Supplementary information

Refeeding with different levels of dietary carbohydrate modulates epigenetic stability through global DNA (de)methylation and histone modifications in juvenile and adult Nile tilapia (*Oreochromis niloticus*)

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Table S2. Nucleotide sequences of cDNA encoding enzymes involved in DNA (de)methylation, histone (de)methylation, and histone (de)acetylation. Underlined letters indicate primer positions. Bold letters indicate start and stop codons.

dnmt1	
NCBI NO.	XM_025906327.1
Position of Coding sequence	139-4671
>XM_025906327.1 PREDICTED: Oreochromis niloticus DNA (cytosine-5)-methyltransferase 1 (LOC100706458), transcript variant X1, mRNA GAATTGCTTATAGCATCCATCTGCACACGACAGACTGTCACCGTGGAGCCGCGCGGTGGTTAATGATAGTGGAGTTTTAAACG GTGTTTTAACGGTTTTAAAACATTTTTAGTCGCTCGTGTCTTACGCTCGTTTACG**ATG**CCAACCAGGACGTCCCTGCCTCTCCCG GACGATGTCAGGAAAAGCTTGCAGAGGTTGGATGAGGAAGGATCTGCAGAAGAGGAACATGTGAAAGAGAAGCTCAAGTTGG TGCAGGACTTTCTGCATGCTGATGCTCAGGATCAGCTGACCAGTCTGGAGGAAAAAATGAAAAGTTCAGAGATCTCAAAGGAG GTCTATATCTCTAAAGTGAAGGCCCTACTTGGAAAAGAACTTCATCTTGAAAATGGCTCCCACGTTGATGACGCAGAGAAGAA TGGAAAGACGAATGGCTTTTCAAATGGTTCGCACAAAGACGAGCATGATGAAGATGTAACCATGAGCGTACAGGAGGAGGAG GAGGAATCTTTCAAGTCACCAACTGCTTCGAAGGGGAAGGGTGGACGGAGGAGCAAGGCAAATTCTGACACAAAAAAGTCTC CAGCAAGTACCAGGGTTACCAGAAACAGTGGGAAACAGCCAACCATCTTGTCAATGTTCACTAAAGTTCAGAAGCGCAAGTCA GAGGACTTGAATGGAGAAGCTGTCAACGGACAGAATGAACCGAAGAAAGATGATGACGTTGAGGAGTCTCGGGAGGAGAAG CGTCTCAAAGTGGAGTCGGATGAAAATGCTGCTCCAGAAGAATCCAAGAGTGACATTGCAAAGCCGGTTTCTGCTGTAAAGAC GCCACCACCCAAATGTCAAGACTGTAGACAATACCTAGATGATTCTGACCTGAAGTTTTTTCAAGGGGATCCTGATAATGCGCT GGATGAGCCTGAAATGTTAACAGATGAGCGCCTCTCACTGTTTGACTCCAATGAGGATGGATTTGAGAGCTATGAGGATCTGC CACAGCACAAGATCACAAACTTCAGTGTTTATGACAAGCGTGGCCATCTCTGTCCATTCGACTCTGGACTTATTGAGAAGAATG TTGAGCTTTACTTCAGCTGTGTTGTCAAACCCATCTATGATGACAACCCTTGTATGGATGGTGGTGTTCCTGCCAAAAAGCTGG	

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dnmt3aa	
NCBI NO.	XM_005475084.4
Position of Coding sequence	357-2885
>XM_005475084.4 PREDICTED: Oreochromis niloticus DNA (cytosine-5)-methyltransferase 3A (LOC100702269), transcript variant X3, mRNA GAGAGATTGAGTTGTGTGTGAGAGAGAACGCCGACGGGAGCGCGCAGCAACGGAGAGAGAAGACCCGTTTGAACGCGAGGA GAGAGAGAGAGGGAGAGAGAGTTTGAGTGTGTGTGGGTGTGAGAGAGAGAGATCGAGAGTGAACGAGAGGAGAGAGAGCGA CGACCGTGAGGGTCCGGGTGCCTGAGGGACGGACGACACGGAGAGGGGGAGGTCTGAGGGAGCGAGTTATCGTCTGACAGAC CGAGACAGGTTGAATGAAGCTGCACCTGGTGCTTCTGAGGGCATTTCCCATGTTTTGATTTGCTCTGTTTTTTTATCTTTCTAAA CTTGGTTTCACCGAGCTGTTCCCTGCC**ATG**CCGTCCAACAGTCCTGCTACTGGTGAACCACCCCAGACACCAGAGAACGACAC CTCTAACGATCTGAGTGAAGATGGTGCAGACCAGGACAGTCCAGAGGAGGGGACACCGGCGAGCCCCCGCAACAAGCGCAGA GTGGGTCGTCCCAGCAGGAAACGCAAACAGCTGCTTCCTGAGATGGCAACCTCTGACCCCTGTGCAAACGCCCCCCCAACTCC GCCTGAGGAGCCGGCGCCTTCACCTTCCCCTCGCAAGAAGCGCGGGCGTCGGAAACAAGAGCCAGCGGAGAGGAATAAGGAC GAGCCAGATGACAGAAACTGTGACTCCCCCAGAGAGGGAGAGACTGGGAGGCTGCGGAGAAGGCCAGTCCCCAGAGTAACTT TTCAGGCTGGAGATCCATACTATATCAGCAGGAGACAGAGAGAAGAATGGCTCAGCCGCTGGAAGATGGAGGCAGAGCGACG GGCCTACCGAGAGGCAGAGATAAACATGATGGATGACCTCTCAGAAGCTGACTTTCAGAAAGAGGAGGAGCCCGCCAGCCCT GCCCCTCCCCCTTCACAACAACACACAGACCCTGCCTCTCCGACGGTCGCCGTGACACCCGAGCCAGTCGCCAGGGGAGAACA GCCCACGCCCAGTGAGATTGAATACCAGGATGGTCGGGGCTTTGGCATCGGGACTCTGGTGTTTGGAAAGCTGCGAGGTTTCT	

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dnmt3ab

NCBI NO.	XM_005477258.3
Position of Coding sequence	280-3228

>XM_005477258.3 PREDICTED: Oreochromis niloticus DNA (cytosine-5)-methyltransferase 3A (LOC100693331), mRNA AGCAGGCACACTTCAGGCCCCTGCAGTCAGAGCGGCGCATCTGGAAGAGAGCTGGCCGGCTGGGGAGGTGGAGGACGGGGAG AGAAGAGGAAGGAGGCTCCGGGAGCAAGCGAGACAAAAAGGGTCAGGCCTGGGACTTGGGAAAACCGGGAGAGCAGGAAG

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dnmt3ba

NCBI NO.	XM_025901732.1
Position of Coding sequence	184-4581

>XM_025901732.1 PREDICTED: Oreochromis niloticus DNA (cytosine-5-)-methyltransferase 3 beta, duplicate a (dnmt3ba), transcript variant X3, mRNA

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NCBI NO.	XM_025901790.1
Position of Coding sequence	378-2843

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NCBI NO.	XM_025897345.1
Position of Coding sequence	300-6794

>XM_025897345.1 PREDICTED: Oreochromis niloticus tet methylcytosine dioxygenase 1 (tet1), mRNA

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NCBI NO.	XM_005457001.3

Position of Coding sequence	545-5947

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NCBI NO.	XM_019365521.2
Position of Coding sequence	3585-9461

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setd1a	
NCBI NO.	XM_005468973.4
Position of Coding sequence	62-6679

>XM_005468973.4 PREDICTED: Oreochromis niloticus SET domain containing 1A, histone lysine methyltransferase (setd1a), transcript variant X1, mRNA

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setd1ba	
NCBI NO.	XM_005470275.4
Position of Coding sequence	890-6325

>XM_005470275.4 PREDICTED: Oreochromis niloticus SET domain containing 1B, histone lysine methyltransferase a (setd1ba), transcript variant X1, mRNA

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kmt2a	
NCBI NO.	XM_013274782.3
Position of Coding sequence	50-13726

>XM_013274782.3 PREDICTED: Oreochromis niloticus lysine (K)-specific methyltransferase 2A (kmt2a), mRNA

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kmt2ba	
NCBI NO.	XM_013275905.3
Position of Coding sequence	95-9511

>XM_013275905.3 PREDICTED: Oreochromis niloticus lysine (K)-specific methyltransferase 2Ba (kmt2ba), transcript variant X1, mRNA

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kmt2bb	
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Position of Coding sequence	76-11661

>XM_013277028.3 PREDICTED: Oreochromis niloticus lysine (K)-specific methyltransferase 2Bb (kmt2bb), transcript variant X1, mRNA

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>XM_005451728.4 PREDICTED: Oreochromis niloticus lysine demethylase 5A (kdm5a), transcript variant X1, mRNA

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NCBI NO.	XM_005475002.4
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suv39h1b	
NCBI NO.	XM_003459875.5
Position of Coding sequence	87-1322

>XM_003459875.5 PREDICTED: Oreochromis niloticus histone-lysine N-methyltransferase SUV39H1 (LOC100693758), mRNA
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kdm4aa	
NCBI NO.	XM_005457300.3
Position of Coding sequence	179-3472

>XM_005457300.3 PREDICTED: Oreochromis niloticus lysine (K)-specific demethylase 4A, genome duplicate a (kdm4aa), mRNA

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NCBI NO.	XM_005476068.4

Position of Coding sequence	208-3738

>XM_005476068.4 PREDICTED: Oreochromis niloticus lysine (K)-specific demethylase 4A, genome duplicate b (kdm4ab), transcript variant X1, mRNA

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NCBI NO.	XM_005453970.4
Position of Coding sequence	184-3897

>XM_005453970.4 PREDICTED: Oreochromis niloticus lysine (K)-specific demethylase 4B (kdm4b), mRNA

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kat2a	
NCBI NO.	XM_025906390.1
Position of Coding sequence	163-2559

>XM_025906390.1 PREDICTED: Oreochromis niloticus K(lysine) acetyltransferase 2A (kat2a), transcript variant X1, mRNA

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kat2b	
NCBI NO.	XM_003444058.3
Position of Coding sequence	493-2871

>XM_003444058.3 PREDICTED: Oreochromis niloticus K(lysine) acetyltransferase 2B (kat2b), mRNA

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kat6a	
NCBI NO.	XM_005472980.3
Position of Coding sequence	865-7641

>XM_005472980.3 PREDICTED: Oreochromis niloticus K(lysine) acetyltransferase 6A (kat6a), mRNA

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gtf3c4

NCBI NO.	XM_003440231.5
Position of Coding sequence	43-2358

>XM_003440231.5 PREDICTED: Oreochromis niloticus general transcription factor IIIC, polypeptide 4 (gtf3c4), mRNA

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sirt2	
NCBI NO.	XM_003449264.5
Position of Coding sequence	153-1301

>XM_003449264.5 PREDICTED: Oreochromis niloticus sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae) (sirt2), transcript variant X1, mRNA

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Table S3. Data for the analysis of global DNA (de)methylation in liver tissue in the present study.

Stages	Treatments	Replication	Concentration (nmol/ng DNA)					Cytosines composition (%)				
			5-mdC	5-hmdC	5-fdC	5-cadC	dC	5-mdC	5-hmdC	5-fdC	5-cadC	dC
Juvenile	Fasted	F1	24.70	0.43	0.46	0.28	343.78	6.58	0.11	0.14	0.08	93.08
		F2	22.45	0.64	0.34	0.10	318.06	6.69	0.19	0.10	0.03	92.99
		F3	23.63	0.62	0.13	0.07	270.55	8.05	0.21	0.05	0.03	91.67
		F4	24.29	0.57	0.03	0.12	320.94	7.07	0.17	0.01	0.03	92.72
		F5	21.25	0.82	0.07	0.12	256.30	7.87	0.30	0.03	0.05	91.76
		F6	21.83	0.93	0.21	0.09	296.53	6.82	0.29	0.07	0.03	92.80
	HC/LP	H1	24.83	0.08	0.14	0.05	305.11	7.54	0.02	0.04	0.02	92.38
		H2	33.39	0.16	0.16	0.02	387.74	7.93	0.04	0.04	0.00	91.99
		H3	21.10	0.17	0.14	0.14	248.16	7.95	0.06	0.05	0.05	91.89
		H4	25.47	0.14	0.17	0.36	294.35	8.00	0.05	0.06	0.12	91.78
		H5	35.19	0.14	0.13	0.15	332.12	9.19	0.04	0.04	0.04	90.70
		H6	35.42	0.35	0.19	0.46	409.02	7.93	0.08	0.04	0.10	91.85
	LC/HP	L1	24.56	0.12	0.19	0.17	251.31	8.95	0.04	0.07	0.06	90.87
		L2	32.94	0.26	0.16	0.16	368.07	8.18	0.07	0.04	0.04	91.66
		L3	38.31	0.30	0.20	0.04	486.09	7.28	0.06	0.04	0.01	92.61
		L4	38.92	0.33	0.21	0.08	490.92	7.34	0.06	0.04	0.02	92.54
		L5	42.60	0.40	0.22	0.18	501.31	7.82	0.07	0.04	0.03	92.03
		L6	42.94	0.26	0.21	0.14	473.44	8.31	0.05	0.04	0.03	91.58
Adult	Fasted	F1	20.25	0.78	0.29	0.17	253.64	7.36	0.30	0.11	0.06	92.17
		F2	17.97	1.01	0.07	0.12	239.41	7.45	0.39	0.03	0.05	92.07
		F3	19.94	0.94	0.23	0.29	225.81	8.32	0.38	0.08	0.14	91.09
		F4	19.72	0.78	0.21	0.14	201.47	8.92	0.35	0.10	0.06	90.57
		F5	21.52	0.73	0.10	0.21	206.25	9.35	0.32	0.05	0.08	90.20
		F6	24.89	1.04	0.10	0.15	262.93	8.82	0.37	0.03	0.05	90.73
	HC/LP	H1	32.64	0.93	0.15	0.05	355.90	8.27	0.24	0.04	0.01	91.44
		H2	47.42	0.64	0.24	0.06	456.51	9.12	0.11	0.05	0.01	90.71
		H3	23.20	1.02	0.13	0.12	241.42	8.84	0.38	0.05	0.04	90.69
		H4	27.06	0.20	0.15	0.12	245.65	9.78	0.08	0.05	0.04	90.05
		H5	20.65	0.74	0.13	0.04	219.25	8.88	0.35	0.05	0.02	90.70
		H6	42.27	0.85	0.18	0.07	451.62	8.54	0.17	0.04	0.01	91.24
	LC/HP	L1	30.08	0.76	0.20	0.27	325.19	8.59	0.22	0.06	0.08	91.05
		L2	22.16	0.64	0.14	0.13	212.24	9.48	0.27	0.06	0.05	90.13
		L3	26.70	0.24	0.15	0.06	280.18	8.66	0.08	0.05	0.02	91.19
		L4	27.98	0.85	0.16	0.06	246.57	10.05	0.30	0.06	0.02	89.57
		L5	33.96	1.10	0.21	0.09	345.03	8.93	0.29	0.05	0.02	90.70
		L6	28.45	0.40	0.23	0.15	264.23	9.71	0.14	0.08	0.05	90.03

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S4. Data for the analysis of global DNA (de)methylation in muscle tissue in the present study.

Stages	Treatments	Replication	Concentration (nmol/ng DNA)					Cytosines composition (%)				
			5-mdC	5-hmdC	5-fdC	5-cadC	dC	5-mdC	5-hmdC	5-fdC	5-cadC	dC
Juvenile	Fasted	F1	27.49	2.55	0.43	0.18	350.68	7.31	0.66	0.11	0.05	91.87
		F2	27.31	2.92	0.37	0.20	315.79	7.93	0.84	0.12	0.08	91.03
		F3	22.78	2.43	0.43	0.29	294.46	7.13	0.73	0.13	0.09	91.92
		F4	29.15	1.06	0.55	0.60	340.39	7.89	0.27	0.16	0.16	91.52
		F5	34.39	1.67	0.56	0.38	336.91	9.21	0.46	0.14	0.09	90.10
		F6	22.10	1.50	0.53	0.33	267.38	7.57	0.53	0.18	0.11	91.60
	HC/LP	H1	5.72	0.53	0.19	0.06	92.57	5.75	0.54	0.17	0.07	93.47
		H2	10.00	1.27	0.06	0.01	180.29	5.38	0.74	0.03	0.00	93.85
		H3	12.69	1.21	0.21	0.15	137.48	8.43	0.81	0.14	0.10	90.52
		H4	11.21	1.77	0.10	0.11	196.96	5.24	0.86	0.03	0.09	93.77
		H5	6.66	0.75	0.16	0.13	84.44	7.02	0.78	0.17	0.10	91.92
		H6	13.66	1.78	0.16	0.05	190.26	7.05	0.83	0.13	0.03	91.96
	LC/HP	L1	11.50	0.64	0.08	0.06	139.63	7.64	0.33	0.04	0.03	91.96
		L2	7.40	0.42	0.05	0.09	83.85	7.95	0.36	0.05	0.08	91.56
		L3	17.86	2.10	0.17	0.14	247.69	7.00	0.83	0.07	0.14	91.95
		L4	20.25	2.28	0.10	0.22	267.18	7.16	0.76	0.03	0.08	91.97
		L5	32.06	1.99	0.19	0.32	482.18	6.41	0.50	0.03	0.08	92.97
		L6	11.45	1.19	0.04	0.04	147.73	6.74	0.83	0.05	0.02	92.36
Adult	Fasted	F1	20.10	0.33	0.07	0.07	273.40	7.04	0.13	0.03	0.03	92.77
		F2	24.48	0.27	0.08	0.06	326.22	6.94	0.08	0.02	0.02	92.95
		F3	22.25	1.03	0.12	0.12	301.38	6.97	0.33	0.03	0.04	92.63
		F4	18.45	0.29	0.08	0.09	248.28	6.90	0.11	0.03	0.04	92.93
		F5	25.96	0.53	0.10	0.12	326.96	7.41	0.16	0.03	0.04	92.36
		F6	12.67	0.51	0.07	0.09	224.15	4.98	0.20	0.03	0.04	94.75
	HC/LP	H1	9.03	0.23	0.04	0.11	149.11	5.69	0.15	0.02	0.06	94.07
		H2	10.56	0.23	0.05	0.03	174.17	5.65	0.13	0.03	0.02	94.17
		H3	10.09	0.22	0.08	0.06	137.64	6.82	0.15	0.05	0.04	92.94
		H4	14.27	0.39	0.25	0.11	226.32	6.01	0.12	0.09	0.03	93.76
		H5	20.52	0.82	0.72	0.15	284.44	6.70	0.27	0.23	0.05	92.74
		H6	7.60	0.44	0.14	0.11	113.13	6.64	0.30	0.17	0.16	92.74
	LC/HP	L1	18.16	0.36	0.19	0.10	209.28	8.01	0.15	0.09	0.04	91.70
		L2	18.08	0.46	0.05	0.20	207.95	8.10	0.20	0.02	0.09	91.60
		L3	16.34	0.51	0.13	0.11	190.51	7.84	0.25	0.07	0.06	91.79
		L4	12.48	1.34	0.01	0.04	170.00	6.73	0.71	0.01	0.02	92.54
		L5	18.14	1.31	0.02	0.14	221.26	7.54	0.55	0.01	0.06	91.85
		L6	21.57	1.74	0.08	0.16	250.22	7.87	0.63	0.03	0.06	91.41

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S5. Data used for the analysis of global histone modification in liver tissue in the present study.

Stages	Treatments	Replication	H3K4me3/H3	H3K9me3/H3	H3K36me3/H3	H3K9ac/H3
Juvenile	Fasted	F1	1.20	0.89	1.05	0.86
		F2	1.24	1.47	1.52	1.30
		F3	0.97	0.84	0.92	0.94
		F4	1.13	0.85	0.87	1.13
		F5	0.65	1.35	1.16	1.22
		F6	0.85	1.85	1.90	2.61
	HC/LP	H1	0.60	0.93	1.04	0.50
		H2	0.82	1.11	0.95	0.46
		H3	1.06	0.86	0.87	0.51
		H4	0.86	0.79	0.52	0.00
		H5	2.90	2.17	0.00	0.00
		H6	1.10	1.95	0.68	0.00
	LC/HP	L1	1.45	1.80	1.56	1.79
		L2	1.01	1.16	1.07	1.41
		L3	1.06	0.98	1.25	2.24
		L4	1.07	0.78	0.95	1.45
		L5	1.08	1.50	1.59	1.76
		L6	0.88	1.67	1.59	4.03
Adult	Fasted	F1	0.10	0.94	0.66	0.50
		F2	0.21	1.04	0.65	1.28
		F3	1.11	1.71	1.57	2.98
		F4	2.50	1.34	1.23	1.57
		F5	0.63	1.27	1.07	1.03
		F6	0.87	1.67	1.58	1.60
	HC/LP	H1	0.15	0.54	0.74	0.14
		H2	0.72	1.13	1.55	0.20
		H3	1.32	1.54	1.18	1.70
		H4	0.67	1.01	0.90	1.09
		H5	2.57	1.76	2.48	1.11
		H6	0.30	0.89	0.73	1.03
	LC/HP	L1	1.60	0.89	0.83	0.50
		L2	2.94	1.05	0.96	0.57
		L3	34.04	15.05	6.21	121.18
		L4	10.24	1.25	1.49	8.25
		L5	0.63	1.36	1.20	1.29
		L6	7.87	1.70	2.50	5.54

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S6. Data used for the analysis of global histone modification in muscle tissue in the present study.

Stages	Treatments	Replication	H3K4me3/H3	H3K9me3/H3	H3K36me3/H3	H3K9ac/H3
Juvenile	Fasted	F1	0.54	1.21	0.52	1.23
		F2	0.32	0.69	0.46	0.87
		F3	0.63	1.21	0.92	0.75
		F4	0.73	1.52	1.02	1.16
		F5	0.98	0.89	1.41	0.88
		F6	0.80	0.75	1.07	0.71
	HC/LP	H1	0.79	1.18	1.56	2.42
		H2	3.21	2.38	4.23	4.57
		H3	1.11	1.29	2.45	1.16
		H4	1.18	1.41	3.21	1.37
		H5	0.86	0.56	1.40	0.91
		H6	0.55	0.27	1.19	0.73
	LC/HP	L1	0.52	0.91	0.51	1.01
		L2	0.51	0.60	0.60	0.89
		L3	1.31	1.18	2.65	1.30
		L4	0.55	0.96	0.95	1.23
		L5	0.98	1.16	0.46	1.08
		L6	0.88	0.71	0.79	0.74
Adult	Fasted	F1	0.23	0.25	0.22	0.09
		F2	0.80	0.66	0.98	0.32
		F3	0.24	0.51	0.22	0.31
		F4	4.46	2.49	0.79	1.19
		F5	0.53	0.31	0.61	0.72
		F6	0.24	0.47	0.60	0.43
	HC/LP	H1	2.51	2.02	1.79	1.03
		H2	1.12	0.47	0.75	0.34
		H3	0.97	1.19	0.00	0.24
		H4	0.40	0.57	0.08	0.35
		H5	1.17	1.07	2.21	1.42
		H6	0.35	0.31	0.37	0.24
	LC/HP	L1	12.34	12.00	19.61	3.85
		L2	1.95	1.14	1.63	0.66
		L3	0.87	2.36	1.47	2.31
		L4	0.15	1.00	0.19	1.07
		L5	1.79	1.25	2.00	1.82
		L6	8.85	2.27	6.63	7.00

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S7. Data used for the analysis of mRNA expression of genes involved in (de)methylation in liver tissue in the present study.

			DNA methylation writer					DNA methylation eraser		
Stages	**Treatments**	**Replication**	***dnmt1***	***dnmt3aa***	***dnmt3ab***	***dnmt3ba***	***dnmt3bb***	***tet1***	***tet2***	***tet3***
Juvenile	Fasted	F1	0.49	0.53	nd	0.16	0.20	0.76	0.60	0.79
		F2	0.41	0.49	nd	0.14	0.20	0.87	0.65	0.76
		F3	0.37	0.43	nd	0.28	0.18	0.82	0.64	0.77
		F4	0.41	0.57	nd	0.25	0.20	0.62	0.65	0.76
		F5	0.40	0.55	nd	0.23	0.23	0.47	0.82	0.78
		F6	0.39	0.55	nd	0.27	0.25	0.59	0.85	0.92
	HC/LP	H1	1.78	0.94	nd	0.59	0.59	0.38	0.41	0.65
		H2	1.63	0.78	nd	0.50	0.51	0.32	0.57	0.66
		H3	1.74	0.86	nd	0.85	0.85	0.64	0.45	0.66
		H4	1.86	0.90	nd	0.70	0.70	0.41	0.52	0.83
		H5	1.66	0.72	nd	0.61	0.61	0.34	0.39	0.56
		H6	1.85	0.81	nd	0.74	0.75	0.45	0.76	1.09
	LC/HP	L1	0.95	0.72	nd	0.13	0.50	0.35	0.51	0.54
		L2	1.02	0.70	nd	0.14	0.43	0.28	0.43	0.61
		L3	0.95	0.52	nd	0.12	0.57	0.40	0.46	0.47
		L4	1.01	0.70	nd	0.12	0.38	0.23	0.38	0.46
		L5	0.87	0.51	nd	0.13	0.54	0.42	0.33	0.43
		L6	0.95	0.57	nd	0.11	0.56	0.44	0.42	0.48
Adult	Fasted	F1	1.33	1.53	nd	0.25	0.34	1.00	1.32	1.20
		F2	1.80	1.49	nd	0.31	0.38	1.09	1.18	1.09
		F3	2.34	1.31	nd	0.37	0.36	1.29	1.06	1.42
		F4	1.54	1.13	nd	0.30	0.36	1.45	2.13	0.97
		F5	2.09	1.26	nd	0.33	0.24	1.05	1.89	1.27
		F6	1.60	1.17	nd	0.37	0.29	1.08	1.91	1.23
	HC/LP	H1	1.20	0.69	nd	0.84	0.85	0.33	0.68	0.66
		H2	1.39	0.72	nd	0.72	0.72	0.26	0.72	1.03
		H3	1.44	0.65	nd	1.15	1.16	0.47	0.69	0.58
		H4	1.21	0.67	nd	0.87	0.87	0.32	0.57	0.57
		H5	1.38	0.57	nd	0.78	0.79	0.27	0.72	0.84
		H6	1.22	0.69	nd	0.99	1.00	0.36	0.88	0.72
	LC/HP	L1	0.32	0.35	nd	0.59	0.60	0.21	0.30	0.44
		L2	0.27	0.41	nd	0.54	0.55	0.23	0.45	0.56
		L3	0.28	0.32	nd	0.64	0.65	0.30	0.24	0.28
		L4	0.31	0.40	nd	0.54	0.54	0.16	0.27	0.50
		L5	0.31	0.41	nd	0.58	0.59	0.23	0.20	0.32
		L6	0.54	0.40	nd	0.41	0.41	0.20	0.37	0.61

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S8. Data used for the analysis of mRNA expression of genes involved in (de)methylation in muscle tissue in the present study.

			DNA methylation writer					DNA methylation eraser		
Stages	**Treatments**	**Replication**	***dnmt1***	***dnmt3aa***	***dnmt3ab***	***dnmt3ba***	***dnmt3bb***	***tet1***	***tet2***	***tet3***
Juvenile	Fasted	F1	2.09	0.86	nd	1.96	0.93	1.44	1.67	1.48
		F2	3.07	0.83	nd	1.87	0.72	1.41	1.59	1.39
		F3	2.29	0.80	nd	1.87	0.97	1.46	1.64	1.44
		F4	2.04	0.83	nd	2.40	0.82	1.40	1.63	1.53
		F5	2.13	0.82	nd	1.75	0.77	1.34	1.54	1.48
		F6	1.97	0.88	nd	1.92	0.77	1.28	1.45	1.41
	HC/LP	H1	1.66	1.52	nd	1.22	1.63	1.47	0.98	1.21
		H2	1.78	1.57	nd	1.52	1.70	1.48	1.03	1.17
		H3	1.82	1.55	nd	1.29	1.92	1.61	1.03	1.13
		H4	1.70	1.55	nd	0.90	1.94	1.51	1.02	1.14
		H5	1.79	1.50	nd	1.02	1.76	1.27	0.88	1.13
		H6	1.78	1.54	nd	1.10	1.78	1.38	0.95	1.11
	LC/HP	L1	1.39	1.24	nd	0.98	1.44	1.35	0.87	0.90
		L2	1.37	1.29	nd	1.19	1.43	1.46	0.86	0.89
		L3	1.53	1.31	nd	0.94	1.46	1.30	0.84	0.93
		L4	1.74	1.36	nd	1.21	1.51	1.37	0.86	0.93
		L5	1.52	1.31	nd	0.96	1.40	1.38	0.85	0.90
		L6	1.41	1.26	nd	1.02	1.46	1.41	0.88	0.91
Adult	Fasted	F1	0.95	0.93	nd	0.87	0.55	1.06	1.15	1.03
		F2	0.97	0.92	nd	1.14	0.57	1.05	1.29	1.04
		F3	0.94	0.95	nd	1.41	0.60	1.06	1.29	1.11
		F4	1.12	0.95	nd	1.17	0.65	0.98	1.34	1.07
		F5	1.06	0.97	nd	0.96	0.56	1.04	1.34	1.11
		F6	0.99	0.97	nd	1.24	0.70	1.05	1.38	1.14
	HC/LP	H1	1.61	1.02	nd	1.31	1.37	1.41	1.13	1.21
		H2	1.53	1.04	nd	1.06	1.28	1.21	0.93	1.14
		H3	1.55	1.00	nd	0.98	1.26	1.22	0.93	1.13
		H4	2.15	1.01	nd	1.19	1.24	1.22	1.05	1.32
		H5	2.05	0.94	nd	1.09	1.33	1.28	1.12	1.49
		H6	2.02	0.95	nd	1.12	1.18	1.15	1.07	1.23
	LC/HP	L1	1.21	1.41	nd	0.65	0.82	1.03	0.73	0.73
		L2	1.14	1.39	nd	0.86	0.79	1.05	0.77	0.76
		L3	0.95	1.36	nd	0.85	0.77	1.03	0.74	0.75
		L4	1.26	1.38	nd	0.99	0.84	0.99	0.71	0.78
		L5	1.72	1.37	nd	0.73	0.85	0.97	0.79	0.73
		L6	1.24	1.41	nd	0.97	0.82	0.94	0.81	0.83

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S9. Data used for the analysis of mRNA expression of genes involved in H3K4me3 modification in liver tissue in the present study.

			H3K4me3 writer					H3K4me3 eraser				
Stages	**Treatments**	**Replication**	***setd1a***	***setd1ba***	***kmt2a***	***kmt2ba***	***kmt2bb***	***kdm5a***	***kdm5ba***	***kdm5bb***	***kdm5c***	***riox1***
Juvenile	Fasted	F1	0.64	0.42	0.95	0.99	0.83	0.47	0.79	0.37	0.32	0.12
		F2	0.59	0.50	0.96	0.97	0.79	0.44	0.75	0.31	0.28	0.07
		F3	0.64	0.47	0.94	0.94	0.78	0.49	0.84	0.29	0.25	0.06
		F4	0.63	0.45	0.93	0.95	0.75	0.50	0.72	0.30	0.30	0.16
		F5	0.68	0.47	1.13	0.94	0.89	0.54	0.93	0.35	0.31	0.06
		F6	0.78	0.73	1.16	1.08	0.99	0.33	0.91	0.42	0.37	0.09
	HC/LP	H1	0.76	0.36	0.55	0.64	0.79	1.02	1.28	0.73	0.50	0.79
		H2	0.64	0.39	0.48	0.72	0.79	1.30	1.25	0.77	0.43	0.56
		H3	0.72	0.32	0.48	0.49	0.62	1.31	1.21	0.60	0.39	0.79
		H4	0.75	0.39	0.53	0.54	0.73	1.24	1.45	0.60	0.33	1.08
		H5	0.59	0.28	0.44	0.46	0.71	1.18	0.88	0.47	0.34	1.43
		H6	0.62	0.39	0.42	0.59	0.72	1.05	1.39	0.68	0.49	0.36
	LC/HP	L1	0.48	0.47	0.35	0.56	0.77	0.48	0.69	0.26	0.31	0.39
		L2	0.51	0.43	0.37	0.57	0.70	0.53	0.63	0.29	0.27	0.59
		L3	0.45	0.43	0.31	0.48	0.59	0.58	0.63	0.18	0.22	0.31
		L4	0.52	0.36	0.43	0.68	0.76	0.52	0.70	0.29	0.29	0.36
		L5	0.40	0.28	0.34	0.56	0.53	0.51	0.45	0.21	0.16	0.24
		L6	0.46	0.34	0.52	0.60	0.67	0.51	0.72	0.24	0.28	0.16
Adult	Fasted	F1	1.36	2.36	1.66	1.68	1.86	2.24	1.37	0.79	0.67	0.48
		F2	1.39	1.99	1.49	1.52	2.15	1.98	1.54	0.62	0.53	0.48
		F3	2.14	2.66	2.04	2.07	2.12	1.87	3.28	1.34	0.49	1.20
		F4	2.03	1.54	1.27	1.57	1.47	1.85	3.60	0.96	1.33	1.20
		F5	2.41	2.51	1.70	2.11	2.50	1.81	3.47	1.30	0.97	0.77
		F6	2.31	2.18	1.49	1.84	2.29	1.96	3.01	1.20	0.88	0.69
	HC/LP	H1	0.29	0.44	0.39	0.56	0.50	0.60	0.68	0.22	0.26	0.12
		H2	0.66	0.96	0.97	0.69	0.96	0.51	1.29	0.34	0.36	0.21
		H3	0.58	0.64	0.92	0.93	0.82	0.84	0.96	0.37	0.25	0.25
		H4	0.84	1.33	0.91	0.81	1.12	0.71	1.12	0.44	0.43	0.57
		H5	0.79	1.05	0.90	0.99	0.88	0.68	1.17	0.46	0.43	0.52
		H6	0.92	0.87	0.70	0.89	0.94	0.53	0.88	0.44	0.40	0.85
	LC/HP	L1	0.23	0.43	0.49	0.39	0.40	0.21	0.32	0.08	0.11	0.04
		L2	0.37	0.49	0.83	0.60	0.57	0.14	0.42	0.14	0.19	0.01
		L3	0.21	0.28	0.66	0.37	0.41	0.17	0.29	0.08	0.10	0.03
		L4	0.40	0.94	0.79	0.93	0.77	0.11	0.43	0.18	0.23	0.06
		L5	0.15	0.14	0.30	0.28	0.26	0.25	0.12	0.04	0.06	0.11
		L6	0.38	0.42	0.76	0.75	0.75	0.16	0.33	0.13	0.18	0.15

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S10. Data used for the analysis of mRNA expression of genes involved in H3K9me3, H3K36me3 and H3K9ac modification in liver tissue in the present study.

			H3K9me3 writer	H3K9me3 and H3K36me3 eraser				H3K36me3 eraser	H3K9ac writer				H3K9ac eraser	
Stages	**Treatments**	**Replication**	***suv39h1b***	***kdm4aa***	***kdm4ab***	***kdm4b***	***kdm4c***	***setd2***	***kat2a***	***kat2b***	***kat6a***	***gtf3c4***	***sirt2***	***sirt5***
Juvenile	Fasted	F1	0.17	0.47	0.25	0.40	0.28	0.49	0.19	0.44	0.52	0.44	0.15	0.43
		F2	0.17	0.44	0.27	0.32	0.23	0.39	0.21	0.39	0.68	0.36	0.14	0.45
		F3	0.19	0.47	0.24	0.31	0.27	0.45	0.16	0.37	0.80	0.39	0.16	0.45
		F4	0.21	0.44	0.28	0.37	0.27	0.48	0.19	0.63	0.67	0.52	0.17	0.43
		F5	0.25	0.41	0.22	0.37	0.23	0.42	0.20	0.55	0.77	0.40	0.20	0.47
		F6	0.14	0.46	0.27	0.34	0.25	0.45	0.31	0.42	0.70	0.41	0.18	0.43
	HC/LP	H1	1.04	0.55	0.64	0.82	0.65	0.54	0.76	0.82	0.25	0.59	0.95	0.64
		H2	0.94	0.55	0.50	0.73	0.59	0.45	0.42	0.78	0.23	0.53	0.90	0.56
		H3	0.93	0.52	0.52	0.76	0.56	0.42	0.37	0.57	0.21	0.46	1.79	0.63
		H4	1.02	0.53	0.45	0.68	0.57	0.40	0.25	0.33	0.12	0.43	1.83	0.67
		H5	0.95	0.49	0.52	0.74	0.59	0.39	0.41	0.48	0.11	0.68	1.22	0.64
		H6	0.88	0.54	0.46	0.78	0.49	0.42	0.49	0.50	0.42	0.45	0.76	0.63
	LC/HP	L1	0.70	0.38	0.40	0.40	0.33	0.42	0.41	0.54	0.25	0.54	0.37	0.38
		L2	0.59	0.38	0.31	0.41	0.30	0.40	0.47	0.44	0.23	0.58	0.39	0.45
		L3	0.62	0.38	0.33	0.37	0.29	0.40	0.45	0.24	0.26	0.49	0.35	0.37
		L4	0.67	0.39	0.33	0.34	0.32	0.38	0.34	0.19	0.37	0.50	0.30	0.27
		L5	0.72	0.34	0.30	0.36	0.28	0.38	0.45	0.32	0.25	0.50	0.28	0.31
		L6	0.73	0.32	0.26	0.36	0.31	0.40	0.48	0.29	0.29	0.45	0.28	0.28
Adult	Fasted	F1	0.73	1.83	1.02	1.24	0.85	1.40	0.86	1.81	0.97	0.95	1.13	1.04
		F2	1.26	1.88	1.19	1.26	0.92	1.41	0.79	1.74	1.15	0.89	1.15	0.87
		F3	0.60	2.11	1.16	1.32	0.82	1.47	0.72	0.83	1.35	0.94	1.52	1.28
		F4	1.10	1.85	1.06	1.11	0.83	1.46	1.24	0.89	1.00	0.83	1.20	0.96
		F5	1.23	1.98	1.09	1.12	0.87	1.40	1.00	1.36	0.91	0.60	0.83	0.91
		F6	1.13	1.76	1.08	1.28	0.78	1.42	0.65	0.84	0.88	0.45	1.09	1.12
	HC/LP	H1	0.38	0.80	0.60	1.23	0.62	0.42	0.66	1.54	0.39	0.80	0.35	0.42
		H2	0.34	0.65	0.50	1.29	0.60	0.45	0.61	0.94	0.40	0.77	0.31	0.28
		H3	0.34	0.69	0.41	1.30	0.54	0.46	0.74	0.70	0.16	0.71	0.36	0.36
		H4	0.59	0.76	0.50	1.17	0.61	0.46	0.52	0.64	0.24	0.51	0.31	0.30
		H5	0.40	0.76	0.54	1.38	0.62	0.43	1.02	0.38	0.50	0.31	0.27	0.31
		H6	0.16	0.70	0.51	1.15	0.56	0.41	0.36	0.45	0.56	0.44	0.32	0.41
	LC/HP	L1	0.53	0.26	0.17	0.28	0.15	0.33	0.23	0.44	0.20	0.61	0.07	0.13
		L2	0.29	0.28	0.18	0.26	0.21	0.29	0.20	0.54	0.20	0.41	0.05	0.13
		L3	0.31	0.29	0.18	0.24	0.19	0.28	0.22	0.43	0.28	0.29	0.06	0.15
		L4	0.24	0.25	0.18	0.30	0.19	0.28	0.21	0.26	0.68	0.31	0.07	0.10
		L5	0.17	0.18	0.21	0.16	0.15	0.25	0.37	0.28	0.43	0.19	0.04	0.10
		L6	0.17	0.21	0.15	0.21	0.21	0.31	0.40	0.26	0.30	0.14	0.05	0.13

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S11. Data used for the analysis of mRNA expression of genes involved in H3K4me3 modification in muscle tissue in the present study.

			H3K4me3 writer					H3K4me3 eraser				
Stages	**Treatments**	**Replication**	***setd1a***	***setd1ba***	***kmt2a***	***kmt2ba***	***kmt2bb***	***kdm5a***	***kdm5ba***	***kdm5bb***	***kdm5c***	***riox1***
Juvenile	Fasted	F1	1.62	1.75	1.50	1.35	2.04	1.85	1.16	1.94	1.43	0.80
		F2	1.82	1.95	1.57	1.34	1.89	2.00	1.24	1.91	1.46	0.86
		F3	1.62	1.80	1.52	1.32	1.88	2.09	1.18	1.89	1.45	0.82
		F4	1.66	1.83	1.52	1.40	1.97	2.21	1.20	1.85	1.43	0.82
		F5	1.43	1.64	1.47	1.35	1.77	1.50	1.28	1.52	1.18	0.83
		F6	1.52	1.72	1.47	1.25	1.72	1.49	1.09	1.72	1.33	0.79
	HC/LP	H1	1.51	1.62	0.80	1.04	1.24	1.25	1.20	0.96	1.08	1.78
		H2	1.30	1.60	0.71	1.00	1.15	1.20	1.40	0.97	1.07	1.89
		H3	1.20	1.63	0.83	1.12	1.21	1.18	1.14	1.01	1.10	1.87
		H4	1.28	1.64	0.80	0.97	1.19	1.12	1.27	1.00	1.21	1.93
		H5	1.22	1.49	0.74	0.96	1.21	1.10	1.24	0.94	1.02	1.99
		H6	1.19	1.46	0.82	0.98	1.15	1.26	1.28	0.99	1.09	1.80
	LC/HP	L1	1.30	1.27	0.71	0.88	1.13	0.94	1.00	0.95	0.93	1.38
		L2	1.27	1.44	0.78	0.90	1.26	0.96	0.96	1.00	1.18	1.51
		L3	1.29	1.36	0.72	0.82	1.00	0.93	0.95	0.97	1.11	1.42
		L4	1.30	1.38	0.78	0.84	1.15	1.01	0.94	0.98	1.19	1.47
		L5	1.20	1.39	0.85	0.88	0.99	0.91	0.98	0.75	0.89	1.34
		L6	1.14	1.42	0.90	0.83	1.22	0.91	0.93	0.97	1.11	1.41
Adult	Fasted	F1	1.14	0.96	0.92	0.94	1.03	1.33	0.78	1.16	1.06	0.83
		F2	1.19	1.04	1.00	0.98	0.98	1.37	0.71	1.13	1.07	0.86
		F3	1.15	0.98	1.03	0.99	0.98	1.50	0.74	1.22	1.09	0.84
		F4	1.17	1.02	1.02	0.98	1.03	1.39	0.74	1.07	1.09	0.88
		F5	1.10	1.04	0.91	0.98	1.12	1.30	0.67	1.18	1.06	0.87
		F6	1.23	1.04	1.03	0.97	1.08	1.28	0.71	1.14	0.70	0.79
	HC/LP	H1	1.14	1.18	0.87	1.00	1.25	1.19	0.90	0.88	0.91	1.28
		H2	1.10	1.21	0.98	1.02	1.46	1.19	0.85	0.89	0.89	1.29
		H3	1.17	1.24	1.09	1.07	1.38	1.24	0.79	0.93	0.88	1.22
		H4	1.05	1.19	0.88	0.91	1.34	1.17	0.67	0.89	0.90	1.26
		H5	1.43	1.15	0.93	0.86	1.23	1.02	0.73	0.84	0.84	1.30
		H6	1.38	1.08	0.86	0.89	1.15	1.04	0.74	0.85	0.85	1.17
	LC/HP	L1	1.24	0.95	0.75	0.79	0.92	0.97	0.67	0.83	0.94	0.89
		L2	1.24	0.97	0.78	0.87	0.97	1.18	0.72	0.90	0.95	0.96
		L3	1.21	0.98	0.79	0.82	1.05	1.08	0.67	0.86	0.65	0.94
		L4	1.25	0.96	0.71	0.79	0.88	1.04	0.63	0.86	0.75	0.96
		L5	1.17	1.06	0.65	0.84	0.89	0.99	0.58	0.81	0.60	0.87
		L6	1.17	1.06	0.70	0.79	1.06	1.02	0.61	0.89	0.82	0.88

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.

Table S12. Data used for the analysis of mRNA expression of genes involved in H3K9me3, H3K36me3 and H3K9ac modification in muscle tissue in the present study.

			H3K9me3 writer	H3K9me3 and H3K36me3 eraser				H3K36me3 eraser	H3K9ac writer				H3K9ac eraser	
Stages	**Treatments**	**Replication**	***suv39h1b***	***kdm4aa***	***kdm4ab***	***kdm4b***	***kdm4c***	***setd2***	***kat2a***	***kat2b***	***kat6a***	***gtf3c4***	***sirt2***	***sirt5***
Juvenile	Fasted	F1	1.95	1.40	nd	1.22	1.61	1.56	0.74	1.88	1.65	1.69	1.17	1.42
		F2	1.76	1.43	nd	1.21	1.68	1.59	0.76	1.94	1.67	1.80	1.15	1.40
		F3	1.71	1.35	nd	1.22	1.72	1.58	0.80	2.01	1.65	1.63	1.24	1.49
		F4	1.77	1.36	nd	1.24	1.58	1.46	0.72	1.76	1.65	1.60	1.20	1.43
		F5	1.40	1.27	nd	1.19	1.53	1.48	0.76	1.98	1.40	1.45	1.20	1.35
		F6	1.36	1.27	nd	1.12	1.49	1.37	0.71	1.67	1.56	1.42	1.12	1.26
	HC/LP	H1	1.07	1.00	nd	0.91	1.19	1.32	1.67	0.63	1.12	1.19	1.04	1.12
		H2	1.09	1.09	nd	0.99	1.22	1.47	1.79	0.65	1.09	1.23	1.07	1.10
		H3	1.02	1.08	nd	0.95	1.14	1.40	1.56	0.60	1.03	1.13	1.03	1.05
		H4	0.91	1.05	nd	0.99	1.22	1.40	1.76	0.76	1.04	1.12	0.85	0.89
		H5	1.04	1.25	nd	1.01	1.18	1.39	1.82	0.73	1.12	1.04	0.90	0.91
		H6	0.90	1.09	nd	0.98	1.14	1.37	1.73	0.70	1.12	0.97	0.84	0.84
	LC/HP	L1	0.72	1.11	nd	0.91	1.12	1.26	1.45	0.67	0.88	0.89	0.94	0.98
		L2	0.82	0.93	nd	0.94	1.23	1.37	1.49	0.70	0.98	1.00	0.99	1.00
		L3	0.75	0.87	nd	0.93	1.13	1.38	1.41	0.63	0.88	0.93	0.91	0.87
		L4	0.86	0.94	nd	1.02	1.20	1.37	1.49	0.69	0.97	1.01	0.97	0.94
		L5	0.84	0.70	nd	0.94	1.19	1.36	1.50	0.72	0.96	1.00	0.95	0.96
		L6	0.95	0.85	nd	0.93	1.15	1.31	1.37	0.62	0.90	0.92	0.92	0.83
Adult	Fasted	F1	0.83	1.07	nd	0.80	0.99	1.24	0.66	1.27	1.18	1.07	0.94	1.05
		F2	0.78	1.07	nd	0.82	0.96	1.19	0.74	1.43	1.11	0.99	0.98	0.95
		F3	0.60	1.14	nd	0.85	0.97	1.14	0.84	1.56	1.21	1.01	0.96	0.95
		F4	0.64	1.06	nd	0.78	0.96	1.14	0.71	1.34	1.23	1.08	0.99	1.01
		F5	0.67	1.09	nd	0.80	0.95	1.12	0.71	1.21	1.20	0.99	0.87	0.98
		F6	0.73	1.24	nd	0.85	1.03	1.20	0.72	1.28	1.23	0.95	0.94	1.01
	HC/LP	H1	1.74	0.88	nd	1.26	1.16	1.36	1.22	0.86	0.93	1.39	0.73	0.97
		H2	1.68	0.91	nd	1.21	1.16	1.32	1.18	1.01	1.05	1.30	0.93	0.87
		H3	1.76	1.00	nd	1.15	1.04	1.19	1.20	1.14	1.00	1.27	0.96	0.86
		H4	1.64	0.90	nd	1.21	1.12	1.32	1.18	0.86	0.93	1.34	0.99	0.91
		H5	2.08	0.91	nd	1.21	0.94	1.14	1.18	0.93	0.90	1.38	0.94	0.85
		H6	1.73	0.87	nd	1.24	1.05	1.21	1.19	0.91	0.89	1.20	0.89	0.82
	LC/HP	L1	0.99	0.67	nd	0.83	1.00	1.22	1.18	0.59	0.71	0.90	0.76	0.79
		L2	1.04	0.67	nd	0.89	1.02	1.22	1.18	0.60	0.76	0.97	1.02	0.82
		L3	1.11	0.67	nd	0.83	0.99	1.16	1.14	0.55	0.73	0.89	0.71	0.79
		L4	1.01	0.66	nd	0.86	1.01	1.20	1.18	0.60	0.74	0.81	0.70	0.78
		L5	1.08	0.62	nd	0.77	0.87	1.10	1.18	0.57	0.73	0.89	0.67	0.73
		L6	1.19	0.61	nd	0.82	0.91	1.12	1.15	0.58	0.71	0.81	0.71	0.76

Red letters indicate the outliers of each experimental group, which were not included in the statistical analysis of significance.