Description of Additional Supplementary Files

Supplementary Data 1: The information of the samples used in this study.

Supplementary Data 2: 12 detected OMIA variants in the 1KCIGP dataset.

Supplementary Data 3: The 262 public samples were used to evaluate 1KCIGP imputation performance.

Supplementary Data 4: 106 additional public samples were used for population structure and introgression analyses.

Supplementary Data 5: The result of f_4 statistic to detect admixture between European domestic pigs and Chinese domestic pig populations.

Supplementary Data 6: The enriched KEGG pathways for 225 genes located in the introgression regions from ET to European domestic pigs.

Note: The KEGG enrichment analyses were performed with KOBAS. The P value was calculated using a hypergeometric distribution. False discovery rate (FDR) correction was performed to adjust for multiple testing. Pathways with an FDR-corrected P value of < 0.05 were considered statistically significantly enriched.

Supplementary Data 7: The result of f_4 statistic to detect admixture among Chinese domestic pig populations.

Supplementary Data 8: The expected frequency of European Y chromosomes in Chinese domestic pig populations.

Supplementary Data 9: The breed information is used for the selection signature detection of different traits.

Supplementary Data 10: Overlapped regions under selection of high-altitude adaptation population.

Supplementary Data 11: Overlapped regions under selection of large ear size population.

Supplementary Data 12: Overlapped regions under selection of small body size population.

Supplementary Data 13: The phenotypes collected for the Chinese domestic pigs in this study.

Supplementary Data 14: The GWAS results of biological traits.

Note: P-values are derived from two-sided statistical tests. Only loci with P-values smaller

than the Bonferroni-corrected significance threshold of P = 2.29×10^{-9} are shown in the table.

Supplementary Data 15: The public long-reads are used to validate SVs.

Supplementary Data 16: SV validation.

Supplementary Data 17: 36 genes overlapped to the SVs had high LD with tag SNPs.

Supplementary Data 18: The 277 TWBSVs.

Supplementary Data 19: 104 genes affected by TWBSVs.

Supplementary Data 20: The primer information of SVs related to *CASP10*, *NAV2*, and *POLD3* genes.