

Supplementary Materials

Supplementary Table 1. Ingredients and composition of the basal diet (air-dried base).

Ingredients	Percentage (%)	Nutrient	Content
Corn	64.73	Digestible energy (MJ/kg)	12.98
Soybean meal	12.50	Crude protein (%)	14.04
Wheat bran	20.45	Total Ca (%)	0.53
Limestone	0.80	Available P (%)	0.22
CaHCO ₃	0.30	Lysine (%)	0.84
NaCl	0.30	Methionine (%)	0.20
Lysine	0.40	Cystine (%)	0.44
Methionine	0.02	Threonine (%)	0.49
Threonine	0.10	Tryptophan (%)	0.15
Tryptophan	0.01		
Choline chloride	0.15		
Vitamin premix ¹	0.04		
Mineral premix ²	0.20		
Total	100.00		

¹ The vitamin premix provides per kg: 2,250 IU vitamin A, 220 IU vitamin D₃, 16 mg vitamin E, 0.5 mg vitamin K, 2 mg vitamin B₁, 5 mg vitamin B₂, 4 mg vitamin B₆, 0.03 mg vitamin B₁₂, 30 mg niacin, 20 mg pantothenic acid, 0.3 mg folic acid, and 0.2 mg biotin.

² The mineral premix provides per kg: 80 mg iron, 5 mg copper, 80 mg zinc, 3 mg manganese, 0.14 mg iodine, and 0.25 mg selenium.

Supplementary Table 2. Primers for real-time quantitative PCR.

Gene names	Primers	Sequences (5'–3')	Product size (bp)
<i>ACC</i>	Forward	AGCAAGGTCGAGACCGAAAG	169
	Reverse	TAAGACCACCGGCGGATAGA	
<i>Akt</i>	Forward	CTGCCCTTCTACAACCAGGA	214
	Reverse	CATACACATCCTGCCACACG	
<i>ATGL</i>	Forward	CAACGCCAAGCACATCTACG	84
	Reverse	CCAGTATCACCCAGGCAGAC	
<i>CAT</i>	Forward	CAGATGAAGCATTGGAAGGAGC	83
	Reverse	TTGTCTCCTATCGGATTCCCAG	
<i>CPT1</i>	Forward	GACAAGTCCTTACCCTCATCGC	170
	Reverse	GGGTTTGGTTTGCCAGACAG	
<i>FABP4</i>	Forward	TGGAAACTTGTCTCCAGTG	227
	Reverse	GGTACTTTCTGATCTAATGGTG	
<i>FATP1</i>	Forward	ACCACTCCTACCGCATGCAG	78
	Reverse	CCACGATGTTCCCTGCCGAGT	
<i>FOXO1</i>	Forward	GCCCTGGCTCTCACAGCAAC	292
	Reverse	GGTGAAGACTGGGTGGAAAC	
<i>GAPDH</i>	Forward	GGAGCGAGATCCCGCCAACA	158
	Reverse	ACATGGGGGCATCGGCAGAA	
<i>GHR</i>	Forward	GGAAAGAGTGCCCTGATTATGTC	119
	Reverse	ATCCACAGTCCCACCATTGC	
<i>GPX1</i>	Forward	GTGAATGGCGCAAATGCTCA	126
	Reverse	ATTGCGACACACTGGAGACC	
<i>HSL</i>	Forward	CACAAGGGCTGCTTCTACGG	167
	Reverse	AAGCGGCCACTGGTGAAGAG	
<i>IGF-1R</i>	Forward	GACTTCACAGTCAAATCGG	154
	Reverse	ACCAGACATCAGAGTGCCT	
<i>IRS1</i>	Forward	CCTAGCACCAACAGGACTCA	239
	Reverse	GAAGAGATGAAACCGCCGTC	
<i>JAK2</i>	Forward	GCCACTGCCAGAACTTGAA	165
	Reverse	TGACCACTGAATTCCACCGT	
<i>LDH</i>	Forward	ACAGTGCTGACACTCTGTGG	179
	Reverse	CTGGGAGCCCACATTCACAT	
<i>LPL</i>	Forward	CTCGTGCTCAGATGCCCTAC	148
	Reverse	GGCAGGGTGAAAGGGATGTT	
<i>MAFbx</i>	Forward	CCAGAGAGTTCGGCAAGT	374
	Reverse	GAGGGTAGCATCGCACAAAGT	
<i>MSTN</i>	Forward	GTCCCGTGGATCTGAATG	293
	Reverse	TTCCGTCGTAGCGTGATA	
<i>mTOR</i>	Forward	TGATGCCCTGAAGTTCCAT	201
	Reverse	TGGTACTTCTTCCCAGCTG	
<i>MuRF1</i>	Forward	AGCACGAAGACGAGAAAATC	150
	Reverse	TGCGGTTACTCAGCTCAGTC	
<i>Myf6</i>	Forward	GCTCGTGATGACTGCCAAGGAAG	80
	Reverse	CGATGGAAGAAAGGCACCGAAGG	
<i>MyHC I</i>	Forward	GGCCCCTTCCAGCTTGA	63
	Reverse	TGGCTGCGCCTTGGTTT	
<i>MyHC IIa</i>	Forward	TTAAAAAGCTCCAAGAAGTGTTC	100

	Reverse	CCATTTCTGGTCGGAACTC	
<i>MyHC IIb</i>	Forward	CACTTTAAGTAGTTGTCTGCCTTGAG	80
	Reverse	GGCAGCAGGGCACTAGATGT	
<i>MyHC IIx</i>	Forward	AGCTTCAAGTTCTGCCCCACT	76
	Reverse	GGCTGCGGGTTATTGATGG	
<i>MyoD</i>	Forward	CAACAGCGGACGACTTCTATG	383
	Reverse	GCGCAAGATTTCCACCTT	
<i>MyoG</i>	Forward	GCAGGGTGCTCCTCTTCA	230
	Reverse	AGGCTACGAGCGGACTGA	
<i>PFKFB3</i>	Forward	CCGCATCGTGTACTACCTGAT	223
	Reverse	CGTCTGGATGGTGCTCTTCA	
<i>PGK1</i>	Forward	GGTGGAATGGCCTTTACCTT	186
	Reverse	GCCAATCTTGGCATTCTCAT	
<i>PPARγ</i>	Forward	CCAGCATTTCCACTCCACACTA	124
	Reverse	GACACAGGCTCCACTTTGATG	
<i>SOD1</i>	Forward	AGACCTGGGCAATGTGACTG	102
	Reverse	GTGCGGCCAATGATGGAATG	
<i>SREBP1c</i>	Forward	GCGACGGTGCCCTCTGGTAGT	218
	Reverse	CGCAAGACGGCGGATTTA	
<i>β-actin</i>	Forward	TGCGGGACATCAAGGAGAAG	216
	Reverse	AGTTGAAGGTGGTCTCGTGG	

Note: *ACC*, acetyl-CoA carboxylase; *Akt*, AKT serine/threonine kinase 1; *ATGL*, adipose tissue triglyceride lipase; *CAT*, catalase; *CPT1*, carnitine palmitoyl transferase 1; *FABP4*, fatty acid binding protein 4; *FATP1*, fatty acid transport protein 1; *FOXO1*, forkhead box O1; *GAPDH*, glyceraldehyde-3-phosphate dehydrogenase; *GHR*, growth hormone receptor; *GPX1*, glutathione peroxidase 1; *HSL*, hormone-sensitive triglyceride lipase; *IGF-IR*, insulin-like growth factor 1 receptor; *IRS1*, insulin receptor substrate 1; *JAK2*, janus kinase 2; *LDH*, lactate dehydrogenase; *LPL*, lipoprotein lipase; *MAFbx*, muscle atrophy F-box; *MSTN*, myostatin; *mTOR*, mechanistic target of rapamycin kinase; *MuRF1*, muscle RING finger 1; *Myf6*, myogenic factor 6; *MyHC I*, myosin heavy-chain I; *MyHC IIa*, myosin heavy-chain IIa; *MyHC IIb*, myosin heavy-chain IIb; *MyHC IIx*, myosin heavy-chain IIx; *MyoD*, myogenic differentiation 1; *MyoG*, myogenin; *PFKFB3*, 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; *PGK1*, phosphoglycerate kinase 1; *PPAR γ* , peroxisome proliferation-activated receptor- γ ; *SOD1*, superoxide dismutase 1; *SREBP1c*, sterol regulatory elementbinding protein 1c.

Supplementary Table 3. Contents of metabolites that differ in one-way ANOVA in the *longissimus dorsi* muscle of Duroc, TB, and XB pigs at 185 days of age.

Items, $\mu\text{mol/g}$	Duroc Pigs	TB Pigs	XB Pigs	SEM	<i>P</i> -values
Amino acids					
5-aminolevulinic acid	0.011 ^b	0.019 ^a	0.014 ^{ab}	0.001	0.018
L-glutamic acid	0.717 ^b	1.293 ^a	1.049 ^{ab}	0.094	0.034
L-homocitrulline	0.003 ^b	0.004 ^a	0.004 ^a	0.000	0.027
L-isoleucine	0.826 ^b	1.277 ^a	0.861 ^b	0.085	0.048
Phosphoserine	1.592 ^b	1.937 ^a	1.790 ^{ab}	0.053	0.021
Pyroglutamic acid	0.757 ^b	1.214 ^a	1.038 ^{ab}	0.074	0.032
Bile acids					
D-ribose-5-phosphate	10.684 ^b	14.444 ^a	13.808 ^{ab}	0.683	0.048
Carbohydrates					
N-acetyl-D-glucosamine	0.032 ^b	0.051 ^a	0.038 ^{ab}	0.003	0.027
N-acetylneuraminic acid	0.100 ^b	0.153 ^a	0.126 ^{ab}	0.008	0.015
Carnitines					
3-hydroxyisovalerylcarnitine	0.030 ^b	0.048 ^a	0.053 ^a	0.004	0.022
Decanoylcarnitine	0.003 ^b	0.003 ^b	0.006 ^a	0.001	0.020
Glutaryl carnitine	0.003 ^b	0.005 ^a	0.002 ^c	0.000	<0.001
Lauroyl carnitine	0.005 ^b	0.008 ^{ab}	0.012 ^a	0.001	0.028
Methylmalonylcarnitine	0.812 ^b	1.147 ^a	1.202 ^a	0.069	0.036
Octanoylcarnitine	0.004 ^b	0.006 ^b	0.011 ^a	0.001	0.012
Fatty acids					
10-trans-heptadecenoic acid	0.033 ^b	0.060 ^a	0.042 ^b	0.004	0.012
10Z-heptadecenoic acid	0.065 ^b	0.116 ^a	0.083 ^{ab}	0.008	0.022
2-hydroxy-3-methylbutyric acid	0.222 ^a	0.191 ^{ab}	0.144 ^b	0.011	0.010
8-11-14-eicosatrienoic acid	0.327 ^b	0.557 ^a	0.351 ^b	0.041	0.031
Arachidonic acid	1.176 ^b	1.975 ^a	1.404 ^{ab}	0.131	0.029
Eicosapentaenoic acid EPA	0.048 ^b	0.089 ^a	0.055 ^b	0.007	0.038
Oleic acid	24.513 ^b	37.954 ^a	29.808 ^{ab}	2.106	0.024
Petroselinic acid	1.256 ^b	1.935 ^a	1.493 ^{ab}	0.108	0.025

Data are presented as means with their SEM ($n = 8$). ^{a-c} Mean values with different superscript letters indicate significant differences ($P < 0.05$). TB, Taoyuan black pigs; XB, Xiangcun black pigs.

Supplementary Table 4. Differential metabolites enrichment in the *longissimus dorsi* muscle of Duroc, TB, and XB pigs at 185 days of age.

Pathways	Total¹	Hits²	P-values³	Differential metabolites
Phenylalanine metabolism	10	2	0.009	Phenylacetic acid; Hippuric acid
Glycerolipid metabolism	16	2	0.023	Glyceraldehyde; Glyceric acid
β -alanine metabolism	21	2	0.039	Hydroxypropionic acid; β -alanine
Propanoate metabolism	23	2	0.046	β -alanine; Hydroxypropionic acid
Pyrimidine metabolism	39	2	0.116	Ureidosuccinic acid; β -alanine
Nicotinate and nicotinamide metabolism	15	1	0.205	Nicotinic acid
Pantothenate and CoA biosynthesis	19	1	0.253	β -alanine
Fructose and mannose metabolism	20	1	0.264	Glyceraldehyde
Pentose phosphate pathway	22	1	0.286	Glyceric acid
Alanine, aspartate and glutamate metabolism	28	1	0.350	Ureidosuccinic acid
Glyoxylate and dicarboxylate metabolism	32	1	0.389	Glyceric acid
Glycine, serine, and threonine metabolism	33	1	0.398	Glyceric acid
Cysteine and methionine metabolism	33	1	0.398	L- α -aminobutyric acid
Fatty acid degradation	39	1	0.452	L-palmitoylcarnitine

¹ Total number of metabolites in this pathway.

² Number of differential metabolites in the present study.

³ Raw *P*-values of enrichment analysis.