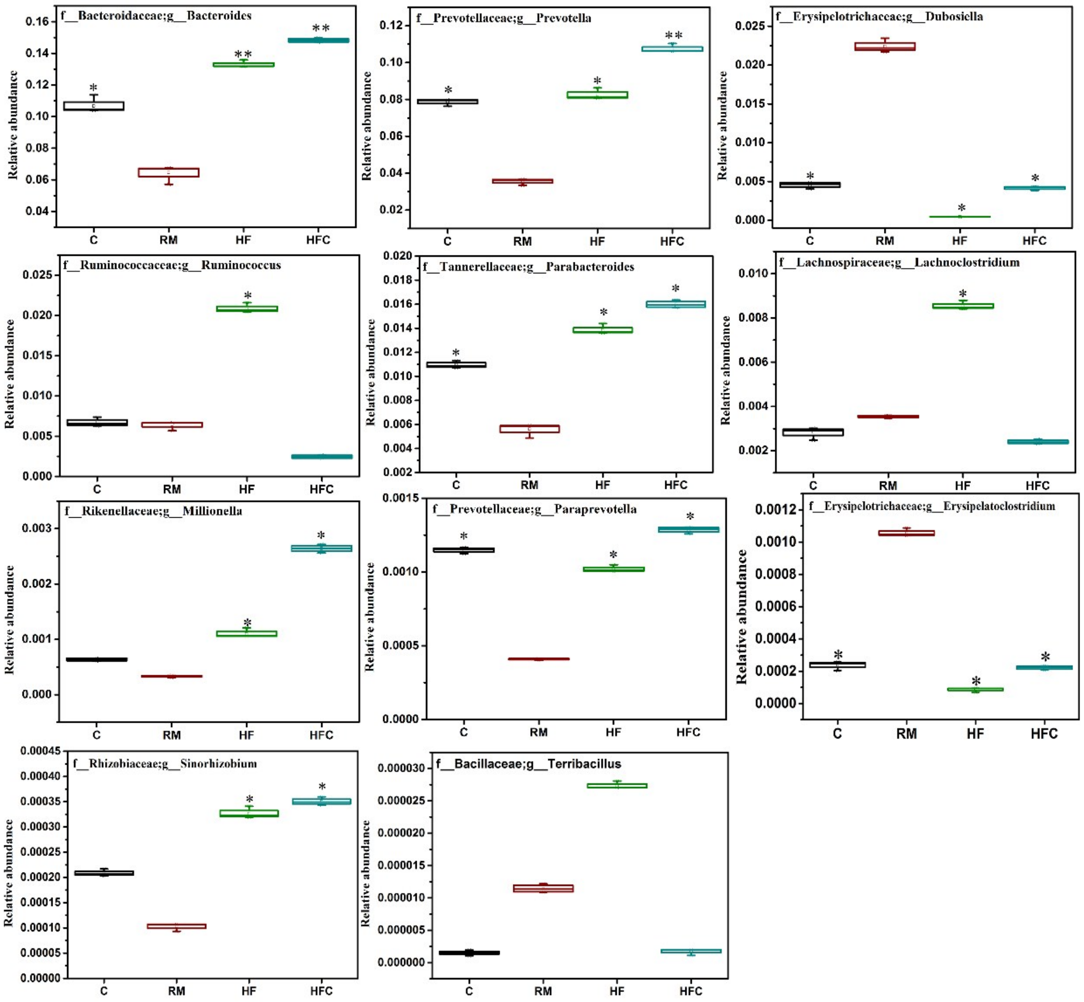

Figure 2. The significant difference of species relative to the diet groups. Note: * and ** indicate significant ($p < 0.05$) and highly significant differences ($p < 0.01$) with RM group.

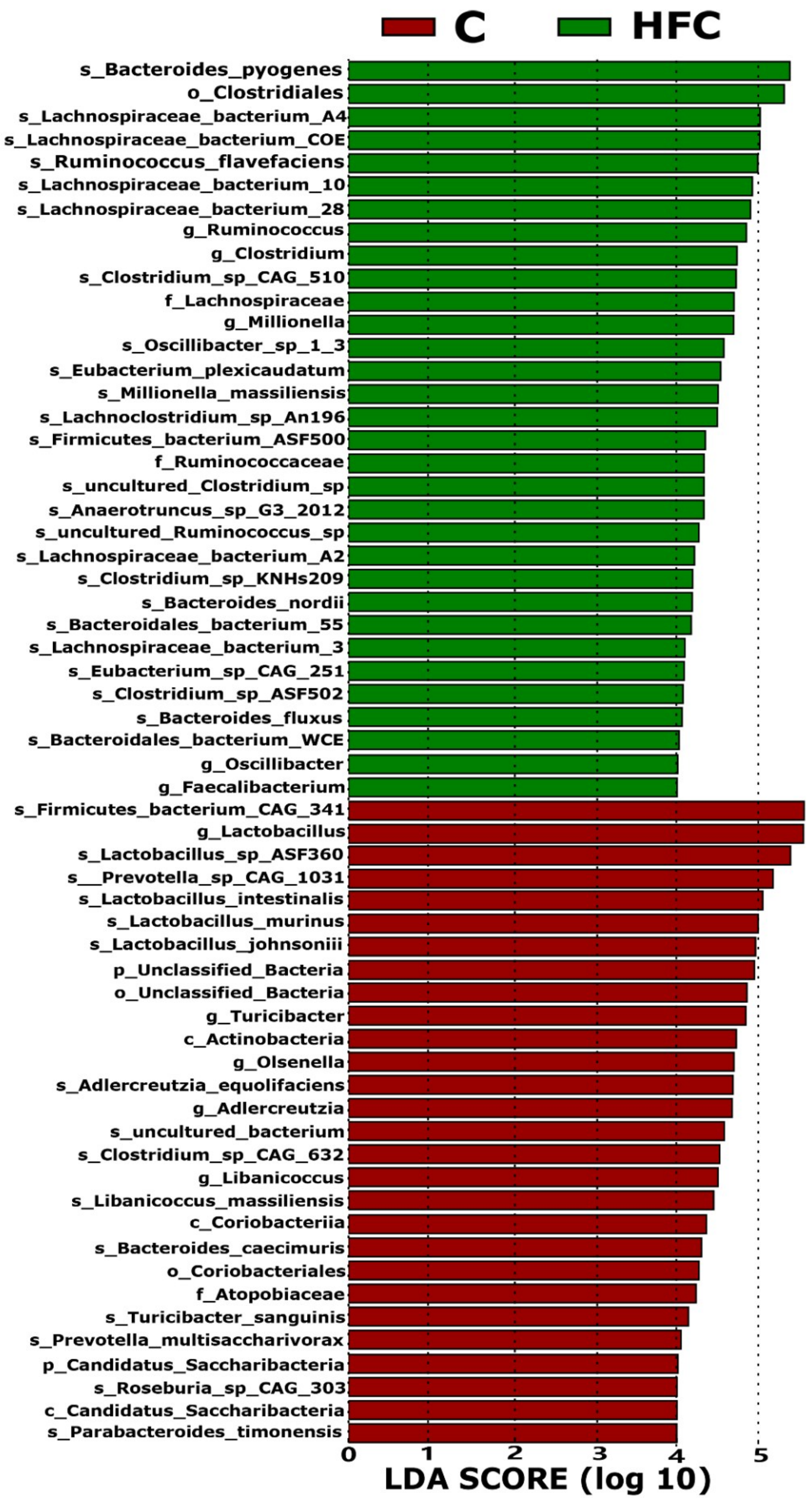

Figure 3. The linear discriminant analysis (LDA) value distribution histogram (default setting is 4) of the C (control diet) and HFC (fiber-rich diet with an AMPK restriction) groups.

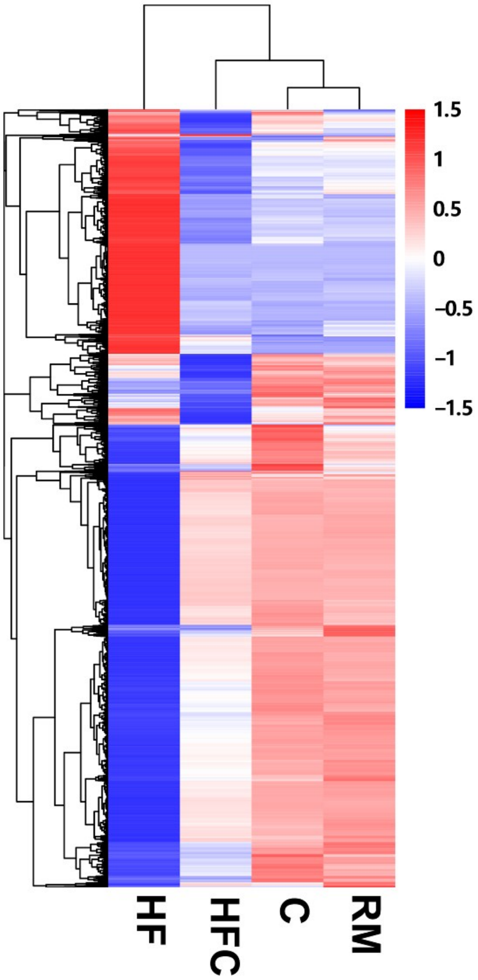

Figure 4. The heat map depicting transcript profiling of genes expressed in intestinal epithelial tissue. The color ranges represents expression level, where red represents highly expressed genes, blue represents poorly expressed genes.

Supplymentary Table

Table 1 Ingredient lists daily intake for the designed diets

	C	RM	HF	HFC
Dietary fiber (g/kg)	1.53%	1.11%	7.87%	7.87%
Red meat (g/kg)	-	21.45%	20.08%	20.08%
Tallow (g/kg)	5.90%	6.38%	5.83%	5.83%
Total food intake (g)	53.86	109.35	78.63	58.12
Daily food intake (g)	1.92	3.91	2.81	2.08
Fiber intake (g)	0.03	0.04	0.22	0.16
Fat intake (g)	0.11	0.25	0.16	0.12
Protein intake (g)	0.35	1.09	0.80	0.59

Note: Data are presented as the mean values (n =10); The capital letter combinations represent the different diet group. Expressed as % of sample dry matter. Dietary fiber, fat and protein intake contributions to total food intake were estimated by assuming from the diet composition and logs database.

Table 2 Analysis of species diversity within samples on each diet

Sample name	observed_ species	chao1	ACE	shannon	simpson	goods_ coverage	PD_whole_ tree
C	650	724	742	5.404	0.906	0.998	44.60
RM	670	748	762	4.672	0.883	0.998	48.61
HF	689	814	790	5.811	0.951	0.998	53.65
HFC	676	775	785	5.604	0.938	0.998	51.98

Note: The diversity index represents the richness and evenness of species in microbal community.The increased figure of observed_species, Chao1, ACE and PD_whole_tree indicate an upward trend in abundance of species; the increase in shannon and simpson suggests an enhanced evenness of species. The goods_coverage is an index of sequencing depth in the method.

Table 3 The difference of each individual's gut microbiota based on their diet communities (α diversity)

	Wilcoxon-test					**Tukey-test**			
	difference	*p*-value	sig.	LCL	UCL	difference	lwr	upr	*p*-adjust
shannon									
RM-C	-3.667	0.104		-8.279	0.945	-0.600	-1.781	0.581	0.416
HF-C	4.667	0.048	*	0.055	9.279	0.907	-2.088	0.274	0.042
C-HFC	-2.333	0.277		-6.945	2.279	-0.432	-1.613	0.749	0.660
RM-HF	-7.000	0.008	**	-11.612	-2.388	-1.339	-2.520	0.158	0.003
RM-HFC	-6.000	0.017	*	-10.612	-1.388	-1.032	-0.149	2.213	0.038
HF-HFC	1.000	0.631		-3.612	5.612	0.306	-1.487	0.875	0.839
simpson									
C-HF	1.000	0.766		-6.492	8.492	-22.840	-158.743	113.062	0.947
C-HFC	1.333	0.692		-6.159	8.825	-43.225	-179.128	92.677	0.744
C-RM	-1.667	0.022	*	-9.159	5.825	4.566	-131.336	140.468	0.015
HF-HFC	0.333	0.921		-7.159	7.825	-20.385	-156.287	115.517	0.961
HF-RM	-2.667	0.055		-10.159	4.825	27.406	-108.496	163.309	0.914
HFC-RM	-3.000	0.018	*	-10.492	4.492	47.791	-88.111	183.694	0.012

Note: Asterisks indicate significant differences: * only means significant difference ($p < 0.05$); ** means highly significant difference ($p < 0.01$). LCL and lwr, lower confidence limits for difference; UCL and upr, upper confidence limits for difference.

Table 4 The Operational Taxonomic Units (OUTs) relative abundances for groups at phylum level

Taxonomy	Firmicutes	Bacteroidetes	Verrucomicrobia	Proteobacteria	Actinobacteria	unidentified_Bacteria	Tenericutes	Fusobacteria	Spirochaetes	Gracilibacteria	Others
C	0.322273	0.492552	0.14607	0.020003	0.012282	0.004621	0.000598	0.000329	0.000056	0.000005	0.001211
RM	0.557199	0.43611	0.001705	0.00494	0.001000	0.002474	0.001545	0.000334	0.000172	0.000015	0.000005
HF	0.345813	0.559322	0.053700	0.02469	0.011614	0.001995	0.001443	0.000628	0.000111	0.000091	0.000593
HFC	0.29623	0.61645	0.061068	0.011045	0.012065	0.001141	0.000618	0.000846	0.000066	0.000005	0.000466

Table 5 The Operational Taxonomic Units (OUTs) relative abundances for groups at genus level

Taxonomy	**C**	**RM**	**HF**	**HFC**	**Tax_detail**
Akkermansia	3.99%	0.17%	10.60%	6.87%	p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae
Lactobacillus	5.48%	14.35%	9.34%	19.66%	p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae
Dubosiella	9.69%	14.08%	7.63%	10.18%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae
Turicibacter	10.60%	1.75%	0.47%	0.41%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae
Alloprevotella	3.04%	0.67%	4.09%	3.19%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae
unidentified_Lachnospiraceae	0.69%	1.75%	2.08%	3.12%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Lachnoclostridium	0.42%	0.51%	1.73%	0.23%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Desulfovibrio	0.42%	1.39%	0.27%	0.14%	p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae
Bacteroides	0.54%	1.22%	2.53%	2.33%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae
unidentified_Ruminococcaceae	0.90%	1.50%	0.91%	0.97%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Faecalibaculum	1.04%	0.06%	0.07%	0.05%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae
Muribaculum	0.63%	0.62%	0.83%	1.31%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae
Alistipes	1.54%	1.51%	0.72%	0.47%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae
Bifidobacterium	0.35%	0.34%	0.74%	0.54%	p__Actinobacteria;c__unidentified_Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae
Parabacteroides	0.24%	0.44%	0.77%	0.29%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae
Blautia	0.52%	0.05%	0.71%	0.59%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Odoribacter	0.26%	0.64%	0.25%	0.11%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae
Millionella	0.27%	0.16%	0.41%	0.05%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae
Streptococcus	0.22%	0.16%	0.45%	0.15%	p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae
Neisseria	0.14%	0.07%	0.42%	0.09%	p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Neisseriaceae
Rikenella	0.18%	0.34%	0.33%	0.05%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae
Helicobacter	0.27%	0.32%	0.15%	0.14%	p__unidentified_Bacteria;c__unidentified_Bacteria;o__Campylobacterales;f__Helicobacteraceae
Oscillibacter	0.04%	0.29%	0.13%	0.22%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Erysipelatoclostridium	0.06%	0.32%	0.07%	0.13%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae
Roseburia	0.08%	0.05%	0.45%	0.36%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Porphyromonas	0.13%	0.37%	0.20%	0.12%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae
Intestinimonas	0.05%	0.08%	0.25%	0.13%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Parasutterella	0.06%	0.34%	0.24%	0.24%	p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae
Ruminiclostridium	0.07%	0.21%	0.12%	0.15%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Anaerostipes	0.00%	0.18%	0.03%	0.00%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
unidentified_Enterobacteriaceae	0.02%	0.03%	0.01%	0.16%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;

					o__Enterobacteriales;f__Enterobacteriaceae;
unidentified_Prevotellaceae	0.15%	0.08%	0.28%	0.07%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales; f__Prevotellaceae
Enterorhabdus	0.17%	0.29%	0.27%	0.14%	p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales; f__Eggerthellaceae
Faecalibacterium	0.00%	0.03%	0.24%	0.09%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Phyllobacterium	0.00%	0.01%	0.00%	0.16%	p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales; f__Rhizobiaceae
Prevotella	0.08%	0.13%	0.15%	0.03%	p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae
Lachnospira	0.00%	0.00%	0.22%	0.04%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Anaerotruncus	0.02%	0.15%	0.19%	0.05%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
unidentified_Clostridiales	0.19%	0.20%	0.14%	0.10%	p__Firmicutes;c__Clostridia;o__Clostridiales; f__unidentified_Clostridiales
Veillonella	0.11%	0.04%	0.10%	0.06%	p__Firmicutes;c__Negativicutes;o__Selenomonadales; f__Veillonellaceae
Fusicatenibacter	0.00%	0.21%	0.00%	0.06%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Gemella	0.06%	0.06%	0.14%	0.05%	p__Firmicutes;c__Bacilli;o__Bacillales;f__unidentified_Bacillales
Corynebacterium	0.05%	0.00%	0.00%	0.10%	p__Actinobacteria;c__unidentified_Actinobacteria; o__Corynebacteriales;f__Corynebacteriaceae
Granulicatella	0.10%	0.03%	0.14%	0.14%	p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae
Actinomyces	0.05%	0.00%	0.03%	0.09%	p__Actinobacteria;c__unidentified_Actinobacteria; o__Actinomycetales;f__Actinomycetaceae
Tyzzerella	0.02%	0.12%	0.06%	0.03%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Acinetobacter	0.00%	0.00%	0.04%	0.07%	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Moraxellaceae
Marvinbryantia	0.09%	0.09%	0.08%	0.07%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Subdoligranulum	0.00%	0.07%	0.02%	0.00%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Lautropia	0.07%	0.01%	0.04%	0.06%	p__Proteobacteria;c__Gammaproteobacteria; o__unidentified_Gammaproteobacteria;f__Burkholderiaceae
Romboutsia	0.06%	0.08%	0.06%	0.06%	p__Firmicutes;c__Clostridia;o__Clostridiales; f__Peptostreptococcaceae
Rothia	0.03%	0.01%	0.03%	0.06%	p__Actinobacteria;c__unidentified_Actinobacteria; o__Micrococcales;f__Micrococcaceae
Megamonas	0.00%	0.00%	0.00%	0.05%	p__Firmicutes;c__Negativicutes;o__Selenomonadales; f__Veillonellaceae
unidentified_Erysipelotrichaceae	0.00%	0.05%	0.01%	0.01%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales; f__Erysipelotrichaceae
Abiotrophia	0.05%	0.01%	0.05%	0.01%	p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae
Dialister	0.00%	0.06%	0.01%	0.04%	p__Firmicutes;c__Negativicutes;o__Selenomonadales; f__Veillonellaceae
Candidatus_Saccharimonas	0.06%	0.02%	0.01%	0.00%	p__unidentified_Bacteria;c__unidentified_Bacteria; o__unidentified_Bacteria;f__unidentified_Bacteria
Delftia	0.00%	0.00%	0.00%	0.05%	p__Proteobacteria;c__Gammaproteobacteria; o__unidentified_Gammaproteobacteria;f__Burkholderiaceae

Collinsella	0.00%	0.05%	0.05%	0.02%	p__Actinobacteria;c__Coriobacteriia; o__Coriobacteriales;f__Coriobacteriaceae
Candidatus_Arthromitus	0.03%	0.05%	0.01%	0.06%	p__Firmicutes;c__Clostridia;o__Clostridiales; f__unidentified_Clostridiales
Gordonibacter	0.01%	0.01%	0.08%	0.02%	p__Actinobacteria;c__Coriobacteriia; o__Coriobacteriales;f__Eggerthellaceae
Leptotrichia	0.02%	0.01%	0.02%	0.04%	p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales; f__Leptotrichiaceae
Capnocytophaga	0.03%	0.02%	0.03%	0.05%	p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales; f__Flavobacteriaceae
Comamonas	0.01%	0.01%	0.00%	0.03%	p__Proteobacteria;c__Gammaproteobacteria; o__unidentified_Gammaproteobacteria;f__Burkholderiaceae
Bergeyella	0.01%	0.03%	0.01%	0.01%	p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales; f__unidentified_Flavobacteriales
Staphylococcus	0.00%	0.03%	0.02%	0.00%	p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae
Fusobacterium	0.02%	0.02%	0.05%	0.03%	p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales; f__Fusobacteriaceae
Cardiobacterium	0.01%	0.00%	0.00%	0.04%	p__Proteobacteria;c__Gammaproteobacteria; o__Cardiobacteriales;f__Cardiobacteriaceae
Butyricicoccus	0.01%	0.00%	0.07%	0.05%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Pediococcus	0.01%	0.00%	0.03%	0.01%	p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae
Peptostreptococcus	0.00%	0.00%	0.01%	0.03%	p__Firmicutes;c__Clostridia;o__Clostridiales; f__Peptostreptococcaceae
Adlercreutzia	0.02%	0.03%	0.02%	0.04%	p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales; f__Eggerthellaceae
Catonella	0.01%	0.02%	0.03%	0.02%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Flavonifractor	0.00%	0.02%	0.03%	0.02%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Pseudomonas	0.01%	0.00%	0.01%	0.02%	p__Proteobacteria;c__Gammaproteobacteria; o__Pseudomonadales;f__Pseudomonadaceae
Anaeroplasma	0.00%	0.02%	0.00%	0.01%	p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales; f__Anaeroplasmataceae
Bacillus	0.00%	0.00%	0.01%	0.02%	p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae
Dorea	0.00%	0.04%	0.02%	0.01%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Faecalitalea	0.00%	0.03%	0.00%	0.00%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales; f__Erysipelotrichaceae
Lachnoanaerobaculum	0.02%	0.01%	0.02%	0.02%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
Planococcus	0.00%	0.00%	0.00%	0.02%	p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae
Harryflintia	0.01%	0.02%	0.03%	0.01%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
Solobacterium	0.01%	0.00%	0.04%	0.02%	p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales; f__Erysipelotrichaceae
Acetatifactor	0.00%	0.02%	0.00%	0.00%	p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
unidentified_Veillonellaceae	0.02%	0.00%	0.01%	0.00%	p__Firmicutes;c__Negativicutes;o__Selenomonadales; f__Veillonellaceae
Sutterella	0.00%	0.04%	0.00%	0.02%	p__Proteobacteria;c__Gammaproteobacteria;

					o__unidentified_Gammaproteobacteria; f__Burkholderiaceae
Oribacterium	0.02%	0.00%	0.01%	0.01%	p__Firmicutes;c__Clostridia;o__Clostridiales; f__Lachnospiraceae
unidentified_Spirochaetaceae	0.01%	0.02%	0.01%	0.01%	p__Spirochaetes;c__Spirochaetia;o__Spirochaetales; f__Spirochaetaceae
Campylobacter	0.02%	0.01%	0.03%	0.02%	p__unidentified_Bacteria;c__unidentified_Bacteria; o__Campylobacterales;f__Campylobacteraceae
Candidatus_Stoquefichus	0.00%	0.02%	0.00%	0.02%	p__Firmicutes;c__Erysipelotrichia; o__Erysipelotrichales;f__Erysipelotrichaceae
Asteroleplasma	0.00%	0.01%	0.00%	0.00%	p__Firmicutes;c__Erysipelotrichia; o__Erysipelotrichales;f__Erysipelotrichaceae
Bilophila	0.00%	0.01%	0.02%	0.00%	p__Proteobacteria;c__Deltaproteobacteria; o__Desulfovibrionales;f__Desulfovibrionaceae
Stenotrophomonas	0.00%	0.00%	0.01%	0.01%	p__Proteobacteria;c__Gammaproteobacteria; o__Xanthomonadales;f__Xanthomonadaceae
Others	56.35%	53.74%	50.02%	44.18%	Others

Table 6 The KEGG Ortholog groups (KOs) and enzymes (ECs) associated with short chain fatty acids (SCFAs) metabolism

KO ID	C	RM	HF	HFC	KO EC	C	RM	HF	HFC	KEGG Description
Acetate										
K01284	0.000320	0.00019	0.00037	0.00046	2.7.1.40	0.00025	0.00047	0.00021	0.00024	pyk | pyruvate kinase
K00656	0.00025	0.00051	0.00016	0.00018	2.3.1.54	0.00025	0.00051	0.00016	0.00018	pflD | formate C-acetyltransferase
K00172	3.3E-05	4.1E-05	5.7E-05	2.1E-05	1.2.7.1	0.00013	0.00016	0.00019	7.6E-05	porG | pyruvate ferredoxin oxidoreductase gamma subunit
K00158	6.5E-05	4.8E-05	2E-06	5E-06	1.2.3.3	6.5E-05	4.8E-05	2E-06	5E-06	poxL | pyruvate oxidase
K04073	1E-06	3E-06	1E-06	0	1.2.1.10	1E-06	3E-06	1E-06	0	mhpF | acetaldehyde dehydrogenase
K01895	7.1E-05	6.7E-05	0.00013	0.00012	6.2.1.1	6.7E-05	7.1E-05	0.00013	0.00012	acs | acetyl-CoA synthetase
K00625	0.0003	0.00029	0.00024	0.00031	2.3.1.8	0.00034	0.00031	0.00025	0.00032	pta | phosphate acetyltransferase
K01026	7.4E-05	0.0002	1.1E-05	4.4E-05	2.8.3.1	7.4E-05	0.0002	1.1E-05	4.4E-05	pct | propionate CoA-transferase
K00128	7.3E-05	0.00024	4.8E-05	6.5E-05	1.2.1.3	7.3E-05	0.00024	4.8E-05	6.5E-05	ALDH | aldehyde dehydrogenase (NAD+)
K00925	0.00036	0.00036	0.00028	0.00031	2.7.2.1	0.00036	0.00036	0.00028	0.00031	ackA | acetate kinase
K01512	9.7E-05	0.00013	2.4E-05	3.4E-05	3.6.1.7	9.7E-05	0.00013	2.4E-05	3.4E-05	acyP | acylphosphatase
Butanoate										
K00626	0.00013	0.00021	6.2E-05	5.6E-05	2.3.1.9	0.00013	0.00021	6.2E-05	5.6E-05	atoB | acetyl-CoA C-acetyltransferase
K00074	0.000110	0.00024	5.7E-05	6.5E-05	1.1.1.157	0.00011	0.00024	5.7E-05	6.5E-05	paaH, hbd, fadB, mmgB | 3-hydroxybutyryl-CoA dehydrogenase
K01715	7.2E-05	0.00014	5.7E-05	0.00004	4.2.1.17	7.2E-05	0.00014	6.2E-05	0.00004	crt | enoyl-CoA hydratase
K00248	0.000030	0.000040	0.000080	0.000020	1.3.8.1	0.000030	0.000040	0.000080	0.000020	bcd | butyryl-CoA dehydrogenase
K00634	2.1E-05	1.9E-05	4.1E-05	2.5E-05	2.3.1.19	2.1E-05	1.9E-05	4.1E-05	2.5E-05	ptb | phosphate butyryltransferase
K00929	8.8E-05	6.7E-05	0.00012	0.00011	2.7.2.7	8.8E-05	6.7E-05	0.00012	0.00011	buk | butyrate kinase
Propionate (succinate decarboxylation pathway)										
K01610	0.00026	0.00017	0.00025	0.00027	4.1.1.49	0.00026	0.00017	0.00025	0.00027	pckA | phosphoenolpyruvate carboxykinase (ATP)
K0159	1.6E-05	2.6E-05	3.8E-05	2.7E-05	4.1.1.32	1.6E-05	2.6E-05	3.8E-05	2.7E-05	pckA | phosphoenolpyruvate

6										carboxykinase (GTP)
K01595	8.8E-05	3.6E-05	3E-06	1.6E-05	4.1.1.31	8.8E-05	3.6E-05	3E-06	1.6E-05	ppc | phosphoenolpyruvate carboxylase
K01960	0.00016	8.5E-05	0.00017	0.00022	6.4.1.1	0.00017	9.8E-05	0.000180	0.00023	pycB | pyruvate carboxylase subunit B
K01572	0.00018	0.00014	0.00023	0.00023	4.1.1.3	0.00024	0.00021	0.000320	0.00029	oadB | oxaloacetate decarboxylase, beta subunit
K00024	0.00029	0.00016	0.000280	0.00035	1.1.1.37	0.00029	0.00016	0.000280	0.00035	mdh | malate dehydrogenase
K01676	0.00015	9.2E-05	0.00017	0.00023	4.2.1.2	0.00032	0.00035	0.00032	0.00032	fumA, fumB | fumarate hydratase, class I
K00244	0.00015	0.00017	4.9E-05	0.000170	1.3.5.4	0.00016	0.00019	5.3E-05	0.00018	frdA | fumarate reductase flavoprotein subunit
K01902	3.7E-05	1.8E-05	1.6E-05	2.6E-05	6.2.1.5	7.2E-05	3.5E-05	3.1E-05	5.3E-05	sucD | succinyl-CoA synthetase alpha subunit
K01847	0.00032	0.00019	0.00035	0.0005	5.4.99.2	0.00032	0.00019	0.00035	0.0005	MUT | methylmalonyl-CoA mutase
K05606	0.00015	8.9E-05	0.00014	0.0002	5.1.99.1	0.00015	8.9E-05	0.00014	0.0002	MCEE, epi | methylmalonyl-CoA/ethylmalonyl-CoA epimerase
K01966	1.3E-05	1.1E-05	2.1E-05	2.8E-05	6.4.1.3	1.3E-05	1.1E-05	2.1E-05	2.8E-05	pccB | propionyl-CoA carboxylase beta chain
K01026	7.4E-05	0.0002	1.1E-05	4.4E-05	2.8.3.1	7.4E-05	0.0002	1.1E-05	4.4E-05	pct | propionate CoA-transferase
K00625	0.0003	0.00029	0.00024	0.00031	2.3.1.8	0.00034	0.00031	0.00025	0.00032	pta | phosphate acetyltransferase
K00925	0.00036	0.00036	0.00028	0.00031	2.7.2.1	0.00036	0.00036	0.00028	0.00031	ackA | acetate kinase
K00656	0.00025	0.00051	0.00016	0.00018	2.3.1.54	0.00025	0.00051	0.00016	0.00018	pflD | formate C-acetyltransferase
K00172	3.3E-05	4.1E-05	5.7E-05	2.1E-05	1.2.7.1	0.00013	0.00016	0.00019	7.6E-05	porG | pyruvate ferredoxin oxidoreductase gamma subunit
K01895	6.7E-05	7.1E-05	0.00013	0.00012	6.2.1.1	6.7E-05	7.1E-05	0.00013	0.00012	acs | acetyl-CoA synthetase
Propionate (acrylate pathway)										
K03778	0.00035	0.00052	6.7E-05	0.0001	1.1.1.28	0.00035	0.00052	6.7E-05	0.0001	ldhA | D-lactate dehydrogenase
K00016	0.00013	0.00017	7.1E-05	3.5E-05	1.1.1.27	0.00013	0.00017	7.1E-05	3.5E-05	ldh | L-lactate dehydrogenase
K20627	0	0	0	1E-06	4.2.1.54	0	0	0	1E-06	lactoyl-CoA dehydratase subunit alpha
K00249	0	0	0	0	1.3.8.7	0	0	0	0	acyl-CoA dehydrogenase

Table 7 The statistical summary of the densitometric analysis of intestinal epithelial pAMPK-α levels from three experimental replicates of western blot analysis

	Intestinal epithelial pAMPK-α level/β-actin level ratio
C	0.38 ± 0.01^{c}
RM	0.06 ± 0.00^{d}
HF	1.06 ± 0.02^{a}
HFC	0.69 ± 0.01^{b}

Note: Data are presented as mean ± standard deviation (n = 3); The different lower case letters in the same column indicate significant difference ($p < 0.05$).

Table 8 The pearson correlation analysis between KOs related to SCFAs metabolism and AMPK expression in intestinal epithelial cells

KO_ID	Pearson Correlation	*Sig.*
Acetate		
K01284	.799**	.002
K00656	-.877**	.000
K00172	.247	.439
K00158	-.825**	.001
K04073	-.732**	.007
K01895	.898**	.000
K00625	-.503	.096
K01026	-.916**	.000
K00128	-.823**	.001
K00925	-.909**	.000
K01512	-.966**	.000
Butanoate		
K00626	-.924**	.000
K00074	-.894**	.000
K01715	-.831**	.001
K00248	.426	.168
K00634	.858**	.000
K00929	.705*	.010
Propionate (succinate decarboxylation pathway)		
K01610	.724**	.008
K01596	.642*	.024
K01595	-.596*	.041
K01960	.771**	.003
K01572	.929**	.000
K00024	.697*	.012
K01676	.700*	.011
K00244	-.720**	.008
K01902	-.228	.475
K01847	.710**	.010
K05606	.634*	.027
K01966	.786**	.002
K01026	-.916**	.000
K00625	-.503	.096
K00925	-.909**	.000
K00656	-.877**	.000
K00172	.247	.439
K01895	.898**	.000
Propionate (acrylate pathway)		
K03778	-.916**	.000
K00016	-.503	.096

Note: *p* value < 0.05 (*) means the correlation is significant difference. *p* value < 0.01 (**) means the correlation is highly significant difference.

Table 9 The pearson correlation analysis between KOs related to SCFAs metabolism and serum concentrations of TMAO, TG and GLU

KO_ID	correlation (TMAO)	Sig.	correlation (TG)	Sig.	correlation (GLU)	Sig.
Acetate						
K01284	-.277	.383	-.529	.077	-.981**	.000
K00656	.543	.068	.762**	.004	.958**	.000
K00172	-.005	.987	.015	.962	.287	.365
K00158	-.318	.313	-.035	.914	.600*	.039
K04073	.468	.125	.672*	.017	.955**	.000
K01895	.154	.633	-.129	.690	-.681*	.015
K00625	-.025	.938	.044	.893	-.038	.907
K01026	.545	.067	.761**	.004	.916**	.000
K00128	.673*	.017	.855**	.000	.929**	.000
K00925	-.033	.919	.227	.477	.646*	.023
K01512	.177	.581	.456	.136	.871**	.000
Butanoate						
K00626	.311	.325	.574	.051	.956**	.000
K00074	.515	.087	.742**	.006	.954**	.000
K01715	.470	.123	.698*	.012	.994**	.000
K00248	.022	.946	-.048	.883	.055	.866
K00634	-.120	.711	-.305	.335	-.439	.153
K00929	-.803**	.002	-.894**	.000	-.616*	.033
Propionate (succinate decarboxylation pathway)						
K01610	-.640*	.025	-.820**	.001	-.963**	.000
K01596	.374	.231	.178	.580	-.173	.590
K01595	-.608*	.036	-.373	.233	.249	.434
K01960	-.347	.270	-.587*	.045	-.986**	.000
K01572	-.266	.403	-.534	.074	-.944**	.000
K00024	-.472	.121	-.680*	.015	-.975**	.000
K01676	-.211	.510	-.454	.138	-.952**	.000
K00244	.274	.388	.388	.213	.279	.380
K01902	-.730**	.007	-.619*	.032	-.275	.388
K01847	-.187	.561	-.435	.158	-.950**	.000
K05606	-.321	.310	-.540	.070	-.939**	.000
K01966	.067	.836	-.214	.503	-.863**	.000
K01026	.545	.067	.761**	.004	.916**	.000
K00625	-.025	.938	.044	.893	-.038	.907
K00925	-.033	.919	.227	.477	.646*	.023
K00656	.543	.068	.762**	.004	.958**	.000
K00172	-.005	.987	.015	.962	.287	.365
K01895	.154	.633	-.129	.690	-.681*	.015
Propionate (acrylate pathway)						
K03778	.545	.067	.761**	.004	.916**	.000
K00016	-.025	.938	.044	.893	-.038	.907

Note: p value < 0.05 (*) means the correlation is significant difference. p value < 0.01 (**) means the correlation is highly significant difference. TMAO, trimethylamine N-oxide; TG, triglyceride; GLU, blood glucose. All indexes were tested for serum of animals on different diets for 28 days.

Table 10 The cluster analysis of differentially expressed genes in intestinal epithelial cells

Pathway	Input number	Background number	*p-value*
Up-regulated genes found in pathways			
Peroxisome	43	45	8.24E-09
Glutamatergic synapse	82	98	9.25E-09
Retinol metabolism	71	88	2.55E-07
Carbon metabolism	82	111	4.26E-07
Axon guidance	93	129	5.04E-07
Complement and coagulation cascades	63	77	8.46E-07
Dopaminergic synapse	93	133	1.29E-06
Biosynthesis of amino acids	60	78	5.93E-06
Retrograde endocannabinoid signaling	74	103	7.59E-06
Long-term potentiation	54	66	1.03E-05
Gap junction	65	87	1.10E-05
Cholinergic synapse	78	113	1.23E-05
Fatty acid degradation	43	49	1.39E-05
Glycolysis/Gluconeogenesis	49	65	5.79E-05
GABAergic synapse	62	89	7.51E-05
Pentose and glucuronate interconversions	33	36	7.64E-05
Nicotine addiction	36	40	8.00E-05
AMPK signaling pathway	59	129	0.00011
Propanoate metabolism	27	27	0.00013
Fatty acid metabolism	39	50	0.00019
cGMP-PKG signaling pathway	96	170	0.00038
Neuroactive ligand-receptor interaction	145	282	0.00041
Phosphatidylinositol signaling system	54	81	0.00046
Regulation of actin cytoskeleton	116	217	0.00050
Gastric acid secretion	50	74	0.00058
PPAR signaling pathway	53	84	0.00113

Glutathione metabolism	41	53	0.00015
Melanogenesis	68	118	0.00156
Thyroid hormone signaling pathway	53	89	0.00171
Endocytosis	115	231	0.00337
Pyruvate metabolism	28	39	0.00342
Synaptic vesicle cycle	107	214	0.00354
Serotonergic synapse	45	74	0.00416
Glyoxylate and dicarboxylate metabolism	21	26	0.00417
Primary bile acid biosynthesis	14	16	0.01152
Alanine, aspartate and glutamate metabolism	24	37	0.01508
Inositol phosphate metabolism	35	61	0.02101
Butanoate metabolism	18	26	0.02161
ErbB signaling pathway	46	87	0.02489
Neurotrophin signaling pathway	61	123	0.02780
Pantothenate and CoA biosynthesis	13	17	0.02908
2-Oxocarboxylic acid metabolism	14	19	0.02913
Glycerolipid metabolism	30	55	0.03570
Tight junction	65	136	0.03958
Down regulated genes found in pathways			
Oxidative phosphorylation	126	135	7.23E-15
Parkinson's disease	131	147	2.22E-14
Alzheimer's disease	139	173	8.05E-13
Non-alcoholic fatty liver disease (NAFLD)	121	154	6.31E-11
Huntington's disease	135	182	8.17E-11
Calcium signaling pathway	125	181	3.61E-08
Chemical carcinogenesis	72	92	4.71E-07
Steroid hormone biosynthesis	68	86	7.48E-07
cAMP signaling pathway	130	198	1.55E-07
Legionellosis	47	58	2.34E-05
Valine, leucine and isoleucine degradation	43	52	3.68E-05
Ascorbate and aldarate metabolism	26	27	0.00026
Glycine, serine and threonine metabolism	33	40	0.00029
Porphyrin and chlorophyll metabolism	33	40	0.00029
Staphylococcus aureus infection	38	51	0.00044
Cysteine and methionine metabolism	32	40	0.00052

Hippo signaling pathway	87	154	0.00069
Wnt signaling pathway	82	143	0.00070
Ras signaling pathway	120	229	0.00072
Fatty acid elongation	22	24	0.00116
Protein processing in endoplasmic reticulum	88	169	0.00190
Biosynthesis of unsaturated fatty acids	21	25	0.00304
Starch and sucrose metabolism	35	54	0.00391
Rap1 signaling pathway	72	133	0.00411
Tryptophan metabolism	31	46	0.00423
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	45	74	0.00466
Long-term depression	38	61	0.00666
Vascular smooth muscle contraction	68	128	0.00719
Hedgehog signaling pathway	32	49	0.00748
Vasopressin-regulated water reabsorption	29	44	0.00968
Arginine and proline metabolism	35	59	0.01047
Focal adhesion	99	207	0.01380
Basal cell carcinoma	33	55	0.01591
Proteoglycans in cancer	95	205	0.02746
Protein export	18	28	0.03446
Antigen processing and presentation	30	55	0.03639
ABC transporters	26	46	0.03661
Glioma	18	28	0.03865
HIF-1 signaling pathway	53	111	0.04039
Apoptosis	41	82	0.04125
Type II diabetes mellitus	28	50	0.04391
Measles	63	137	0.04550
Steroid biosynthesis	13	19	0.04981

Note: *p-value* < 0.05 indicates significant difference.

Table 11 The differentially expressed genes list typically in intestinal epithelial cells

Gene_id	readcount _HF	readcount_ RM	log2FoldChange	*p-value*	Gene name
Up-regulated genes found in pathways					
Gap junction					
ENSMUSG00000068615	136.23	0.00	-	2.56E-29	Gjd2
ENSMUSG00000021536	3683.77	6.73	9.10	4.27E-149	Adcy2
ENSMUSG00000033910	824.94	206.82	2.00	2.84E-08	Gucy1a1
ENSMUSG00000020431	30767.54	23.36	10.36	2.95E-226	Adcy1
ENSMUSG00000062380	8437.10	2.76	11.58	3.29E-198	Tubb3
ENSMUSG00000030137	390.70	203.72	0.94	0.0003240	Tuba8
ENSMUSG00000025856	1073.30	387.77	1.47	7.04E-10	Pdgfa
ENSMUSG00000027646	6484.56	231.58	4.81	3.40E-82	Src
ENSMUSG00000022376	734.15	6.27	6.87	3.94E-23	Adcy8
ENSMUSG00000052920	318.30	15.73	4.34	3.34E-32	Prkg1
ENSMUSG00000028005	3115.29	171.81	4.18	1.74E-62	Gucy1b1
ENSMUSG00000036752	5158.00	3261.96	0.66	0.002284	Tubb4b
ENSMUSG00000034801	726.47	461.80	0.65	0.006348	Sos2
ENSMUSG00000029334	65.20	3.11	4.39	1.59E-06	Prkg2
ENSMUSG00000057614	6162.24	71.15	6.44	6.05E-121	Gnai1
ENSMUSG00000029231	1310.61	301.60	2.12	1.82E-18	Pdgfra
ENSMUSG00000019828	2429.08	0.00	-	1.21E-136	Grm1
ENSMUSG00000024620	764.40	410.81	0.90	0.0002253	Pdgfrb
ENSMUSG00000072235	14597.04	124.08	6.88	6.79E-141	Tuba1a
ENSMUSG00000050965	8518.94	427.60	4.32	4.32E-42	Prkca
ENSMUSG00000005034	7338.86	1988.23	1.88	5.97E-08	Prkacb
ENSMUSG00000005469	5744.77	3655.86	0.65	0.002387	Prkaca
ENSMUSG00000005580	3328.48	1098.80	1.60	4.85E-12	Adcy9
ENSMUSG00000038668	835.88	50.47	4.05	2.76E-28	Lpar1
ENSMUSG00000026202	10548.37	5987.51	0.82	0.0001409	Tuba4a
ENSMUSG00000001525	13629.14	2693.37	2.34	4.08E-26	Tubb5
ENSMUSG00000059923	5443.41	3149.70	0.79	0.0002542	Grb2
ENSMUSG00000063065	5253.94	2659.95	0.98	5.77E-06	Mapk3
ENSMUSG00000045136	4418.35	16.28	8.08	1.13E-143	Tubb2b
ENSMUSG00000041380	865.83	0.00	-	1.70E-96	Htr2c
ENSMUSG00000020654	1210.77	30.04	5.33	7.30E-71	Adcy3
ENSMUSG00000030265	2354.72	1166.46	1.01	5.45E-06	Kras
ENSMUSG00000049583	6879.75	0.00	-	1.91E-197	Grm5
ENSMUSG00000063358	15494.06	3133.85	2.31	1.17E-25	Mapk1
ENSMUSG00000000489	1258.07	119.05	3.40	3.56E-39	Pdgfb
ENSMUSG00000004936	9536.33	2098.37	2.18	4.27E-23	Map2k1
ENSMUSG00000030102	8670.76	1685.99	2.36	2.98E-20	Itpr1
ENSMUSG00000021478	60.04	0.00	-	5.50E-14	Drd1
ENSMUSG00000034997	257.50	0.00	-	5.38E-47	Htr2a

ENSMUSG00000027523	4461.86	1339.52	1.74	3.78E-15	Gnas
ENSMUSG00000062591	24440.76	5.95	12.01	9.84E-241	Tubb4a
ENSMUSG00000030516	2527.63	1251.43	1.01	5.09E-06	Tjp1
ENSMUSG00000001034	1661.74	185.08	3.17	4.71E-37	Mapk7
ENSMUSG00000039943	471.94	72.14	2.71	1.40E-20	Plcb4
ENSMUSG00000035283	710.73	89.31	2.99	1.22E-12	Adrb1
ENSMUSG00000023004	4726.61	434.17	3.44	7.43E-48	Tuba1b
ENSMUSG00000032259	56.82	0.00	-	4.26E-14	Drd2
ENSMUSG00000058672	17166.43	1899.51	3.18	1.65E-44	Tubb2a
ENSMUSG00000035725	414.57	133.04	1.64	3.59E-09	Prkx
ENSMUSG00000022840	5118.46	88.62	5.85	4.43E-105	Adcy5
ENSMUSG00000032006	96.58	42.20	1.19	0.002907	Pdgfd
ENSMUSG00000024639	8149.14	687.50	3.57	1.62E-52	Gnaq
ENSMUSG00000051177	5302.29	370.45	3.84	8.46E-58	Plcb1
ENSMUSG00000052889	8448.44	61.18	7.11	1.13E-139	Prkcb
Fatty acid degradation					
ENSMUSG00000029455	237804.24	3484.73	6.09	7.44E-124	Aldh2
ENSMUSG00000063929	3804.04	0.00	Inf	7.98E-101	Cyp4a32
ENSMUSG00000029098	1307.31	751.83	0.80	5.48E-04	Acox3
ENSMUSG00000036880	62572.04	496.39	6.98	4.68E-149	Acaa2
ENSMUSG00000078597	6799.69	0.42	14.00	1.94E-218	Cyp4a12b
ENSMUSG00000037797	5099.63	0.00	Inf	3.29E-107	Adh4
ENSMUSG00000053644	42877.43	2616.80	4.03	1.18E-41	Aldh7a1
ENSMUSG00000026003	13332.69	738.33	4.17	9.26E-68	Acadl
ENSMUSG00000028712	3150.79	0.00	Inf	6.58E-19	Cyp4a31
ENSMUSG00000025465	13536.10	1007.87	3.75	2.96E-40	Echs1
ENSMUSG00000028715	163484.94	0.21	19.59	9.25E-59	Cyp4a14
ENSMUSG00000059447	10913.21	1214.40	3.17	2.45E-35	Hadhb
ENSMUSG00000022853	35763.05	76.54	8.87	9.23E-48	Ehhadh
ENSMUSG00000035561	4764.38	355.71	3.74	7.04E-37	Aldh1b1
ENSMUSG00000020777	155799.36	5027.43	4.95	1.58E-52	Acox1
ENSMUSG00000030861	5854.34	1478.66	1.99	9.07E-19	Acadsb
ENSMUSG00000024981	13439.19	1097.20	3.61	2.23E-53	Acsl5
ENSMUSG00000066072	101081.53	0.83	16.89	5.89E-82	Cyp4a10
ENSMUSG00000066071	12769.29	0.00	Inf	3.03E-150	Cyp4a12a
ENSMUSG00000074207	65414.74	16.20	11.98	1.33E-279	Adh1
ENSMUSG00000003809	40755.44	829.82	5.62	5.26E-90	Gcdh
ENSMUSG00000029545	10970.93	152.57	6.17	1.48E-120	Acads
ENSMUSG00000010651	77271.07	24.30	11.64	1.19E-208	Acaa1b
ENSMUSG00000028138	26612.17	1314.32	4.34	6.93E-73	Adh5
ENSMUSG00000023832	1737.11	657.64	1.40	1.41E-09	Acat2
ENSMUSG00000018796	81360.02	1265.19	6.01	1.44E-93	Acsl1
ENSMUSG00000018574	11685.65	723.39	4.01	7.45E-11	Acadvl
ENSMUSG00000028607	12100.91	125.52	6.59	7.98E-86	Cpt2

ENSMUSG00000026687	24431.86	1007.14	4.60	1.00E-79	Aldh9a1
ENSMUSG00000055301	989.04	0.79	10.30	3.70E-53	Adh7
ENSMUSG00000024900	31713.88	763.44	5.38	1.83E-23	Cpt1a
ENSMUSG00000062908	28621.83	921.92	4.96	6.73E-62	Acadm
ENSMUSG00000025745	21873.97	1837.13	3.57	2.11E-36	Hadha
ENSMUSG00000036138	22720.34	2020.76	3.49	7.67E-51	Acaa1a
ENSMUSG00000032047	28143.38	2324.48	3.60	4.56E-49	Acat1
Glycolysis/Gluconeogenesis					
ENSMUSG00000025877	195.45	62.34	1.65	0.00048394	Hk3
ENSMUSG00000097148	2012.55	27.40	6.20	8.82E-101	Gm3839
ENSMUSG00000028307	332072.99	55.68	12.54	8.63E-312	Aldob
ENSMUSG00000021456	11.73	0.00	Inf	0.020481	Fbp2
ENSMUSG00000062070	17004.48	10083.76	0.75	0.0004982	Pgk1
ENSMUSG00000010025	22376.22	1378.54	4.02	5.79E-30	Aldh3a2
ENSMUSG00000041798	1849.00	65.23	4.83	1.26E-20	Gck
ENSMUSG00000020664	5533.83	3018.83	0.87	0.0094344	Dld
ENSMUSG00000037797	5099.63	0.00	Inf	3.29E-107	Adh4
ENSMUSG00000053644	42877.43	2616.80	4.03	1.18E-41	Aldh7a1
ENSMUSG00000041237	5522.87	2.75	10.97	1.14E-38	Pklr
ENSMUSG00000027605	7006.81	1399.54	2.32	5.36E-12	Acss2
ENSMUSG00000063229	59700.20	8150.72	2.87	8.45E-37	Ldha
ENSMUSG00000035561	4764.38	355.71	3.74	7.04E-37	Aldh1b1
ENSMUSG00000078650	18053.94	0.00	Inf	4.28E-66	G6pc
ENSMUSG00000027513	317662.74	0.00	Inf	0	Pck1
ENSMUSG00000074207	65414.74	16.20	11.98	1.33E-279	Adh1
ENSMUSG00000063524	39663.66	22545.59	0.81	1.47E-04	Eno1
ENSMUSG00000028692	25792.80	8202.53	1.65	7.87E-10	Akr1a1
ENSMUSG00000028138	26612.17	1314.32	4.34	6.93E-73	Adh5
ENSMUSG00000069805	74926.45	5.01	13.87	2.30E-68	Fbp1
ENSMUSG00000026687	24431.86	1007.14	4.60	1.00E-79	Aldh9a1
ENSMUSG00000025236	881.30	446.25	0.98	4.27E-05	Adpgk
ENSMUSG00000055301	989.04	0.79	10.30	3.70E-53	Adh7
ENSMUSG00000023456	33307.07	18228.93	0.87	5.46E-05	Tpi1
ENSMUSG00000035473	6164.43	77.06	6.32	6.48E-45	Galm
ENSMUSG00000029455	237804.24	3484.73	6.09	7.44E-124	Aldh2
AMPK signaling pathway					
ENSMUSG00000020053	29367.91	166.83	7.46	1.62E-116	Igf1
ENSMUSG00000074064	13246.88	940.39	3.82	1.65E-58	Mlycd
ENSMUSG00000027936	2464.55	1132.02	1.12	6.64E-07	Crtc2
ENSMUSG00000029513	1834.71	497.53	1.88	9.67E-16	Prkab1
ENSMUSG00000021456	11.73	0.00	Inf	2.05E-02	Fbp2
ENSMUSG00000020538	5140.69	1912.39	1.43	3.45E-05	Srebf1
ENSMUSG00000003037	4253.10	1019.95	2.06	1.05E-19	Rab8a
ENSMUSG00000028518	1218.10	626.25	0.96	2.16E-03	Prkaa2

ENSMUSG00000005534	6416.71	1653.22	1.96	2.50E-18	Insr
ENSMUSG00000067713	768.36	440.96	0.80	8.09E-04	Prkag1
ENSMUSG00000026457	6777.13	2165.40	1.65	1.08E-13	Adipor1
ENSMUSG00000026027	1638.80	612.87	1.42	1.05E-09	Stradb
ENSMUSG00000032058	831.27	423.33	0.97	6.28E-05	Ppp2r1b
ENSMUSG00000041769	2554.46	1326.83	0.95	2.27E-05	Ppp2r2d
ENSMUSG00000038648	994.96	490.20	1.02	3.02E-05	Creb3l2
ENSMUSG00000045875	263.25	138.37	0.93	1.38E-03	Adra1a
ENSMUSG00000034994	179244.85	42781.79	2.07	6.96E-21	Eef2
ENSMUSG00000078650	18053.94	0.00	Inf	4.28E-66	G6pc
ENSMUSG00000027513	317662.74	0.00	Inf	0.00E+00	Pck1
ENSMUSG00000030168	18899.45	1259.58	3.91	1.80E-54	Adipor2
ENSMUSG00000006542	13.29	0.00	Inf	1.33E-03	Prkag3
ENSMUSG00000037071	546216.28	3665.14	7.22	1.69E-21	Scd1
ENSMUSG00000030244	9262.72	1.14	12.99	2.28E-99	Gys2
ENSMUSG00000003068	8984.52	2796.96	1.68	2.01E-14	Stk11
ENSMUSG00000003123	991.65	250.40	1.99	6.05E-16	Lipe
ENSMUSG00000028466	2774.22	1146.80	1.27	1.42E-08	Creb3
ENSMUSG00000024900	31713.88	763.44	5.38	1.83E-23	Cpt1a
ENSMUSG00000021981	2797.21	677.13	2.05	9.25E-14	Cab39l
ENSMUSG00000069805	74926.45	5.01	13.87	2.30E-68	Fbp1
ENSMUSG00000035041	19393.82	18.51	10.03	8.96E-221	Creb3l3
ENSMUSG00000042010	3017.34	289.83	3.38	4.26E-45	Acacb
ENSMUSG00000017950	40868.05	0.00	Inf	1.85E-306	Hnf4a
ENSMUSG00000025271	2696.00	10.45	8.01	1.86E-130	Pfkfb1
ENSMUSG00000002944	2664.93	18.24	7.19	7.96E-34	Cd36
Propanoate metabolism					
ENSMUSG00000074064	13246.88	940.39	3.82	1.65E-58	Mlycd
ENSMUSG00000033429	3303.71	426.81	2.95	3.18E-36	Mcee
ENSMUSG00000023921	7649.67	898.45	3.09	1.45E-09	Mut
ENSMUSG00000025465	13536.10	1007.87	3.75	2.96E-40	Echs1
ENSMUSG00000022853	35763.05	76.54	8.87	9.23E-48	Ehhadh
ENSMUSG00000063229	59700.20	8150.72	2.87	8.45E-37	Ldha
ENSMUSG00000027605	7006.81	1399.54	2.32	5.36E-12	Acss2
ENSMUSG00000032527	13203.36	1896.44	2.80	5.22E-12	Pccb
ENSMUSG00000022110	5652.40	3291.99	0.78	9.18E-03	Sucla2
ENSMUSG00000052738	13231.01	2027.90	2.71	8.65E-33	Suclg1
ENSMUSG00000061838	10825.70	288.81	5.23	4.41E-40	Suclg2
ENSMUSG00000021238	17999.84	1304.65	3.79	2.51E-25	Aldh6a1
ENSMUSG00000032047	28143.38	2324.48	3.60	4.56E-49	Acat1
ENSMUSG00000057880	22159.03	5737.95	1.95	7.23E-05	Abat
ENSMUSG00000062908	28621.83	921.92	4.96	6.73E-62	Acadm
ENSMUSG00000023832	1737.11	657.64	1.40	1.41E-09	Acat2
ENSMUSG00000042010	3017.34	289.83	3.38	4.26E-45	Acacb

ENSMUSG00000035948	443.36	20.01	4.47	2.70E-06	Acss3
ENSMUSG00000025745	21873.97	1837.13	3.57	2.11E-36	Hadha
ENSMUSG00000041650	4827.88	790.49	2.61	4.35E-10	Pcca
PPAR signaling pathway					
ENSMUSG00000022853	35763.05	76.54	8.87	9.23E-48	Ehhadh
ENSMUSG00000028712	3150.79	0.00	Inf	6.58E-19	Cyp4a31
ENSMUSG00000066072	101081.53	0.83	16.89	5.89E-82	Cyp4a10
ENSMUSG00000078597	6799.69	0.42	14.00	1.94E-218	Cyp4a12b
ENSMUSG00000028715	163484.94	0.21	19.59	9.25E-59	Cyp4a14
ENSMUSG00000066071	12769.29	0.00	Inf	3.03E-150	Cyp4a12a
ENSMUSG00000063929	3804.04	0.00	Inf	7.98E-101	Cyp4a32
ENSMUSG00000024900	31713.88	763.44	5.38	1.83E-23	Cpt1a
ENSMUSG00000028607	12100.91	125.52	6.59	7.98E-86	Cpt2
ENSMUSG00000010651	77271.07	24.30	11.64	1.19E-208	Acaa1b
ENSMUSG00000036138	22720.34	2020.76	3.49	7.67E-51	Acaa1a
ENSMUSG00000026003	13332.69	738.33	4.17	9.26E-68	Acadl
ENSMUSG00000028603	172430.31	1917.76	6.49	2.80E-36	Scp2
ENSMUSG00000062908	28621.83	921.92	4.96	6.73E-62	Acadm
ENSMUSG00000021751	15109.93	8.93	10.72	1.33E-135	Acox2
ENSMUSG00000020777	155799.36	5027.43	4.95	1.58E-52	Acox1
ENSMUSG00000029098	1307.31	751.83	0.80	0.0005477	Acox3
Pyruvate metabolism					
ENSMUSG00000010025	22376.22	1378.54	4.02	5.79E-30	Aldh3a2
ENSMUSG00000020664	5533.83	3018.83	0.87	9.43E-03	Dld
ENSMUSG00000053644	42877.43	2616.80	4.03	1.18E-41	Aldh7a1
ENSMUSG00000024158	16980.86	2022.30	3.07	6.04E-41	Hagh
ENSMUSG00000063229	59700.20	8150.72	2.87	8.45E-37	Ldha
ENSMUSG00000027605	7006.81	1399.54	2.32	5.36E-12	Acss2
ENSMUSG00000035561	4764.38	355.71	3.74	7.04E-37	Aldh1b1
ENSMUSG00000020321	32185.67	11871.90	1.44	4.06E-11	Mdh1
ENSMUSG00000021620	7363.81	11.61	9.31	2.02E-186	Acot12
ENSMUSG00000027513	317662.74	0.00	Inf	0.00E+00	Pck1
ENSMUSG00000032418	7094.51	1354.01	2.39	8.90E-07	Me1
ENSMUSG00000023832	1737.11	657.64	1.40	1.41E-09	Acat2
ENSMUSG00000026687	24431.86	1007.14	4.60	1.00E-79	Aldh9a1
ENSMUSG00000042010	3017.34	289.83	3.38	4.26E-45	Acacb
ENSMUSG00000026526	15160.97	1722.28	3.14	5.32E-29	Fh1
ENSMUSG00000031958	16198.08	421.60	5.26	9.31E-19	Ldhd
ENSMUSG00000024892	58606.34	2485.02	4.56	8.22E-51	Pcx
ENSMUSG00000035637	26743.09	1134.76	4.56	8.86E-79	Grhpr
ENSMUSG00000032047	28143.38	2324.48	3.60	4.56E-49	Acat1
ENSMUSG00000024026	16618.15	2391.03	2.80	4.79E-35	Glo1
ENSMUSG00000029455	237804.24	3484.73	6.09	7.44E-124	Aldh2
Butanoate metabolism					

ENSMUSG00000027984	17579.39	499.89	5.14	1.05E-23	Hadh
ENSMUSG00000028672	20671.75	737.55	4.81	5.24E-85	Hmgcl
ENSMUSG00000030972	5187.54	1.98	11.36	5.48E-123	Acsm5
ENSMUSG00000030935	2631.96	8.88	8.21	4.03E-21	Acsm3
ENSMUSG00000030945	27.54	0.26	6.72	7.12E-06	Acsm2
ENSMUSG00000046598	14679.61	1143.34	3.68	3.56E-55	Bdh1
ENSMUSG00000029545	10970.93	152.57	6.17	1.48E-120	Acads
ENSMUSG00000025465	13536.10	1007.87	3.75	2.96E-40	Echs1
ENSMUSG00000027875	210175.79	196.27	10.07	7.76E-243	Hmgcs2
ENSMUSG00000057880	22159.03	5737.95	1.95	7.23E-05	Abat
ENSMUSG00000022853	35763.05	76.54	8.87	9.23E-48	Ehhadh
ENSMUSG00000035936	2579.09	1781.89	0.53	1.68E-02	Aldh5a1
ENSMUSG00000025745	21873.97	1837.13	3.57	2.11E-36	Hadha
ENSMUSG00000032047	28143.38	2324.48	3.60	4.56E-49	Acat1
ENSMUSG00000020988	2599.90	468.81	2.47	9.26E-26	L2hgdh
ENSMUSG00000023832	1737.11	657.64	1.40	1.41E-09	Acat2
ENSMUSG00000033533	17103.89	0.00	Inf	3.20E-266	Acsm1
Tight junction					
ENSMUSG00000022831	438.55	152.38	1.53	0.0002139	Hcls1
ENSMUSG00000023906	14.92	0.21	6.17	0.002118	Cldn6
ENSMUSG00000068876	1542.95	212.11	2.86	2.99E-31	Cgn
ENSMUSG00000004085	404.08	141.53	1.51	2.76E-08	Map3k20
ENSMUSG00000018569	63.52	0.92	6.11	0.0002574	Cldn7
ENSMUSG00000030189	2603.23	1377.36	0.92	0.00003348	Ybx3
ENSMUSG00000047109	437.34	26.68	4.04	7.78E-37	Cldn14
ENSMUSG00000047230	2883.71	106.12	4.76	5.98E-20	Cldn2
ENSMUSG00000041769	2554.46	1326.83	0.95	0.00002270	Ppp2r2d
ENSMUSG00000000001	2841.67	880.26	1.69	4.56E-06	Gnai3
ENSMUSG00000004056	6733.45	3958.10	0.77	0.0004006	Akt2
ENSMUSG00000032058	831.27	423.33	0.97	0.00006284	Ppp2r1b
ENSMUSG00000027935	472.22	132.13	1.84	1.11E-11	Rab13
ENSMUSG00000014932	641.38	255.97	1.33	1.45E-07	Yes1
ENSMUSG00000025812	3488.71	670.43	2.38	5.36E-25	Pard3
ENSMUSG00000038235	5249.80	271.27	4.27	9.80E-68	F11r
ENSMUSG00000024048	3911.94	818.16	2.26	4.57E-23	Myl12a
ENSMUSG00000054808	13376.61	4516.68	1.57	9.27E-13	Actn4
ENSMUSG00000024387	3861.56	1670.78	1.21	4.67E-08	Csnk2b
ENSMUSG00000037815	6251.10	1630.28	1.94	4.67E-18	Ctnna1
ENSMUSG00000070473	15417.79	41.84	8.53	4.16E-39	Cldn3
ENSMUSG00000074698	3473.83	1968.62	0.82	0.0002100	Csnk2a1
ENSMUSG00000061859	579.22	135.26	2.10	2.76E-15	Patj
ENSMUSG00000050520	13.79	0.71	4.28	0.001168	Cldn8
ENSMUSG00000034917	3193.86	124.76	4.68	1.37E-45	Tjp3
ENSMUSG00000020782	3016.45	84.34	5.16	1.66E-85	Llgl2

ENSMUSG00000044641	383.82	153.76	1.32	1.31E-06	Pard6b
ENSMUSG00000038387	2531.15	367.23	2.79	4.94E-32	Rras
ENSMUSG00000030739	2651.81	1781.01	0.57	0.009270	Myh14
ENSMUSG00000028906	6906.46	846.54	3.03	4.17E-28	Epb41
ENSMUSG00000047501	10.59	0.24	5.46	0.001707	Cldn4
ENSMUSG00000000159	1330.29	3.68	8.50	3.53E-76	Igsf5
ENSMUSG00000006728	1891.37	1205.63	0.65	0.003827	Cdk4
ENSMUSG00000021638	854.83	326.53	1.39	1.14E-08	Ocln
Down regulated genes found in pathways					
Calcium signaling pathway					
ENSMUSG00000030376	0.48	16450.01	-15.07	8.30E-237	Slc8a2
ENSMUSG00000079055	7.76	516.15	-6.06	1.35E-29	Slc8a3
ENSMUSG00000054640	6.95	1382.13	-7.64	1.23E-101	Slc8a1
ENSMUSG00000031633	423.96	16604.88	-5.29	4.04E-99	Slc25a4
ENSMUSG00000025537	16.12	631.74	-5.29	1.77E-55	Phkg1
cAMP signaling pathway					
ENSMUSG00000041329	29.07	9565.54	-8.36	4.57E-167	Atp1b2
ENSMUSG00000032412	1303.85	2054.23	-0.66	0.003386	Atp1b3
ENSMUSG00000007097	57.41	30008.14	-9.03	7.99E-200	Atp1a2
ENSMUSG00000059412	5.85	101.14	-4.11	2.80E-14	Fxyd2
ENSMUSG00000040907	5.46	86228.65	-13.95	3.22E-299	Atp1a3
ENSMUSG00000026576	2321.32	43885.12	-4.24	2.21E-72	Atp1b1
ENSMUSG00000028698	64.92	923.26	-3.83	6.11E-43	Pik3r3
ENSMUSG00000039936	270.97	1237.36	-2.19	2.90E-19	Pik3cd
ENSMUSG00000032462	676.63	1091.89	-0.69	0.002842	Pik3cb
ENSMUSG00000019699	86.06	4626.47	-5.75	1.58E-101	Akt3
ABC transporters					
ENSMUSG00000022822	254.94	6396.79	-4.65	5.04E-78	Abcc5
ENSMUSG00000029408	198.39	1087.56	-2.45	1.07E-22	Abcb9
ENSMUSG00000028125	15.43	179.69	-3.54	0.01368	Abca4
ENSMUSG00000024130	1422.89	2340.54	-0.72	0.001003	Abca3
ENSMUSG00000035722	498.25	1290.57	-1.37	5.02E-09	Abca7
ENSMUSG00000023088	56.67	665.53	-3.55	9.36E-35	Abcc1
ENSMUSG00000040136	0.00	1983.47	-	1.43E-136	Abcc8
ENSMUSG00000032131	0.45	2476.64	-12.42	1.29E-145	Abcg4
ENSMUSG00000026944	1945.57	11583.44	-2.57	1.06E-30	Abca2
ENSMUSG00000035435	0.00	24.52	-	1.04E-06	Abca17
ENSMUSG00000024030	261.58	1749.98	-2.74	1.40E-29	Abcg1
ENSMUSG00000018800	263.60	1033.18	-1.97	7.79E-16	Abca5
ENSMUSG00000032849	110.60	446.59	-2.01	3.71E-13	Abcc4
ENSMUSG00000040584	129.05	758.70	-2.56	4.56E-22	Abcb1a
HIF-1 signaling pathway					
ENSMUSG00000028645	1269.53	2927.93	-1.21	5.44E-08	Slc2a1
ENSMUSG00000034330	77.72	190.89	-1.30	8.38E-05	Plcg2

ENSMUSG00000021820	640.67	5053.73	-2.98	4.64E-31	Camk2g
ENSMUSG00000057897	624.95	39149.14	-5.97	8.62E-121	Camk2b
ENSMUSG00000053819	321.46	1086.40	-1.76	1.60E-04	Camk2d
ENSMUSG00000024617	0.44	118361.49	-18.03	0.00E+00	Camk2a
ENSMUSG00000030339	258.16	7467.35	-4.85	1.76E-83	Ltbr
ENSMUSG00000022797	1091.58	2137.0232	-0.97	3.86E-03	Tfrc
ENSMUSG00000022521	1114.32	2294.664	-1.04	3.04E-06	Crebbp
ENSMUSG00000029648	252.46	1704.7936	-2.76	1.12E-29	Flt1
ENSMUSG00000022309	22.73	108.52872	-2.26	1.74E-07	Angpt1
ENSMUSG00000001131	6.25	37.95	-2.60	2.51E-04	Timp1

Note: *p-value* < 0.05 indicates significant difference.