Supplemental Table S13. Functional candidate genes under breed-specific selection in Rongchang (nine fat deposition genes), Jinhua pigs (six fat deposition genes) and Tibetan wild boar (16 high-altitude adaptation genes).

Chr.	Start	End	FDR	Gene symbol	Gene name	Associated phenotypes	Functional description
Rongchang (9 genes)							
6	65,800,001	65,830,000	7.96E-03	*NPPA*	Natriuretic peptide A	Feed intake and energy homeostasis	*NPPA* encoding the precursor of atrial natriuretic peptide, may serve as a part of the extended endocrine network that regulates cardiovascular and metabolic homeostasis[46], and is associated with hypertension[47], stroke, heart failure[48], type II diabetes and obesity[49].
8	55,220,001	55,360,000	0.00E+00	*NPY1R*	Neuropeptide Y receptor Y1		Hypothalamus plays a key role in energy homeostasis and a number of hypothalamic neuropeptides are involved in physiological control of feeding regulation and energy homeostasis[50,51]. *NPY1R* and *NPY5R* are two transmembrane proteins being abundantly expressed in the hypothalamus and mediate the function of neuropeptide Y (NPY)[52]. Both *NPY5R* and *NPY1R* are implicated in the orexigenic effects of NPY[53], and are positively correlated with energy intake and weight gain[54,55].
8	55,220,001	55,360,000	0.00E+00	*NPY5R*	Neuropeptide Y receptor Y5		See functional description for *NYP1R*.
8	1,820,001	1,850,000	1.99E-02	*LRPAP1*	Low density lipoprotein receptor-related protein-associated protein 1	Lipid metabolism	As a lipid metabolizing gene, *LRPAP1* interacts with the low density lipoprotein (LDL) receptor-related protein and facilitates its proper folding and localization by preventing the binding of ligands[56]. The polymorphisms of *LPRAP1* have been associated with body mass index in human[57,58] and carcass composition traits in chicken[59].
11	70,680,001	70,720,000	1.04E-03	*ABCC4*	ATP-binding cassette sub-family C member 4		*ABCC4*, also known as the multidrug resistance-associated protein 4 (*MRP4*) or multi-specific organic anion transporter B, is a basolateral efflux transporter that pumps various endogenous and exogenous chemicals from hepatocytes to blood[60,61]. The expression of *ABCC4* in liver was associated with residual feed intake (a measure of feed efficiency) in beef cattle[62], and fat mass in mouse[63].
8	1,240,001	1,290,000	4.70E-04	*ADD1*	Adducin α	Obesity-induced	*ADD1*, a family of cytoskeleton proteins, is known to increase renal sodium reabsorption and may be involved in the

						hypertension, inflammatory signaling and insulin resistance	pathophysiology of essential hypertension, which is a common comorbidity of obesity[64-66].
13	1,410,001	1,480,000	0.00E+00	*PIK3R4*	Phosphoinositide-3-kinase, regulatory subunit 4		*PIK3R4* plays a regulatory role in the phosphoinositide 3 kinase complex[67], are is involved in cellular response to glucose starvation[68] and insulin receptor signaling pathway[69].
15	112,470,001	112,530,000	0.00E+00	*HSPD1*	Heat shock 60kDa protein 1		*HSPD1*, also known as *HSP60*, exerts autocrine/paracrine effects on adipocytes characterized by an increased release of proinflammatory adipokines[70], increased obesity-related inflammatory signaling[71] and insulin resistance[72].
17	64,900,001	64,930,000	6.86E-03	*RAE1*	Ribonucleic acid export 1		*RAE1*, a high affinity ligand of the natural killer group 2, member D (*NKG2D)* receptor, is highly expressed under stressful environments[73]. The activating receptor *NKG2D* is thought to be directly involved in the progression of type I diabetes[74]. The delivered therapeutic *RAE1* plasmid showed a delay in the incidence of diabetes without a sharp decline of body weight and survival rate in mouse model[75].
Jinhua (6 genes)							
2	132,180,001	132,240,000	8.93E-06	*CEP120*	Centrosomal protein of 120 kDa	Feed intake and energy homeostasis	*CEP120*, a centrosomal protein, is preferentially expressed in neural progenitors, is involved in controlling interkinetic nuclear migration[76], and is also essential for centriole assembly[77,78].
8	38,180,001	38,220,000	1.73E-03	*GABRA2*	γ-amino butyric acid α2 receptor subunit		*GABRA2*, a major inhibitory neurotransmitter in the mammalian brain, is a predictor for alcoholism[79,80], and associated with elevated body mass index regardless of the presence/absence of obesity and impulsiveness[81].
15	42,760,001	42,830,000	0.00E+00	*ANGPT2*	Angiopoietin-2	Lipid metabolism	*ANGPT2*, a marker of endothelial cell activation[82], is crucial for controlling adipose vascular function, which is part of an adaptation to increased adipose tissue metabolism[83,84].
18	6,110,001	6,150,000	9.25E-04	*PRKAG2*	AMP-activated, γ-2 non-catalytic subunit		*PRKAG2*, a member of the AMP-activated protein kinase (AMPK) *γ* subunit family[85]. AMPK is a metabolic regulator that monitors cellular energy status and functions by inactivating key enzymes involved in regulating *de novo* biosynthesis of fatty acid and cholesterol[86,87], making it a key gene in the molecular regulation of feed efficiency[88,89].
2	88,180,001	88,220,000	5.27E-04	*TBCA*	Tubulin-specific chaperone A	Obesity-induced hypertension, inflammatory signaling and insulin resistance	*TBCA* interacts with *β* tubulin and is involved in the folding and dimerization of new tubulin heterodimers, the building blocks of microtubules[90]. The deletion variations of *TBCA* has been shown to contribute to genetic susceptibility of common childhood obesity[91,92].
6	27,500,001	27,530,000	3.10E-02	*MMP2*	Matrix metallopeptidase 2		*MMP2* is suggested to be involved in the development of various clinical factors of metabolic syndrome, which plays an important

							role in adipose tissue development by cleave insulin-like growth factor-binding proteins and release insulin-like growth factors[93]. Additionally, tissue degradation by *MMP2* is pivotal to inflammation[94] and obesity is associated with low grade inflammation[95-97].
Tibetan wild boar (16 genes)							
2	75,150,001	75,190,000	7.43E-03	*MAP2K2*	Mitogen-activated protein kinase kinase 2	Hypoxic response	*MAP2K2*, also known as *MEK2*, activates the ERK1 and ERK2 MAP kinases[98]. In the MAPK pathway[99], *MAP2K2* has been shown to be down-regulated in the hypoxia condition[100].
2	82,690,001	82,730,000	7.43E-03	*UNC5A*	Unc-5 netrin receptor A		*UNC5A* belongs to a family of netrin-1 receptors[101], which could promote neuronal apoptosis during spinal cord development[102]. The neuronal guidance molecule netrin 1 could be induced by hypoxia-inducible factor 1α (*HIF-1α*) under the hypoxic condition[103].
8	9,990,001	10,010,000	6.56E-01	*CPEB2*	Cytoplasmic polyadenylation element binding protein 2		*CPEB2* encodes an RNA-binding protein that participates in translational control[104], which interacts with eukaryotic elongation factor 2 to modulate the translation of *HIF-1α* (a master regulator of oxygen homeostasis) by bind to *HIF-1α* mRNA 3'-UTR[105 106].
13	32,160,001	32,190,000	1.64E-02	*CXCR6*	Chemokine (C-X-C motif) receptor 6		*CXCR6* encodes a member of chemokine receptor families, could facilitate immune responses via cell-cell contact, and guide the trafficking of T-cells[107,108]. *CXCR6* has important roles in tumorigenesis[109] and contributes significantly to cell migration during hypoxia by regulated expression of the *HIF-1α*[110].
13	32,580,001	32,610,000	1.64E-02	*LTF*	Lactotransferrin		Lactotransferrin, also known as lactoferrin, is the cationic transferrin of exocrine secretions (milk, lacrimal fluid, saliva, etc.) and a key component of innate immune defense[111,112]. Lactoferrin plays crucial roles in hypoxic pulmonary hypertension and vascular remodeling[113]. Apo-form of lactoferrin performs as a normoxic mimetic of hypoxia, capable of stabilizing *HIF-1α*[114].
6	112,290,001	112,360,000	0.00E+00	*RPRD1A*	Regulation of nuclear pre-mRNA domain containing 1A	Content of hemoglobin	*RPRD1A*, also known as *p15RS*[115], encodes a regulatory nuclear pre-mRNA domain containing protein, which inhibits Wnt signaling by interrupting the formation of the *β*-catenin·TCF4 complex[116,117]. Mutations in *RPRD1A* of mouse have been associated with the increased hemoglobin content and decreased circulating amylase level (Mouse Genome Informatics, Supplemental URLs).
17	39,120,001	39,150,000	2.21E-02	*SLC52A3*	Solute carrier family 52 (riboflavin		*SLC52A3* encodes a vitamin B2 transporter protein that plays a role in intestinal absorption of vitamin B2[118,119]. Mutations in *SLC52A3* are associated with increased mean corpuscular

					transporter), member 3		hemoglobin concentration (Mouse Genome Informatics, Supplemental URLs), which probably contribute to the metabolically active form of vitamin B2, aids in the synthesis of hemoglobin and enhances oxygen binding[120].
12	23,250,001	23,300,000	2.57E-03	*CDK12*	Cyclin-dependent kinase 12	Maintaining genomic stability against solar UV	*CDK12*, a member of cyclin-dependent kinase, acts as a key regulator of transcription via phosphorylating the C-terminal domain of the large subunit of RNA polymerase II[121]. *CDK12* promotes homologous recombination repair[122] and maintains genomic stability via regulation of expression of DNA damage response genes[123,124].
3	55,770,001	55,800,000	4.06E-02	*TBC1D8*	TBC1 domain family, member 8	Hair follicle maturation	*TBC1D8* acts as a GTPase-activating protein for Rab family proteins[125] and is involved in hair follicle maturation[36].
15	104,080,001	104,150,000	5.78E-06	*COL3A1*	Collagen, type III, *α* 1	Assembly of collagen in skin	*COL3A1* and *COL5A* encode two fibrillar collagens that are found in extensible connective tissues such as skin, lung, uterus, intestine and the vascular system[126]. Mutations in *COL3A1* are associated with Ehlers-Danlos syndrome (EDS) type IV characterized by thin, pale and translucent skin and fragile blood vessels[127,128]. Mutations in *COL5A2* are associated with EDS types I and II characterized by severe skin involvement for type 1 and mild to moderate skin involvement for type 2[129,130].
15	104,080,001	104,150,000	5.78E-06	*COL5A2*	Collagen, type V, *α* 2		See functional description for *COL3A1*.
1	6,400,001	6,430,000	1.77E-02	*QKI*	KH domain containing, RNA binding	Development of cardiovascular system	*QKI* belongs to the family of highly conserved RNA binding proteins[131], which regulate circRNA formation during epithelial-mesenchymal transition[132]; and is a critical regulator of vascular smooth muscle cell phenotype[133,134].
3	7,310,001	7,350,000	1.89E-03	*STAG3*	Stromal antigen 3		*STAG3* encodes a subunit of cohesin, a large protein complex that is essential for proper pairing and segregation of chromosomes during meiosis[135], and is associated with female infertility[136] and Williams–Beuren syndrome characterized by supravalvular aortic stenosis, multiple peripheral pulmonary arterial stenoses,'elfin face', mental and statural deficiency[137].
9	13,070,001	13,110,000	2.43E-03	*PAK1*	P21 protein (Cdc42/Rac)-activated kinase 1		*PAK1* encodes a family member of serine/threonine p21-activating kinases, is a critical effector that link RhoGTPases to cytoskeleton reorganization and nuclear signaling[138]. *PAK1* is essential for protective physiological cardiac remodeling by maintaining ventricular Ca^{2+} homeostasis and electrophysiological stability under hypertrophic stress condition[139-141].
12	23,250,001	23,300,000	2.57E-03	*MED1*	Mediator complex subunit 1		*MED1*, a key subunit of the mediator complex, interacts with nuclear receptors to target gene-specific transcription[142], which

						is critical for postnatal cardiac growth and development[143,144]. Mutations in *MED1* of mouse have been associated with abnormal heart morphology (Mouse Genome Informatics, Supplemental URLs).
15	96,990,001	97,030,000	3.00E-03	*PDE1A*	Phosphodiesterase 1A	*PDE1A*, a member of the PDE1 family, is a Ca^{2+}/calmodulin-dependent phosphodiesterase that plays a role in signal transduction by regulating intracellular cyclic nucleotide concentrations[145] and is involved in aging-related loss of vasodilator function, vascular smooth muscle cells senescence, increased blood pressure and vascular hypertrophy [146,147].