

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: **The number of unique mapped reads and filtered reads for ChIP-seq experiments.** “Filtered reads” indicates the mapped reads that removed low MAPQ reads (< 25), unmapped reads, mate unmapped reads, not primary alignments, reads failing platform, and duplicates.

File Name: Supplementary Data 2

Description: **Quality control values for ChIP-seq experiments.** “NSC” represents normalized strand cross-correlation coefficient. “RSC” represents relative strand cross-correlation coefficient. “FRiP” represents fraction of all mapped reads that fall into the called peak regions.

File Name: Supplementary Data 3

Description: **The tissue-specific expressed genes identified in pig tissues.**

File Name: Supplementary Data 4

Description: **The top 5 GO terms of tissue-specific genes relevant to function of corresponding tissues.** The *P*-values were calculated by a two-side modified fisher exact test without adjustments.

File Name: Supplementary Data 5

Description: **The information of newly identified transcripts in pig.**

File Name: Supplementary Data 6

Description: **The tissue-specific expressed enhancers identified in pig tissues (susScr11.1 reference genome assembly).**

File Name: Supplementary Data 7

Description: **The top 5 GO terms of tissue-specific enhancers relevant to function of corresponding tissues.** The twoside binomial statistic method without adjustment was adopted to calculate the *P*-value.

File Name: Supplementary Data 8

Description: **The enhancers conserved with VISTA enhancers.**

File Name: Supplementary Data 9

Description: **Significantly differential expressed genes from four pig breeds.** The two-side Wald statistics test with FDR adjustment was adopted to identify the significantly differential expression genes.

File Name: Supplementary Data 10

Description: **Pig-human rearranged TAD of head and face phenotype related gene, Related to Figures 5G and 5H.**

File Name: Supplementary Data 11

Description: **The HPO of human genes in the pig-human rearranged TADs.** A two side thypergeometric test were adopted to estimate the *P*-value.

File Name: Supplementary Data 12

Description: **The information of primer and genomic location of reporter assay.**