

Supplementary Tables

Table S1 The phenotype value of experimental animal

Samples	Initial weight(g)	Final weight(g)	Daily feed intake(g)	Daily body weight gain(g)	FCR	RFI
MH1	950	1355	93.2	20.25	4.60	14.92
MH2	1100	1585	103.5	24.25	4.27	13.75
MH3	920	1350	90.85	21.5	4.23	12
ML1	845	1295	66.4	22.5	2.95	-14.02
ML2	1100	1730	87	31.5	2.76	-12.84
ML3	820	1390	72.5	28.5	2.54	-12.21
FH1	720	1090	83.85	18.5	4.53	13.68
FH2	810	1170	84	18	4.67	11.45
FH3	750	1110	81	18	4.50	10.53
FL1	800	1245	63.8	22.25	2.87	-14.72
FL2	690	1105	62	20.75	2.99	-10.48
FL3	870	1320	71.1	22.5	3.16	-10.16

FCR = Daily feed intake/Daily body weight gain.

Table S2 Summary of metagenomic sequencing data

Sample	Raw data(Mbp)	Non host data(Mbp)	Clean data(Mbp)	Assembled scaftig length (bp)	Scaftig number	Average length of scaftigs (bp)	N50 (bp)
M-HFE1	6,149	6,101	6,129	219,381,694	133,514	1,643	2,409
M-HFE2	6,861	6,428	6,847	215,772,014	136,786	1,577	2,244
M-HFE3	6,722	6,142	6,697	197,940,659	123,144	1,607	2,295
M-LFE1	7,274	6,790	7,231	213,076,618	149,025	1,430	1,729
M-LFE2	6,266	6,108	6,249	187,104,352	124,199	1,506	2,076
M-LFE3	7,867	7,659	7,828	231,896,541	157,680	1,471	1,945
F-HFE1	6,238	5,952	6,218	173,764,110	108,892	1,596	2,357
F-HFE2	7,134	6,407	7,100	213,848,248	147,553	1,449	1,840
F-HFE3	6,704	6,284	6,685	184,127,692	117,558	1,566	2,223
F-LFE1	6,557	6,055	6,545	190,280,485	151,136	1,259	1,414
F-LFE2	6,934	6,853	6,920	191,680,602	132,638	1,445	1,890
F-LFE3	6,560	6,257	6,546	234,644,760	155,694	1,507	1,997

M-HFE, M-LFE, F-HFE, F-LFE denote the high feed efficiency group in male chickens, the low feed efficiency group in male chickens, the high feed efficiency group in female chickens, the low feed efficiency group in female chickens, respectively.

Table S3 The LDA score of potential biomarkers in the cecum for the different FE groups

Group	Taxonomy	LDA_score
F-LFE	<i>g__Blautia</i>	5.017
F-LFE	<i>s__Campylobacter_avium</i>	4.826
F-LFE	<i>g__Faecalibacterium</i>	4.808
F-LFE	<i>s__Parabacteroides_sp_CAG_409</i>	4.669
F-LFE	<i>o__Veillonellales</i>	4.337
F-LFE	<i>g__Collinsella</i>	4.297
F-LFE	<i>s__Bacteroides_sp_Marseille_P3166</i>	4.262
F-LFE	<i>g__Erysipelatoclostridium</i>	4.221
F-LFE	<i>s__Blautia_sp_An46</i>	4.109
F-LFE	<i>s__Bacteroidales_bacterium_WCE2004</i>	4.103
F-LFE	<i>s__Bacteroides_sp_CAG_598</i>	4.090
F-LFE	<i>g__Butyricimonas</i>	4.006
F-HFE	<i>f__Enterobacteriaceae</i>	4.376
F-HFE	<i>p__Proteobacteria</i>	4.122
M-HFE	<i>s__Barnesiella_sp_An22</i>	4.511
M-HFE	<i>s__Lactobacillus_oris</i>	4.275
M-LFE	<i>s__Bacteroides_sp_An322</i>	4.987
M-LFE	<i>s__Subdoligranulum_variabile</i>	4.486
M-LFE	<i>s__Helicobacter_pullorum</i>	4.342
M-LFE	<i>f__Unclassified_Lentisphaerae</i>	4.233
M-LFE	<i>c__Unclassified_Lentisphaerae</i>	4.182
M-LFE	<i>o__Unclassified_Lentisphaerae</i>	4.170

Table S4 The significantly different KEGG pathway between high FE and low FE group of chickens

Group	Ko_ID	Pathway	P-value
M-HFE	ko00361	Chlorocyclohexane and chlorobenzene degradation	0.006
M-HFE	ko04512	ECM-receptor interaction	0.018
M-HFE	ko04933	AGE-RAGE signaling pathway in diabetic complications	0.023
M-HFE	ko00982	Drug metabolism - cytochrome P450	0.039
F-HFE	ko05146	Amoebiasis	0.004
F-HFE	ko02040	Flagellar assembly	0.047
F-LFE	ko00040	Pentose and glucuronate interconversions	0.047

Supplementary Figures

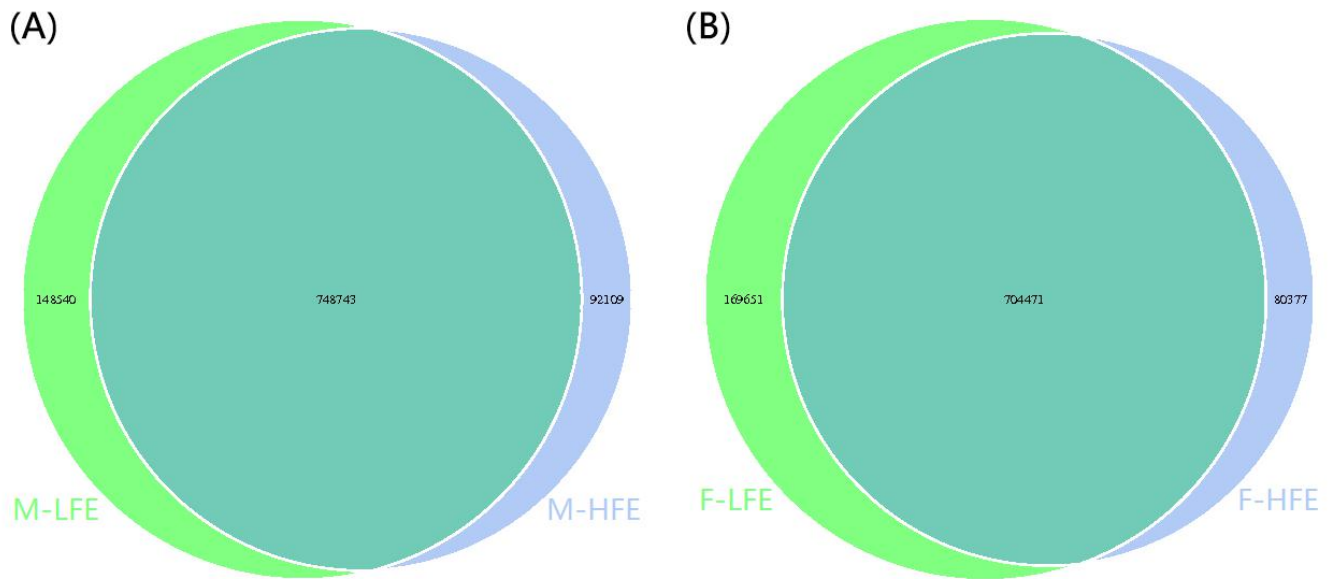


Figure S1 Venn diagram of intersection between the genes in the high FE group and low FE group. (A) Venn diagram of male chickens. (B) Venn diagram of female chickens.

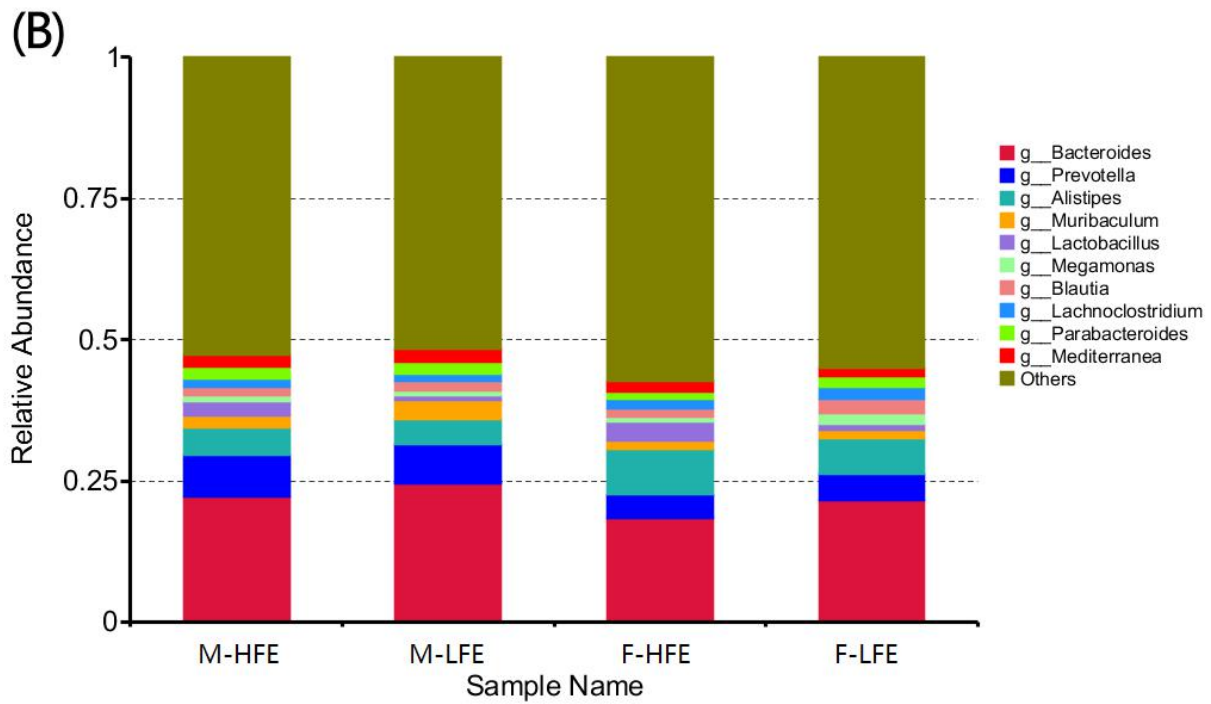
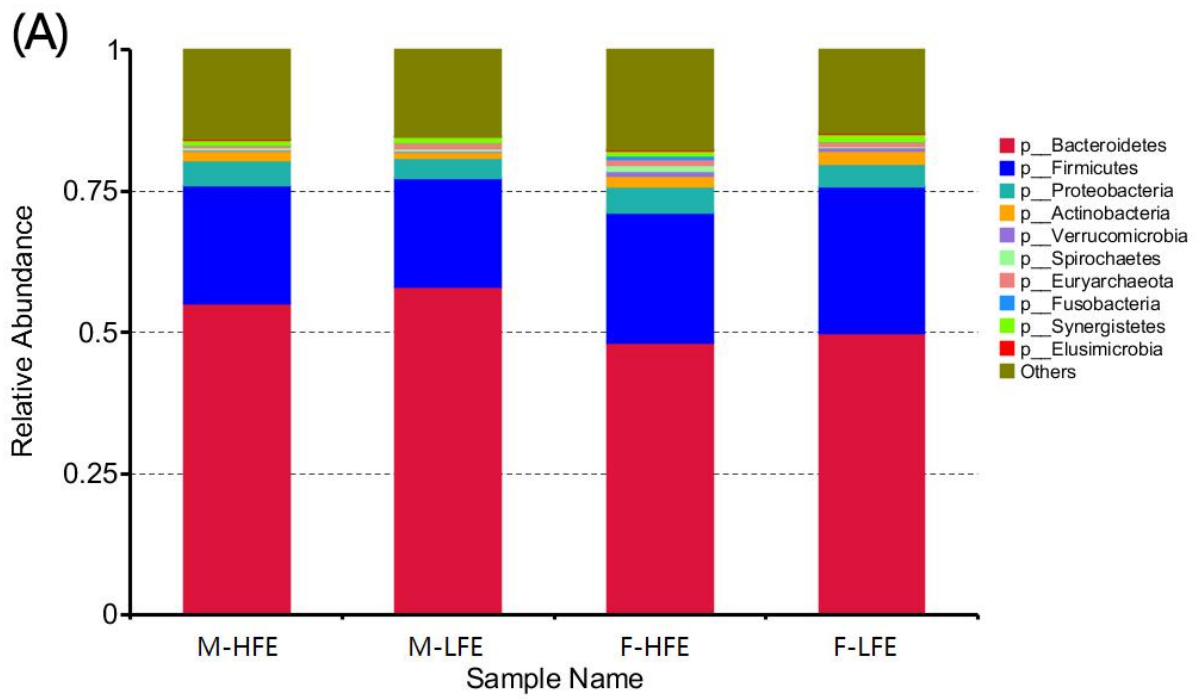


Figure S2 Predominant microbes in caecum at (A) phyla and (B) genus level

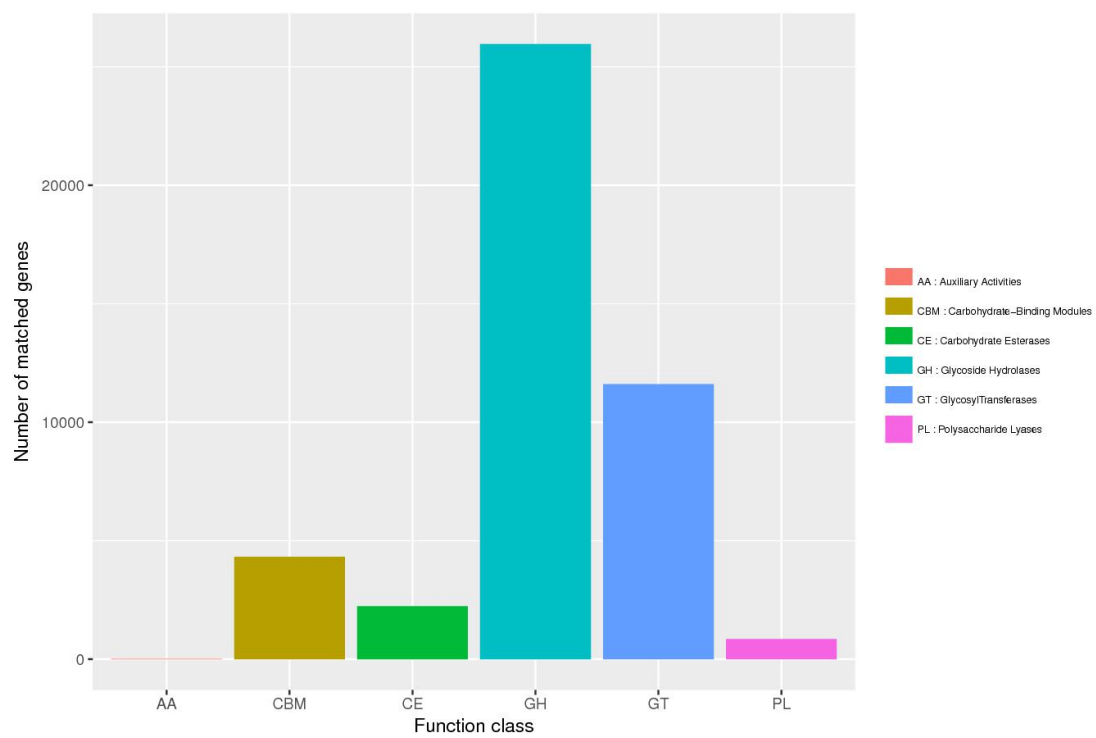


Figure S3 Functional composition of genes in the CAZy database for high and low FE groups.

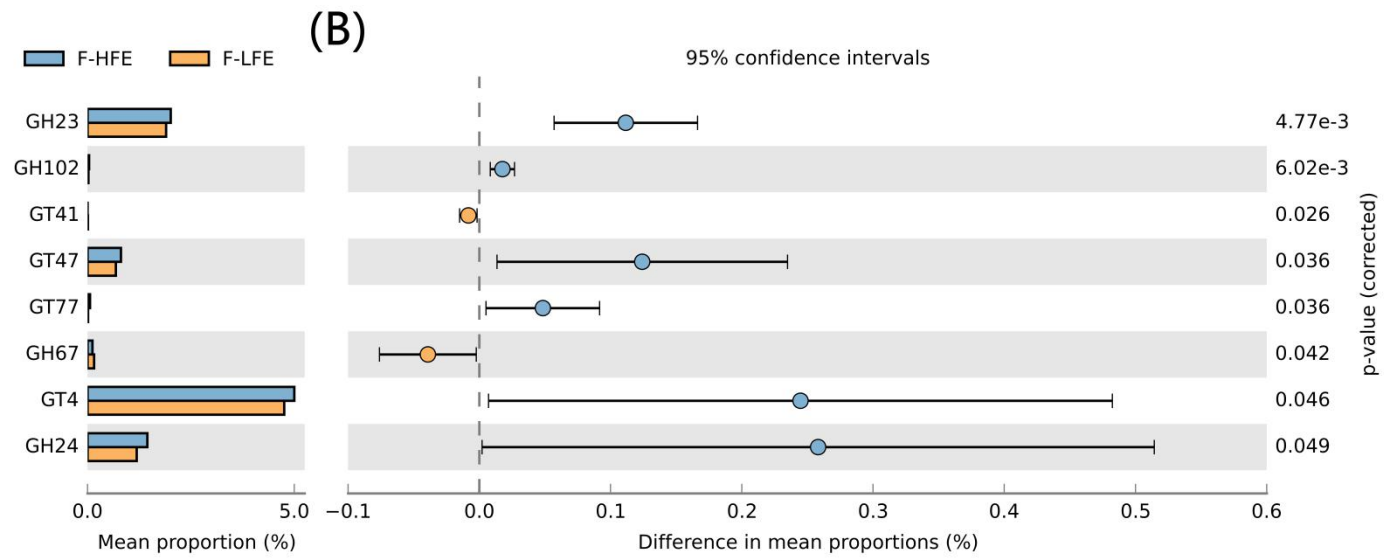
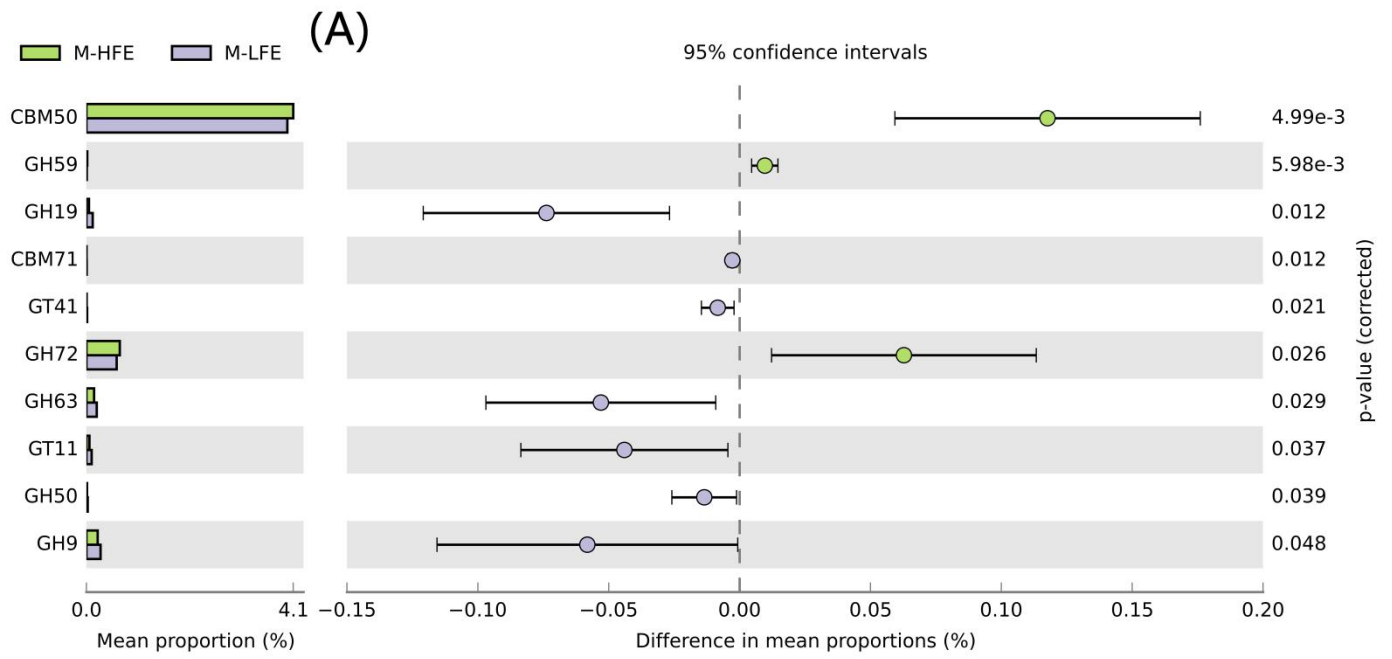


Figure S4 Differential CAZy families between high and low FE groups

(A) The CAZy families detected in male chickens. (B) The CAZy families detected in female chickens.