

Supplementary Table S1. Descriptive statistics of blood BHB trait for individuals with genotypes in different parity.

Parity ¹	num	Mean	SD	Min	Max
BHB ₂	844	0.792	0.437	0.100	5.000
BHB ₃	695	0.876	0.461	0.100	3.900
aBHB _{II} ⁴	1030	-0.087	0.099	-0.310	0.594

¹represents the number of individuals with both genotype and phenotype values; ² BHB₂ and BHB₃ represent phenotypic values for blood BHB; ⁴ aBHB_{II} represents DMU-estimated breeding values for BHB.

Supplementary Table S2. The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways and Gene Ontology (GO)involved in candidate genes($P<0.05$).

Term	Database	ID	P-Value	Input
Fatty acid elongation	KEGG PATHWAY	bta00062	1.16×10 ⁻³	HADHB, HADHA
beta-Alanine metabolism	KEGG PATHWAY	bta00410	1.74×10 ⁻³	HADHA, SMOX
Fatty acid degradation	KEGG PATHWAY	bta00071	2.33×10 ⁻³	HADHB, HADHA
Valine, leucine and isoleucine degradation	KEGG PATHWAY	bta00280	3.37×10 ⁻³	HADHB, HADHA
Fatty acid metabolism	KEGG PATHWAY	bta01212	4.29×10 ⁻³	HADHB, HADHA
Metabolic pathways	KEGG PATHWAY	bta01100	9.21×10 ⁻³	PANK2, SMOX, HADHB, HADHA, NDST4, SELENOI, DNMT3A
Progesterone-mediated oocyte maturation	KEGG PATHWAY	bta04914	9.42×10 ⁻³	ANAPC1, CDC25B
MicroRNAs in cancer	KEGG PATHWAY	bta05206	9.88×10 ⁻³	CDC25B, DNMT3A, BCL2L11
Phosphonate and phosphinate metabolism	KEGG PATHWAY	bta00440	1.13×10 ⁻²	SELENOI
Cell cycle	KEGG PATHWAY	bta04110	1.76×10 ⁻²	ANAPC1, CDC25B
Pantothenate and CoA biosynthesis	KEGG PATHWAY	bta00770	3.20×10 ⁻²	PANK2
Transcriptional misregulation in cancer	KEGG PATHWAY	bta05202	3.81×10 ⁻²	RUNX2, SUPT3H

Glycosaminoglycan biosynthesis-heparan sulfate/heparin	KEGG PATHWAY	bta00534	3.98×10 ⁻²	<i>NDST4</i>
Butanoate metabolism	KEGG PATHWAY	bta00650	4.60×10 ⁻²	<i>HADHA</i>
chromatin binding	Gene Ontology	GO:0003682	2.66×10 ⁻⁴	<i>RUNX2,</i> <i>ASXL2,</i> <i>SATB2,</i> <i>DNMT3A,</i> <i>CENPB</i>
osteoblast development	Gene Ontology	GO:0002076	3.45×10 ⁻⁴	<i>RUNX2,</i> <i>SATB2</i>
histone acetyltransferase activity	Gene Ontology	GO:0004402	9.47×10 ⁻⁴	<i>PHF10,</i> <i>SUPT3H</i>
T cell homeostasis	Gene Ontology	GO:0043029	9.47×10 ⁻⁴	<i>ZC3H8,</i> <i>BCL2L11</i>
positive regulation of mitotic cell cycle	Gene Ontology	GO:0045931	1.02×10 ⁻³	<i>CDC25B,</i> <i>SMOC2</i>
odontogenesis of dentin-containing tooth	Gene Ontology	GO:0042475	2.23×10 ⁻³	<i>RUNX2,</i> <i>BCL2L11</i>
odontogenesis of dentin-containing tooth	Gene Ontology	GO:0042475	2.23×10 ⁻³	<i>RUNX2,</i> <i>BCL2L11</i>
endosomal transport	Gene Ontology	GO:0016197	2.44×10 ⁻³	<i>AP5S1,</i> <i>RAB10</i>
microtubule binding	Gene Ontology	GO:0008017	3.69×10 ⁻³	<i>SPEF1,</i> <i>BCL2L11,</i> <i>KIF3C</i>
cellular response to insulin stimulus	Gene Ontology	GO:0032869	3.88×10 ⁻³	<i>RAB10,</i> <i>INSIG2</i>
roof of mouth development	Gene Ontology	GO:0060021	4.02×10 ⁻³	<i>INSIG2,</i> <i>SATB2</i>
spermatogenesis	Gene Ontology	GO:0007283	4.26×10 ⁻³	<i>DNMT3A,</i> <i>BCL2L11,</i> <i>MERTK</i>
