a





Figure S1. Overview of Luchuan genome assembly.

(a) The flowchart of the contig, scaffold, and chromosome assembly in this study. (b) Hi-C contact heatmap. Genome-wide analysis of chromatin interactions in Luchuan genome. The numbering of a chromosome is based on the chromosome length from the longest to the shortest.



Additional file 2 Figure S2. Circos plot shows the genome characterization of the Luchuan and Duroc pigs.

I: Syntenic alignments between the Luchuan and Duroc genome based on one-to-one orthologous genes.

II: GC content in non-overlapping 1 Mb windows.

III: Percent coverage of TEs in non-overlapping 1Mb windows.

IV: Gene density calculated on the basis of the number of genes in non-overlapping 1Mb windows.

V: The length of pseudo-chromosome, light red, and light purple ideograms represent the chromosomes of Luchuan and Duroc pigs, respectively. Each ticket above the ideograms is on a scale of 50 Mb.



0

Figure S3. Comparative Genomic and Phylogenetic Analyses.

(a) Venn diagram showing shared orthologous groups among genomes of Luchuan, Duroc, goat, and human. (b) Phylogenetic tree with divergence times and history of orthologous gene families. Numbers on the nodes represent divergence times, with the error range shown in parentheses. The numbers of gene families that expanded (red) or contracted (blue) in each lineage after speciation are shown on the corresponding branch. MRCA is the most recent common ancestor.



Figure S4. PCA plots. (a) PCA of the first three principal components. BAMEI, Bamei; BER, Berkshire; BMX, Bamaxiang; CWB, Chinesewild boar; DUR, Duroc; EHL, Erhualian; GST, Tibetan (Gansu); HAM, Hampshire; HTDE, Hetao; JH, Jinhua; KBP, Korean black pig; KWB, Korean wild boar; LD, Landrace; LUC, Luchuan; LW, Large White; LWH, Laiwu; MEI, Meishan; MIN, Min; PTL, Pietrain; RC, Rongchang; SCT, Tibetan (Sichuan); TC, Tongcheng; TT, Tibetan (Tibet); WZS, Wuzhishan; YM, Yucatan Miniature; YNT, Tibetan (Yunnan). (b) PCA plots of the first two principal components by classifying them into seven groups: Chinese wild boar (CWB), Korean wildboar (BWB), Luchuan pig (LUC), Duroc (DUR), Korean black pig (KBP), other Eastern pigs (EST) and Western pigs (WST).







b

Figure S5. LD decay analysis. (a) LD decay determined by squared correlations (r²) of allele frequencies against the distance between polymorphic sites in eastern (EST; orange) and western (WST; green) pig groups. (b) LD decay in DUR (Duroc; red) and LUC (Luchuan; blue) pig groups.

Figure S6. Enrichment pattern of genes under potential selection in GWAS regions associated with some economic traits. Red represents genes located in selective regions of eastern pigs while blue represents those of western pigs. * represents FDR < 0.05. ** represents FDR < 0.01.



Adipose_up

Adipose_down

Figure S7.



Heart_down

RNA metabolic process

RNA biosynthetic process

regulation of gene expression

mRNA processing

gene expression

cell cycle process

cell cycle

mRNA metabolic process

DNA metabolic process

cellular response to stress

nucleic acid-templated transcription

heterocycle biosynthetic process

cellular response to DNA damage stimulus

cellular macromolecule biosynthetic process

aromatic compound biosynthetic process

regulation of transcription, DNA-templated

regulation of nucleic acid-templated transcription

regulation of nitrogen compound metabolic process

regulation of macromolecule biosynthetic process

regulation of cellular macromolecule biosynthetic process

nucleobase-containing compound biosynthetic process

protein modification by small protein conjugation or removal

egulation of nucleobase-containing compound metabolic process

regulation of RNA metabolic process

regulation of RNA biosynthetic process

regulation of symbiosis, encompassing mutualism through parasitism

- ribonucleoside triphosphate metabolic process ribonucleoside monophosphate metabolic process
 - ribonucleoside metabolic process
- purine ribonucleoside triphosphate metabolic process
- purine ribonucleoside monophosphate metabolic process
- purine ribonucleoside metabolic process
- purine nucleoside triphosphate metabolic process
- purine nucleoside monophosphate metabolic process
 - purine nucleoside metabolic process
- purine-containing compound metabolic process
 - oxidation-reduction process
 - nucleotide metabolic process
- nucleoside triphosphate metabolic process
- nucleoside phosphate metabolic process
- nucleoside monophosphate metabolic process
 - nucleoside metabolic process
- nucleobase–containing small molecule metabolic process mitochondrial ATP synthesis coupled electron transport
 - glycosyl compound metabolic process
 - generation of precursor metabolites and energy
- energy derivation by oxidation of organic compounds
- - ATP synthesis coupled electron transport
 - ATP metabolic process

0 30 40 –log2(P–value)

-log2 (P-value)

count

• 50

• 100

• 150

• 200

- skeletal muscle contraction single–organism catabolic process single–organism carbohydrate metabolic process ribonucleoside monophosphate metabolic process purine ribonucleoside triphosphate metabolic process purine ribonucleoside monophosphate metabolic process purine nucleoside monophosphate metabolic process polysaccharide metabolic process oxoacid metabolic process oxidation-reduction process organic acid metabolic process nucleoside monophosphate metabolic process muscle system process monocarboxylic acid metabolic process glycogen metabolic process glucan metabolic process generation of precursor metabolites and energy energy reserve metabolic process energy derivation by oxidation of organic compounds cellular polysaccharide metabolic process cellular glucan metabolic process
 - cellular carbohydrate metabolic process
 - carboxylic acid metabolic process
 - ATP metabolic process

Muscle_down



S

Cerebellum_down



Liver_down

Stomach_down





-log2 (P-value)

count

• 20

• 30

• 40

• 50

60

coun

• 20

• 50

-log2 (P-value)

•

•

-log2(P-value)

cell adhesion biological adhesion ATP metabolic process

Heart_up

electron transport chain cellular respiration

Muscle_up

30 33 3

-log2(P-value)



muscle contraction

Cerebrum_down



response to other organism response to external stimulus response to external biotic stimulus response to biotic stimulus regulation of immune system process regulation of immune response regulation of defense response regulation of cytokine productio positive regulation of response to stimulus positive regulation of immune system process positive regulation of immune response positive regulation of defense response positive regulation of cytokine production leukocyte cell–cell adhesion leukocyte activation innate immune response immune response-regulating signaling pathway immune response immune effector process defense response to other organism defense respon cytokine producti

cell activation

- antigen processing and presentation
- activation of immune response

-log2 (P-value) 4 5 6 7 -log2(P-value)

stem cell proliferation renal system development regulation of stem cell proliferation regulation of epithelial cell differentiation regulation of transmembrane receptor protein serine/threonine kinase signaling pathway positive regulation of protein metabolic process positive regulation of epithelial cell differentiation organic anion transport 🔶 • negative regulation of epithelial cell proliferation monosaccharide transport monocarboxylic acid transport mesonephros development mesonephric tubule development mesonephric epithelium development lipid transport lipid localization kidney epithelium development kidney development hexose transport glucose transport fatty acid transport

Cerebellum_up

urogenital system development

ureteric bud development

- carbohydrate transport

-log2 (P-value

count

• 40

60

Liver_up

steroid metabolic process

oxoacid metabolic process

oxidation-reduction process

lipid oxidatior

lipid metabolic process

lipid catabolic process

lipid biosynthetic process

fatty acid metabolic process

fatty acid catabolic proces

cellular lipid metabolic process

cellular lipid catabolic process

carboxylic acid metabolic process

carboxylic acid catabolic process

carbohydrate metabolic process

fatty acid beta-oxidatio

lipid homeostasis

fatty acid oxidation

organic acid metabolic process

organic acid catabolic process

monosaccharide metabolic process

monocarboxylic acid metabolic process

monocarboxylic acid catabolic process

small molecule catabolic process

small molecule biosynthetic process

single-organism catabolic process

- sister chromatid segregation -
- RNA metabolic process
- regulation of nucleobase-containing compound metabolic process regulation of nitrogen compound metabolic process
 - regulation of gene expression 🔸
 - recombinational repair
 - protein modification by small protein removal
- protein modification by small protein conjugation or removal
 - protein deubiquitination -
 - nuclear chromosome segregation
 - mitotic cell cycle process
 - microtubule organizing center organization
- double-strand break repair via homologous recombination double-strand break repair
 - DNA repair
 - DNA metabolic process
 - chromosome segregation
 - chromosome organization +•
 - centrosome organization
 - centrosome cycle
 - cellular response to stress cellular response to DNA damage stimulus
 - - cell cycle process

Small intestine_down



Stomach_up

30

-log2(P-value)

Cerebrum_up



Lung_down





Lung_up





- nervous system developmen movement of cell or subcellular component
 - locomotion
 - localization of cell
 - extracellular structure organization extracellular matrix organization chemotaxis
 - cellular component morphogenesis
 - cell projection organization
 - cell projection morphogenesis cell motility
 - cell migration
 - cell adhesion
 - cell-substrate adhesion
 - cell–cell adhesion
 - biological adhesion
- anatomical structure formation involved in morphogenesis



Small intestine_up



single–organism catabolic process ribonucleoside triphosphate metabolic process ribonucleoside monophosphate metabolic process ribonucleoside metabolic process pyridine nucleotide metabolic process pyridine-containing compound metabolic process purine ribonucleoside triphosphate metabolic process purine ribonucleoside monophosphate metabolic process purine ribonucleoside metabolic process purine nucleoside triphosphate metabolic process purine nucleoside monophosphate metabolic process purine nucleoside metabolic process oxidoreduction coenzyme metabolic process oxidation-reduction process organic acid metabolic process nucleoside triphosphate metabolic process nucleoside monophosphate metabolic process nucleoside metabolic process nucleobase–containing small molecule metabolic process nicotinamide nucleotide metabolic process monocarboxylic acid metabolic process glycosyl compound metabolic process

generation of precursor metabolites and energy

carbohydrate derivative metabolic process

ATP metabolic process





-log2(P-value)

С

Cell Cycle



b



Figure S8. DEG in skeletal muscle tissues.

(a) The number of DEG in different tissues. Duroc: the expression level is higher in Duroc pigs compared to Luchuan pigs. Luchuan: the expression level is higher in Luchuan pigs compared to Duroc pigs. (b) Heatmap showing the expression of DEG related to "muscle contraction" in skeletal muscle tissues. (c) Heatmap showing the expression of DEG related to "DEG related to "cell cycle" in skeletal muscle tissues.



Figure S9. Frequencies of the Luchuan promoter allele across different pig breeds. DUR: Duroc pig; LW: Large White pig; LD: Landrace pig; YM: Yucatan miniature pig; YNT: Tibetan pig (Yunnan); TC: Tongcheng pig; TT: Tibetan pig (Qinghai-Tibetan); HTDE: Hetaodaer pig; SCT: Tibetan pig (Sichuan); WZS: Wuzhishan pig; BMX: Bamaxiang pig; EHL: Erhualian pig; LUC: Luchuan pig; LWH: Laiwu black pig; MIN: Min pig (Shandong).







Figure S10. QC of ATACseq peaks. Heatmap of reads density around TSS for five tissues. **Figure S11. Muscle fiber differences between Duroc and Luchuan pigs.** Proportions of slow muscle fiber.



Figure S12. Knockdown and overexpression efficiency of *Tnnc1* **in C2C12 cells and in vivo.** (a) *Tnnc1* expression after siRNA knockdown in C2C12 cells. (b) *Tnnc1* expression after overexpression in C2C12 cells. (c) *Tnnc1* expression after in vivo siRNA knockdown in mouse skeletal muscle.

а

b

С





b

Figure S13. (a) Expression of *Ho-1* after overexpression of *Tnnc1*.(b) Expression of *Ho-1* after siRNA konckdown of *Tnnc1*. (c) Expression of *Ogg1* afteroverexpression of *Tnnc1*. (d) Expression of *Ogg1* after siRNA knockdown of *Tnnc1*.



Figure S14. (a). Expression of slow muscle (*Myh7*) and fast muscle (*Myh2*, *Myh4*, *Myh1*) markers after siRNA knockdown of *Sema3g* in mouse C2C12 cells (b). Measuring the same markers as (a) after overexpression of *Sema3g* in mouse C2C12 cells. (c). Choosing siRNAs with the best knockdown efficiency. (d). Evaluation of the overexpression efficiency. (e). Comparing the expression level of *Sema3g* before and after knocking down *Cebpa*. * represents p value < 0.05. ** represents p value < 0.01.