Appendix A Fatty acid composition (mg 100 g^{-1} of diet) of the experimental diets

Item	Control	Waxy corn starch	Pea starch
C12:0	0.22	0.21	0.20
C13:0	0.01	0.01	0.01
C14:0	0.99	0.85	0.83
C14:1	0.30	0.37	0.33
C16:0	40.90	36.70	36.65
C16:1	0.93	1.30	1.09
C17:0	0.36	0.26	0.27
C17:1	0.16	0.21	0.18
C18:0	14.92	12.50	13.31
C18:1	42.08	29.07	30.77
C18:2	75.66	56.04	57.25
C18:3n3	3.71	2.60	2.95
C20:0	1.01	0.58	0.62
C20:1	0.67	0.42	0.42
C20:2	0.14	0.10	0.10
C20:3n6	0.07	0.04	0.03
C20:4n6	0.07	0.04	0.03
C22:1n9	0.48	0.35	0.34
SFA	59.7	51.8	52.6
USFA	125.2	91.3	94.1
MUFA	45.0	32.0	33.3
PUFA	80.3	59.3	60.8

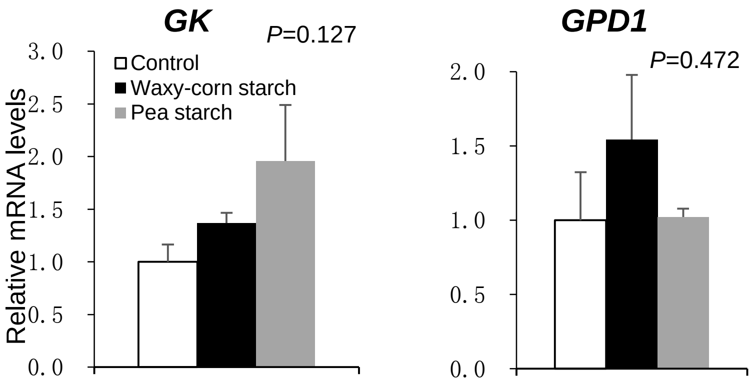
SFA, saturated fatty acid; USFA, unsaturated fatty acid; MUFA, monounsaturated fatty acid; PUFA, polyunsaturated fatty acid.

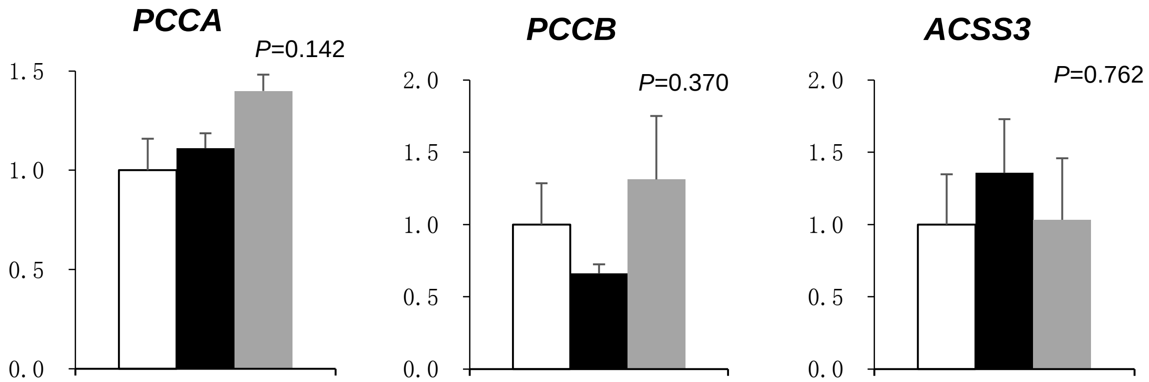
Appendix B Primer sequences (5' to 3') for quantitative real-time PCR

Gene name	GenBank ID	Primer	Sequence	Length (bp)
Pyruvate carboxylase (*PC*)	NM_177946.4	Forward	GACTGCAGCAAGTTCGGTTG	343
		Reverse	TCAGCTTTCTGTCGGTGCAT	
Fructose 1,6-bisphosphatase (*FBP1*)	NM_001034447.2	Forward	CTGCTGGCTATGCGCTCTAT	200
		Reverse	GACATACTCGGTGAGGGCAG	
Pyruvate kinase (*PKLR*)	NM_001076176.1	Forward	CAAGGGGCATTCCCATGACT	472
		Reverse	AGTGCGTATCTCTGGTCCCT	
Lactate dehydrogenase B (*LDHB*)	NM_001316338.1	Forward	AGTGGATTACCCAAGCACCG	170
		Reverse	GCCACATTCACTCCACTCCA	
Glycerol-3-phosphate dehydrogenase-1 (*GPD1*)	NM_001035354.1	Forward	TCAGCCATCGCCAAGATTGT	102
		Reverse	CTTTCTGCCCCCGATGTCTT	
Glycerol kinase (*GK*)	NM_001075236.1	Forward	GCCTTGGAAGGTGTGCCAAT	390
		Reverse	TGCACTGGGCTCCCAATAAG	
Acetyl-CoA synthetase short-chain family member 3 (*ACSS3*)	NM_001102137.2	Forward	TGCAAGGAGTTGGGGAGGAAG	587
		Reverse	GTACATCGCCTGTGGGATCA	
Propionyl CoA carboxylase alpha (*PCCA*)	NM_001083509.1	Forward	ACCGCAGAAGCTGCTACATA	198
		Reverse	AGGATACGCACCTTGTACACT	
Propionyl CoA carboxylase beta (*PCCB*)	NM_001038548.2	Forward	CGAACGCATCGAGAACAAGC	222
		Reverse	CCAGTGACCACACTGTCTCC	
Ribosomal protein S9 (*RPS9*)	NM_001101152.2	Forward	TTCCAGAGCGTTGGCTTAGG	167
		Reverse	CCATACTCGCCGATCAGCTT	

PCR, polymerase chain reaction.

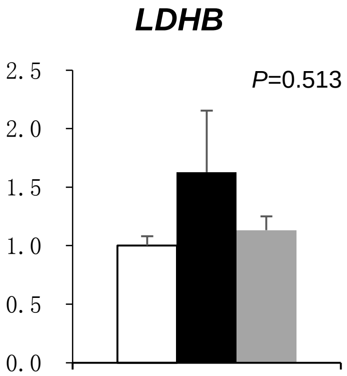
(A) Glycerol





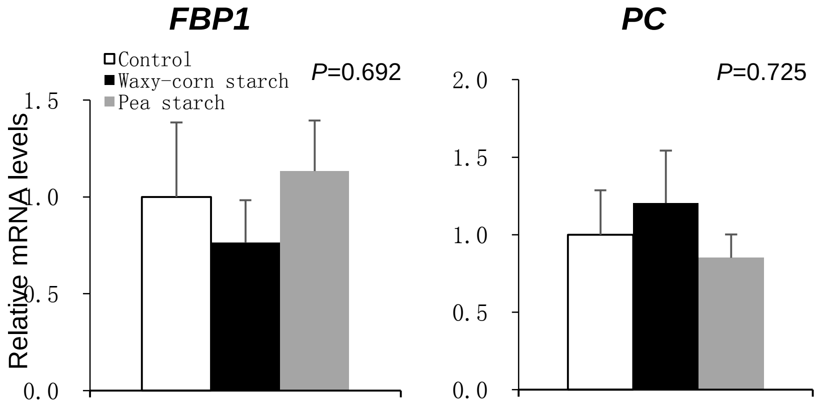
(B) Propionate

(C) Lactate/pyruvate

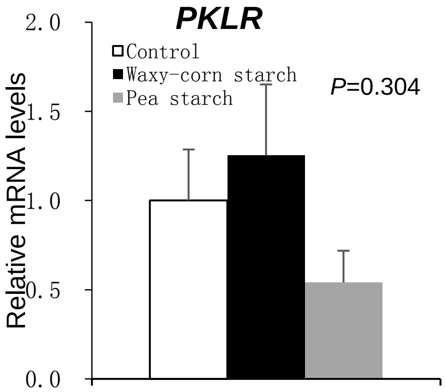


Appendix C Hepatic mRNA levels of genes for glucogenic substrate incorporation in gluconeogenesis pathway in Chinese Qinchuan breed bulls.

mRNA levels were determined by real-time polymerase chain reaction and normalized with a control ribosomal protein s9 gene. mRNA levels in bulls were normalized to 1.0. Values are expressed as the mean+standard error (n=6). *GK*, glycerol kinase; *GPD1*, glycerol-3-phosphate dehydrogenase-1; *LDHB*, lactate dehydrogenase B; *PCCA*, propionyl CoA carboxylase alpha; *PCCB*, propionyl CoA carboxylase beta; *ACSS3*, acetyl-CoA synthetase short-chain family member 3.



Appendix D Hepatic mRNA levels of genes for gluconeogenesis from glucose to pyruvate in Chinese Qinchuan breed bulls. mRNA levels were determined by real-time polymerase chain reaction and normalized with a control ribosomal protein s9 gene. mRNA levels in bulls were normalized to 1.0. Values are expressed as the mean+standard error (n=6). *FBP1*, fructose 1,6-bisphosphatase; *PC*, pyruvate carboxylase.



Appendix E Hepatic mRNA level of glucose transporter and glycolysis gene in Chinese Qinchuan breed bulls. mRNA levels were determined by real-time polymerase chain reaction and normalized with a control ribosomal protein s9 gene. mRNA levels in bulls were normalized to 1.0. Values are expressed as the mean+standard error (n=6). *PKLR*, pyruvate kinase.