

Supplementary Material

Comprehensive analysis of lncRNAs and circRNAs reflects the metabolic specialization in oxidative and glycolytic skeletal muscles

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Supplementary Table S1. The measured weight of Qingyu pigs

Age	0 day	23 day	35 day	50 day	70 day
BW	0.76±0.08	4.63±0.88	6.91±0.93	9.70±1.48	14.13±0.85
Age	90 day	120 day	150 day	165 day	180 day
BW	22.78±2.95	39.37±3.14	55.36±4.71	63.54±5.28	69.32±6.30
Age	195 day	225 day	255 day	270 day	300 day
BW	75.60±7.81	85.15±6.64	99.22±8.26	105.17±7.66	113.13±7.52
Age	330 day	360 day	385 day	400 day	
BW	128.32±9.75	137.94±7.78	143.04±7.49	146.65±6.26	

BW, body weight.

Supplementary Table S2. Fitting parameters of Logistic nonlinear curves

Model	k	a	b	R ²	Age (MGR)	Index (MGR)
Logistic	130.404	24.613	0.018	0.974	177.960	65.202

MGR, the point of maximum growth rate

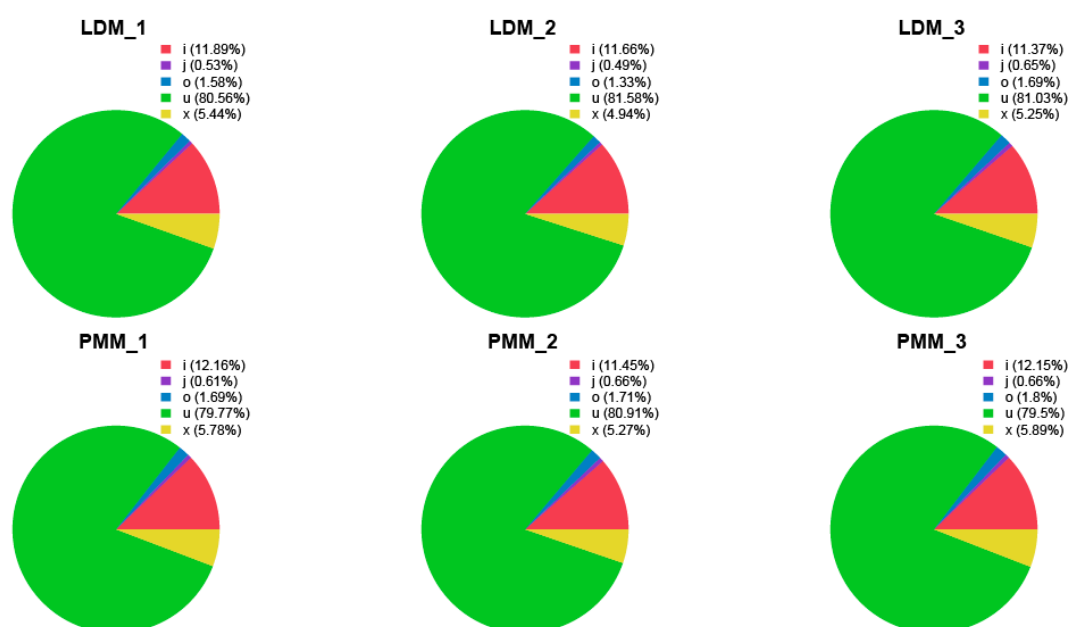
Supplementary Table S3. Summary of transcriptome data

Sample	LDM_1	LDM_2	LDM_3	PMM_1	PMM_2	PMM_3
Valid reads	86930486	86411128	86581698	86844958	85596078	86113732
Mapped reads	71.91%	71.66%	75.01%	71.96%	72.09%	72.24%
Unique Mapped reads	61.51%	63.15%	58.98%	62.43%	61.42%	60.62%
Multi Mapped reads	10.40%	8.51%	16.03%	9.53%	10.67%	11.61%
PE Mapped reads	32.47%	32.38%	34.08%	32.54%	32.16%	32.51%
Mapped left reads	37.22%	36.79%	38.55%	37.22%	37.12%	37.39%
Mapped right reads	34.70%	34.87%	36.46%	34.74%	34.97%	34.84%
Reads map to sense strand	30.75%	31.76%	29.68%	31.22%	31.03%	30.46%
Reads map to antisense strand	30.76%	31.39%	29.30%	31.21%	30.38%	30.17%
Non-splice reads	36.06%	40.56%	33.66%	39.49%	38.88%	36.57%
Splice reads	25.45%	22.58%	25.32%	22.94%	22.54%	24.06%
Back-spliced junctions reads	0.85%	0.74%	1.10%	0.72%	0.98%	0.87%

Supplementary Table S4. Statistics of identified lncRNAs

Sample	"i"	"j"	"o"	"u"	"x"
LDM_1	293	13	39	1985	134
LDM_2	333	14	38	2329	141
LDM_3	262	15	39	1867	121
PMM_1	280	14	39	1837	133
PMM_2	261	15	39	1844	120
PMM_3	256	14	38	1675	124

J: Potentially novel isoform (fragment): at least one splice junction is shared with a reference transcript; I: A transfrag falling entirely within a reference intron; O: Generic exonic overlap with a reference transcript; U:Unknown, intergenic transcript; X:Exonic overlap with reference on the opposite strand



Supplementary Fig.S1. The type and distribution of identified lncRNAs. J: Potentially novel isoform (fragment): at least one splice junction is shared with a reference transcript; I:A transfrag falling entirely within a reference intron; O: Generic exonic overlap with a reference transcript; U:Unknown, intergenic transcript; X:Exonic overlap with reference on the opposite strand.

Supplementary Table S8. Ingredient composition and nutrient levels of experimental diets (as fed basis,%)

Ingredients	7-11kg	11-25kg	25-50kg	50-75kg	>75kg
Corn grain	27.19	35.00	68.57	75.13	78.03
Expand corn	25.00	23.68	0.00	0.00	0.00
Soybean oil	2.50	1.80	3.00	3.00	3.00
Sucrose	2.00	2.00	2.00	0.00	0.00
Wheat bran	0.00	0.00	3.00	3.00	5.00
Whey powder	12.00	7.00	0.00	0.00	0.00
Soybean meal	8.00	12.00	18.20	15.50	10.90
Full-fat soybean	5.00	8.00	0.00	0.00	0.00
Soy protein concentrate	5.00	3.00	0.00	0.00	0.00
Whole milk powder	3.00	0.00	0.00	0.00	0.00
Fishmeal (CP 62.5 %)	4.00	3.00	2.00	0.00	0.00
Plasma protein powder	3.00	1.00	0.00	0.00	0.00
L-Lys·HCl	0.45	0.46	0.42	0.44	0.40
DL-Met	0.15	0.16	0.14	0.12	0.10
L-Thr	0.15	0.16	0.14	0.15	0.14
L-Try	0.01	0.02	0.03	0.03	0.03
Choline chloride 50%	0.15	0.10	0.10	0.10	0.10
CaCO ₃	1.00	0.92	0.90	0.89	0.80
CaHPO ₄	0.10	0.40	0.70	0.84	0.70
NaCl	0.30	0.30	0.30	0.30	0.30
Premix ¹	1.00	1.00	0.50	0.50	0.50
Total	100.00	100.00	100.00	100.00	100.00
Nutrient levels²					
DE (Kcal/kg)	3.58	3.48	3.39	3.40	3.39
CP (%)	19.55	18.35	15.68	13.73	12.18
Ca (%)	0.79	0.71	0.66	0.59	0.52
STTD P (%)	0.39	0.34	0.31	0.27	0.25
SID Lys (%)	1.36	1.23	0.98	0.85	0.73
SID Met+cys (%)	0.74	0.69	0.55	0.55	0.42
SID Thr (%)	0.80	0.73	0.58	0.52	0.46
SID Trp (%)	0.22	0.20	0.17	0.15	0.13

Note 1: Contents per kg of diet for 7-25 kg BW Period: Fe, 150 mg; Cu, 195 mg; Zn, 150 mg; Mn, 30 mg; I, 0.3 mg; Se, 0.3 mg; vitamin A, 12000 IU; vitamin D, 3200 IU; vitamin E, 80 mg; vitamin K₃, 32.50 mg; vitamin B₁, 2.30 mg; vitamin B₂, 6.50 mg; vitamin B₆, 5 mg; vitamin B₁₂, 50 µg; nicotinic acid, 45 mg; pantothenic acid, 20 mg; folic acid, 1.50 mg; biotin, 0.15 mg; enzyme preparation and preservatives. Contents per kg of diet for 7-25 kg BW Period: Fe, 120 mg; Cu, 17 mg; Zn, 100 mg; Mn, 25 mg; I, 0.3 mg; Se, 0.2 mg; vitamin A, 5512 IU; vitamin D, 2250 IU; vitamin E, 24 mg; vitamin K₃, 3 mg; vitamin B₂, 6 mg; vitamin B₆, 3 mg; vitamin B₁₂, 24 µg; pantothenic acid, 15 mg; folic acid, 1.20 mg; biotin, 0.15 mg; enzyme preparation and preservatives. Note 2: Nutrient levels were calculated values.

Supplementary Table S9. Information of primers used to perform q-PCR

Gene symbol	Forward primer (5'-3')	Reverse primer (5'-3')
<i>COX2</i>	GCACCCCGACATAGAGAGC	CTGCGGAGTGCAGTGTCT
<i>ND1</i>	CCACTACCAATACCCTACCCTC	TGCGTATTTTGAGTTGGATGCT
<i>ATP6</i>	AAACATCACTAGCCCACTTTCT	TAATGTTGGCTGTCAGTCGTAC
<i>GCG</i>	GAATCAACACCATCGGTCAAAT	CTCCACCCATAGAATGCCCAGT
<i>LncRNA14704</i>	CAAGCCTCATCTGAATCCTCTA	GTCCCACTATCCTCACTGCTAA
<i>LncRNA3569</i>	GAGGAGCAAGATTTAAGAGGCG	CCCTGAGTAGATGATACCCACA
<i>LncRNA6176</i>	ATCTGGTGTGTCTACTGCTTGG	TTAGGAAATATCCATTGTTTGG
<i>Foxj3</i>	GAAACCTCCATACAGTTACGCC	CACTTGTTGAGGGACAGATTAT
<i>MEF2C</i>	GGGTATGGCAATCCCCGAAACT	TTGCTGCCTGGTGGGAATAAGAA
<i>SIRT1</i>	TCTTCCCTGAAAGTAAGACCAG	GGCATATTCACCTCCTAACCTA
<i>miR-27b</i>	TTCACAGTGGCTAAGTTCTGC	R-primer (Uni-miR qPCR Primer)
<i>miR-23a</i>	ATCACATTGCCAGGGATTTC	R-primer (Uni-miR qPCR Primer)
<i>miR-217</i>	TACTGCATCAGGAAGTATTGGAT	R-primer (Uni-miR qPCR Primer)
<i>circRNA290</i>	GATGTGGAATGATTTCTTCTGG	ATCAGATCCAAGTCACGGTCGC
<i>circRNA9210</i>	ACAAACTATTATGGTAATGGAA	CCACAGTTCAACAACAGACCAA
<i>circRNA41</i>	TGGGTTCAATTTCTGACCTTAC	AAACGCATTACACAGGTATTCA
<i>circRNA118</i>	TCCCGCTCAAATCACATCAAG	TGCAACTTGCAAACCGCCAGG
<i>circRNA1208</i>	ATATCTATGCAGACACCATCCT	TCTCCTGTGCCCATCATTGTGTG
<i>circRNA154</i> (Divergent)	TACAAATAAATCCCTGCGTAAA	CCTCCTGTCTGGCATAAAGTAA
<i>circRNA154</i> (Convergent)	GTGAGGACGGAAGTGTGGG	CCTCTGCGGTGCGCACCTTATT
<i>ACTB</i> (Divergent)	ACTCGTCGTAATCCTGCTTGCT	CCCCTGCGCTTCTGCTTTCCTC
<i>ACTB</i> (Convergent)	TCTGGCACCACACCTTCT	TGATCTGGGTCATCTTCTCAC
<i>TBP</i>	GATGGACGTTTCGGTTTGG	AGCAGCACAGTACGAGCAA
<i>TOP2B</i>	AACTGGATGATGCTAATGATGCT	TGGAAAACTCCGTATCTGTCTC

COX2: cytochrome c oxidase subunit 2; *ND1*: NADH dehydrogenase subunit 1; *ATP6*: ATP synthase F0 subunit 6; *GCG*: glucagon; *Foxj3*: forkhead box J3; *MEF2C*: myocyte enhancer factor 2C; *SIRT1*: sirtuin 1; *ACTB*: actin beta; *TBP*: TATA-box binding protein; *TOP2B*: DNA topoisomerase II beta. Uni-miR qPCR Primer included in commercial kits.