

Supplementary Table S1 Primers information for the qPCR study on mtDNA and lipid metabolism-related genes in this work

Primer	Sequence (5'-3')	GenBank reference	PL (bp)
mtDNA			
16S rRNA-F	ATGTGGACCTGTATGAATGGC	NC_004299.1	119
16S rRNA-R	CTCCATAGGGTCTTCTCGTCTT		
CTYB-F	CCTCCTGGGCTTCACAATCA	NC_004299.1	123
CTYB-R	TTAATGTGGGCGGGGGTAAC		
lipid metabolism gene			
Lipogenesis			
<i>acacβ</i> -F	GAAAGGTTTGCTGTGCGACTA	XM_011615767.1	154
<i>acacβ</i> -R	TTACATCAGCGACCATTTCAGT		
<i>fas</i> -F	CTTTGCCGCTGTCAATCG	XM_011619859.1	78
<i>fas</i> -R	TGTCTCAACCCATTTGTAGTCG		
β-oxidation			
<i>cpt-1</i> -F	GGGGTTTGTGGTCAAGTTAGG	XM_011607269.1	186
<i>cpt-1</i> -R	ATAGATCCGTGGCGCTCAT		
<i>vlc</i> -qF	CGCTGTTCTTGGTGTGGAC	XM_003969871.3	276
<i>vlc</i> -qR	GAGATTTGCTGCGGATGTTG		
<i>acox1</i> -qF	GCACGGCATCGCAAGTAAC	XM_029850253.1	145
<i>acox1</i> -qR	GAGATCGAAGGCATCCACC		
<i>acox3</i> -qF	GACTGTGGCTATCCGCTTCT	XM_029839734.1	214
<i>acox3</i> -qR	TTCCTGTGCGTCACTCTTGT		
<i>ehhadh</i> -qF	GGCACAATGGGAAGAGGCATT	XM_003961946.3	185
<i>ehhadh</i> -qR	TGGACGGTTTCGCTGTAGGTA		
<i>acaa1</i> -qF	GGACAACAGCAAAGCAAGAG	XM_029849183.1	110
<i>acaa1</i> -qR	ACCAGAAAAAACAGCCAAAA		
<i>acaa2</i> -qF	ACGGGGGTGTTTTGAAGGA	XM_003975006.3	159

<i>acaa2-qR</i>	CATGACGGGCAATGTAGGG		
<i>dgat1-F</i>	TGGTTTGTGAGCCGTTTCC		
<i>dgat1-R</i>	CTGGCATTCGTTTGACTTCG	XM_003969352.2	185
<i>mgat2a-F</i>	AAAGGCTTCATTAAATTGGC		
<i>mgat2a-R</i>	TGATGGCTTGTCTGTAGGG	XM_003978609.3	223
Hydrolysis of glycerides			
<i>atgl-F</i>	CCAACCTCTACAGGGTCTCA		
<i>atgl-R</i>	GTTTAGCAGCCCGTTCTTC	XM_003967696.3	119
<i>dagla-F</i>	CTGTTGGTGGAGTTGGTGTATG		
<i>dagla-R</i>	ATCAGAGCACGGCTGGTAAT	XM_011610175.1	72
<i>hsl-F</i>	CTCTTGCTATCGGTCTTGTGG		
<i>hsl-R</i>	TTCTGGGTCAATGGCATACTT	XM_011621066.1	113
<i>mgll-F</i>	CCATCCAGTCAAAGTGGGTCT		
<i>mgll-R</i>	CATCAGCTGCATGCCGAA	XM_003963030.2	110
Lipid digestion			
<i>bsal-F</i>	TTGAAGATGACTGACCCCGA		
<i>bsal-R</i>	GATGTCTGCTGCGTTGTGAA	XM_003978375.2	162
<i>lp-F</i>	CGTTTTCTCCTGTTACCC		
<i>lp-R</i>	GACTCGTCCTCATCCCCT	XM_029832009.1	97
Lipid transport			
<i>lpl-F</i>	AGGGTCCACATCCGCAAA		
<i>lpl-R</i>	GTTTCTCCTTGCGGCTCAT	NM_001305600.1	157
<i>lipc-F</i>	GCGGCTTCAACAGCAGTAA		
<i>lipc-R</i>	GAGGTGCGCTATGTCTTTCC	XM_011610357.1	215
<i>fabp1-F</i>	CCATCGGTCTCCCTGATGAAG		
<i>fabp1-R</i>	TTGACCGTTACCTTCGGTCC	XM_003974807.3	121
<i>fabp10a-F</i>	CTGTGACCAACTCCTTTACCAT		
<i>fabp10a-R</i>	TCTCTCCACCTTTGAGCTCCTG	XM_003965635.3	150

<i>fatp1</i> -F	ATTGCAGACACCACAGGGAG	XM_003964742.3	219
<i>fatp1</i> -R	ATATCGTGACGCTCGTGCAT		
<i>apoa1</i> -F	CGATGACGCCGAGTACAAA	AB183289.1	104
<i>apoa1</i> -R	CGGTTATGGGAGAAACGCTA		
<i>apoa4</i> -F	TGCTTTCTGGGACTATGTTGC	NM_001078591.1	124
<i>apoa4</i> -R	GTTGACTTTGTCTGGCACTCTC		
<i>apob100</i> -F	AGGGACATAGTCAAACCAAGGA	XM_011619944.1	127
<i>apob100</i> -R	AGAACACGAAGGCTGGACAC		
<i>apoel</i> -F	TATTCAGACCCGCACCTCA	NM_001078592.1	201
<i>apoel</i> -R	ATTTCCTCCATCTTGTCCTCC		
<i>mttp</i> -F	ATGCTAAGGGTCTGGTTCTGC	XM_011612378.1	124
<i>mttp</i> -R	ATGTCAGTGCTGCCGATCTT		
Lipid metabolism-related transcriptional factors			
<i>srebf1</i> -F	TTTCAGCATCCCACCTTCC	XM_011603881.1	158
<i>srebf1</i> -R	GGTGAACCGTGAGGACAATA		
<i>ppara1</i> -F	TCAGTAGTTTATGGGTGTTGG	NM_001097630.1	119
<i>ppara1</i> -R	GCGTGGACTCCGTAGTGGTA		
<i>ppara2</i> -F	CCAGAAGAAGAACCGCAACA	NM_001097629.1	149
<i>ppara2</i> -R	CCTCTTTCTCCACCATCTTGTT		
<i>pparβ</i> -F	AGCTGGAATACGACCGATGT	AB275887.1	249
<i>pparβ</i> -R	TCTTCAGGTAGGCGGAGTTG		
<i>pparγ</i> -F	CGCTGTCCCGACATCTGTAT	NM_001097627.1	146
<i>pparγ</i> -R	GAACTGCTCGCCTTCCATT		
<i>fxr</i> -F	GTGAACGACCACAAGTTTACCC	XM_003967283.2	166
<i>fxr</i> -R	AGACCAACAGATTACACCGGAT		
<i>lxra</i> -F	GTGACGCACCACTAACAGCA	XM_011609917.1	191
<i>lxra</i> -R	CTGACAACACCGAGCAAGACT		
<i>hnf4a</i> -F	GAGCCACGGGCAAACACTA	XM_011619034.1	199

<i>hnf4a</i> -R	AGGGTCCTACCTTCTTTCTTCAT		
<i>lrh-1</i> -F	CGCTGACATGCTGCCTAAA		
<i>lrh-1</i> -R	TCTCGTCCAAGTCTTCGTCAT	XM_003974281.2	140
Cholesterol and bile acid biosynthesis			
<i>hmgcr</i> -F	GCTGCTGGCAATCAAGTACAT		
<i>hmgcr</i> -R	AAACATACAACCTCCTTCCTACAGC	XM_003974466.2	143
<i>cyp7a1</i> -F	CCTACCTGCTACCTTCTGGAGT		
<i>cyp7a1</i> -R	TCCTCTTTGGCAACACGAA	XM_003975521.2	237
Reference gene			
β -actin-F	GAGAGGGAAATCGTGCGTGA		
β -actin-R	GAAGGATGGCTGGAAGAGGG	XM_003964421.3	186
<i>ef1a</i> -F	TTGGAGGCATTGGAAGTGT		
<i>ef1a</i> -R	GTTGACGGGAGCAAAGGT	NM_001037873.1	86
Reference gene			
β -actin-F	GACGCAAAACCTCCGAAGT		
β -actin-R	CCTCCAAACGGATCAGCACA	Gene ID 101079312	129
EF1 α -F	TGGCCTTTAGCCGAATGAGG		
EF1 α -R	TGTCGGGCCAATCAATCCAG	Gene ID 653026	117

PL: product length; *acac β* : acetyl-CoA carboxylase beta; *fas*: fatty acid synthase; *cpt-1*: carnitine O-palmitoyltransferase-1; *vlcs*: very long-chain acyl-CoA synthetase; *acox1*: acyl-CoA oxidase 1, palmitoyl; *acox3*: acyl-CoA oxidase 3, pristanoyl; *ehhadh*: enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase; *acaa*: acetyl-CoA acyltransferase; *dgat1*: diacylglycerol O-acyltransferase 1; *mgat2a*: 2-acylglycerol O-acyltransferase 2-A-like (LOC101069338); *atgl*: adipose triglyceride lipase (patatin like phospholipase domain containing 2 (*pnpla2*)); *dagla*: diacylglycerol lipase, alpha; *hsl*: hormone-sensitive lipase; *mgll*: monoglyceride lipase; *bsal*: bile acid activated lipase; *lp*: inactive pancreatic lipase-related protein 1-like (LOC101064949); *lpl*: lipoprotein lipase; *lipc*: lipase, hepatic; *fabp*: fatty acid binding protein; *fatp*: fatty acid transport protein (solute carrier family 27 member 1 (*slc27a1*)); *apo*: apolipoprotein; *mttp*: microsomal triglyceride transfer protein; *srebf1*: sterol regulatory element binding

transcription factor 1; *ppar*: peroxisome proliferators-activated receptor; *fxr*: farnesoid X receptor (nuclear receptor subfamily 1, group H, member 4, *nr1h4*); *lxra*: liver X receptor alpha (nuclear receptor subfamily 1, group H, member 3, *nr1h3*); *hnf4a*: hepatocyte nuclear factor 4, alpha; *lrh-1*: liver receptor homolog-1 (nuclear receptor subfamily 5, group A, member 2, *nr5a2*); *hmgcr*: 3-hydroxy-3-methylglutaryl-CoA reductase; *cyp7a1*: cholesterol 7-alpha-hydroxylase (cytochrome P450 7A1); CYTB: cytochrome B.

Supplementary Table S2 Growth performance of experimental tiger puffer (mean ± standard error)

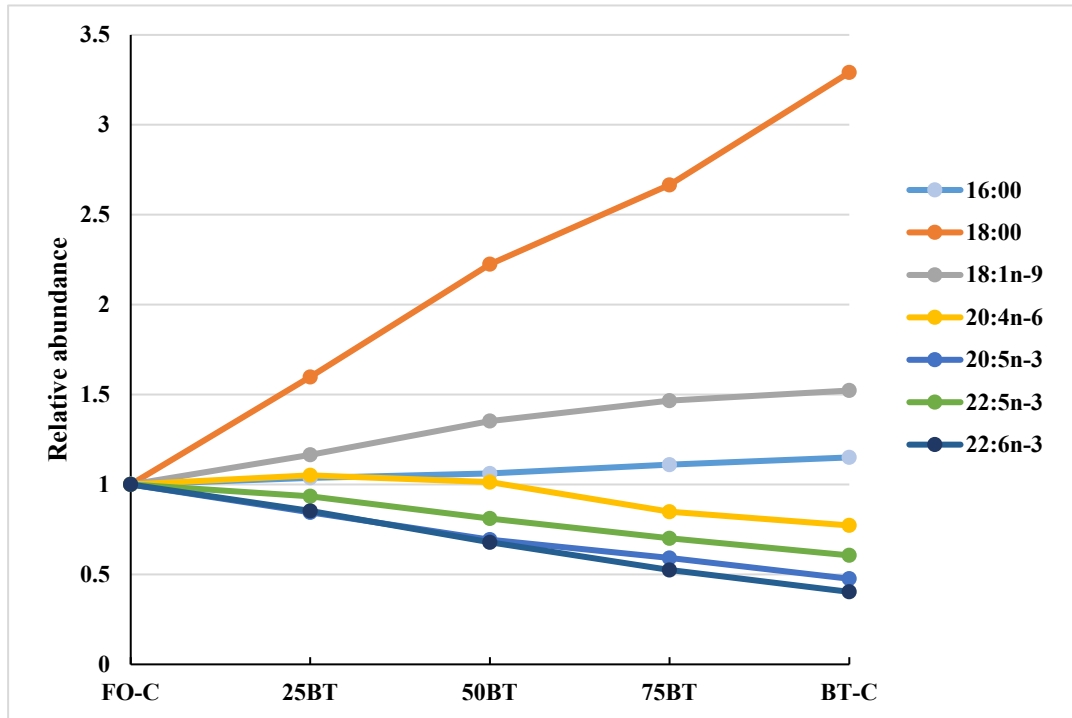
Parameters	FO-C	Graded FO replacement with BT			Alternate feeding between FO and BT			BT-C
		25%	50%	75%	1BT-1FO	2BT-1FO	3BT-1FO	
FBW (g)	75.5±1.36 ^{ab}	68.9±1.07 ^a	68.7±0.67 ^a	83.5±8.02 ^b	70.1±3.31 ^a	70.5±1.33 ^a	74.0±3.10 ^{ab}	75.6±4.26 ^{ab}
FER	0.71±0.03 ^{bc}	0.54±0.03 ^{bc}	0.36±0.09 ^a	0.78±0.18 ^c	0.62±0.03 ^{abc}	0.43±0.14 ^{ab}	0.61±0.05 ^{abc}	0.65±0.06 ^{abc}
WG (%)	628±11.3 ^a	574±8.89 ^{ab}	572±5.62 ^a	696±66.9 ^b	583±27.6 ^a	587±11.1 ^a	616±25.8 ^{ab}	630±35.5 ^{ab}
Survival (%)	59.1±4.76 ^{bc}	40.0±0.00 ^{ab}	32.4±6.87 ^a	48.6±1.65 ^{bc}	38.1±0.95 ^{ab}	30.5±5.30 ^a	45.7±4.36 ^{abc}	50.5±8.30 ^{bc}

Data in a same row sharing same superscript letters are not significantly different ($P>0.05$). FBW: final body weight; FER: feed efficiency ratio; WG: weight gain.

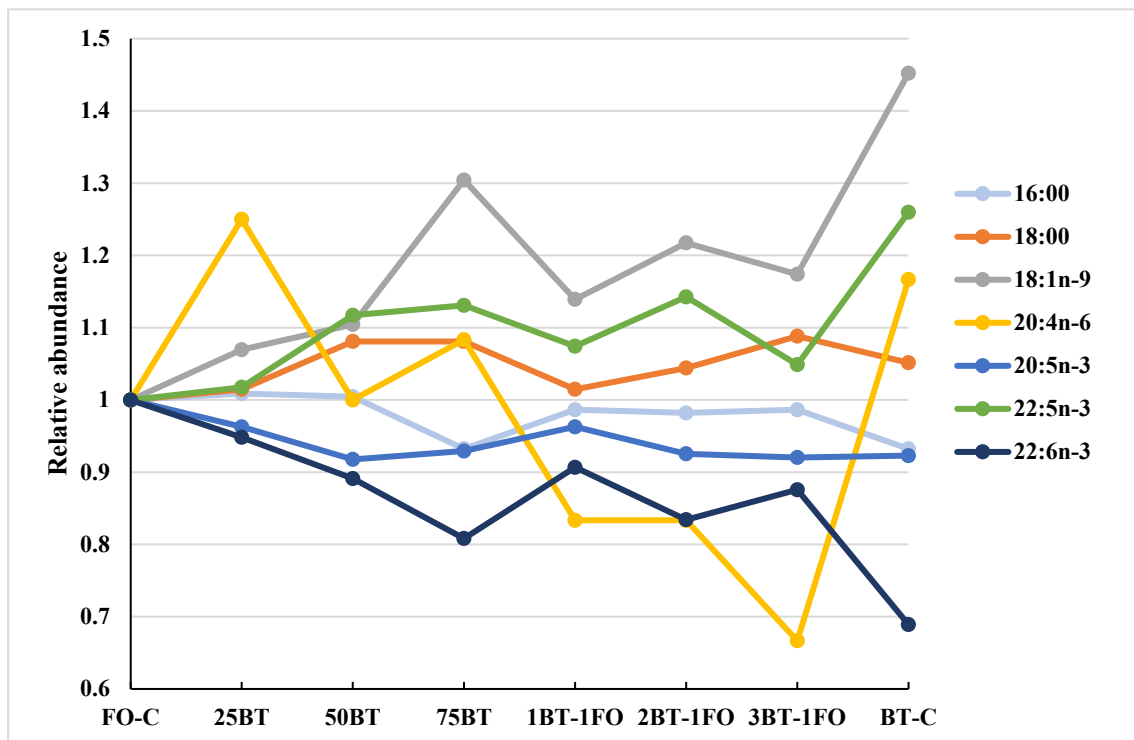
Supplementary Table S3 Lipid metabolism-related biochemical parameters in the serum (mean ± standard error)

Parameters	FO-C	Graded FO replacement with BT			Alternate feeding between FO and BT			BT-C
		25%	50%	75%	1BT-1FO	2BT-1FO	3BT-1FO	
TG (mmol L ⁻¹)	0.76±0.02 ^d	0.58±0.02 ^b	0.58±0.00 ^b	0.58±0.02 ^b	0.65±0.02 ^c	0.50±0.00 ^a	0.55±0.01 ^b	0.57±0.01 ^b
HDL-C (mmol L ⁻¹)	0.77±0.10 ^{bc}	1.05±0.15 ^d	0.37±0.01 ^{ab}	0.29±0.04 ^a	0.58±0.10 ^b	0.13±0.01 ^a	0.64±0.09 ^b	0.92±0.04 ^{cd}
LDL-C (mmol L ⁻¹)	3.08±0.10 ^{ab}	2.97±0.09 ^a	4.31±0.27 ^c	3.27±0.20 ^{ab}	3.01±0.13 ^{ab}	3.53±0.20 ^b	3.21±0.12 ^{ab}	3.12±0.09 ^{ab}
TBA (μmol L ⁻¹)	0.46±0.03 ^a	0.49±0.03 ^a	0.64±0.01 ^b	0.53±0.03 ^{ab}	0.57±0.04 ^{ab}	0.57±0.04 ^{ab}	0.60±0.05 ^b	0.53±0.04 ^{ab}
TC (mmol L ⁻¹)	4.83±0.20 ^{ab}	4.72±0.18 ^{ab}	5.30±0.29 ^b	4.17±0.26 ^a	4.31±0.19 ^a	4.25±0.19 ^a	4.42±0.08 ^a	4.83±0.07 ^{ab}

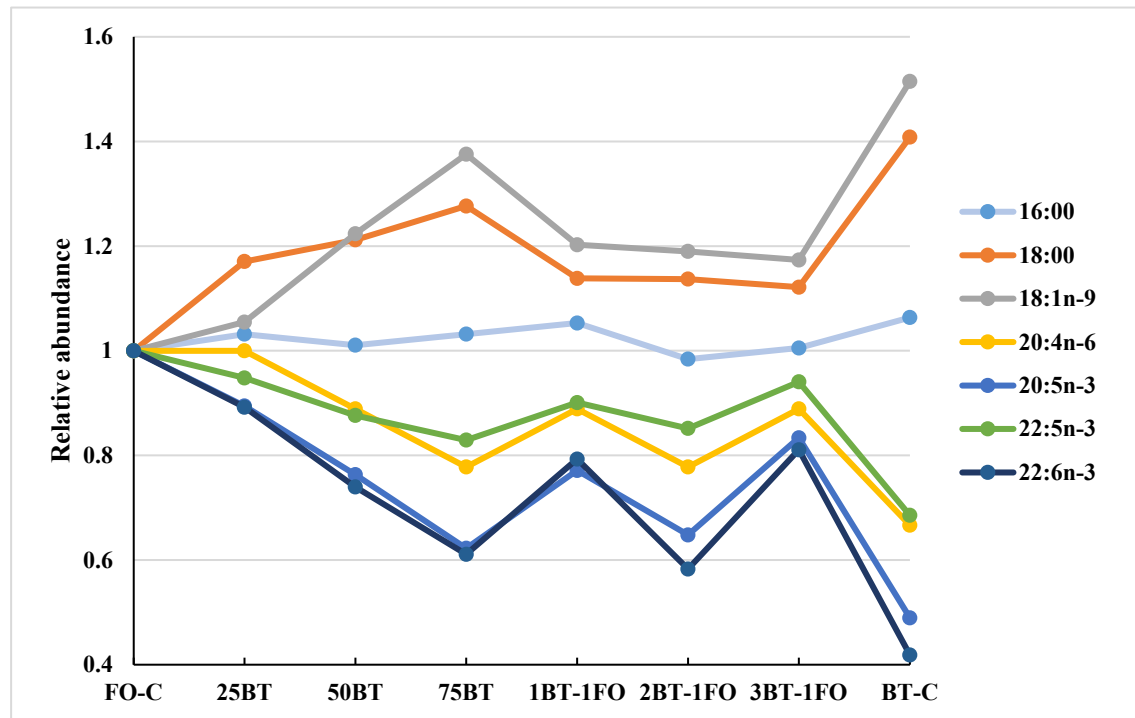
Data in a same row sharing same superscript letters are not significantly different ($P>0.05$). TG: triacylglycerol; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol; TBA: total bile acid; TC: total cholesterol. The concentration of these parameters in serum were measured with commercial kits supplied by Nanjing Jiancheng Bioengineering Institute (Nanjing, China).



Supplementary Figure S1 Relative abundance of main fatty acids in experimental diets. The fatty acid contents in group FO-C were normalized to be 1.



Supplementary Figure S2 Relative abundance of main fatty acids in the muscle of juvenile tiger puffer. The fatty acid contents in group FO-C were normalized to be 1.



Supplementary Figure S3 Relative abundance of main fatty acids in the liver of juvenile tiger puffer. The fatty acid contents in group FO-C were normalized to be 1.