

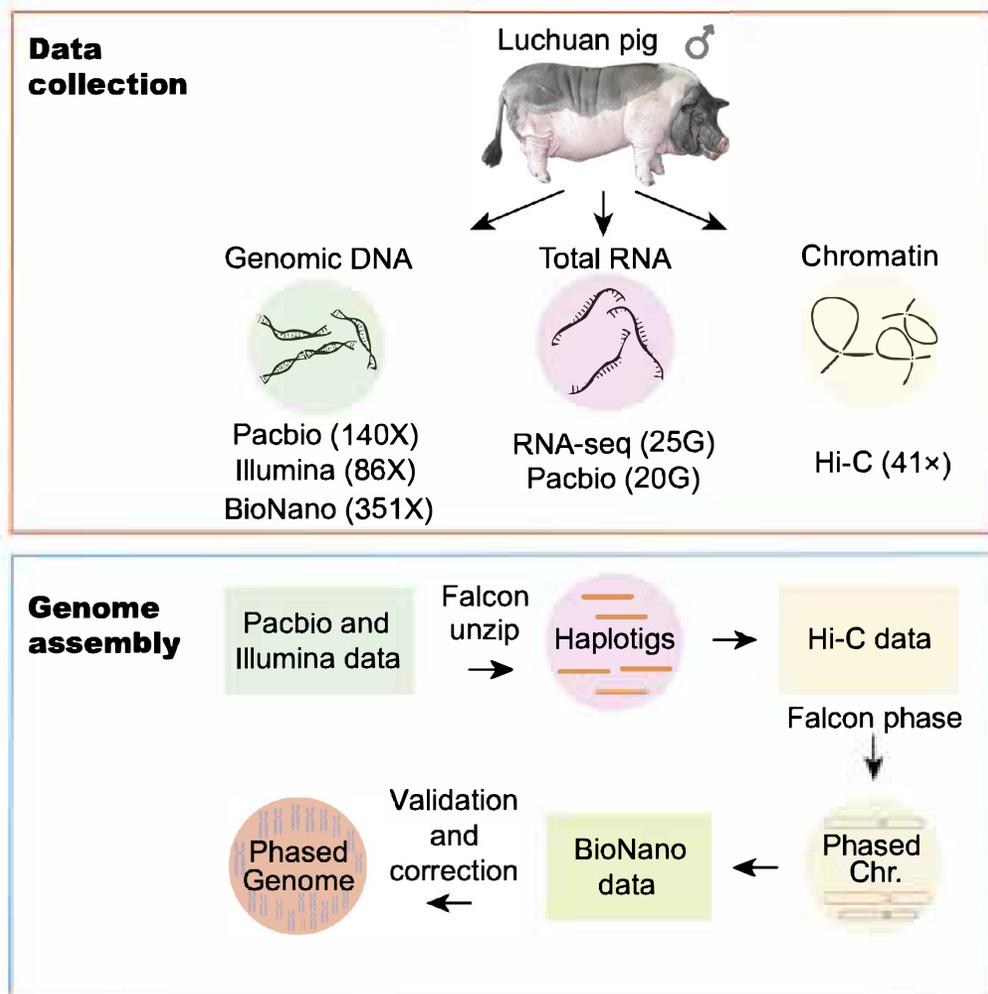
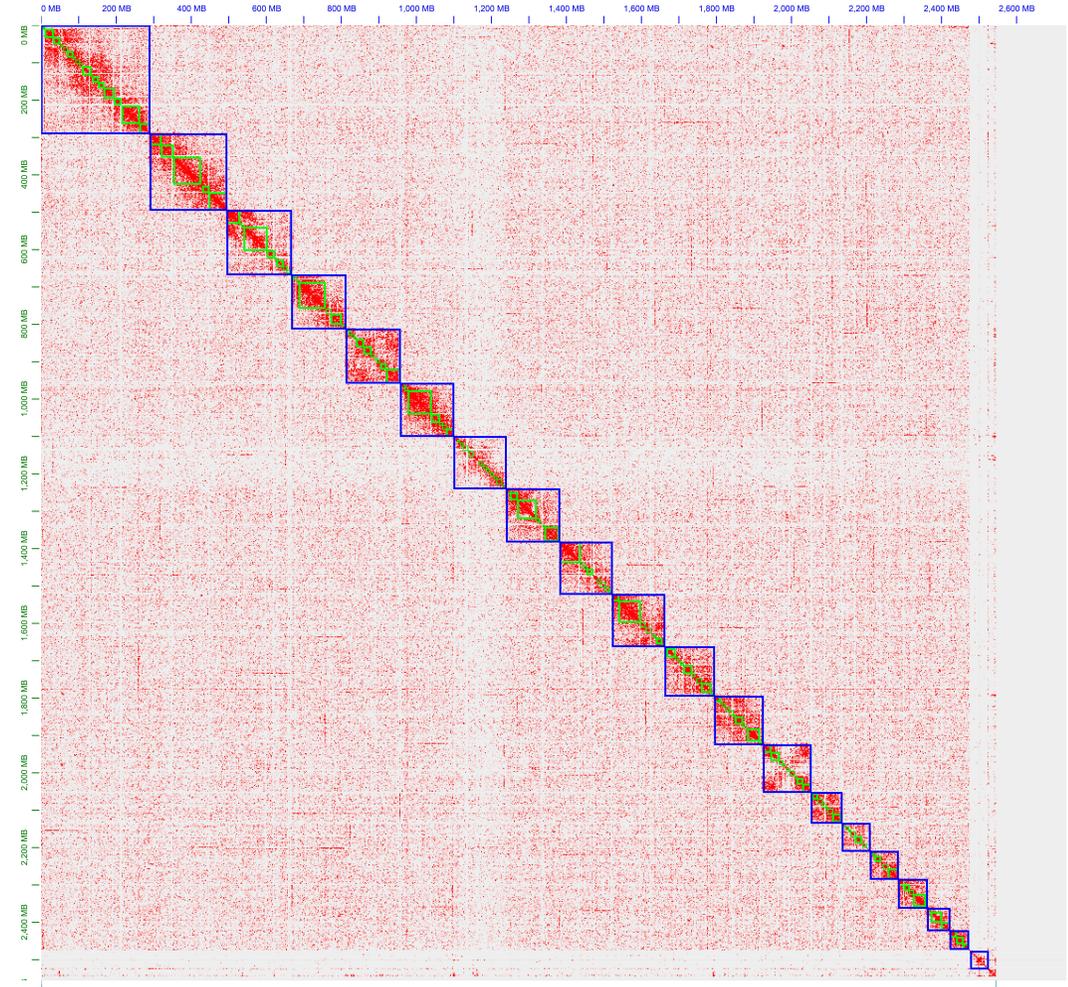
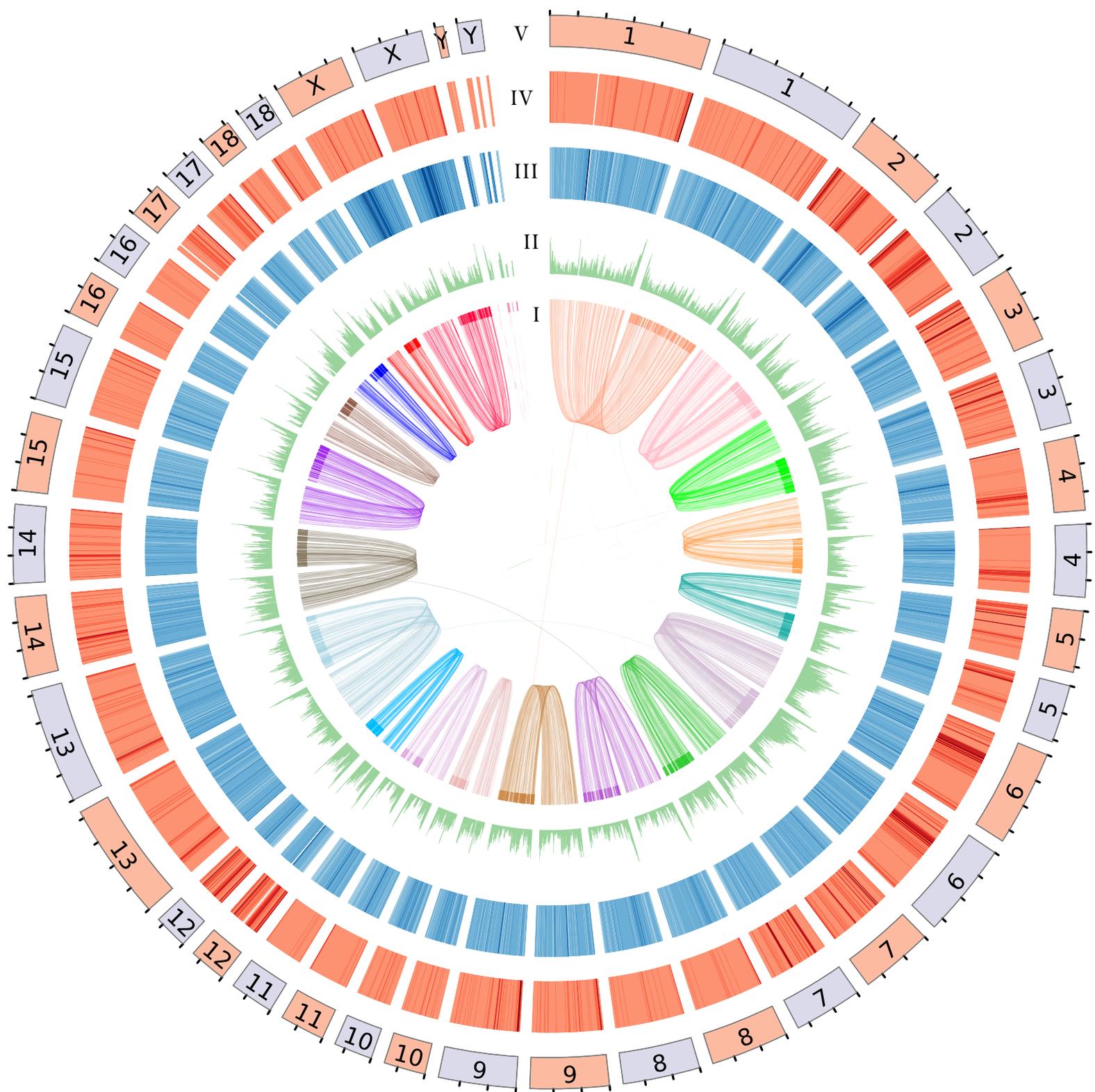
a**b**

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.

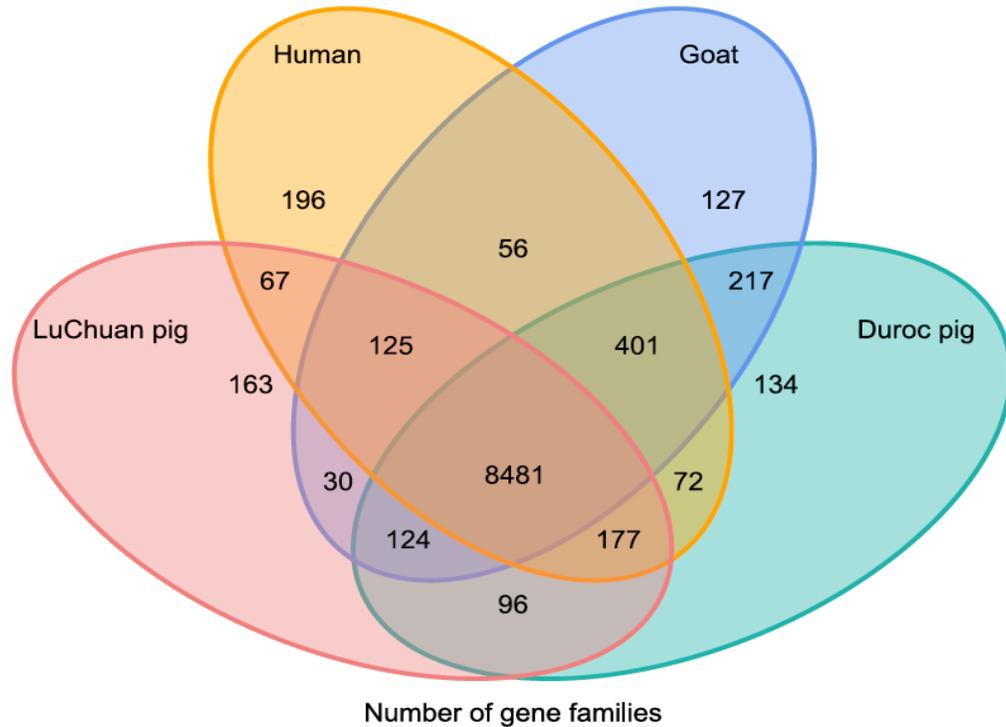
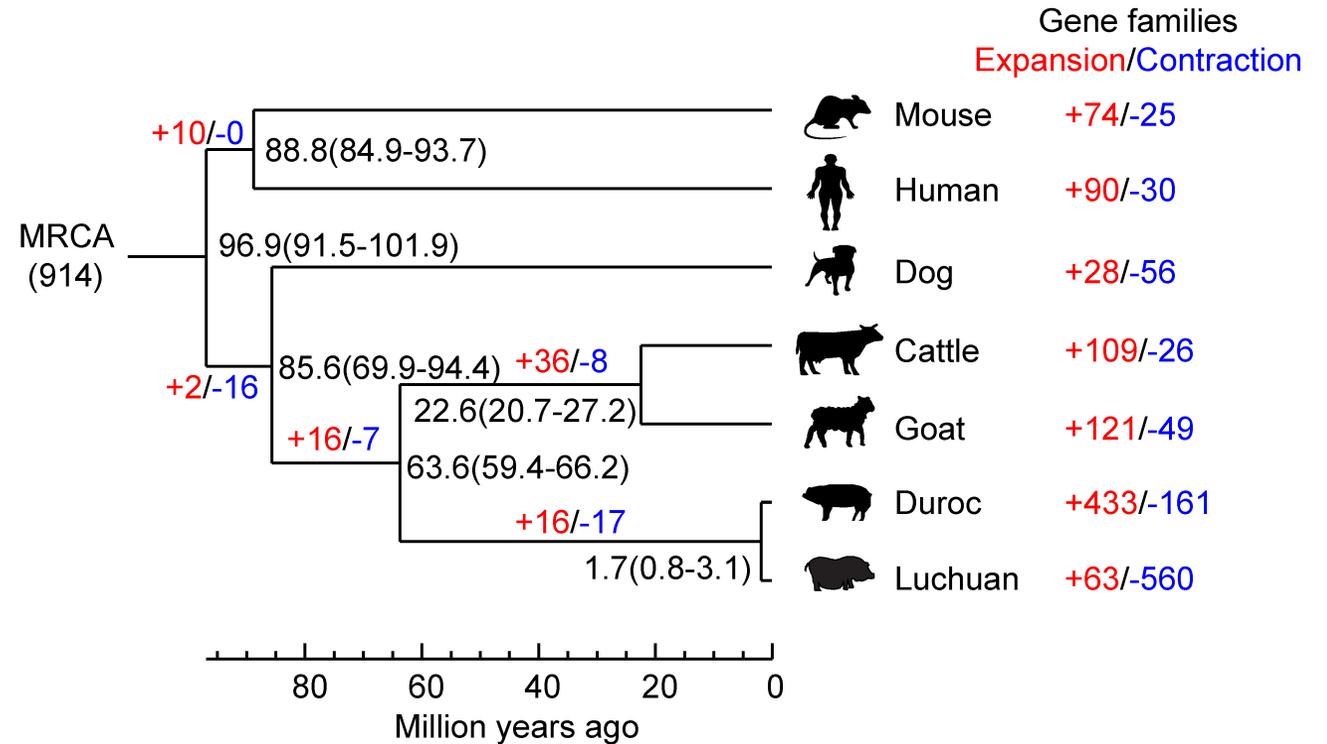
a**b**

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.

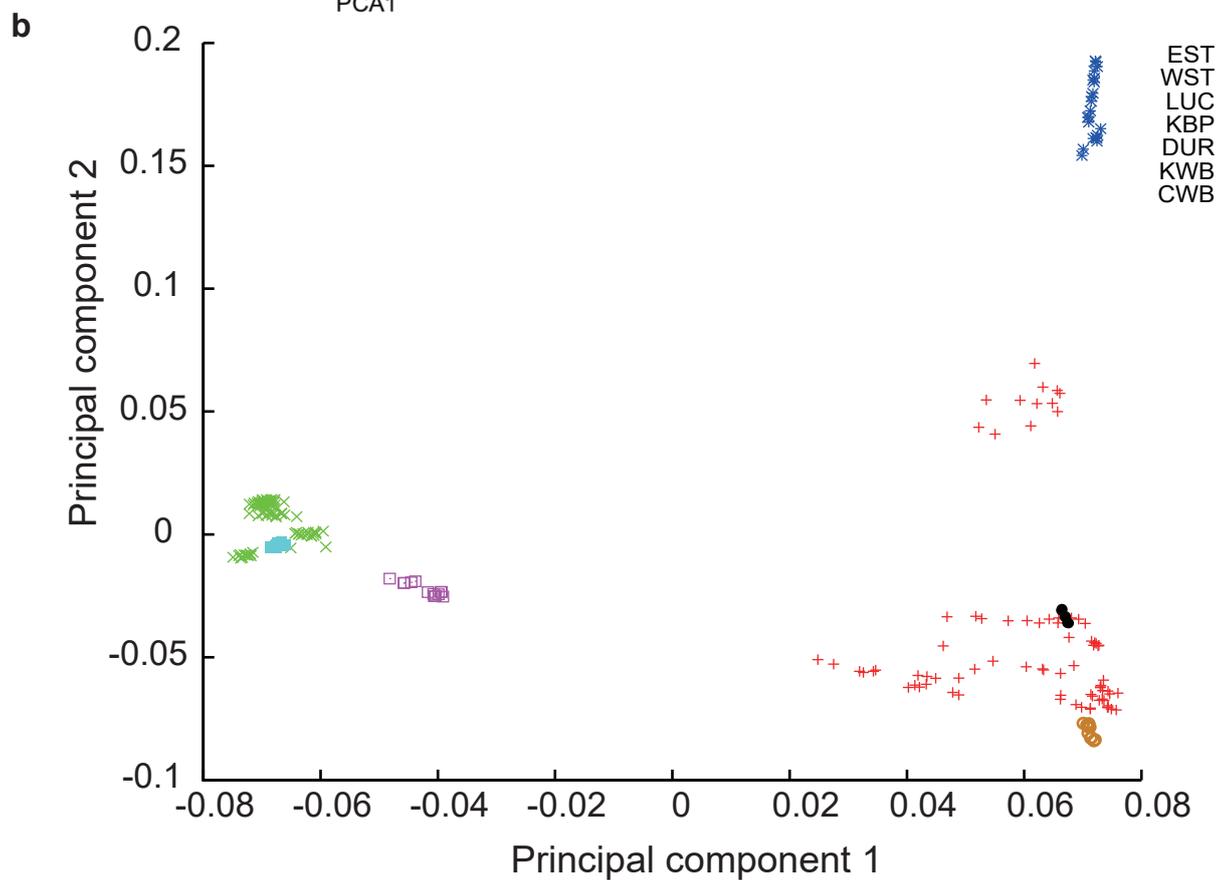
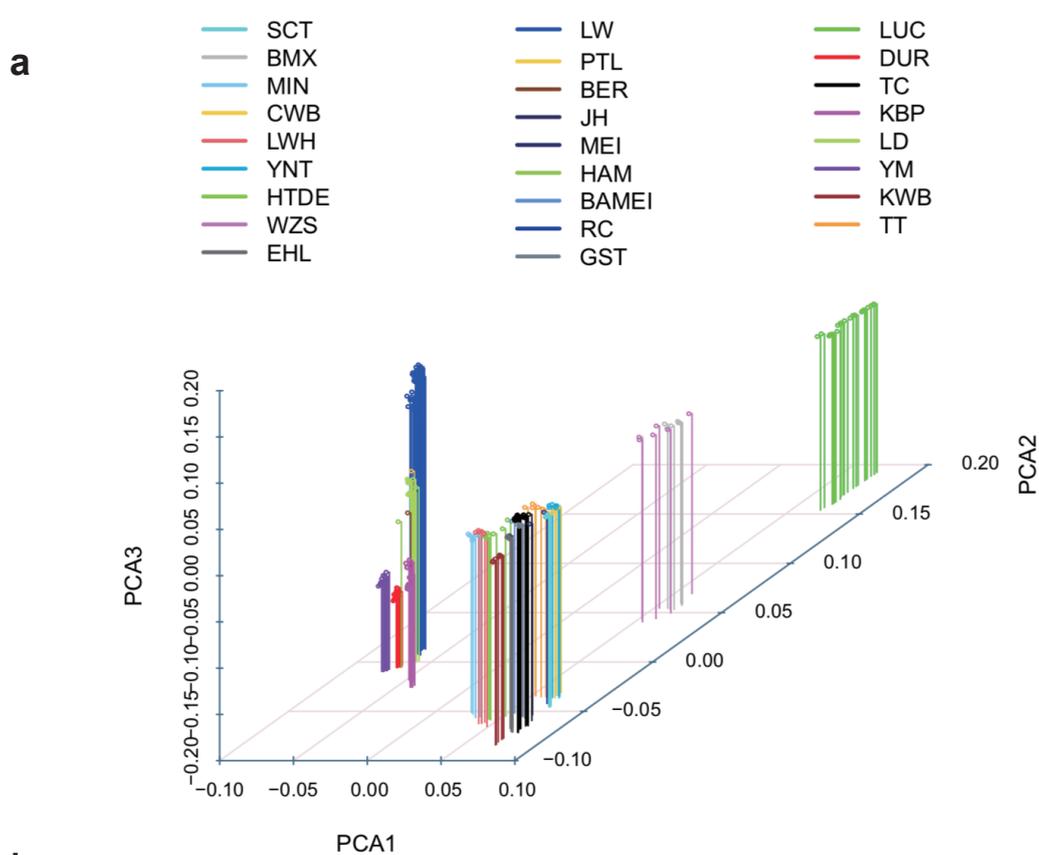


Figure S4. PCA plots. (a) PCA of the first three principal components. BAMEI, Bamei; BER, Berkshire; BMX, Bamaxiang; CWB, Chinesewild boar; DUR, Duroc; EHL, Erhualian; GST, Tibetan (Gansu); HAM, Hampshire; HTDE, Hetao; JH, Jinhua; KBP, Korean black pig; KWB, Korean wild boar; LD, Landrace; LUC, Luchuan; 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).

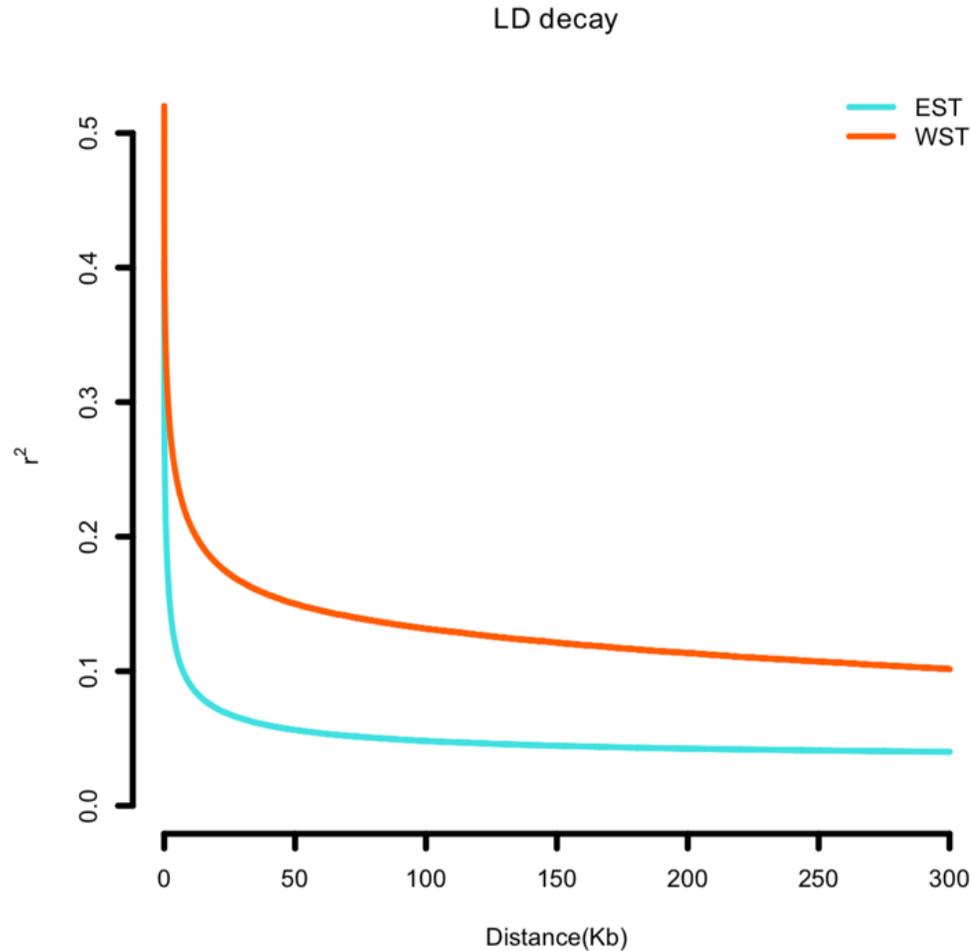
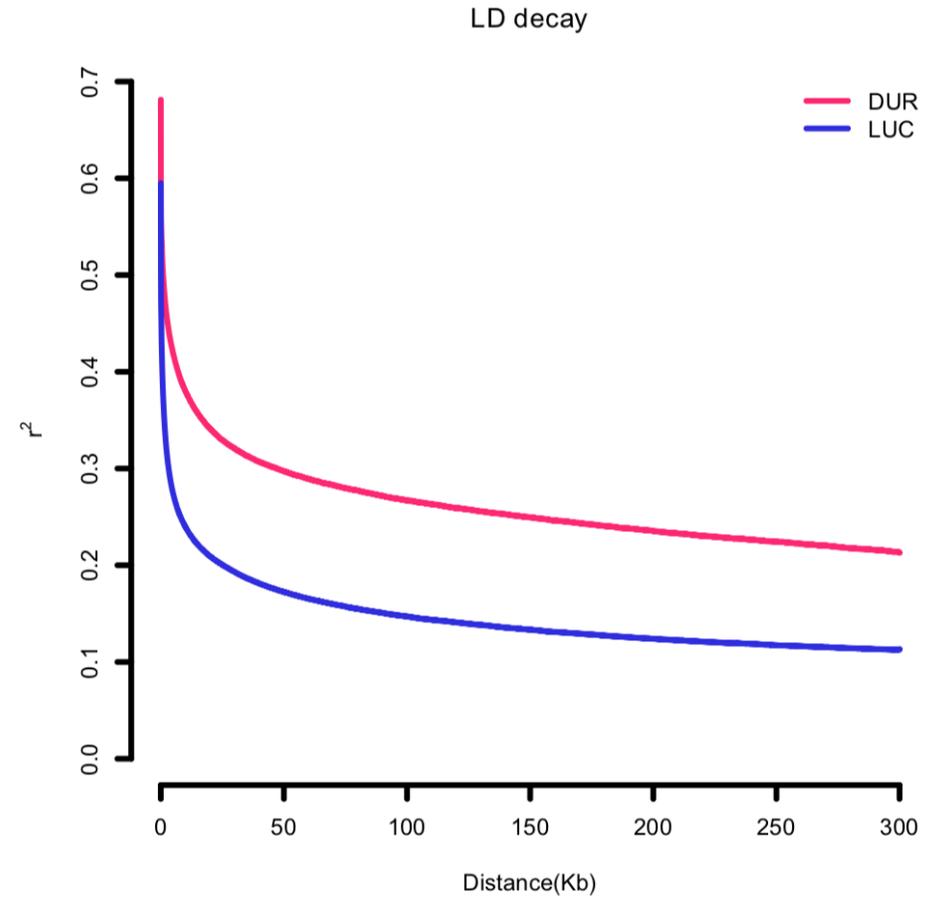
a**b**

Figure S5. LD decay analysis. (a) LD decay determined by squared correlations (r^2) 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.

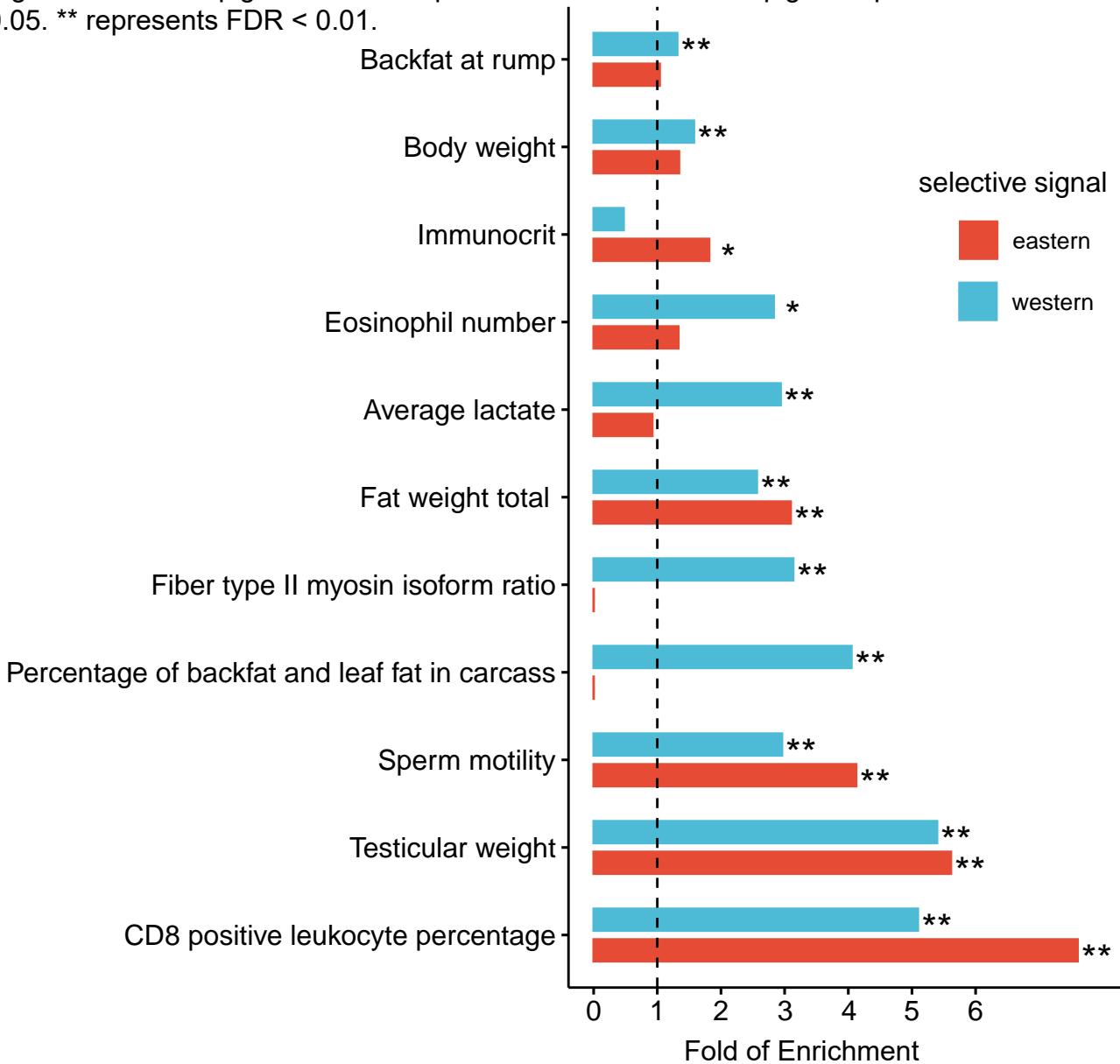


Figure S7.

Adipose_down

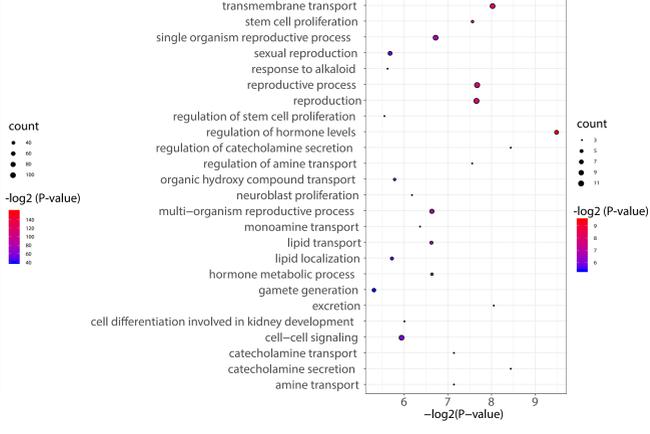
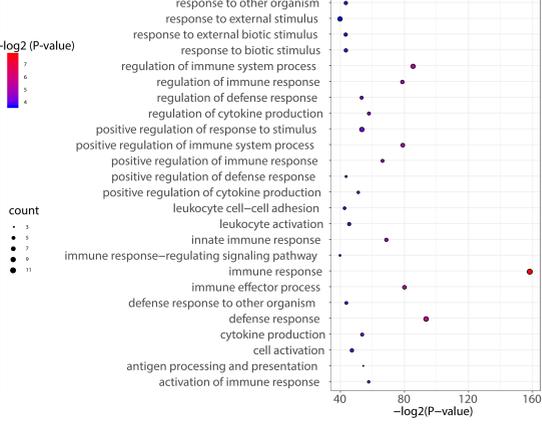
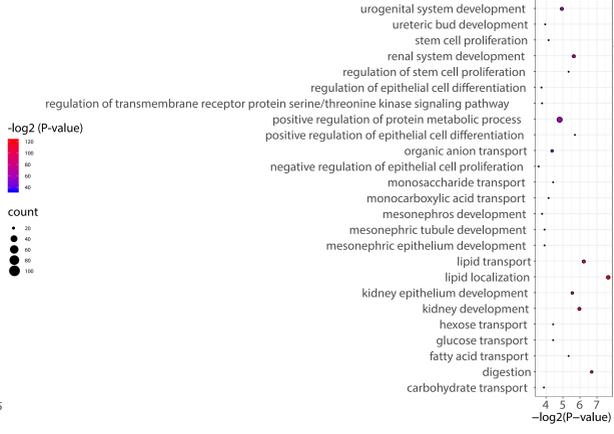
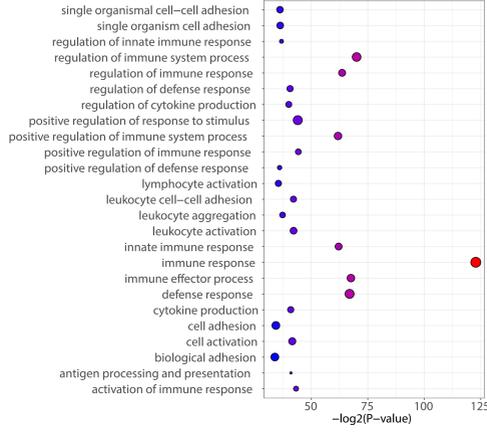
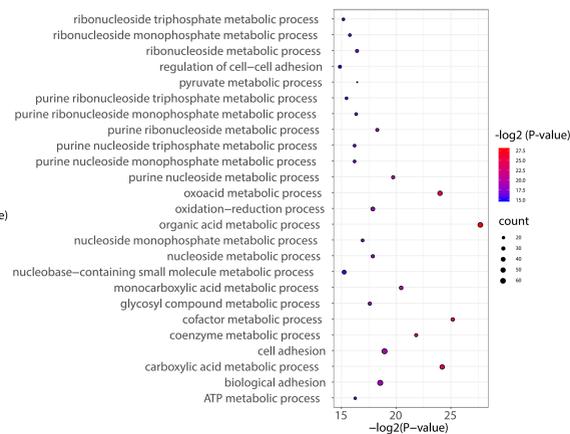
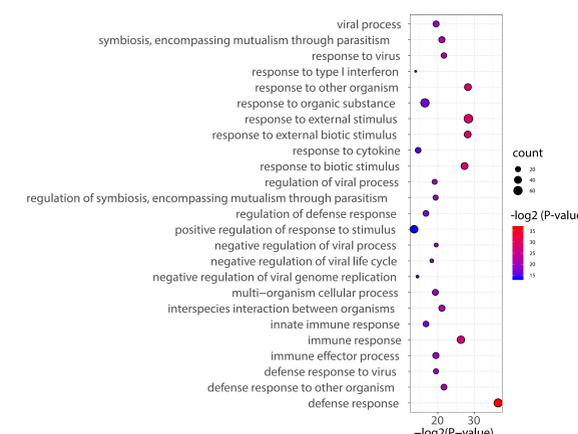
Adipose_up

Cerebellum_down

Cerebellum_up

Cerebrum_down

Cerebrum_up



Heart_down

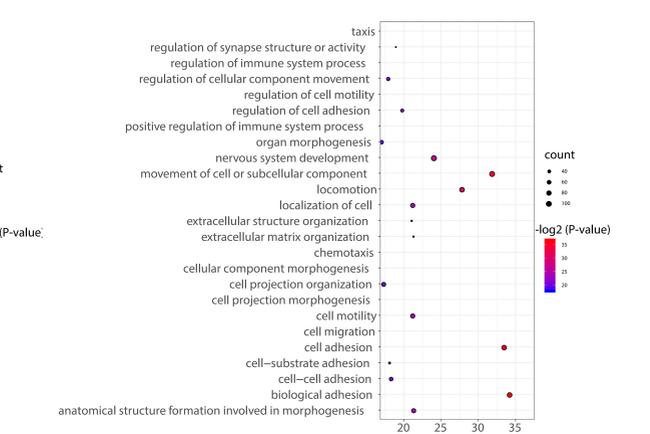
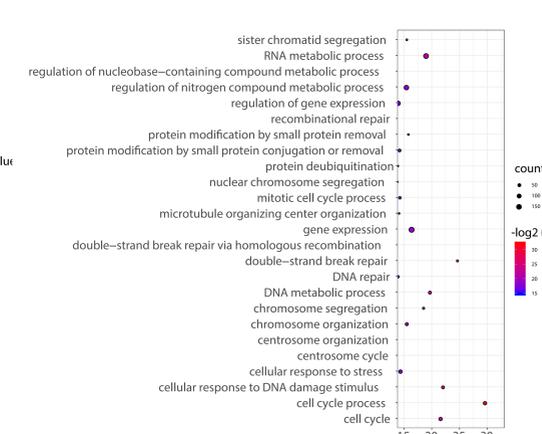
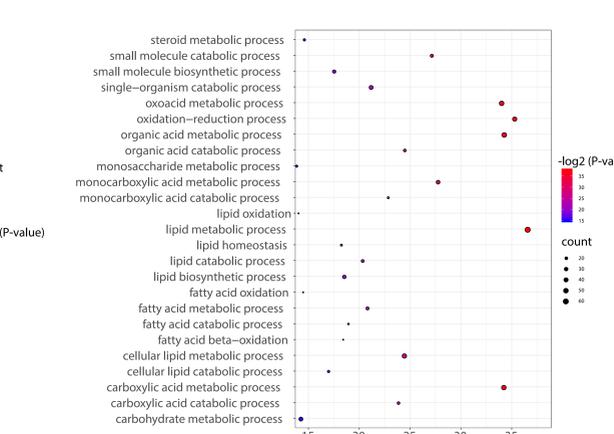
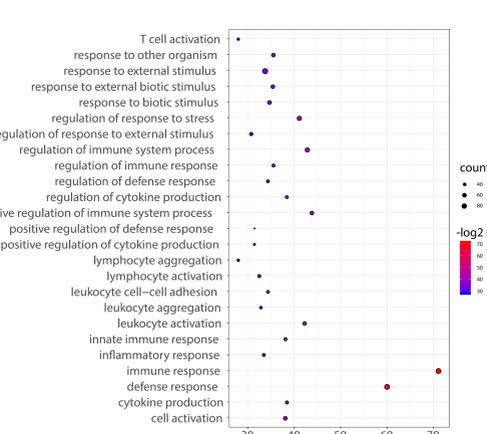
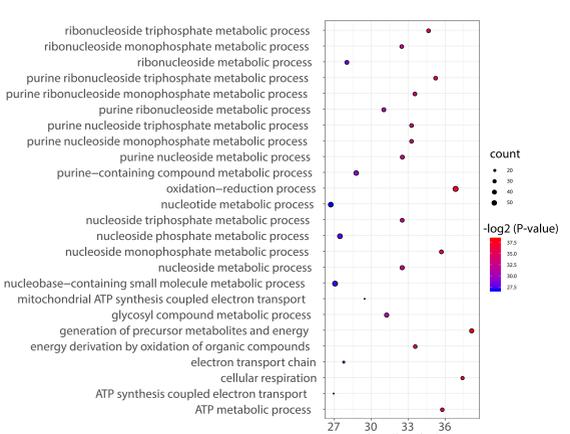
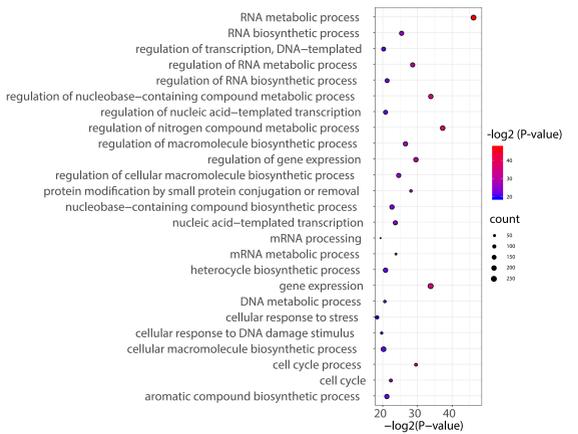
Heart_up

Liver_down

Liver_up

Lung_down

Lung_up



Muscle_down

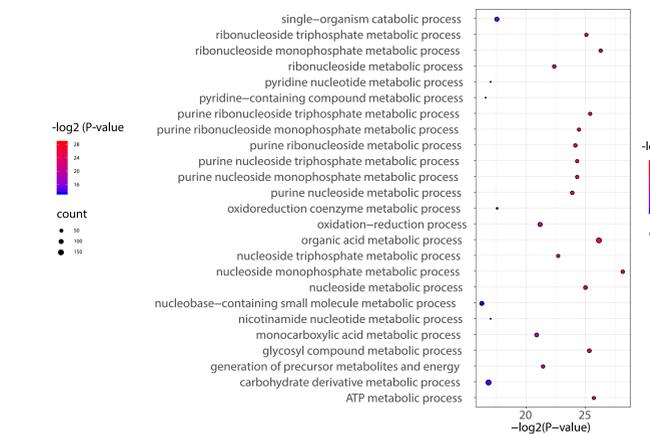
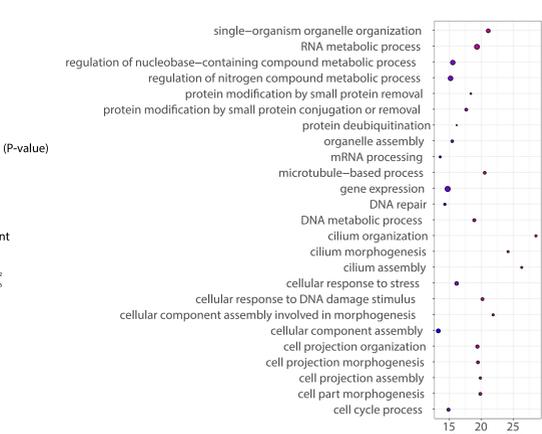
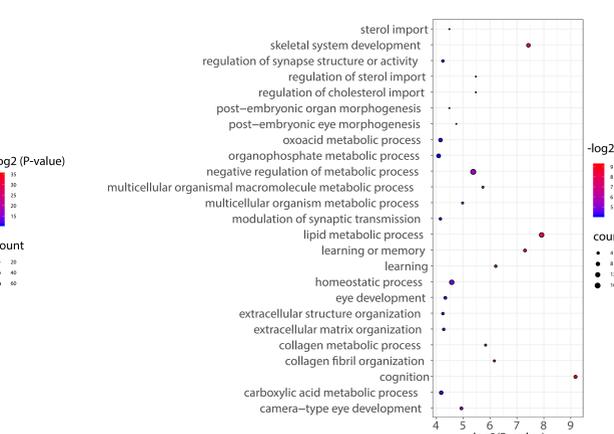
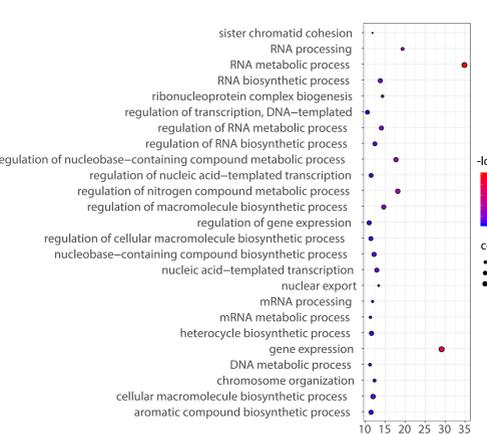
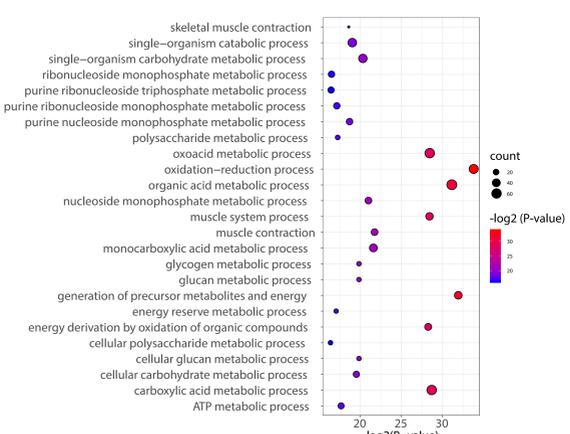
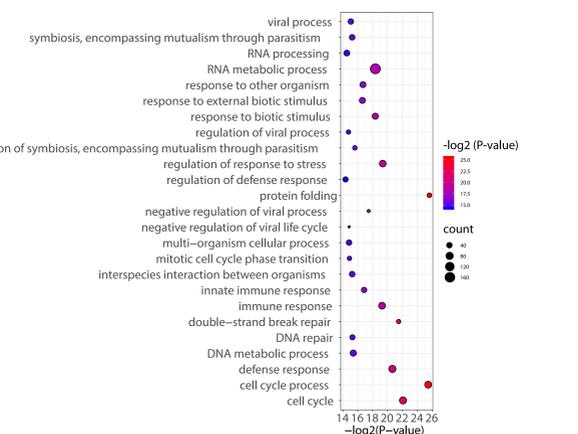
Muscle_up

Stomach_down

Stomach_up

Small intestine_down

Small intestine_up



GO Biological Process

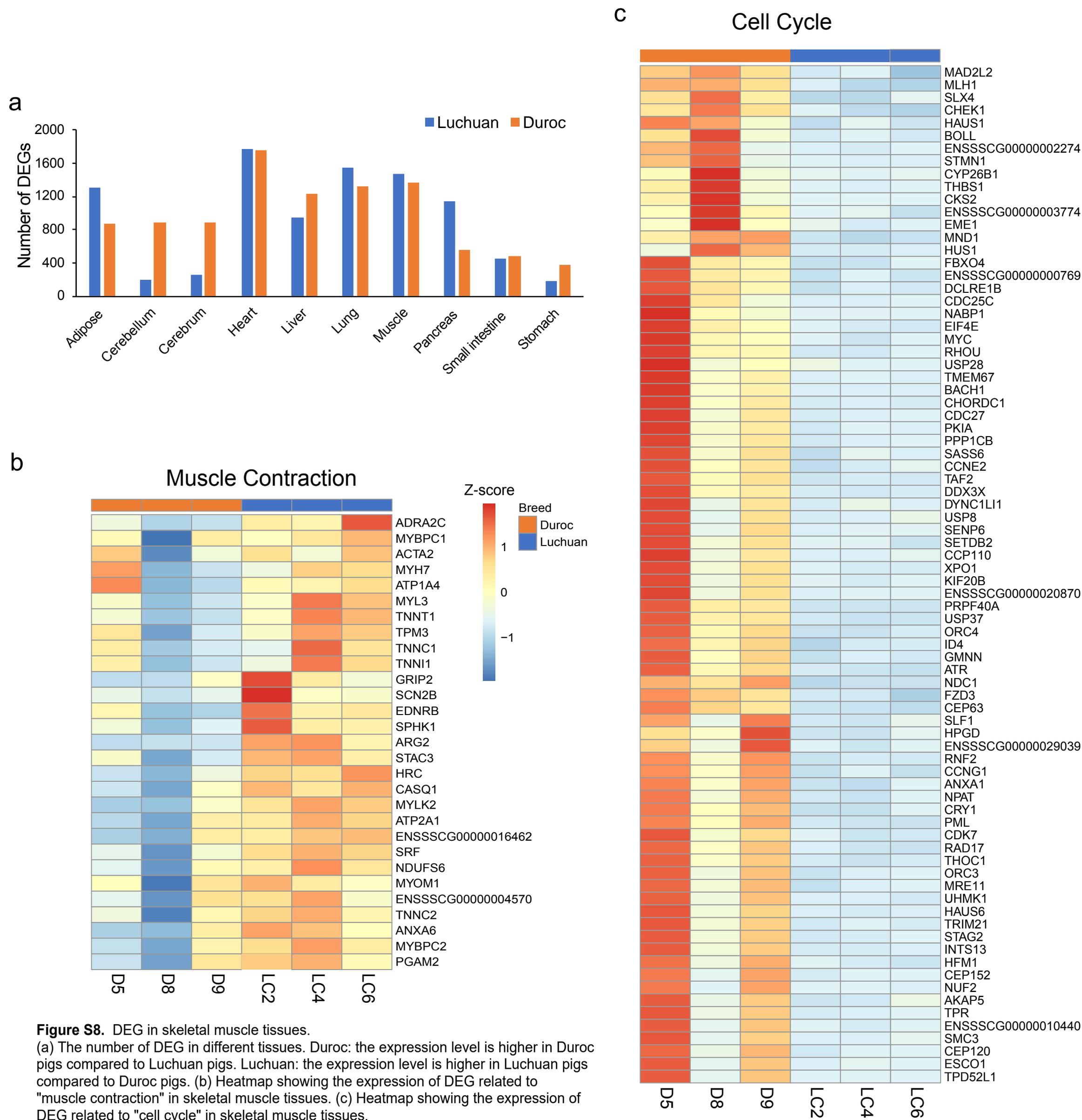
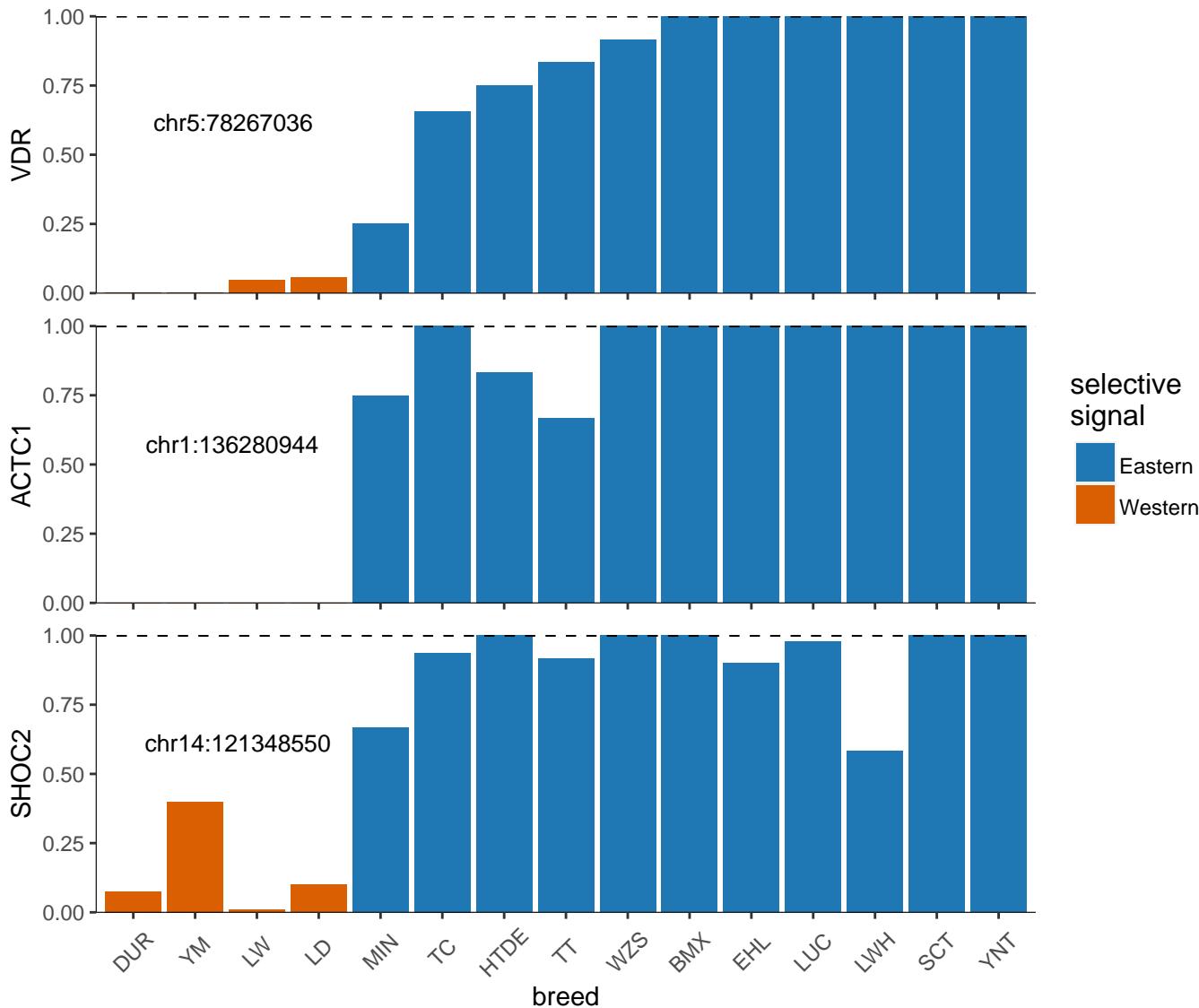


Figure S9. Frequencies of the Luchuan promoter allele across different pig breeds. DUR: Duroc pig; LW: Large White pig; LD: Landrace pig; YM: Yucatan miniature pig ; YNT: Tibetan pig (Yunnan); TC: Tongcheng pig; TT: Tibetan pig (Qinghai-Tibetan); HTDE: Hetaodaer pig; SCT: Tibetan pig (Sichuan); WZS: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



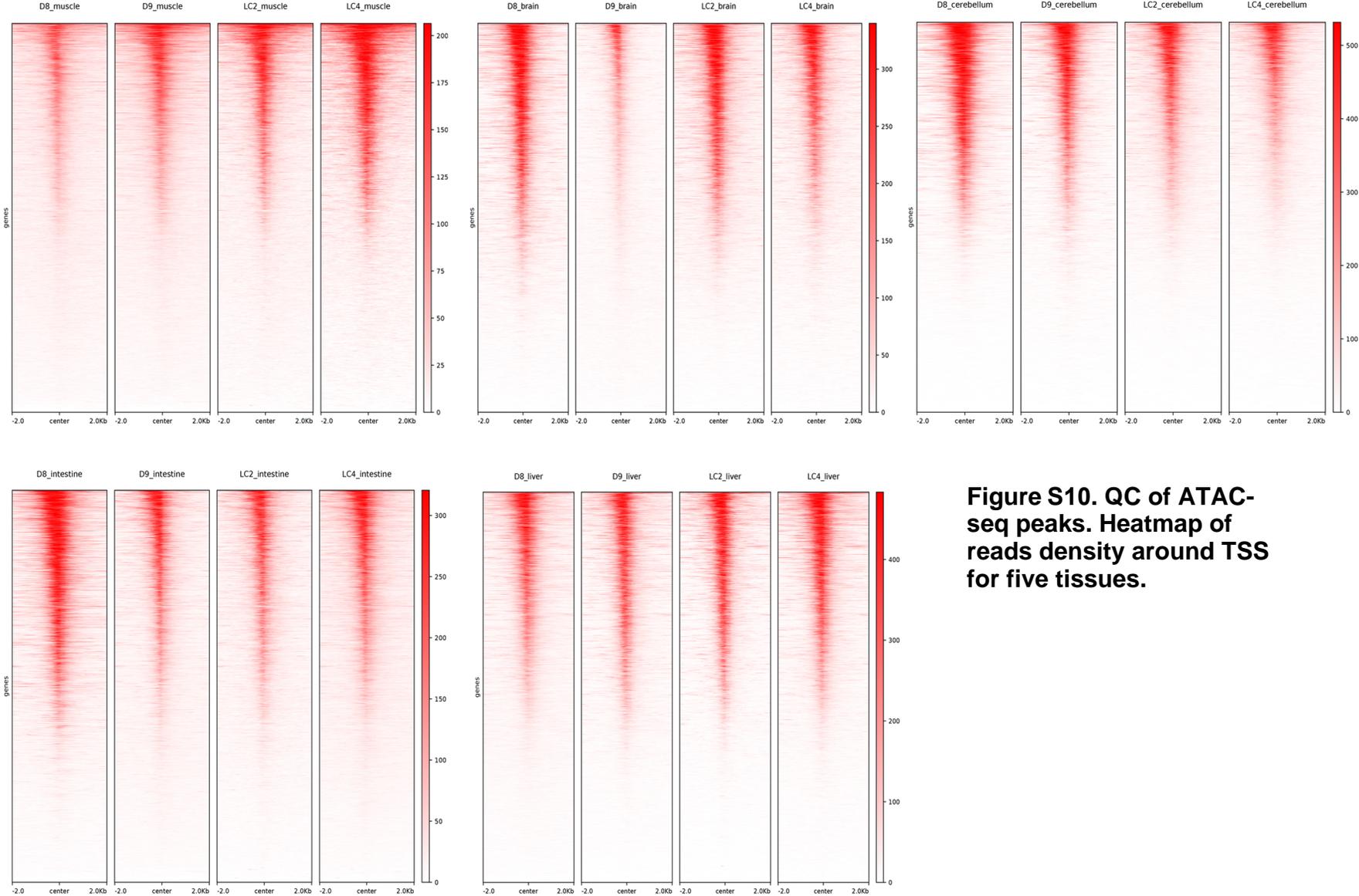


Figure S10. QC of ATAC-seq peaks. Heatmap of reads density around TSS for five tissues.

Figure S11. Muscle fiber differences between Duroc and Luchuan pigs.
Proportions of slow muscle fiber.

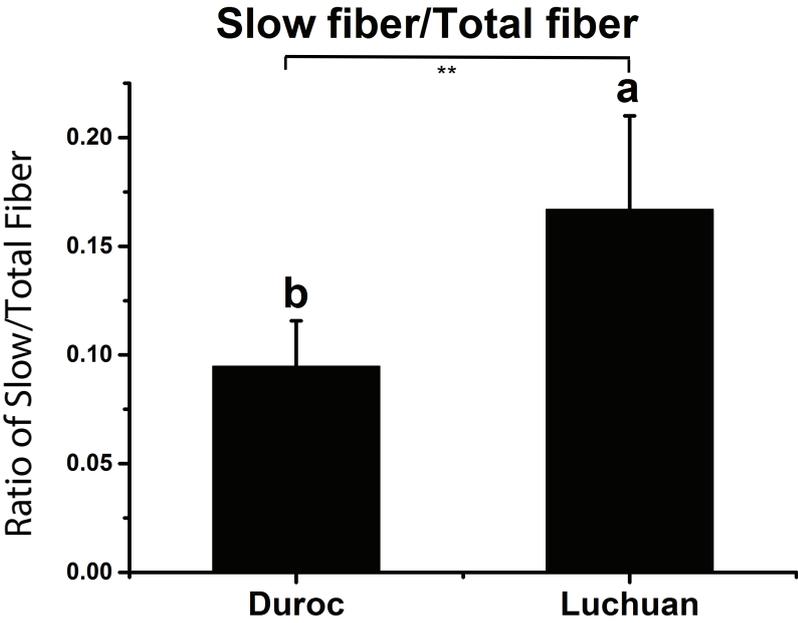
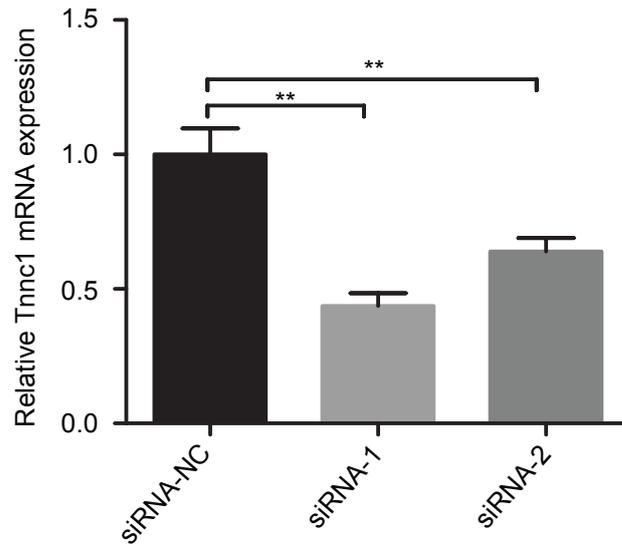
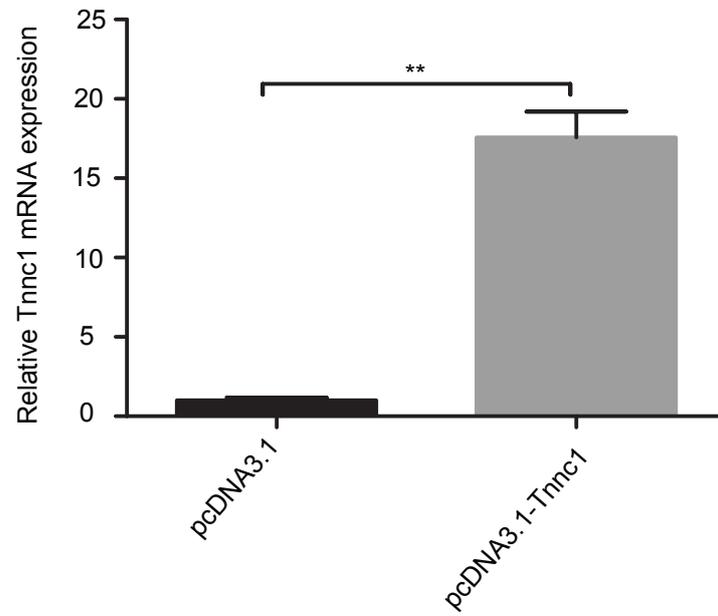


Figure S12. Knockdown and overexpression efficiency of *Tnnc1* in C2C12 cells and in vivo. (a) *Tnnc1* expression after siRNA knockdown in C2C12 cells. (b) *Tnnc1* expression after overexpression in C2C12 cells. (c) *Tnnc1* expression after in vivo siRNA knockdown in mouse skeletal muscle.

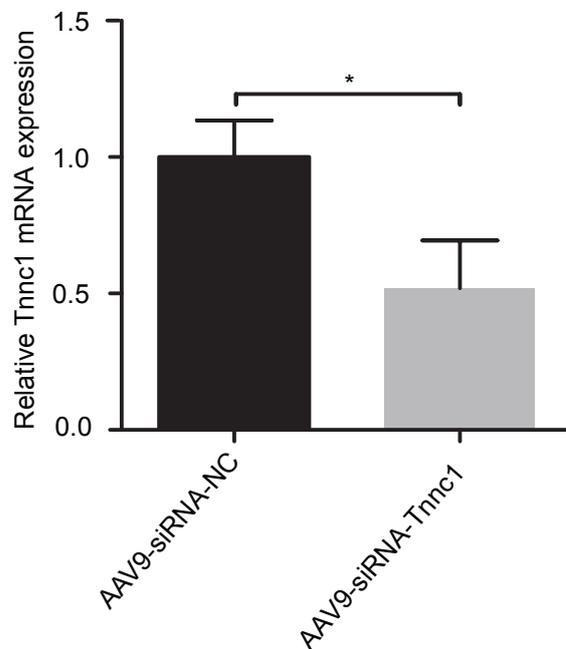
a



b



c



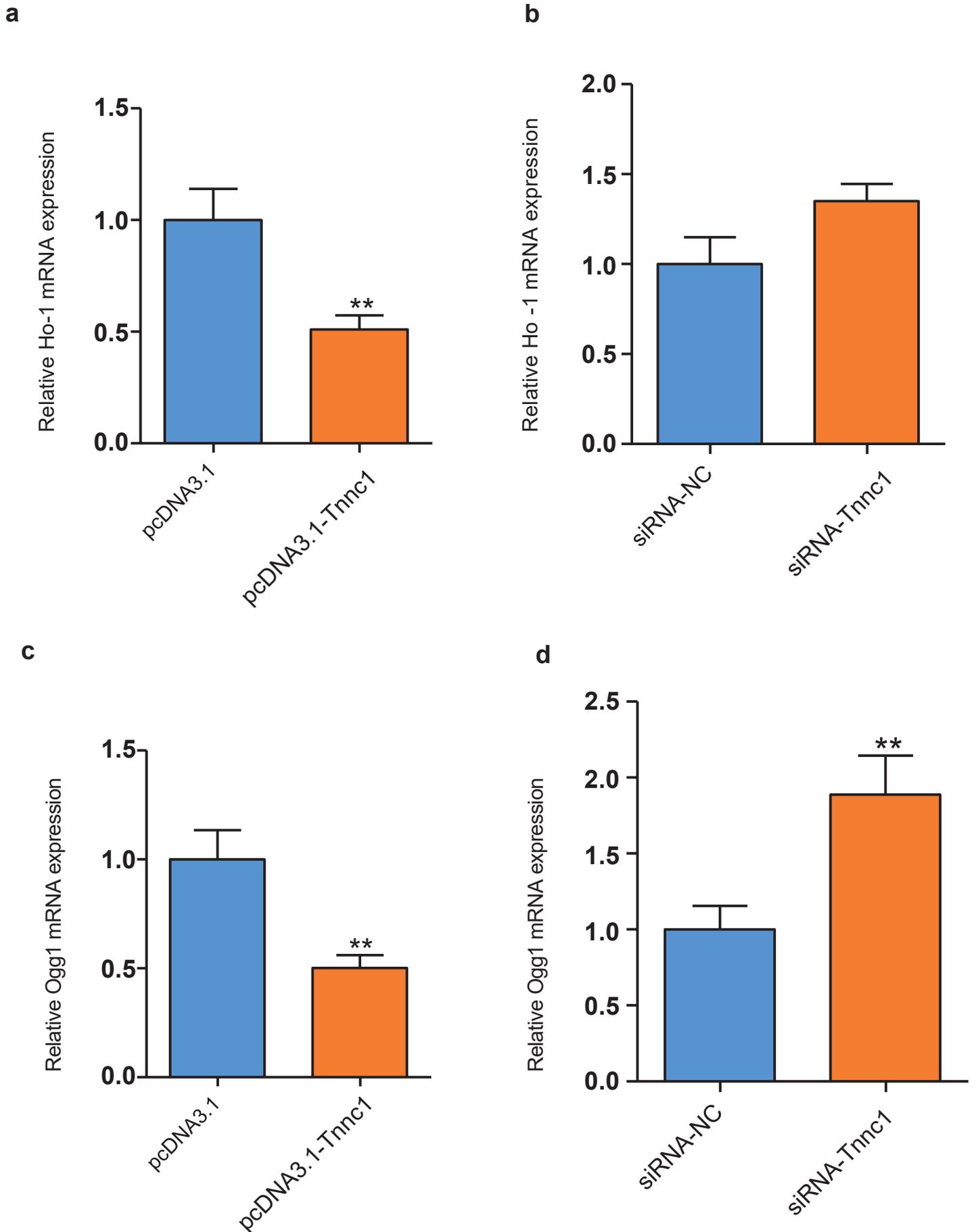


Figure S13. (a) Expression of *Ho-1* after overexpression of *Tnnc1*. (b) Expression of *Ho-1* after siRNA knockdown of *Tnnc1*. (c) Expression of *Ogg1* after overexpression of *Tnnc1*. (d) Expression of *Ogg1* after siRNA knockdown of *Tnnc1*.

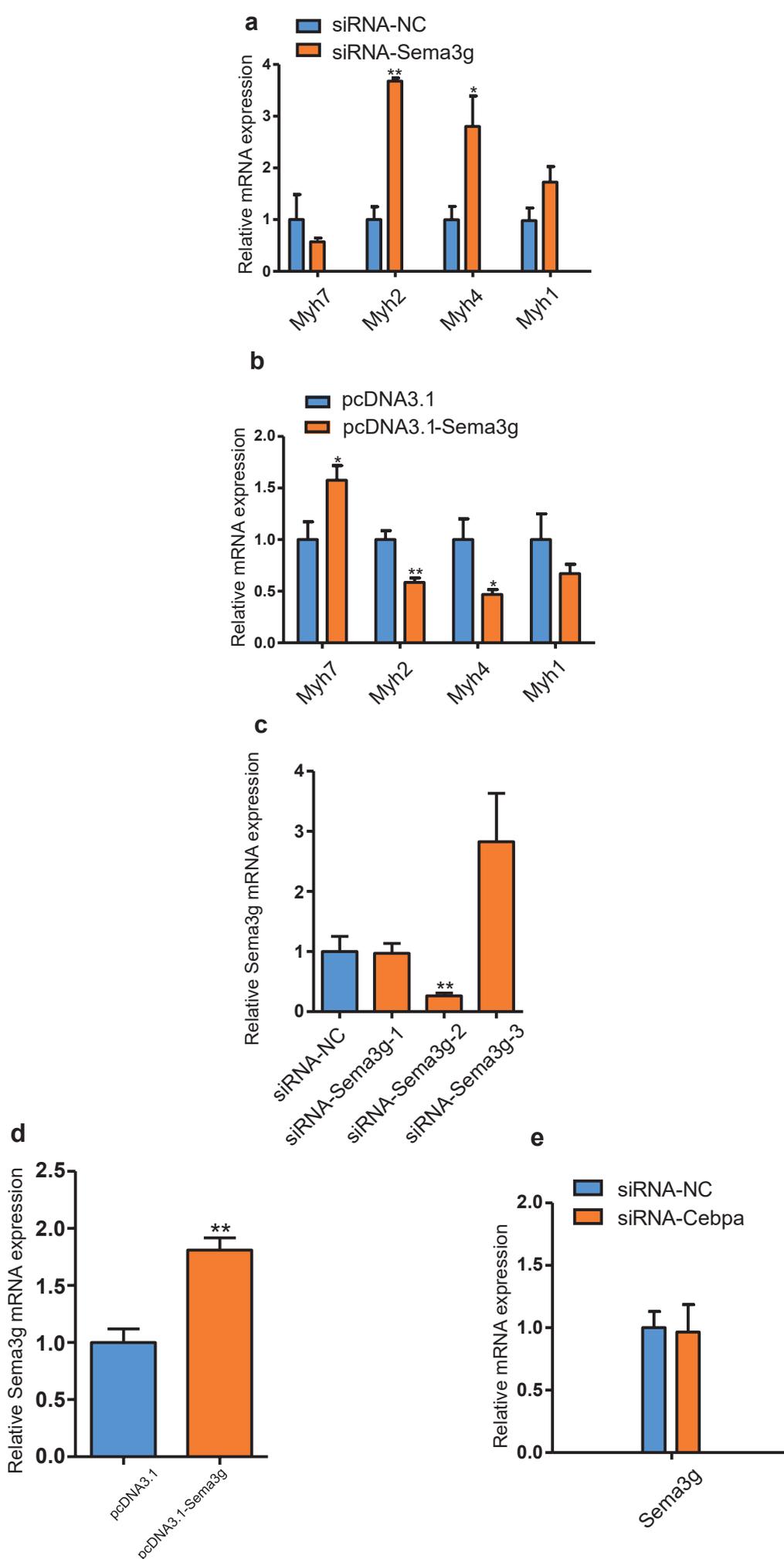


Figure S14. (a). Expression of slow muscle (*Myh7*) and fast muscle (*Myh2*, *Myh4*, *Myh1*) markers after siRNA knockdown of *Sema3g* in mouse C2C12 cells (b). Measuring the same markers as (a) after overexpression of *Sema3g* in mouse C2C12 cells. (c). Choosing siRNAs with the best knockdown efficiency. (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.