

**Table S1. Feed formulation and proximate analysis of experimental diets.**

Ingredients (g kg <sup>-1</sup> )	Control	HFD	CH	HFD + CH
Casein	360	360	360	360
Gelatin	80	80	80	80
Fish oil	30	45	30	45
Corn oil	30	45	30	45
Wheat flour	250	250	250	250
Ascorbyl-2-polyphosphate	10	10	10	10
NaCl	10	10	10	10
Ca (H <sub>2</sub> PO <sub>4</sub> ) <sub>2</sub> ·H <sub>2</sub> O	10	10	10	10
Vitamin premix <sup>1</sup>	5	5	5	5
Mineral premix <sup>2</sup>	5	5	5	5
Cellulose	209.5	179.5	208.5	179.5
Choline chloride	0.5	0.5	1.5	1.5
<i>Proximate analysis (% dry weight)</i>				
Moisture	7.22	7.38	7.29	7.34
Crude protein	39.99	40.86	40.54	40.23
Crude ash	5.37	5.29	5.36	5.38
Crude lipid	10.15	14.61	10.49	14.65
Choline (mg kg <sup>-1</sup> )	563.4	578.9	1650.1	1652.3

<sup>1</sup>Vitamin premix (mg or IU per kg diet): retinylacetate, 10000IU; cholecalciferol, 1000IU; all-rac- $\alpha$ -tocopheryl acetate, 30IU; menadione nicotinamide bisulfite, 7; thiamine hydrochloride, 6; riboflavin, 3; pyridoxine hydrochloride, 12; D-calcium pantothenate, 30; niacin, 50; biotin, 1; folic acid, 6; cyanocobalamin, 0.03.

<sup>2</sup>Mineral mixture (mg per kg diet): Ca(H<sub>2</sub>PO<sub>3</sub>)<sub>2</sub>·H<sub>2</sub>O, 1000; FeSO<sub>4</sub>·7H<sub>2</sub>O, 40; ZnSO<sub>4</sub>·7H<sub>2</sub>O, 40; MnSO<sub>4</sub>·H<sub>2</sub>O, 40; CuSO<sub>4</sub>·5H<sub>2</sub>O, 2; CaIO<sub>3</sub>·6H<sub>2</sub>O, 3; Na<sub>2</sub>SeO<sub>3</sub>, 0.05; CoSO<sub>4</sub>, 0.05.

**Table S2. Effects of dietary high fat and choline supplementation on growth performance and morphological parameters yellow catfish (*Pelteobagrus fulvidraco*) after 10 weeks.**

Diet	Control	HFD	CH	HFD+CH	Two-way ANOVA <i>P</i> -value		
					Fat	Choline	Interaction
IBW, g/fish	3.78±0.05	3.78±0.03	3.80±0.06	3.85±0.01	NS	NS	NS
FBW, g/fish	31.38±0.91 <sup>ab</sup>	35.10±0.14 <sup>c</sup>	30.03±0.63 <sup>a</sup>	32.00±0.50 <sup>b</sup>	<0.001	<0.001	0.034
WG <sup>2</sup> , %	728.60±0.15 <sup>ab</sup>	827.08±0.061 <sup>c</sup>	690.16±0.10 <sup>a</sup>	730.60±0.16 <sup>b</sup>	<0.001	<0.001	0.049
FCR <sup>3</sup>	1.15±0.03	1.08±0.03	1.17±0.02	1.14±0.01	0.025	NS	NS
HSI <sup>4</sup> , %	1.37±0.27	1.43±0.17	1.30±0.25	1.40±0.20	NS	0.007	NS
CF <sup>5</sup> , %	1.70±0.06	1.68±0.30	1.69±0.34	1.72±0.15	NS	NS	NS
Survival <sup>6</sup> , %	98.66±2.30	98.66±2.30	96.00±4.00	97.33±3.21	NS	NS	NS

<sup>1</sup>Values are means ± SEM; n = 3 tanks (30 fish/tank). Labeled means without a common letter differ, *P* < 0.05 (TWO-factor ANOVA, Duncan's post hoc test).

<sup>2</sup>WG = (FBW-IBW)/IBW×100.

<sup>3</sup>FCR = dry feed fed (g)/wet weight gain (g).

<sup>4</sup>HSI = 100×(liver weight)/(body weight);

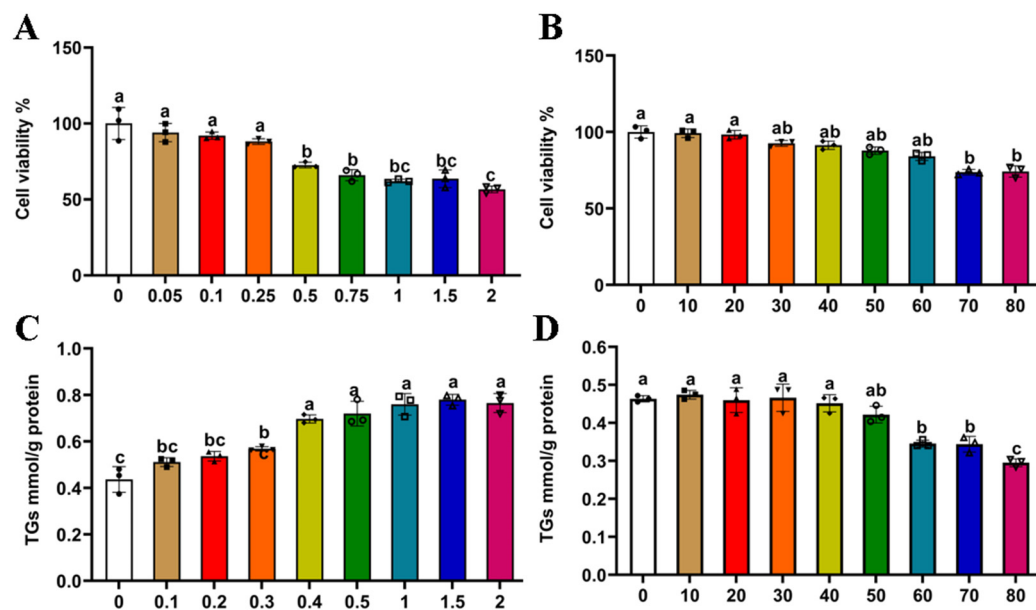
<sup>5</sup>CF = 100×(live weight, g)/(body length, cm)<sup>3</sup>.

<sup>6</sup>Survival = 100 ×final fish number/initial fish number.

**Table S3. Primers used for plasmid construction and RT-qPCR analysis**

Gene	Accession No.	Forward primer (5'-3')	Reverse primer (5'-3')
<b>Bisulfite sequencing for methylation validation</b>			
<i>perk</i>	KP687344.1	TTTAGGGTTGGGTTATTTA GAAATG	ATCTTCTCTCTCATATCAA TCTCATATACA
<b>Plasmid construction</b>			
<i>perk</i>	KP687344.1	ctagcgtttaacttaagcttATGGAG CAAGCAAACCTCTACG	aacggggccctctagactcgagTTAG GCACAGTTACCCATGGC
<b>RT-qPCR analysis</b>			
<i>18s</i>	EU047719	GGCGCGCAAATTACCCAT T	TCCCGAGATCCAACTACA AGC
<i>β-actin</i>	DQ211096.1	ACCCTGAAGTACCCCATC GA	CAGAGGCATACAGGGAC AGC
<i>acca</i>	GU908474.1	GCTTGCGGCGGTTATTAC TG	AGCTGCCTCTCCAACCAT TC
<i>b2m</i>	AB128864.1	GCACTCGTCTCTTTTGCC CT	TTTCGAAGGCCAGGTCAG TC
<i>dnmt1</i>	MN701649	TCATGTGCGGGAACAACA AC	TGCAGCACATGTAGCAGT TC
<i>dnmt3a</i>	MN701650	TGCAGCACTTCTTTGCCA AC	GACAGGACACGAATGGG TTTTC
<i>dnmt3b</i>	MN701651	ACCTGGAATGAACCGACC AC	ATTCATGGTGACCGGCAG AG
<i>fas</i>	GU433188	TCATCCAGCAGTTCCTG GCATT	TGATTAGGTCCACGGCCA CA
<i>6pgd</i>	XM0034449 04.4	GAAGGGCCTGCTGTTTGT TG	CCCAGTCACAACAAGGC TCT
<i>g6pd</i>	XM0054781 06	GAGAAGCCCTTTGGTCGT GA	ATCAAAGTACCCTCCACG GC
<i>dgat1</i>	MN701645	AACGAAAGACTGCGCAA GAG	ACCCATGGCTTTGACAAA CG
<i>dgat2</i>	MN701646	TTCCGGGAACCTTTGACAT GC	GGTTGCGCATTTTGGCTT TG
<i>mgat1</i>	GQ266394.1	CCACCGGCCATCTGATCT AC	GTGTCCAGGGGCATCAAT GA
<i>mgat2</i>	MG241310.1	TTGTGGTCTTCTCCTCGG TC	ACGACACCCACATCTCCA AT
<i>grp78</i>	FJ436356.1	ATTTGTTCCGCTCCACCAT G	AACTCTTTCACCAGCTGC TG
<i>perk</i>	KP687344.1	GGGAAACTGTGGAGGGA TGG	TGCAGCCTTGACCACTTT CT

<i>elf2a</i>	JN195739.1	TCGGCCCCAGTCTCATTC TA	ATACACCACTCGCCTCTC CT
<i>ire1a</i>	KY081668.1	TTCTGCGGGAAACGTTTC AC	ACTACGCATGAACCGTTT GG
<i>xbp1</i>	MN701647	CTCCTGAACAGAAGCAG CCA	CTCGAAGTGCTCTGCCAT GA
<i>atf6</i>	XM0054713 82	TCCCCGGATCATCGTATG GA	TCCTGCAGTGACTCCTAA CG
<i>apob</i>	KF871430	TCCCCGGATCATCGTATG GA	TCCTGCAGTGACTCCTAA CG
<i>apobec1</i>	XM0034479 23.5	GATCCTCACTACTGCCAG CC	CCTTCGACGATGAGAGAG CC
<i>apoe</i>	XM0034502 74.5	GACCAGTTCTGGGCCATG AA	GGTGTATGCGTTGCCTAC AG
<i>mtp</i>	XM0259072 53.1	GATGTTGTGGCACCAGGA GA	CATTCTGTCATCGCTGCT GC
<i>sar1b</i>	XM0054764 33.4	TACTGGTTCACGTGCCTG AG	GCTCGATTGGCAAACAGG AC
<i>cd36</i>	XM0193567 96.2	GTCCAGCAGATCCGTGAG C	TGCCAGGAACTTGGTCTT GTC
<i>vamp7</i>	XM0034394 38.5	GCCTCCAGCTAAACTCCA ACC	CGCTCTCGCTCGTACACC TC
<b>siRNA sequences</b>			
siRNA- <i>perk-376</i>		GCGAGCACCGUGCAGUU UATT	UAAACUGCACGGUGCUC GCTT
NC- siRNA		UUCUCCGAACGUGUCACGU TT	ACGUGACACGUUCGGAGAA TT



**Figure S1. MTT assay and TGs content for the viability of intestinal epithelial cells (IECs) of yellow catfish incubated with FA and choline for 36h. (A-B) MTT assay of FA and choline. (C-D) TG content of FA and choline. Values are means  $\pm$  SEM,  $n \geq 3$ . Letters denote significance at  $P < 0.05$  (One-way ANOVA, Duncan post hoc test).**

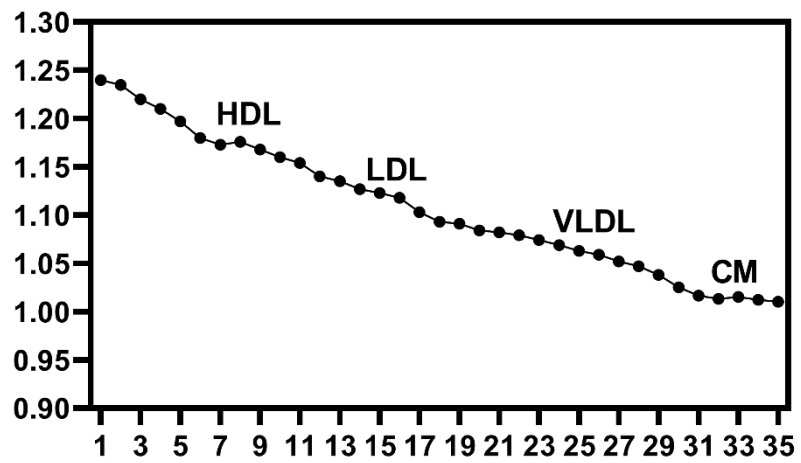
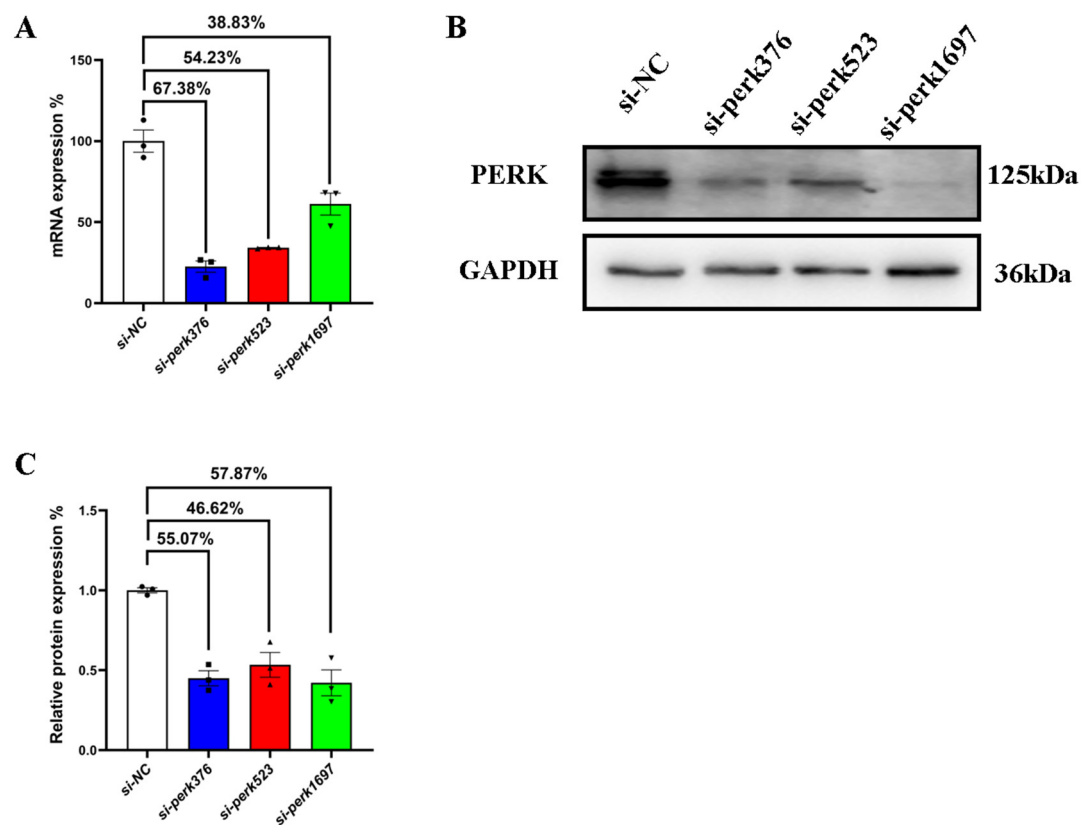
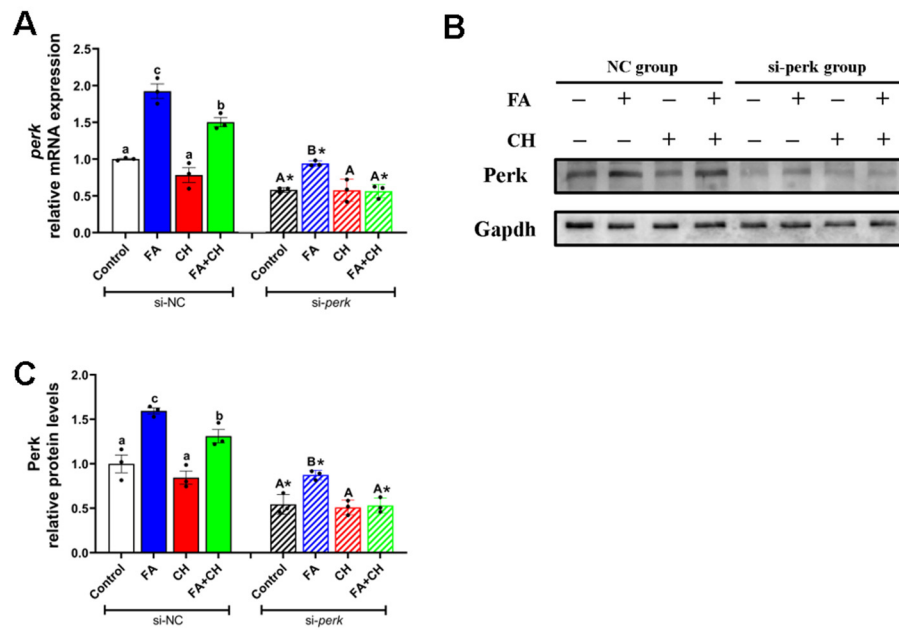


Figure S2. The fraction of density gradient separation for lipoprotein.



**Figure S3. The knockdown efficiency of *perk* gene in IECs.** (A) mRNA levels of *perk*. (B-C) Western blot analysis for PERK. Values are means  $\pm$  SEM,  $n \geq 3$ . Letters denote significance at  $P < 0.05$  (One-way ANOVA, Duncan post hoc test).



**Figure S4. mRNA levels and Western blot analysis of *perk* in the IECs under FA and CH incubation and transfected with si-*perk*.** (A) mRNA levels of *perk*. (B-C) Western blot analysis for Perk. Data are mean  $\pm$  SEM,  $n = 3$   $n = 3$  independent biological experiments; different minuscules indicate significant differences in si-NC groups, different majuscules indicate significant differences in si-*perk* groups ( $p \leq 0.05$ ); asterisks indicate significant differences between si-NC and si-*perk* groups ( $*p \leq 0.05$ ).





Figure S5. Prediction analysis of CpG islands in the sequence range of 2300 bp upstream from the transcriptional start site in the *perk* promoter region (<http://www.urogene.org/>). TSS, transcription start site.

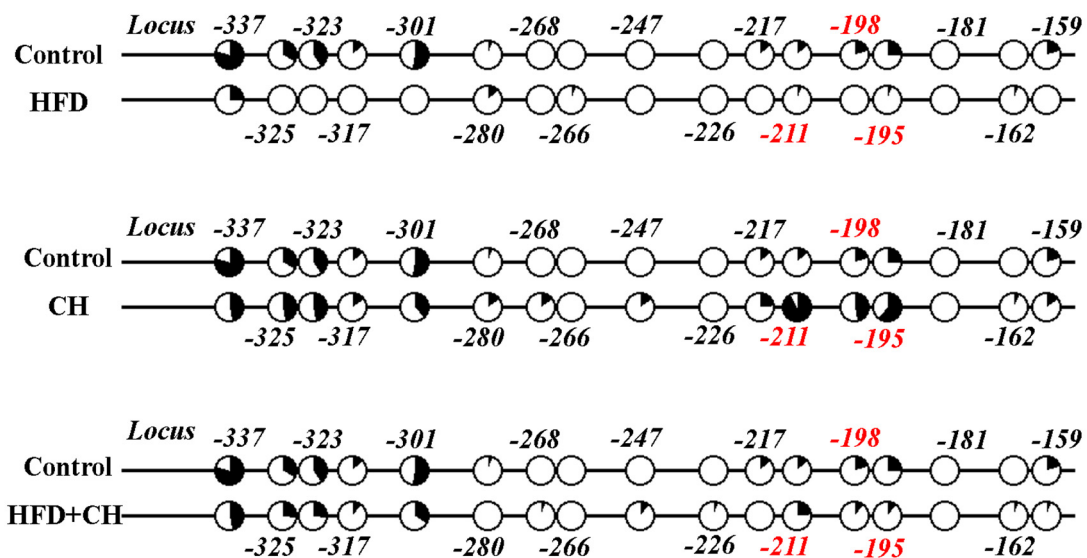


Figure S6. Bisulfite sequencing of the promoters of *perk* between the control, HFD, CH and HFD + CH.

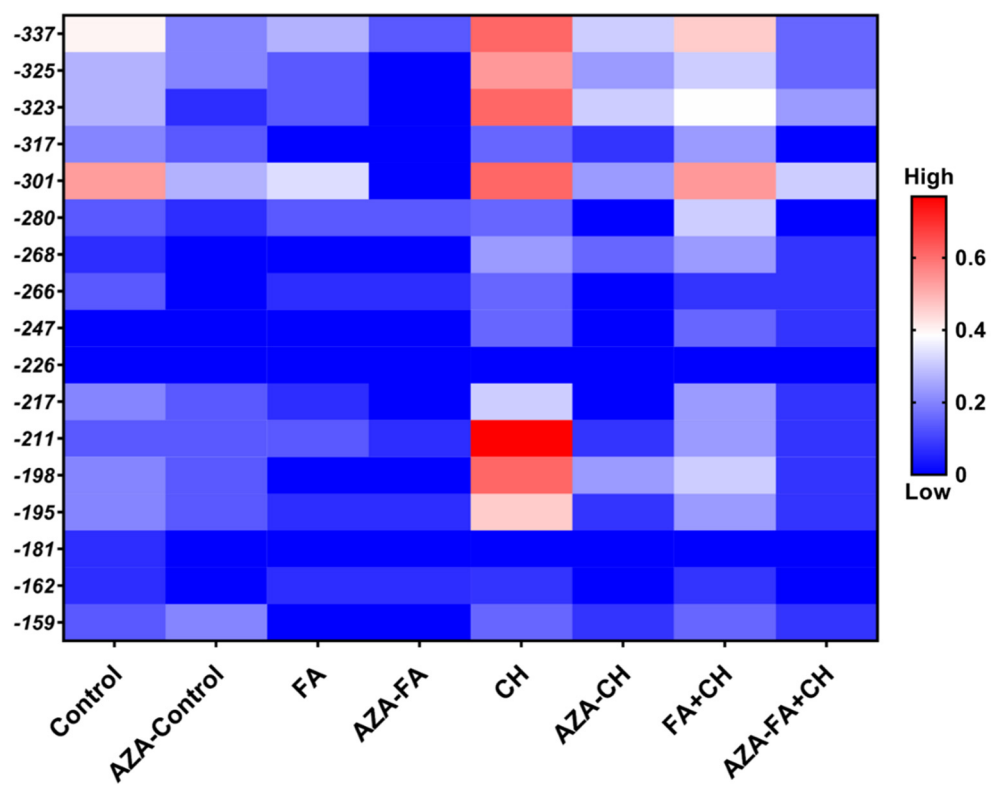
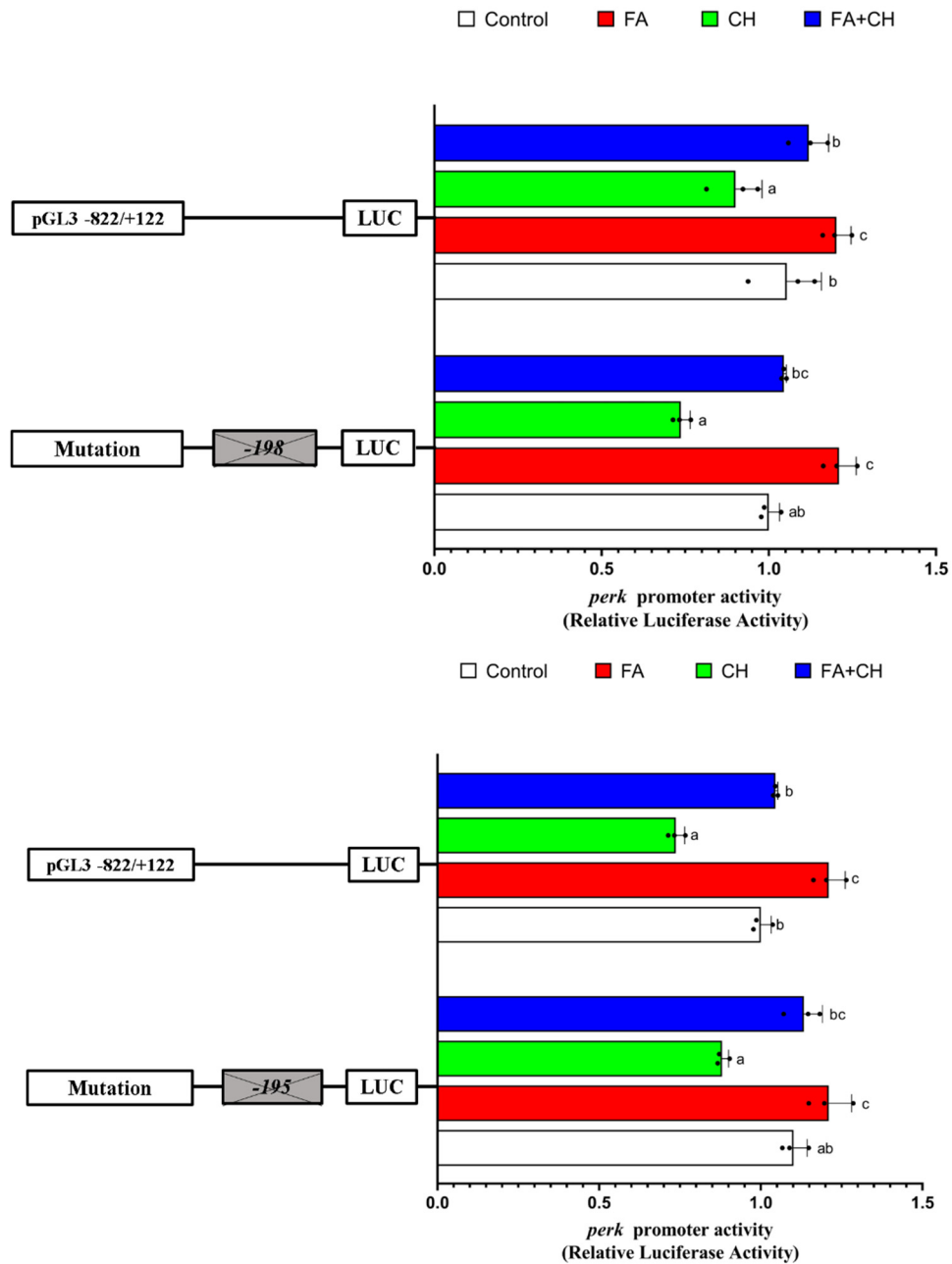


Figure S7. Heat map of methylation percentage of *perk* in the IECs under FA and CH incubation and addition AZA.



**Figure S8. The -198 and -195 methylation sites relative luciferase activities of *perk* in the IECs under FA and CH incubation.** Values are means  $\pm$  SEM,  $n \geq 3$ . Letters denote significance at  $P < 0.05$  (One-way ANOVA, Duncan post hoc test).