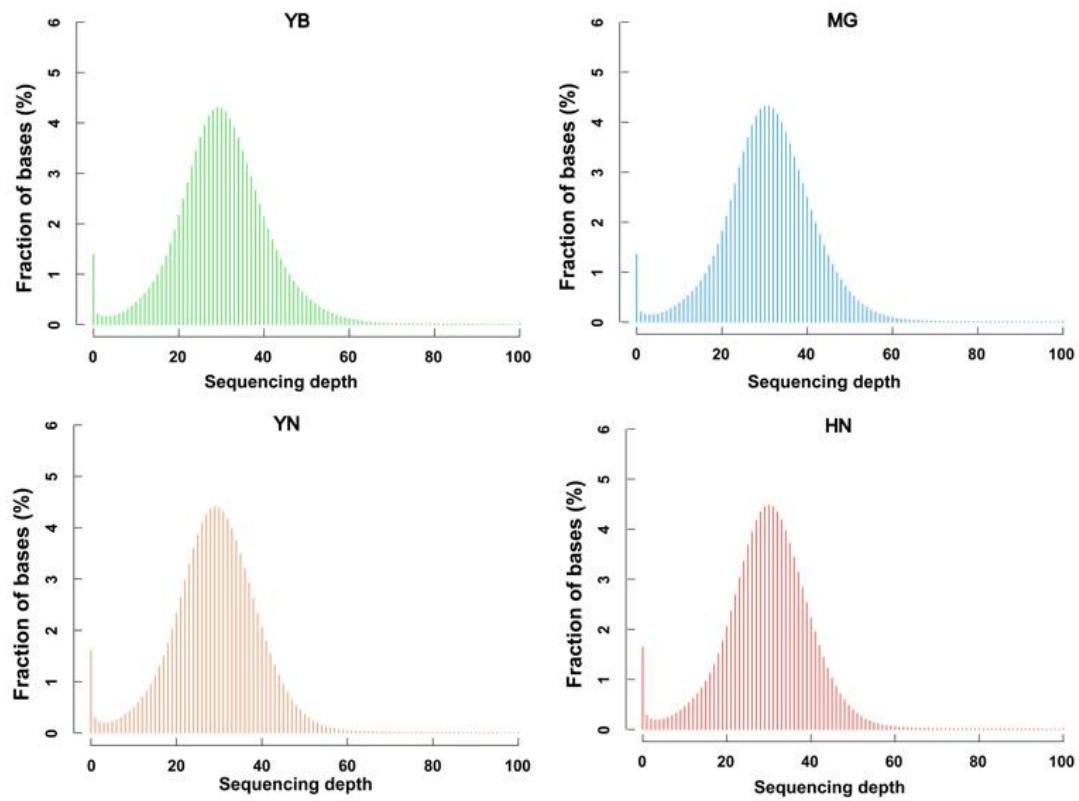


Supplementary Materials



Supplementary Figure S1. Average sequencing depth in four different cattle breeds.

Supplementary Table S1. Information of the worldwide cattle

Sample ID	SRA number	Species
Rashoki1	ERR454987	<i>Bos taurus</i>
Rashoki2	ERR454988	<i>Bos taurus</i>
Rashoki3	ERR454989	<i>Bos taurus</i>
Rashoki4	ERR454991	<i>Bos taurus</i>
Gelbvieh1	SRR1343161	<i>Bos taurus</i>
Gelbvieh2	SRR1343162	<i>Bos taurus</i>
Charolais1	SRR1343167	<i>Bos taurus</i>
Charolais2	SRR1343168	<i>Bos taurus</i>
Charolais3	SRR1343169	<i>Bos taurus</i>
Charolais4	SRR1348571	<i>Bos taurus</i>
Charolais5	SRR1355258	<i>Bos taurus</i>
Charolais6	SRR1365122	<i>Bos taurus</i>
Red Angus1	SRR1343172	<i>Bos taurus</i>
Red Angus2	SRR1355239	<i>Bos taurus</i>
Red Angus3	SRR1365103	<i>Bos taurus</i>
Red Angus4	SRR1365113	<i>Bos taurus</i>
Red Angus5	SRR1425153	<i>Bos taurus</i>
Holstein1	SRR1346386	<i>Bos taurus</i>
Holstein2	SRR1346390	<i>Bos taurus</i>
Holstein3	SRR1346392	<i>Bos taurus</i>
Holstein4	SRR1348583	<i>Bos taurus</i>
Piedmontese1	SRR1525604	<i>Bos taurus</i>
Piedmontese2	SRR1343162	<i>Bos taurus</i>
Simmental1	SRR1525617	<i>Bos taurus</i>
Simmental2	SRR1525618	<i>Bos taurus</i>
Simmental3	SRR1525619	<i>Bos taurus</i>
Simmental4	SRR1525620	<i>Bos taurus</i>
Simmental5	SRR1525621	<i>Bos taurus</i>
Jersey1	SRR2016774	<i>Bos taurus</i>
Jersey2	SRR2016776	<i>Bos taurus</i>
Jersey3	SRR2016799	<i>Bos taurus</i>
Kazakh4	SRR5507253	<i>Bos taurus</i>
Kazakh3	SRR5507254	<i>Bos taurus</i>
Kazakh2	SRR5507255	<i>Bos taurus</i>
Kazakh1	SRR5507256	<i>Bos taurus</i>
Hanwoo1	SRR934415	<i>Bos taurus</i>
Hanwoo2	SRR934417	<i>Bos taurus</i>
Hanwoo3	SRR934418	<i>Bos taurus</i>
Hanwoo4	SRR934419	<i>Bos taurus</i>
Hanwoo5	SRR934432	<i>Bos taurus</i>
Shorthorn Zebu1	ERR320241	<i>Bos taurus x Bos indicus</i>
Shorthorn Zebu2	ERR320244	<i>Bos taurus x Bos indicus</i>
Shorthorn Zebu3	ERR320246	<i>Bos taurus x Bos indicus</i>
Shorthorn Zebu4	ERR320249	<i>Bos taurus x Bos indicus</i>
Ankole1	ERR320247	<i>Bos taurus x Bos indicus</i>
Ankole2	ERR320264	<i>Bos taurus x Bos indicus</i>

Ankole3	ERR320245	<i>Bos taurus x Bos indicus</i>
Zaobei1	SRR5507210	<i>Bos taurus x Bos indicus</i>
zaobei2	SRR5507211	<i>Bos taurus x Bos indicus</i>
zaobei3	SRR5507212	<i>Bos taurus x Bos indicus</i>
Lingnan5	SRR5507215	<i>Bos taurus x Bos indicus</i>
Lingnan4	SRR5507216	<i>Bos taurus x Bos indicus</i>
Lingnan3	SRR5507219	<i>Bos taurus x Bos indicus</i>
Lingnan2	SRR5507220	<i>Bos taurus x Bos indicus</i>
Lingnan1	SRR5507222	<i>Bos taurus x Bos indicus</i>
Luxi1	SRR5507238	<i>Bos taurus x Bos indicus</i>
Luxi2	SRR5507239	<i>Bos taurus x Bos indicus</i>
Luxi3	SRR5507240	<i>Bos taurus x Bos indicus</i>
Luxi4	SRR5507241	<i>Bos taurus x Bos indicus</i>
Luxi5	SRR5507242	<i>Bos taurus x Bos indicus</i>
Wannan1	SRR5507197	<i>Bos indicus</i>
Wannan2	SRR5507196	<i>Bos indicus</i>
Wannan3	SRR5507195	<i>Bos indicus</i>
Jinjiang1	SRR5507274	<i>Bos indicus</i>
Jinjiang2	SRR5507275	<i>Bos indicus</i>
Jinjiang3	SRR5507278	<i>Bos indicus</i>
Guangfeng1	SRR5507283	<i>Bos indicus</i>
Guangfeng2	SRR5507284	<i>Bos indicus</i>
Guangfeng3	SRR5507285	<i>Bos indicus</i>
Guangfeng4	SRR5507286	<i>Bos indicus</i>
Tharparkar	SRR6936538	<i>Bos indicus</i>
Hariana	SRR6936539	<i>Bos indicus</i>
Sahiwal	SRR6936540	<i>Bos indicus</i>
Gir1	SRR2016752	<i>Bos indicus</i>
Gir2	SRR2016753	<i>Bos indicus</i>
Gir3	SRR2016754	<i>Bos indicus</i>
Nelore1	SRR2016757	<i>Bos indicus</i>
Nelore2	SRR2016759	<i>Bos indicus</i>
Brahman1	SRR2016745	<i>Bos indicus</i>
Brahman2	SRR2016748	<i>Bos indicus</i>
Brahman3	SRR2016749	<i>Bos indicus</i>
Brahman4	SRR2016795	<i>Bos indicus</i>

Supplementary Table S2. Primers for RT-PCR

Gene	Forward	Reverse
<i>C/EBPβ</i>	CGCCGCCTTATAAACCTCCC	AGTCGGGCTCGTAGTAGAAGT
<i>CIDEA</i>	TTATCGCCAGCAGAGTGGTC	GATGTAGGTACCAGCCGGTGT
<i>PGC1-α</i>	ACACCAAACCCACAGAGAC	GGGTCAGAGGAAGAGATAAAGATG
<i>PPARγ</i>	CGCTGGGGTATTGGGTCG	TTCAAATCTTGTCTGTACACAGT
<i>PRDM16</i>	GTGCCTACGAGGACGATGAG	GATCCAGCCCCTTCCCAAAA
<i>UCPI</i>	CTAGGGACCATCACCACCCT	GCAGGTGTTTCTCTCCCTGAA

Supplementary Table S3. Overview of sample information and sequencing statistics

	Raw Reads Number	Raw Bases Number	Clean Reads Number	Clean Bases Number	Clean Reads Rate(%)	Mapped Bases	Mapping Rate (%)	Duplication Rate (%)	Uniq Rate(%)	Mean Depth	Coverage Rate (%) (>1X)
Total	20,515,811,754	3,077,371,763,100	17,290,595,634	2,593,589,345,100	84.36	2,568,283,869,214	98.69	19.32	89.56	33.66	97.82
HN1	649,011,786	97,351,767,900	609,599,152	91,439,872,800	93.93	89,704,339,669	97.78	16.68	90.20	32.92	97.79
HN2	653,396,724	98,009,508,600	609,481,156	91,422,173,400	93.28	90,336,957,829	98.33	24.79	88.77	33.1	97.54
HN3	775,395,096	116,309,264,400	722,993,044	108,448,956,600	93.24	107,063,427,621	98.34	18.26	89.44	39.27	97.67
HN4	721,497,970	108,224,695,500	595,130,096	89,269,514,400	82.48	88,170,431,169	98.31	23.17	88.59	32.31	97.56
HN5	613,449,392	92,017,408,800	539,440,756	80,916,113,400	87.94	80,067,074,362	98.6	28.61	91.08	29.38	97.52
HN6	740,426,962	111,064,044,300	618,983,530	92,847,529,500	83.60	91,558,088,804	98.17	24.31	88.92	33.56	97.58
HN7	754,539,172	113,180,875,800	607,414,584	91,112,187,600	80.50	90,125,159,855	98.57	16.42	90.09	33.07	97.61
MG10	882,971,018	132,445,652,700	797,809,522	119,671,428,300	90.36	118,808,256,278	99.01	18.44	89.47	43.63	98.17
MG2	717,619,126	107,642,868,900	596,855,504	89,528,325,600	83.17	88,782,950,880	98.88	18.36	89.6	32.6	98.03
MG3	675,560,088	101,334,013,200	558,396,498	83,759,474,700	82.66	83,100,466,370	98.88	16.03	90.55	30.49	97.95
MG4	706,187,580	105,928,137,000	651,187,466	97,678,119,900	92.21	96,944,784,464	99.02	20.02	88.84	35.61	98.06
MG7	708,055,444	106,208,316,600	588,312,588	88,246,888,200	83.09	87,524,450,326	98.97	19.03	89.54	32.16	98.04
MG9	699,028,982	104,854,347,300	634,833,218	95,224,982,700	90.82	94,442,339,018	98.82	22.5	89.1	34.65	98.14
YB06008	725,501,474	108,825,221,100	582,735,270	87,410,290,500	80.32	86,672,478,935	98.85	19.69	88.62	31.82	97.93
YB09013	728,619,546	109,292,931,900	575,924,356	86,388,653,400	79.04	85,734,265,742	99.01	18.25	87.87	31.49	97.91
YB10001	659,374,326	98,906,148,900	523,981,766	78,597,264,900	79.47	77,986,957,933	98.96	16.92	88.55	28.64	97.88
YB10039	772,927,648	115,939,147,200	652,862,110	97,929,316,500	84.47	96,909,412,974	98.68	17.85	87.92	35.58	98.08
YB13029	987,761,138	148,164,170,700	853,981,668	128,097,250,200	86.46	127,213,545,274	99.05	18.07	88.04	46.72	98.17
YB15015	743,151,368	111,472,705,200	619,907,992	92,986,198,800	83.42	92,356,190,850	99.02	15.86	88.7	33.9	98.00
YB15042	713,104,476	106,965,671,400	649,874,510	97,481,176,500	91.13	96,821,499,628	99.04	19.08	87.61	35.55	98.08
YB50001	654,948,194	98,242,229,100	591,843,470	88,776,520,500	90.36	88,152,918,099	99.05	19.11	88.23	32.38	98.00
YN11	876,014,636	131,402,195,400	631,985,176	94,797,776,400	72.14	93,793,751,574	98.55	18.16	90.85	34.40	97.80
YN12	765,932,126	114,889,818,900	624,668,356	93,700,253,400	81.56	92,668,797,104	98.55	15.93	91.41	34.00	97.56
YN15	689,812,860	103,471,929,000	538,218,930	80,732,839,500	78.02	79,837,996,849	98.53	14.44	91.75	29.29	97.47
YN16	711,650,964	106,747,644,600	589,184,396	88,377,659,400	82.79	87,510,214,862	98.67	19.28	91.94	32.11	97.55
YN18	679,342,948	101,901,442,200	520,090,182	78,013,527,300	76.56	77,243,628,286	98.62	16.89	91.71	28.33	97.55
YN6	799,912,226	119,986,833,900	663,767,888	99,565,183,200	82.98	98,608,221,686	98.77	24.95	89.61	36.21	97.86
YN9	710,618,484	106,592,772,600	541,132,450	81,169,867,500	76.15	80,145,262,773	98.39	20.03	90.89	29.40	97.48

Supplementary Table S4. Summary of SNPs identified from all samples in this study

	Number	Percent (%)
Total	45,271,339	100
UTR5	102,169	0.23
UTR3	275,484	0.61
UTR5;UTR3	278	0
exonic	321,608	0.71
splicing	1,049	0
exonic;splicing	79	0
upstream	244,449	0.54
downstream	271,139	0.60
upstream;downstream	6,408	0.01
intronic	16,183,452	35.75
intergenic	27,844,994	61.51
other	0	0

Supplementary Table S5. The candidate genes were obtained by F_{ST} and Fisher's test analysis

Gene symbol	Gene name	P
<i>ACVRL1</i>	Activin A receptor like type 1	0.0001
<i>ADPRHL1</i>	ADP-ribosylhydrolase like 1	0.0001
<i>AGPAT4</i>	1-acylglycerol-3-phosphate O-acyltransferase 4	0.0007
<i>ALDOB</i>	Aldolase, fructose-bisphosphate B	1.46E-06
<i>ALMS1</i>	ALMS1 centrosome and basal body associated protein	0.0003
<i>ALS2CL</i>	ALS2 C-terminal like	2.84E-09
<i>ANK3</i>	Ankyrin 3	0.0007
<i>APOA5</i>	Apolipoprotein A5	0.0003
<i>APRT</i>	Adenine phosphoribosyltransferase	1.14E-13
<i>ARHGAP21</i>	Rho GTPase activating protein 21	0.0011
<i>ARHGAP26</i>	Rho GTPase activating protein 26	1.46E-06
<i>ARHGAP31</i>	Rho GTPase activating protein 31	1.27E-09
<i>ASAP3</i>	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	0.0018
<i>ASB18</i>	Ankyrin repeat and SOCS box containing 18	0.0001
<i>ASPH</i>	Aspartate beta-hydroxylase	0.0018
<i>ASXL1</i>	ASXL transcriptional regulator 1	0.0018
<i>ATP10B</i>	ATPase phospholipid transporting 10B (putative)	3.11E-05
<i>ATP12A</i>	ATPase H ⁺ /K ⁺ transporting non-gastric alpha2 subunit	0.0003
<i>ATP6V1H</i>	ATPase H ⁺ transporting V1 subunit H	2.77E-11
<i>BAIAP2L2</i>	BAR/IMD domain containing adaptor protein 2 like 2	0.0007
<i>BCAR3</i>	BCAR3 adaptor protein, NSP family member	7.58E-15
<i>BORA</i>	BORA aurora kinase A activator	0.0003
<i>BRCA2</i>	BRCA2 DNA repair associated	1.14E-13
<i>BRD1</i>	Bromodomain containing 1	2.05E-13
<i>BRF1</i>	BRF1 RNA polymerase III transcription initiation factor subunit	1.46E-06
<i>C2CD2</i>	C2 calcium dependent domain containing 2	2.77E-11
<i>CAPN10</i>	Calpain 10	0.0023
<i>CAPN13</i>	Calpain 13	4.00E-05
<i>CCDC141</i>	Coiled-coil domain containing 141	0.0018
<i>CCRL2</i>	C-C motif chemokine receptor like 2	9.40E-12
<i>CD55</i>	CD55 molecule (Cromer blood group)	1.85E-08
<i>CDC16</i>	Cell division cycle 16	1.18E-12
<i>CDC42BPB</i>	CDC42 binding protein kinase beta	1.27E-09
<i>CDC42BPG</i>	CDC42 binding protein kinase gamma	2.05E-13
<i>CDCA5</i>	Cell division cycle associated 5	0.0018
<i>CDKL3</i>	Cyclin dependent kinase like 3	0.0007
<i>CEACAM20</i>	CEA cell adhesion molecule 20	3.98E-05
<i>CFAP65</i>	Cilia and flagella associated protein 65	0.0003
<i>CHML</i>	CHM like Rab escort protein	0.0008
<i>CPLANE1</i>	Ciliogenesis and planar polarity effector 1	6.72E-09
<i>CPT2</i>	Carnitine palmitoyltransferase 2	3.38E-10
<i>CRELD2</i>	Cysteine rich with EGF like domains 2	0.0007
<i>CTC1</i>	CST telomere replication complex component 1	0.0019

<i>DIS3</i>	DIS3 homolog, exosome endoribonuclease and 3'-5'	0.0004
<i>DISP3</i>	dispatched RND transporter family member 3	9.15E-06
<i>DMRTB1</i>	DMRT like family B with proline rich C-terminal 1	0.0001
<i>DNAH12</i>	dynein axonemal heavy chain 12	1.85E-08
<i>DNAH9</i>	dynein axonemal heavy chain 9	0.0007
<i>EIF2AK4</i>	eukaryotic translation initiation factor 2 alpha kinase 4	0.0009
<i>EIF2B5</i>	eukaryotic translation initiation factor 2B subunit epsilon	0.0001
<i>ELL</i>	elongation factor for RNA polymerase II	2.84E-09
<i>EMILIN2</i>	elastin microfibril interfacier 2	0.0007
<i>FAM186B</i>	family with sequence similarity 186 member B	0.0003
<i>FAM214B</i>	family with sequence similarity 214 member B	1.14E-13
<i>FANCA</i>	FA complementation group A	2.77E-11
<i>FBXL21</i>	F-box and leucine rich repeat protein 21, pseudogene	0.0018
<i>FEV</i>	FEV transcription factor, ETS family member	4.13E-05
<i>FGFR4</i>	fibroblast growth factor receptor 4	1.14E-13
<i>FOXL1</i>	forkhead box L1	0.0018
<i>FOXO3</i>	forkhead box O3	2.87E-12
<i>G6PC2</i>	glucose-6-phosphatase catalytic subunit 2	3.76E-11
<i>GATA6</i>	GATA binding protein 6	0.0023
<i>GIPC3</i>	GIPC PDZ domain containing family member 3	1.09E-13
<i>GPCPD1</i>	glycerophosphocholine phosphodiesterase 1	0.0018
<i>GPR1</i>	G protein-coupled receptor 1	0.0003
<i>GPR179</i>	G protein-coupled receptor 179	2.77E-11
<i>GRID2IP</i>	Grid2 interacting protein	1.14E-13
<i>HELB</i>	DNA helicase B	3.96E-05
<i>HEYL</i>	hes related family bHLH transcription factor with YRPW motif like	2.62E-16
<i>HIPK3</i>	homeodomain interacting protein kinase 3	0.0018
<i>HMCN1</i>	hemicentin 1	0.0003
<i>HYDIN</i>	HYDIN axonemal central pair apparatus protein	0.0004
<i>IGFN1</i>	immunoglobulin like and fibronectin type III domain containing 1	0.0023
<i>IL17RC</i>	interleukin 17 receptor C	3.38E-10
<i>IQUB</i>	IQ motif and ubiquitin domain containing	6.21E-11
<i>JCAD</i>	junctional cadherin 5 associated	0.0004
<i>KCNH1</i>	potassium voltage-gated channel subfamily H member 1	0.0004
<i>KIAA1549L</i>	KIAA1549 like	1.31E-07
<i>KIF17</i>	kinesin family member 17	2.87E-12
<i>KLHL5</i>	kelch like family member 5	2.84E-09
<i>KLK4</i>	kallikrein related peptidase 4	0.0001
<i>LDLR</i>	low density lipoprotein receptor	2.87E-12
<i>LOC100140428</i>	-	0.0003
<i>LOC100300760</i>	-	4.13E-05
<i>LOC100336868</i>	-	0.0013
<i>LOC100568284</i>	-	0.0001
<i>LOC100847301</i>	-	0.0011
<i>LOC100847677</i>	-	2.05E-13
<i>LOC100848138</i>	-	0.0011
<i>LOC100848799</i>	-	1.14E-13

<i>LOC101902951</i>	-	0.0007
<i>LOC101903647</i>	-	4.29E-10
<i>LOC101904409</i>	-	9.92E-08
<i>LOC101905308</i>	-	2.87E-12
<i>LOC101907127</i>	-	0.0003
<i>LOC104968820</i>	-	0.0007
<i>LOC112441599</i>	-	7.58E-15
<i>LOC112442245</i>	-	1.13E-07
<i>LOC112442750</i>	-	0.0029
<i>LOC112449110</i>	-	2.84E-09
<i>LOC508455</i>	-	2.84E-09
<i>LOC508459</i>	-	1.85E-08
<i>LOC518134</i>	-	3.38E-10
<i>LOC529488</i>	-	0.0001
<i>LOC540627</i>	-	5.64E-07
<i>LOC614376</i>	-	7.58E-15
<i>LOC616094</i>	-	0.0007
<i>LOC782190</i>	-	0.0008
<i>LOC785804</i>	-	0.0007
<i>LOC787102</i>	-	2.62E-16
<i>LOC787432</i>	-	7.91E-09
<i>LOC787601</i>	-	3.76E-11
<i>LOC787932</i>	-	0.0001
<i>LOC788790</i>	-	1.10E-09
<i>LOC788797</i>	-	0.0019
<i>LOC789504</i>	-	2.84E-09
<i>LOC789929</i>	-	3.76E-11
<i>LRR1Q1</i>	leucine rich repeats and IQ motif containing 1	0.0011
<i>MAST2</i>	microtubule associated serine/threonine kinase 2	1.18E-12
<i>MCMDC2</i>	minichromosome maintenance domain containing 2	0.0009
<i>MERTK</i>	MER proto-oncogene, tyrosine kinase	2.05E-13
<i>MIEF2</i>	mitochondrial elongation factor 2	1.38E-05
<i>MKRN3</i>	makorin ring finger protein 3	0.0003
<i>MLLT11</i>	MLLT11 transcription factor 7 cofactor	0.0018
<i>MORN1</i>	MORN repeat containing 1	0.0007
<i>MRVII</i>	inositol 1,4,5-triphosphate receptor associated 1	0.0011
<i>MUC15</i>	mucin 15, cell surface associated	0.0009
<i>MYCN</i>	MYCN proto-oncogene, bHLH transcription factor	3.76E-11
<i>NACA</i>	nascent polypeptide associated complex subunit alpha	0.0008
<i>NCOA2</i>	nuclear receptor coactivator 2	0.0003
<i>NEK4</i>	NIMA related kinase 4	7.58E-15
<i>NEMPI</i>	nuclear envelope integral membrane protein 1	0.0003
<i>NOP14</i>	NOP14 nucleolar protein	0.0013
<i>NR1P1</i>	nuclear receptor interacting protein 1	2.62E-16
<i>OR2S2</i>	olfactory receptor family 2 subfamily S member 2	2.07E-10
<i>OTOF</i>	otoferlin	0.0018
<i>OXNAD1</i>	oxidoreductase NAD binding domain containing 1	1.14E-13

<i>OXR1</i>	oxidation resistance 1	0.0030
<i>PCDH12</i>	protocadherin 12	2.05E-13
<i>PCDHA13</i>	protocadherin alpha 13	0.0001
<i>PCDHGA2</i>	protocadherin gamma subfamily A, 2	0.0001
<i>PDE3B</i>	phosphodiesterase 3B	0.0033
<i>PEX26</i>	peroxisomal biogenesis factor 26	0.0023
<i>PFAS</i>	phosphoribosylformylglycinamide synthase	0.0019
<i>PHACTR1</i>	phosphatase and actin regulator 1	0.0019
<i>PHLDB2</i>	pleckstrin homology like domain family B member 2	6.67E-08
<i>PIEZO2</i>	piezo type mechanosensitive ion channel component 2	2.05E-13
<i>PKP1</i>	plakophilin 1	0.0003
<i>PKP2</i>	plakophilin 2	0.0008
<i>PLPP2</i>	phospholipid phosphatase 2	7.58E-15
<i>POLRMT</i>	RNA polymerase mitochondrial	1.14E-13
<i>PRDM16</i>	PR/SET domain 16	3.76E-11
<i>PRR23A</i>	proline rich 23A	9.15E-06
<i>PTCD1</i>	pentatricopeptide repeat domain 1	0.0001
<i>PTPRS</i>	protein tyrosine phosphatase receptor type S	1.06E-05
<i>QSER1</i>	glutamine and serine rich 1	0.0001
<i>RASGRP2</i>	RAS guanyl releasing protein 2	4.61E-06
<i>RBM44</i>	RNA binding motif protein 44	3.76E-11
<i>REXO1</i>	RNA exonuclease 1 homolog	0.0004
<i>RFC1</i>	replication factor C subunit 1	0.0009
<i>ROR1</i>	receptor tyrosine kinase like orphan receptor 1	1.06E-05
<i>RTP5</i>	receptor transporter protein 5 (putative)	2.05E-13
<i>RUSC2</i>	RUN and SH3 domain containing 2	1.14E-13
<i>SBF2</i>	SET binding factor 2	1.13E-07
<i>SCP2</i>	sterol carrier protein 2	5.64E-07
<i>SEC24A</i>	SEC24 homolog A, COPII coat complex component	3.76E-11
<i>SEMA3B</i>	semaphorin 3B	2.87E-12
<i>SEMA6C</i>	semaphorin 6C	0.0018
<i>SHANK2</i>	SH3 and multiple ankyrin repeat domains 2	3.76E-11
<i>SHISAL1</i>	shisa like 1	9.15E-06
<i>SMOX</i>	spermine oxidase	1.76E-09
<i>SPIB</i>	Spi-B transcription factor	5.64E-07
<i>SPNS2</i>	sphingolipid transporter 2	2.07E-10
<i>SPTBN5</i>	spectrin beta, non-erythrocytic 5	6.21E-11
<i>SRARP</i>	steroid receptor associated and regulated protein	1.18E-12
<i>STAT5B</i>	signal transducer and activator of transcription 5B	2.42E-06
<i>STK3</i>	serine/threonine kinase 3	0.0001
<i>STOX1</i>	storkhead box 1	2.84E-09
<i>TAGAP</i>	T cell activation RhoGTPase activating protein	0.0001
<i>TAS1R3</i>	taste 1 receptor member 3	0.0018
<i>TCF20</i>	transcription factor 20	0.0023
<i>TEKT3</i>	tektin 3	0.0007
<i>THEG</i>	theg spermatid protein	0.0018
<i>TICAM1</i>	toll like receptor adaptor molecule 1	0.0019

<i>TMEM135</i>	transmembrane protein 135	0.0018
<i>TMEM201</i>	transmembrane protein 201	1.14E-13
<i>TMEM25</i>	transmembrane protein 25	20.5E-13
<i>TRMT13</i>	tRNA methyltransferase 13 homolog	0.0001
<i>TTL8</i>	tubulin tyrosine ligase like 8	2.84E-09
<i>UNC13B</i>	unc-13 homolog B	1.14E-13
<i>VPS72</i>	vacuolar protein sorting 72 homolog	1.18E-12
<i>VPS9D1</i>	VPS9 domain containing 1	0.0037
<i>YEATS2</i>	YEATS domain containing 2	0.0007
<i>ZDHHC3</i>	zinc finger DHHC-type palmitoyltransferase 3	5.22E-06
<i>ZNF366</i>	zinc finger protein 366	0.0037
<i>ZNF469</i>	zinc finger protein 469	0.0024
<i>ZNF827</i>	zinc finger protein 827	0.0011

Supplementary Table S6. The top enriched KEGG pathway of candidate genes

Map	KEGG Pathway	Involved gene	<i>P</i>
map03320	PPAR signaling pathway	<i>SCP2, CPT2, APOA5</i>	0.0165
map04973	Carbohydrate digestion and absorption	<i>TAS1R3, G6PC2</i>	0.0357

Supplementary Table S7. The KEGG pathways associated with fat metabolism and thermogenesis

Map	KEGG Pathway	Involved gene	P
map03320	PPAR signaling pathway	<i>SCP2, CPT2, APOA5</i>	0.0165
map01040	Biosynthesis of unsaturated fatty acids	<i>LOC508455</i>	0.1553
map00051	Fructose and mannose metabolism	<i>ALDOB</i>	0.1918
map04910	Insulin signaling pathway	<i>PDE3B</i>	0.2399
map00071	Fatty acid metabolism	<i>CPT2</i>	0.2656

Supplementary Table S8. GO analysis of candidate genes with $P < 0.5$

GO	Description	<i>P</i>
GO:0071773	cellular response to BMP stimulus	0.0013
GO:0071772	response to BMP	0.0013
GO:0055092	sterol homeostasis	0.0018
GO:0042632	cholesterol homeostasis	0.0018
GO:0060430	lung sacculle development	0.0019
GO:0017025	TBP-class protein binding	0.002
GO:0046660	female sex differentiation	0.0025
GO:2000188	regulation of cholesterol homeostasis	0.0028
GO:0001542	ovulation from ovarian follicle	0.0038
GO:0055088	lipid homeostasis	0.0058
GO:0010649	regulation of cell communication by electrical coupling	0.0065
GO:0008585	female gonad development	0.0076
GO:0031532	actin cytoskeleton reorganization	0.0081
GO:0046545	development of primary female sexual characteristics	0.0086
GO:0030728	ovulation	0.0097
GO:0019199	transmembrane receptor protein kinase activity	0.01
GO:0035257	nuclear hormone receptor binding	0.012
GO:0007493	endodermal cell fate determination	0.0139
GO:0010902	positive regulation of very-low-density lipoprotein particle remodeling	0.0139
GO:1900827	positive regulation of membrane depolarization during cardiac muscle cell action potential	0.0139
GO:1901373	lipid hydroperoxide transport	0.0139
GO:0048386	positive regulation of retinoic acid receptor signaling pathway	0.0139
GO:0032911	negative regulation of transforming growth factor beta1 production	0.0139
GO:0032382	positive regulation of intracellular sterol transport	0.0139
GO:0032385	positive regulation of intracellular cholesterol transport	0.0139
GO:0072658	maintenance of protein location in membrane	0.0139
GO:0046208	spermine catabolic process	0.0139
GO:0051683	establishment of Golgi localization	0.0139
GO:0001543	ovarian follicle rupture	0.0139
GO:0001544	initiation of primordial ovarian follicle growth	0.0139
GO:0072660	maintenance of protein location in plasma membrane	0.0139
GO:0032379	positive regulation of intracellular lipid transport	0.0139
GO:0000126	transcription factor TFIIB complex	0.014
GO:0030689	Noc complex	0.014
GO:0016028	rhabdomere	0.014
GO:0033593	BRCA2-MAGE-D1 complex	0.014
GO:0030692	Noc4p-Nop14p complex	0.014
GO:0032541	cortical endoplasmic reticulum	0.014
GO:0000221	vacuolar proton-transporting V-type ATPase, V1 domain	0.014
GO:0033814	propanoyl-CoA C-acyltransferase activity	0.014
GO:0047389	glycerophosphocholine phosphodiesterase activity	0.014
GO:0003689	DNA clamp loader activity	0.014
GO:0004597	peptide-aspartate beta-dioxygenase activity	0.014

GO:0033695	oxidoreductase activity, acting on CH or CH2 groups, quinone or similar compound as acceptor	0.014
GO:0003875	ADP-ribosylarginine hydrolase activity	0.014
GO:0004642	phosphoribosylformylglycinamide synthase activity	0.014
GO:0052894	norspermine:oxygen oxidoreductase activity	0.014
GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	0.014
GO:0034875	caffeine oxidase activity	0.014
GO:0046592	polyamine oxidase activity	0.014
GO:0052895	N1-acetylspermine:oxygen oxidoreductase (N1-acetylspermidine-forming) activity	0.014
GO:0033170	protein-DNA loading ATPase activity	0.014
GO:0001556	oocyte maturation	0.0156
GO:0060292	long term synaptic depression	0.0156
GO:0001750	photoreceptor outer segment	0.016
GO:0031513	nonmotile primary cilium	0.017
GO:0010644	cell communication by electrical coupling	0.0179
GO:0090314	positive regulation of protein targeting to membrane	0.0179
GO:0051427	hormone receptor binding	0.018
GO:0005929	cilium	0.019
GO:0043966	histone H3 acetylation	0.0191
GO:0030054	cell junction	0.02
GO:0030330	DNA damage response, signal transduction by p53 class mediator	0.0204
GO:0030507	spectrin binding	0.021
GO:0016529	sarcoplasmic reticulum	0.022
GO:0030331	estrogen receptor binding	0.024
GO:0004198	calcium-dependent cysteine-type endopeptidase activity	0.024
GO:0007548	sex differentiation	0.0244
GO:0090313	regulation of protein targeting to membrane	0.0253
GO:0032388	positive regulation of intracellular transport	0.0261
GO:0008406	gonad development	0.0261
GO:1990075	periciliary membrane compartment	0.027
GO:0035517	PR-DUB complex	0.027
GO:0016528	sarcoplasm	0.027
GO:0071439	clathrin complex	0.027
GO:0010650	positive regulation of cell communication by electrical coupling	0.0275
GO:0010901	regulation of very-low-density lipoprotein particle remodeling	0.0275
GO:0016098	monoterpenoid metabolic process	0.0275
GO:0045602	negative regulation of endothelial cell differentiation	0.0275
GO:0032908	regulation of transforming growth factor beta1 production	0.0275
GO:0032905	transforming growth factor beta1 production	0.0275
GO:2000824	negative regulation of androgen receptor activity	0.0275
GO:0060137	maternal process involved in parturition	0.0275
GO:1900825	regulation of membrane depolarization during cardiac muscle cell action potential	0.0275
GO:0010808	positive regulation of synaptic vesicle priming	0.0275
GO:0045760	positive regulation of action potential	0.0275
GO:0048554	positive regulation of metalloenzyme activity	0.0275
GO:0071921	cohesin localization to chromatin	0.0275
GO:0071922	regulation of cohesin localization to chromatin	0.0275

GO:0032380	regulation of intracellular sterol transport	0.0275
GO:0032383	regulation of intracellular cholesterol transport	0.0275
GO:0071447	cellular response to hydroperoxide	0.0275
GO:2000676	positive regulation of type B pancreatic cell apoptotic process	0.0275
GO:0034471	ncRNA 5'-end processing	0.0275
GO:0061144	alveolar secondary septum development	0.0275
GO:0003376	sphingosine-1-phosphate signaling pathway	0.0275
GO:0042264	peptidyl-aspartic acid hydroxylation	0.0275
GO:0018197	peptidyl-aspartic acid modification	0.0275
GO:0051684	maintenance of Golgi location	0.0275
GO:2000563	positive regulation of CD4-positive, alpha-beta T cell proliferation	0.0275
GO:0035359	negative regulation of peroxisome proliferator activated receptor signaling pathway	0.0275
GO:0001547	antral ovarian follicle growth	0.0275
GO:0006598	polyamine catabolic process	0.0275
GO:0000967	rRNA 5'-end processing	0.0275
GO:0032912	negative regulation of transforming growth factor beta2 production	0.0275
GO:0048073	regulation of eye pigmentation	0.0275
GO:0032377	regulation of intracellular lipid transport	0.0275
GO:2000189	positive regulation of cholesterol homeostasis	0.0275
GO:0000480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.0275
GO:0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.0275
GO:0017116	single-stranded DNA-dependent ATP-dependent DNA helicase activity	0.028
GO:0032036	myosin heavy chain binding	0.028
GO:0016647	oxidoreductase activity, acting on the CH-NH group of donors, oxygen as acceptor	0.028
GO:0030368	interleukin-17 receptor activity	0.028
GO:0052901	spermine:oxygen oxidoreductase (spermidine-forming) activity	0.028
GO:0030160	GKAP/Homer scaffold activity	0.028
GO:0052741	(R)-limonene 6-monooxygenase activity	0.028
GO:0035259	glucocorticoid receptor binding	0.028
GO:0032029	myosin tail binding	0.028
GO:0018675	(S)-limonene 6-monooxygenase activity	0.028
GO:0019113	limonene monooxygenase activity	0.028
GO:0018676	(S)-limonene 7-monooxygenase activity	0.028
GO:0010484	H3 histone acetyltransferase activity	0.028
GO:0004714	transmembrane receptor protein tyrosine kinase activity	0.028
GO:0030023	extracellular matrix constituent conferring elasticity	0.028
GO:0010833	telomere maintenance via telomere lengthening	0.0281
GO:0045137	development of primary sexual characteristics	0.0286
GO:0016746	transferase activity, transferring acyl groups	0.031
GO:0097014	ciliary cytoplasm	0.032
GO:0005930	axoneme	0.032
GO:0005085	guanyl-nucleotide exchange factor activity	0.032
GO:0010876	lipid localization	0.0324
GO:0007140	male meiosis	0.0338
GO:2000278	regulation of DNA biosynthetic process	0.0338

GO:0004672	protein kinase activity	0.035
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	0.0369
GO:0042770	signal transduction in response to DNA damage	0.0372
GO:0032391	photoreceptor connecting cilium	0.038
GO:0050805	negative regulation of synaptic transmission	0.04
GO:0071782	endoplasmic reticulum tubular network	0.04
GO:0035363	histone locus body	0.04
GO:0000176	nuclear exosome (RNase complex)	0.04
GO:0070188	Stn1-Ten1 complex	0.04
GO:0031585	regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity	0.041
GO:0090520	sphingolipid mediated signaling pathway	0.041
GO:0034112	positive regulation of homotypic cell-cell adhesion	0.041
GO:0098902	regulation of membrane depolarization during action potential	0.041
GO:0098901	regulation of cardiac muscle cell action potential	0.041
GO:2000823	regulation of androgen receptor activity	0.041
GO:0060486	Clara cell differentiation	0.041
GO:0071043	CUT metabolic process	0.041
GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.041
GO:0071034	CUT catabolic process	0.041
GO:2000279	negative regulation of DNA biosynthetic process	0.041
GO:0006269	DNA replication, synthesis of RNA primer	0.041
GO:0071635	negative regulation of transforming growth factor beta production	0.041
GO:0018214	protein carboxylation	0.041
GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferation	0.041
GO:0006391	transcription initiation from mitochondrial promoter	0.041
GO:0051725	protein de-ADP-ribosylation	0.041
GO:0008215	spermine metabolic process	0.041
GO:0035739	CD4-positive, alpha-beta T cell proliferation	0.041
GO:0022833	mechanically gated channel activity	0.042
GO:0060230	lipoprotein lipase activator activity	0.042
GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	0.042
GO:2001070	starch binding	0.042
GO:0004694	eukaryotic translation initiation factor 2alpha kinase activity	0.042
GO:0035473	lipase binding	0.042
GO:0035939	microsatellite binding	0.042
GO:0048185	activin binding	0.042
GO:0005025	transforming growth factor beta receptor activity, type I	0.042
GO:0008381	mechanically-gated ion channel activity	0.042
GO:0046624	sphingolipid transporter activity	0.042
GO:0004346	glucose-6-phosphatase activity	0.042
GO:0050309	sugar-terminal-phosphatase activity	0.042
GO:0045505	dynein intermediate chain binding	0.042
GO:0003254	regulation of membrane depolarization	0.0433
GO:0071158	positive regulation of cell cycle arrest	0.0433
GO:0048599	oocyte development	0.0433

GO:0002920	regulation of humoral immune response	0.0433
GO:0032838	cell projection cytoplasm	0.044
GO:0010469	regulation of receptor activity	0.0447
GO:0007292	female gamete generation	0.0447
GO:0072372	primary cilium	0.046
GO:0032414	positive regulation of ion transmembrane transporter activity	0.0466
GO:0034358	plasma lipoprotein particle	0.048

Supplementary Table S9. GO category related to fat cell differentiation

GO	Description	P	Significant	Annotated
GO:0045598	Regulation of fat cell differentiation	0.6242	<i>ASXL1</i>	<i>AAMDC, ADIG, ADIPOQ, ADIRF, ANKRD26, ARNTL, ASXL1, ASXL2, ATAT1, AXIN1, CARM1, CCDC85B, CEBPB, CMKLR1, CREB1, CREBL2, DKKL1, FAM57B, FNDC3B, FNDC5, FRZB, GATA3, ID2, ID4, IFT88, INSIG1, JAG1, JDP2, LOC100337001, LOC100337293, LOC104976433, LOC112443458, LOC112449258, LOC112449355, LOC112449366, LOC513969, LOC522845, LOC615768, LOC619000, LOC782348, LOC783893, LPIN1, LRP5, LRP6, MEX3C, MSX2, NOCT, NR1D1, PPAR, PTPRO, RARRES2, RORA, RORC, SIRT1, SIRT2, SOD2, TAF8, TCF7L2, TGFB1, TGFB11, TRIB2, WIF1, WNT3A, WNT5B, WWTR1, ZBTB16, ZC3H12A, ZFPM1, ZFPM2, ZNF385A</i>
GO:0045599	Negative regulation of fat cell differentiation	0.4201	<i>ASXL1</i>	<i>ADIPOQ, ANKRD26, ARNTL, ASXL1, AXIN1, CCDC85B, FAM57B, GATA3, ID4, INSIG1, JAG1, JDP2, LOC100337001, LOC100337293, LOC104976433, LOC112443458, LOC112449258, LOC112449355, LOC112449366, LOC513969, LOC522845, LOC615768, LOC619000, LOC782348, LOC783893, LRP6, MSX2, RORA, SIRT1, SIRT2, SOD2, TCF7L2, TGFB1, TGFB11, TRIB2, WNT3A, WWTR1, ZFPM1, ZFPM2</i>
GO:0050873	Brown fat cell differentiation	0.2003	<i>PRDM16</i>	<i>ADIG, ADIPOQ, ADRB3, ARL4A, ERO1A, FNDC5, LAMA4, LAMB3, LRG1, MRAP, NUDT7, PLAC8, PLAC8-2, PRDM16, RARRES2, SH2B2</i>
GO:0050872	White fat cell differentiation	0.0931	<i>PRDM16</i>	<i>AACS, ADIG, CTBP1, CTBP2, PER2, PRDM16, SIRT1</i>

Supplementary Table S10. SNPs identified by sequence comparison in *PRDM16* gene

Chr	SNP	Position	Amino acid substitution	Exon	Genotypic frequencies							
					Northern cattle			SNP rate	Southern cattle			SNP rate
					Genotypes(n)				Genotypes(n)			
	c.2336 T>C	50871998	L779P	7	TT (12)	TC (2)	CC (0)	0.07	TT (0)	TC (2)	CC (12)	0.93
	c.37 A>G	50899189	T13A	1	AA (13)	AG (1)	GG (0)	0.04	AA (1)	AG (5)	GG (8)	0.75
16	c.354 G>A	51123299	M118I	3	GG (14)	GA (0)	AA (0)	0	GG (2)	GA (8)	AA (4)	0.57
	c.344 T>C	51123300	M115I	3	TT (13)	TC (1)	CC (0)	0.04	TT (1)	TC (8)	CC (5)	0.64
	c.89 C>T	51123555	A30V	3	CC (14)	CT (0)	TT (0)	0	CC (3)	CT (7)	TT (4)	0.54