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Supplementary Information

**Human-mediated admixture and selection shape the diversity on the
modern swine (*Sus scrofa*) Y chromosomes**

26

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104 **1. Supplementary Notes**

105 **Note S1. The quality of SNP calling**

106 We employed BWA to map cleaned reads from 205 samples to Build 11.1 of the *Sus*
107 *scrofa* reference genome and subsequently used Picard and GATK to process the
108 mapped reads. Then we performed a two-round procedure of SNP calling using
109 Platypus (detailed process in **supplementary methods**). Finally, a total of 37,542,852
110 SNPs for the 205 animals were obtained, of which 36,332,442, 1,167,598, 42,288 and
111 524 SNPs were on autosomes, the X chromosome, the Y chromosome and the
112 mitochondrial DNA, respectively.

113 There were two Sumatran wild boars, one Celebes wild boar, one Java warty pig and
114 one African warthog in the present 205 samples. We identified that Sumatran wild boars
115 were largely different from Eurasian pigs. The other three animals were outgroups to
116 *Sus scrofa*, which have many specific SNPs different from *Sus scrofa*.

117 To assess accuracy of the SNP calls, we excluded the above five animals and
118 compared the 200-pig SNP dataset to the SNPs on the porcine 60K BeadChip
119 genotyping array (Illumina) in 98 pigs (**supplementary table S2**). Among the SNPs
120 called from whole-genome resequencing, 53,908 polymorphic loci present in the 60K
121 chip array were extracted. 99.4% of informative SNPs had the same genotypes in the
122 sequencing data as in the 60K chip arrays (**supplementary fig. S1**). In addition, we
123 sequenced six pigs twice and called their SNPs using Platypus. We find that 99.6% were
124 consistent with the SNPs of their duplicate individuals (**supplementary fig. S1**). Both
125 validations demonstrated high quality and reliability of our present SNP calls.

126 We compared our SNP dataset of 200 Eurasian pigs with Build 151 of the *Sus scrofa*
127 dbSNP dataset from the NCBI database. We found that 81.3% (29,554,672) of the SNPs
128 on autosomes were exactly the same as the reference SNPs and 18.7% (6,777,770) were
129 novel (**supplementary fig. S2 and supplementary table S3**). Among these novel

130 SNPs, 53.0% (3,594,384 SNPs) have MAF less than or equal to 0.05 in the 200 Eurasian
131 pigs. Of the 36.3 million SNPs, 14.2% have minor allelic frequency (MAF) less than
132 or equal to 0.02, 33.2% have MAF less than or equal to 0.05, 49.4% have MAF less
133 than or equal to 0.10, and 50.6% have MAF greater than 0.10.

134 **Note S2. The coverage of the Y chromosome**

135 The Y chromosome is notorious for being hard to assemble, with potentially multiple
136 segmental duplications. Recently, a draft assembly of the pig Y chromosome (VEGA62)
137 were generated by sequencing BAC and fosmid clones from the Duroc breed and
138 incorporating information from optical mapping and fiber-FISH (Skinner et al. 2016).
139 The improved porcine sex chromosomes were included in Build 11.1 of the *Sus scrofa*
140 reference genome with comprehensive gene annotation and variant information. These
141 improved assemblies allowed us to generate a comprehensive analysis of the
142 evolutionary history of pigs from the perspective of sex chromosomes, especially from
143 the unique genetic perspective of patrilineal inheritance. Before further analyses, we
144 investigated the landscape of the Y chromosome in the perspective of coverage and
145 depth.

146 In Build 11.1 (VEGA62 version), the total length of the Y chromosome is 43.5Mb,
147 but the actual effective length is 20.5 Mb, which is mainly divided into three segments:
148 0 Mb - 10.5 Mb, 19.5 Mb - 25.5 Mb, 39.5 Mb - 43.5 Mb. In addition, there is a 1.6Mb
149 unplaced Y chromosome sequences contained in Build 11.1.

150 The observed coverage on the Y of certain individual is as expected given the
151 haploid status of the Y and the observed genome-wide coverage for that individual. We
152 calculated the depth of each base covered on the Y chromosome. In the whole effective
153 range (including the unassembled region), the average number of bases across all males
154 is 16,300,379. The average depth (median) is 12X. 13,998,561 bases are with depth
155 greater than or equal to 5X, which accounted for 85.9% of the valid sequences.

156 1,925,952 bases are more than or equal to 2 times of the average depth, accounting for
157 11.8% of the effective sequence, mainly distributed in the HSFY (heat shock
158 transcription factor, Y chromosome) and the PB (proximal block) regions. The average
159 depth in a 100Kb window sliding along the Y chromosomes with a step size of 50Kb
160 across all 103 individuals was plotted (**supplementary fig. S3A**). We also extracted
161 chromosome 18 as the representative of autosomal and drew the corresponding depth
162 map (**supplementary fig. S3B**). The average ratio of Y chromosome depth to those of
163 chromosome 18 across Eurasian male individuals was 0.51 with a standard deviation
164 of 0.047 (**supplementary fig. S3C**). These results show that the coverage of the Y in
165 general is consistent with its haploid state.

166 There are many heterozygous sites observed on the Y, which results from segmental
167 duplications and possible mapping error. We initially obtained a total of 81,057 SNPs.
168 The distribution of heterozygotes is shown in **supplementary fig. S4A**. Furthermore,
169 we use a 150Kb window sliding along the Y chromosome to calculate the
170 heterozygosity rate on the Y (**supplementary fig. S4C**). The heterozygosity rate
171 fluctuates very little in the homologous region of Y chromosome (PAR) and fluctuate
172 greatly in HSFY and PB regions. This disorderly volatility is an indicative of segmental
173 duplications. Subsequently, 12670 SNPs on Y chromosome and on the Y-linked contig
174 of male individuals, which were same as the SNPs called by the reads of female
175 individuals misaligned to Y chromosome reference sequence, were excluded due to the
176 possible bias. We also drew a map showing the distribution of heterozygous loci, the
177 distribution of SNPs, and the change of the heterozygosity rate on Y chromosome after
178 this filtering procedure (**supplementary fig. S5**). Moreover, we found the number of
179 heterozygous sites within Haplogroup A (8748.40 ± 762.08) is significantly larger than
180 that of Haplogroup E (European pigs and Chinese pigs: 6062.68 ± 993.63 and 6903.83

181 ± 704.87 , respectively) with *P* values of $1.05E-17$ and $3.19E-07$, respectively
182 (**supplementary fig. S6**). We specifically extract MSY data from that of the whole Y
183 sequences. We found the number of heterozygous sites within Haplogroup A (5516.38
184 ± 691.31) is significantly larger than that within Haplogroup E (European pigs and
185 Chinese pigs: 2904.61 ± 334.49 and 3146.33 ± 372.40 , respectively) with *P* values of
186 $5.76E-40$ and $1.21E-16$, respectively. The number of heterozygous sites within
187 Haplogroup E (European pigs) and Haplogroup E (Chinese pigs) is not significantly
188 different (**supplementary fig. S7**). When it comes to heterozygous SNPs, we replaced
189 them with missing data on the non-homologous part of Y chromosome for subsequent
190 analyses.

191 The depth of the effectively covered region in the PB interval (19.5 Mb - 25.5 Mb,
192 with grey background in **supplementary fig. S3D**) of individuals within Haplogroup E
193 is abnormally high, while those within Haplogroup A is relatively in a normal range.
194 We calculated the average depth and the average normalized depth in the PB interval.
195 The average depth in PB interval is the average depth derived from the above sliding-
196 window method in this region across individuals. To obtain average normalized depth,
197 the depth in each window of each individual is firstly divided by the average depth of
198 whole chromosome 18 of that individual, then average depth of all windows in this
199 region is obtained, and average depth among individuals is finally calculated.
200 Eventually, the average depth and the average normalized depth in the PB region of
201 individuals within Haplogroup E are 16.25 ± 5.70 and 0.83 ± 0.07 , respectively, while
202 those of individuals within Haplogroup A are 11.82 ± 1.59 and 0.49 ± 0.04 , respectively.
203 The former is significantly higher than the latter ($p=1.55E-07$ and $p=6.81E-053$
204 corresponding to the average depth and the average normalized depth, respectively, T
205 test).

206 **Note S3. South Chinese pigs contribute to the development of modern European**
207 **breeds**

208 Introgression from Asian pigs into European pigs during the Industrial Revolution is
209 well documented (Phillips and Hsu 1944; McLaren 1990; Giuffra et al. 2000; White
210 2011). Previously several research groups detected Asian pig introgression in European
211 pig genomes. Groenen et al. (2012) used the D-statistic to find that ~35% of the
212 genomes of European pig breeds have introgression from Asian pigs; Bosse et al. (2014)
213 estimated ~20% Asian fraction in modern European pigs using a total of 2,377,607
214 autosomal markers; Bianco et al. (2015) used 60K chips to investigate 31 American and
215 European pig populations (or breeds) originating from Europe and found they had 10-
216 30% of introgressed DNA from Asian lineages. We also used 60K chip to investigate
217 39 Chinese and Western pig breeds, and we found that Large White and Landrace had
218 respectively about a 19% and 12% Asian fraction when $K = 2$, but as the K value
219 increased, the Asian fraction slightly declined (Ai et al. 2014). More recently, we
220 resequenced 69 Chinese local pigs with high quality (coverage depth $> 25\times$) and
221 downloaded the whole-genome sequence data for 42 European and Asian pigs
222 submitted by Wageningen University. Using these data, we also detected a ~19%
223 Chinese fraction in European pigs when $K = 2$, and almost all of the introgression in
224 European pig genomes was of South Chinese origin when $K = 3$ (Ai et al. 2015).

225 However, in our present study, 7-13% of the Asian fractions were estimated in several
226 European commercial pigs like Large White, Landrace, Creole, and Pietrain pigs when
227 $K = 2$, which was slightly lower than the previous reports. The introgression in
228 European pig genomes was mainly of South Chinese origin, and tiny amounts of East
229 Chinese origin were also detected when $K > 2$ (**Fig. 1D**). We considered two major
230 reasons possibly contributing to this difference in proportion: (1) different European
231 pig samples and (2) higher-density and high-quality SNPs.

232 In the present study, our test samples included 67 European pigs. Among these
233 European pigs, we resequenced 31 domestic pigs at high coverage (average depth of
234 29.9×), downloaded data for 25 domestic pigs submitted by three different research
235 groups from the NCBI SRA database (**supplementary table S2**), and downloaded data
236 for 11 European wild boars submitted by two groups from Wageningen University and
237 Centre For Research in Agrigenomics from the NCBI SRA database (**supplementary**
238 **table S2**). Except for European wild boars, all European domestic pigs in this study
239 were different from the ones in the previous works described above. In this study, we
240 obtained 36.3 million autosomal SNPs in the 200-pig population. The number of SNPs
241 used here was much higher than in previous studies (i.e. 2,377,607 autosomal markers
242 in (Bosse et al. 2014); 60K SNP chips in (Bianco et al. 2015) and in (Ai et al. 2014)).

243 To further validate our results, we used all autosomal reference variants (n=
244 62,117,429) in *Sus scrofa* dbSNP (build 151) as known variants to guide individual
245 genotyping for the 200 Eurasian pigs via Platypus with the parameters “--
246 source=KnownVariants.vcf.gz --minPosterior=0 --getVariantsFromBAMs=0”. We
247 gained 34,918,325 autosomal SNPs in the 200-pig population. Then, an unsupervised
248 Admixture analysis was computed for the 200 individuals. Similarly, the estimated
249 Asian fractions in European pigs were lower than previous reports, and the introgressed
250 fractions in European pigs were of South Chinese origin with $K = 2$ (**supplementary**
251 **fig. S13**).

252 In summary, we consider that different samples and high-density, high-quality SNPs
253 contribute to the different results for Asian introgression fraction in European pigs. We
254 believe our SNP calling results and demographic and evolutionary history results
255 inferred by autosomal SNPs are reliable and robust.

256 **Note S4. Nucleotide diversity in the Y chromosome haplogroups**

257 To learn more about evolutionary history of the Y chromosome, we calculated

258 nucleotide variability at the genomic level and within the MSY region in sequenced
259 males. The MSY region had a significantly lower level of nucleotide diversity
260 compared to autosomes (**supplementary fig. S11 and supplementary table S5**).
261 Moreover, all nucleotide variability parameters were lower in European pigs in
262 Haplogroup E than in Chinese pigs in Haplogroup A (**supplementary fig. S11**). This
263 could be explained by the fact that European wild boars suffered a more dramatic
264 decrease in population size than Asian wild boars during the Last Glacial period (**Fig.**
265 **1F**).

266 **Note S5. Sex-biased effect may partially contribute to low nucleotide diversity in**
267 **the MSY region.**

268 Although many factors (such as nutrition, season of birth, stress, mother's age and
269 parity, social status, and disease) have been shown to be associated with sex ratio at
270 birth, the male:female ratio of offspring in pigs was consistently around 1:1 (Nishida et
271 al. 1977; Alfonso 2005). However, several reports showed that sex ratio is significantly
272 or slightly skewed towards females in free-roaming wild boar populations. For
273 examples, the male:female ratio of wild boar populations living in southern Poland is
274 approximately 1:2 (Merta et al. 2015); the male:female ratio of wild boars living in a
275 tropical forest, Southwest China, is estimated to be 1:1.2 (Guo et al. 2017).

276 The wild boar (*Sus scrofa*) is a polygynous mammal with large litters (FernaNdez-
277 Llario et al. 1999). Boars are typically social animals living in female-dominated
278 populations, and adult males tend to be solitary outside the breeding season (Marsan
279 and Mattioli 2013). During the breeding season, males drive off young animals and
280 persistently chase the sows in a female-dominated population. Males fiercely fights
281 potential rivals, and a single male can mate with five to 10 sows (Baskin and Danell
282 2003). In the modern pig farming, farmers raise more reproducing sows than boars to
283 keep benign production system. Usually the boar:sow ratio is 1:20 under natural service,

284 and less than 1:150 using artificial insemination (AI) technology (Taylor and Roesse
285 2006; Safranski 2008)

286 In summary, almost no sex-bias exists in the new-birth offspring in pigs, but stronger
287 boars in wild populations are potential rivals, and high-performance boars are
288 artificially selected, and their sperm is used extensive in modern pig farming. These
289 facts might contribute to a sex ratio skewed towards females in pigs. The extent of this
290 sex-bias effect needs to be further investigated.

291 We have observed low nucleotide diversity in the MSY region, and its value is far
292 less than the theoretical ratio of one quarter compared to autosomes (**supplementary**
293 **table S5**). If we roughly treat wild boar sex ratio of 1:2 (Merta et al. 2015) as the sex-
294 bias weight, the observed ratio is still lower than the theoretical one (1:8). Therefore,
295 sex-biased effect may partially contribute to low nucleotide diversity in the MSY region,
296 and there must be other biological mechanisms, such as selection, contributing to low
297 nucleotide diversity as well.

298 **Note S6. The divergence time of the MSY haplotypes**

299 FASTA formatted sequence files were used to construct phylogenetic tree via BEAST.
300 Before constructing the phylogenetic tree, we tested 44 candidate models by
301 jModelTest (Posada 2008). According to the value of Akaike information criterion, the
302 best-fit model was identified as the TVM model, and the second best-fit model was the
303 GTR model (detailed model test in **supplementary table S8**). Because the TVM model
304 is not implemented in BEAST and considering the site heterogeneity model, we
305 selected the GTR+ Γ model as the best-fit model to estimate the divergence time using
306 a strict molecular clock by BEAST. Split times and 95% highest posterior density
307 intervals in the trees were estimated with 10,000,000 MCMC samples. The divergence
308 time between *Sus verucosus* (JWP) and *Sus scrofa* (CB11-2) was set to be 4.2 million
309 years (Frantz et al. 2013) and 1.36 million years (Zhang M. *et al.* manuscript submitted)

310 as the calibration constraint.

311 **Note S7. Introduction to the heterogeneous stock construction**

312 We constructed a heterogeneous pig population crossing eight pig breeds consisting
313 of 4 western commercial pig breeds (including Duroc, Landrace, Large White and
314 Pietrain) and 4 Chinese local breeds (including Erhualian, Laiwu, Bamaxiang and
315 Tibetan), using a disc rotation breeding system. The special breeding system can avoid
316 the increase of inbreeding coefficient and ensure the even genetic contribution of each
317 of eight founder breeds. The details of stock construction were described by (Ji et al.
318 2018). After six years' breeding, the sixth-generation offspring of this population (F6)
319 were composed of 836 progeny, including 448 females and 388 males. We sequenced
320 all 836 piglets to an average genome coverage of 7.8× (Ji et al. 2018; Zhang et al. 2021).
321 As expected, variation was roughly uniformly distributed across the genome of this
322 heterogeneous stock. Also, this was a unique pig population with both Asian and
323 European MSY haplotypes. Among the 388 males, there were 150 individuals with
324 Asian MSY haplotypes and 238 individuals with European MSY haplotypes.

325 **2. Supplementary Methods**

326 **Samples and genome sequencing**

327 We sequenced the genomes of 80 Chinese and European pigs. 83 Chinese pigs were
328 sequenced in our previous study (Ai et al. 2015; Zhu et al. 2017). These pigs include
329 24 South Chinese domestic pigs, 33 North Chinese domestic pigs, 36 West Chinese
330 domestic pigs, 33 East Chinese domestic pigs, six South Chinese wild boars and 31
331 European domestic pigs. Of these animals, Chinese pigs were from 16 geographically
332 diverse breeds, European pigs were from 4 commercial breeds (**supplementary table**
333 **S1**).

334 The genome sequencing was conducted as previously described (Ai et al. 2015).
335 Genomic DNA was extracted from ear tissue using a standard phenol-chloroform
336 method, and then individually sheared into fragments of 200-800 bp using the Covaris
337 system (Life Technologies); DNA fragments were treated according to the Illumina
338 DNA sample preparation protocol. These treated fragments were end-repaired, A-tailed,
339 ligated to paired-end adaptors, and PCR amplified with 500 bp (or 350 bp) inserts for
340 library construction. Sequencing was performed to generate 100 bp (or 125 bp, 150 bp)
341 paired-end reads on a HiSeq 2000 (or 2500) platform (Illumina) according to the
342 manufacture's standard protocols.

343 **SNP calling**

344 We downloaded genome sequence data for 42 pigs, one African warthog
345 (*Phacochoerus africanus*), one Java warty pig (*Sus verrucosus*) and one Celebes warty
346 pig (*Sus celebensis*) from the NCBI SRA database (<https://www.ncbi.nlm.nih.gov/sra>).
347 These data were integrated into the sequence data obtained in this study, resulting in a
348 205-sample high-quality data set (**supplementary table S1 and S2**). Cleaned reads
349 from all individuals were aligned to the *Sus scrofa* reference genome (build 11.1) using
350 BWA (Li and Durbin 2009). The mapped reads were subsequently processed by sorting,
351 duplicate marking, indel realigning, and base quality recalibrating by Picard
352 (<http://picard.sourceforge.net>) and GATK (McKenna et al. 2010). Sequencing coverage
353 and depth of each sample were calculated using genomcov implemented in Bedtools
354 (Quinlan and Hall 2010).

355 A two-round procedure of SNP calling was performed using Platypus (Rimmer et al.
356 2014). In the first round, SNPs were individually called with the default parameters
357 below:

```
358 python Platypus.py callVariants --bamFiles=input.bam --refFile=ref.fa --  
359 output=VariantCalls.vcf
```

360 Detailed default options were shown here: 'assemblyRegionSize': 1500,
361 'trimReadFlank': 0, 'assembleBadReads': 1, 'minVarDist': 9, 'trimSoftClipped': 1,
362 'minReads': 2, 'qualBinSize': 1, 'maxHaplotypes': 50, 'filterVarsByCoverage': 1,
363 'maxSize':1500, 'originalMaxHaplotypes': 50, 'skipDifficultWindows': 0, 'parseNCBI':
364 0, 'skipRegionsFile': None, 'noCycles': 0, 'trimAdapter': 1, 'minPosterior': 0,
365 'assembleAll': 1, 'trimOverlapping': 1, 'filterDuplicates': 1, 'abThreshold': 0.001,
366 'minFlank': 10, 'bufferSize': 100000, 'fileCaching': 0, 'useEMLikelihoods': 0,
367 'coverageSamplingLevel': 30, 'calculateFlankScore': 0, 'filterReadsWithUnmapped
368 Mates': 1, 'qdThreshold': 10, 'maxVariants': 8, 'scThreshold': 0.95,
369 'filterReadsWithDistantMates': 1, 'maxReads': 5000000, 'badReadsWindow': 11,
370 'genIndels': 1, 'largeWindows': 0, 'minMapQual': 20, 'maxVarDist': 15, 'maxGOF': 30,
371 'rlen': 150, 'minGoodQualBases': 20, 'refCallBlockSize': 1000,
372 'countOnlyExactIndelMatches': 0, 'longHaps': 0, 'HLATyping': 0,
373 'filterReadPairsWithSmallInserts': 1, 'minBaseQual': 20, 'getVariantsFromBAMs': 0,
374 'genSNPs': 1, 'assemble': 0, 'assemblerKmerSize': 15, 'minVarFreq': 0.05,
375 'alignScoreFile': "", 'verbosity': 2, 'compressReads': 0, 'rmsmqThreshold': 40,
376 'filteredReadsFrac': 0.70, 'outputRefCalls': 0, 'badReadsThreshold': 15,
377 'hapScoreThreshold': 4, 'sbThreshold': 0.001, 'assembleBrokenPairs': 0,
378 'mergeClusteredVariants': 1, 'maxGenotypes': 1275, 'nInd': 1.

379 In the SNP calling output, the variants were classified into nine categories marked
380 with different FILTER labels, including PASS, HapScore, Q20, MQ, QD, SC, badReads,
381 alleleBias, and strandBias (**supplementary table S11**). High-quality variants were
382 marked with “PASS”; low-quality variants were marked with the other eight labels. The
383 high-quality SNPs marked with “PASS” by Platypus with default parameters were
384 retained. All “PASS” SNPs from all samples were merged together to form a total SNP
385 set (84,923,342 SNPs). We removed the non-biallelic SNPs from this SNP set and

386 obtained 83,702,124 biallelic SNPs. These biallelic SNPs were treated as known
387 variants to guide the second-round individual genotyping for all the samples via
388 Platypus with the parameters “--source=KnownVariants.vcf.gz --minPosterior=0 --
389 getVariantsFromBAMs=0”. SNPs in VCF format were transformed to Plink format by
390 a custom Perl script based on genotype log10-likelihoods of AA, AB and BB genotypes.
391 Low-quality genotypes with likelihood P-value > 0.1 were set as missing genotypes
392 (NA). All SNPs except those on the Y chromosome were filtered with the criteria MAF >
393 0.01 and SNP call rates > 80%. For SNPs on the Y chromosome, only male individuals
394 were used to call SNPs with the criteria MAF > 0.009 and call rates > 80%.

395 **Population genetic analysis using autosomal data**

396 A total of 36,332,442 qualified SNPs on autosomes were used to calculate genetic
397 distance among all individuals using Plink as previously described (Ai et al. 2013). The
398 average proportion of alleles shared was calculated as D_{st} :

$$399 \quad D_{st} = \frac{IBS2 + 0.5 \times IBS1}{N}$$

400 where IBS1 and IBS2 are the number of loci which share either 1 or 2 alleles identical
401 by state (IBS), respectively, and N is the number of loci tested. Genetic distance
402 between all pairwise combinations of individuals was calculated as $1 - D_{st}$. A neighbor-
403 joining tree was then constructed for all individuals using Neighbor in PHYLIP v3.69
404 (Felsenstein 2005) and visualized by FigTree software ([http://beast.bio.
405 ed.ac.uk/FigTree](http://beast.bio.ed.ac.uk/FigTree)).

406 Population genetic structure was inferred using the maximum likelihood approach
407 implemented in ADMIXTURE v1.20 (Alexander et al. 2009). The ADMIXTURE
408 program was run in an unsupervised manner with a variable number of clusters (K = 2
409 to 6). Principal component (PC) analysis was conducted using Smartpca in
410 EIGENSOFT v6.0 (Price et al. 2006). To avoid artifacts caused by linkage

411 disequilibrium (LD), we excluded SNPs with $r^2 \geq 0.4$ in the PC analysis.

412 TreeMix (Pickrell and Pritchard 2012) was used to infer the patterns of historical
413 splits and mixture among Eurasian pig populations in the context of *Suidae*, with 1,000
414 SNPs grouped together in an LD block (-k 1000) and migration events from 0 to 10,
415 respectively. The data was pruned using PLINK toolset (version: 1.90) with parameters
416 "--indep-pairwise 50 10 0.4" before TreeMix analyses. We further used *qpDstat* from
417 AdmixTools (Patterson et al. 2012) to calculate D-statistics in form of $D(\text{H1}, \text{H2}; \text{H3},$
418 **Outgroup**) with default parameters to show if population H1 is symmetrically related
419 to H2 and H3 or shares an excess of alleles with either of the two, with standard errors
420 computed with a block jackknife. Based on the result of more symmetrically relation
421 between EHL and JH compared to MIN, which was inferred by $D(\text{EHL}, \text{JH}; \text{MIN}, \text{JWP})$
422 equal to 0.015 with Z value 7.971, and other possible migration implied by D statistics
423 (**supplementary table S4**), we preferred the result of TreeMix with 4 migration events
424 based on the result of the R package OptM (Fitak 2019) with the linear method
425 (**supplementary fig. S9**). Then 1000 bootstrap were performed with parameter "--
426 bootstrap" to validate the pattern with 4 migration events when running TreeMix.

427 **Evolutionary history analysis using Y chromosome data**

428 For the SNPs-calling procedure on Y chromosome and on a 1.6 Mb unmapped Y-
429 linked contig, some additional quality control was conducted. We exclude the reads
430 containing the "SA:Z" and "XA:Z" flags, so that the reads aligned uniquely to the Y
431 chromosome can be extracted, reducing the error of the alignment on Y-chromosome.
432 Then, the two-round SNP calling was performed using Platypus (Rimmer et al. 2014),
433 as it was as for autosomal SNPs. Additionally, for SNPs on the Y chromosome, we
434 replace the heterozygous SNPs with missing on the Y chromosome and then filter under
435 the criterion $\text{MAF} > 0.009$ and SNP call rates $> 80\%$. Moreover, parts of SNPs on Y

436 chromosome and on the Y-linked contig of male individuals, which were same as the
437 SNPs called by the reads of female individuals misaligned to Y chromosome reference
438 sequence, were excluded due to the possible bias. Finally, a total of 42,288 high-quality
439 SNPs on Y chromosome and the Y-linked contig in the 103 male individuals passed the
440 criteria $MAF > 0.009$ and call rates $> 80\%$, which were used to show the Y chromosome
441 haplotype, reconstruct the phylogenic tree, perform haplotype network and estimate Y
442 chromosome divergence time.

443 Pairwise nucleotide differences per site within (d_x) and between (d_{xy}) populations
444 were calculated by the following formulas as previously described (Ai et al. 2015):

445
$$d_x = \frac{2}{n_x(n_x-1)l} \sum_{i=1}^{n_x-1} \sum_{i'=i+1}^{n_x} k_{ii'}$$

446
$$d_{xy} = \frac{1}{n_x n_y l} \sum_{i=1}^{n_x} \sum_{j=1}^{n_y} k_{ij}$$

447 where k represents the number of differences among haplotypes within a target region,
448 i and j denote haplotypes from populations x and y , respectively, with primes indicating
449 additional haplotypes from the same population. The expression for d_y is identical to
450 that for d_x but with i replaced by j and n_x replaced by n_y . l denotes the effective length
451 of the sequence without gaps in the target region.

452 To investigate global distribution of the haplotypes within the distal and proximal
453 regions on the Y chromosome, we employed six tag SNPs representing these regions
454 from Illumina Porcine 60K Chip in 426 Eurasian pigs from 82 geographically diverse
455 populations. Segregating sites, Theta and Pi values were calculated for autosomes and
456 the MSY region in 50 kb windows with a step size of 25 kb using VariScan (Hutter et
457 al. 2006).

458

459

460 **3. Supplementary Tables**

461 **Supplementary Table S1. Samples Information.**

No	Breed	Population code	Sample Size	Origin	Group	References
Chinese pigs						
1	Bama Xiang	BMX	6	Bama, Guangxi	South Chinese domestic pig (SCDP)	Ai, et al., 2015, Nature genetics
	Bama Xiang	BMX	6	Bama, Guangxi	South Chinese domestic pig (SCDP)	This study
2	Wuzhishan	WZS	6	Qiongsan, Hainan	South Chinese domestic pig (SCDP)	Ai, et al., 2015, Nature genetics
3	Luchuan	LUC	6	Luchan, Guangxi	South Chinese domestic pig (SCDP)	Ai, et al., 2015, Nature genetics
4	Min	MIN	6	Lanxi, Heilongjiang	North Chinese domestic pig (NCDP)	Ai, et al., 2015, Nature genetics
5	Laiwu	LWU	6	Laiwu, Shandong	North Chinese domestic pig (NCDP)	Ai, et al., 2015, Nature genetics
			9	Laiwu, Shandong	North Chinese domestic pig (NCDP)	This study
6	Hetao	HT	6	Wuyuan, Inner Mongolia	North Chinese domestic pig (NCDP)	Ai, et al., 2015, Nature genetics
7	Bamei	BAM	6	Huangzhong, Qinghai	North Chinese domestic pig (NCDP)	Zhu,et al., 2017, Genomic evolution and selection
8	Baoshan	BS	6	Baoshan, Yunnan	West Chinese domestic pig (WCDP)	Zhu,et al., 2017, Genomic evolution and selection
9	Neijiang	NJ	6	Neijiang, Sichuan	West Chinese domestic pig (WCDP)	Zhu,et al., 2017, Genomic evolution and selection
10	Jinhua	JH	6	Jinhua, Zhejiang	East Chinese domestic pig (ECDP)	Zhu,et al., 2017, Genomic evolution and selection
11	Erhualian	EHL	5	Wuxi, Jiangsu	East Chinese domestic pig (ECDP)	Ai, et al., 2015, Nature genetics
			22	Wuxi, Jiangsu	East Chinese domestic pig (ECDP)	This study
14	Tibetan (Sichuan)	SCT	6	Litan, Sichuan	West Chinese domestic pig (WCDP)	Ai, et al., 2015, Nature genetics
			6	Litan, Sichuan	West Chinese domestic pig (WCDP)	This study
			1	Sichuan	West Chinese domestic pig (WCDP)	Li, et al., 2013, Nature genetics
15	Tibetan (Yunnan)	YNT	6	Diqing, Yunnan	West Chinese domestic pig (WCDP)	Ai, et al., 2015, Nature genetics
			6	Diqing, Yunnan	West Chinese domestic pig (WCDP)	This study
16	South Chinese Wild Boar	CWB	2	Jiangxi, Nanchang	Chinese wild boar (CWB)	Ai, et al., 2015, Nature genetics
			2	Jiangxi, Shangyou	Chinese wild boar (CWB)	Ai, et al., 2015, Nature genetics
			2	Zhejiang, Xiangshan	Chinese wild boar (CWB)	Ai, et al., 2015, Nature genetics
European pigs						
17	White Duroc	WDU	10	USA (Originated from Europe)	European domestic pig (EDP)	This study
18	Large White	LW	7	France, Europe	European domestic pig (EDP)	This study
			6	Europe	European domestic pig (EDP)	Kim, et al., 2015, Plos one
19	Duroc	DU	11	Europe	European domestic pig (EDP)	Kim, et al., 2015, Plos one
	Pietrain	PT	6	Europe	European domestic pig (EDP)	This study
20	Iberian	Ib	1	Spain, Europe	European domestic pig (EDP)	Ramírez, et al., 2014, Heredity
21	Creole	Cr	1	Europe	European domestic pig (EDP)	Ramírez, et al., 2014, Heredity
22	Landrace	LR	3	Europe	European domestic pig (EDP)	Kim, et al., 2015, Plos one
			8	Europe	European domestic pig (EDP)	This study
23	Mangalica	MG	3	Hungary, Europe	European domestic pig (EDP)	Molnár, et al., 2014, BMC Genomics
24	European Boar	Wild EUW	1	Europe	European wild boar (EWB)	Ramírez, et al., 2014, Heredity
			10	Europe	European wild boar (EWB)	Frantz, et al., 2015, Nature Genetics
Sumatran pig						

25	Sumatran Boar	Wild	SWB	2	\	Sumatran wild boar (SWB)	Groenen, et al., 2012, Nature
Outgroups							
26	Celebes Wild Boar		CWP	1	\	Outgroup	Groenen, et al., 2012, Nature
27	Java Warty Pig		JWP	1	\	Outgroup	Groenen, et al., 2012, Nature
28	African Warthog	Common	AWP	1	\	Outgroup	Groenen, et al., 2012, Nature

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463

464 **Supplementary Table S2.** Sequencing Statistics of 205 samples.

No	Breed	Sample ID	Population code	Inferred Sex	mtDNA Origin	Y haplogroup	Coverage ^a	Depth (×)	ChrY Depth (×)	60Kchip	References
Chinese pigs											
1	South Chinese Wild Boar	CB11-1	CWB	Female	Chinese	/	0.977	25.9	/	Scanned	Ai, et al., 2015, Nature genetics
2	South Chinese Wild Boar	CB11-2	CWB	Male	Chinese	Asian	0.981	28.2	13.5	Scanned	Ai, et al., 2015, Nature genetics
3	South Chinese Wild Boar	CB11-3	CWB	Female	Chinese	/	0.977	27.6	/	Scanned	Ai, et al., 2015, Nature genetics
4	South Chinese Wild Boar	CB11-4	CWB	Male	Chinese	Asian	0.979	21.7	10.7	Scanned	Ai, et al., 2015, Nature genetics
5	South Chinese Wild Boar	CB11-5	CWB	Male	Chinese	Asian	0.975	20.5	9.8	Scanned	Ai, et al., 2015, Nature genetics
6	South Chinese Wild Boar	CB11-6	CWB	Male	Chinese	Asian	0.975	21.8	10.3	Scanned	Ai, et al., 2015, Nature genetics
7	Wuzhishan	CB1-1	WZS	Female	Chinese	/	0.977	26.1	/	Scanned	Ai, et al., 2015, Nature genetics
8	Wuzhishan	CB1-2	WZS	Female	Chinese	/	0.976	26.2	/	Scanned	Ai, et al., 2015, Nature genetics
9	Wuzhishan	CB1-3	WZS	Female	Chinese	/	0.976	25.7	/	Scanned	Ai, et al., 2015, Nature genetics
10	Wuzhishan	CB1-4	WZS	Male	Chinese	European	0.981	25.5	13.5	Scanned	Ai, et al., 2015, Nature genetics
11	Wuzhishan	CB1-5	WZS	Male	Chinese	European	0.981	26.2	13.9	Scanned	Ai, et al., 2015, Nature genetics
12	Wuzhishan	CB1-6	WZS	Female	Chinese	/	0.975	26.9	/	Scanned	Ai, et al., 2015, Nature genetics
13	Luchuan	CB12-1	LUC	Female	Chinese	/	0.972	23.9	/	Scanned	Ai, et al., 2015, Nature genetics
14	Luchuan	CB12-2	LUC	Female	Chinese	/	0.977	26.6	/	Scanned	Ai, et al., 2015, Nature genetics
15	Luchuan	CB12-3	LUC	Female	Chinese	/	0.978	28.5	/	Scanned	Ai, et al., 2015, Nature genetics
16	Luchuan	CB12-4	LUC	Female	Chinese	/	0.974	27.2	/	Scanned	Ai, et al., 2015, Nature genetics
17	Luchuan	CB12-5	LUC	Female	Chinese	/	0.976	27.0	/	Scanned	Ai, et al., 2015, Nature genetics
18	Luchuan	CB12-6	LUC	Female	Chinese	/	0.977	25.0	/	Scanned	Ai, et al., 2015, Nature genetics
19	Bama Xiang	CB8-1	BMX	Female	Chinese	/	0.976	26.7	/	Scanned	Ai, et al., 2015, Nature genetics
20	Bama Xiang	CB8-2	BMX	Female	Chinese	/	0.977	28.5	/	Scanned	Ai, et al., 2015, Nature genetics
21	Bama Xiang	CB8-3	BMX	Female	Chinese	/	0.977	26.0	/	Scanned	Ai, et al., 2015, Nature genetics

22	Bama Xiang	CB8-4	BMX	Female	Chinese	/	0.977	27.2	/	Scanned	Ai, et al., 2015, Nature genetics
23	Bama Xiang	CB8-5	BMX	Female	Chinese	/	0.977	27.3	/	Scanned	Ai, et al., 2015, Nature genetics
24	Bama Xiang	CB8-6	BMX	Female	Chinese	/	0.977	27.2	/	Scanned	Ai, et al., 2015, Nature genetics
25	Bama Xiang	CB8-7	BMX	Female	Chinese	/	0.992	30.7	/	/	This study
26	Bama Xiang	CB8-8	BMX	Female	Chinese	/	0.992	30.1	/	/	This study
27	Bama Xiang	CB8-9	BMX	Female	Chinese	/	0.976	26.6	/	/	This study
28	Bama Xiang	CB8-10	BMX	Male	Chinese	Asian	0.980	30.4	14.7	/	This study
29	Bama Xiang	CB8-11	BMX	Male	Chinese	Asian	0.979	26.6	12.9	/	This study
30	Bama Xiang	CB8-12	BMX	Male	Chinese	Asian	0.980	29.8	9.7	/	This study
31	Baoshan	CB27-1	BS	Male	Chinese	European	0.982	25.5	14.0	/	Zhu,et al., 2017, Genomic evolution and selection
32	Baoshan	CB27-2	BS	Male	Chinese	European	0.981	25.1	13.7	/	Zhu,et al., 2017, Genomic evolution and selection
33	Baoshan	CB27-3	BS	Male	Chinese	European	0.981	25.5	14.0	/	Zhu,et al., 2017, Genomic evolution and selection
34	Baoshan	CB27-4	BS	Female	Chinese	/	0.978	25.8	/	/	Zhu,et al., 2017, Genomic evolution and selection
35	Baoshan	CB27-5	BS	Female	Chinese	/	0.977	29.2	/	/	Zhu,et al., 2017, Genomic evolution and selection
36	Baoshan	CB27-6	BS	Female	Chinese	/	0.977	27.8	/	/	Zhu,et al., 2017, Genomic evolution and selection
37	Neijiang	CB25-1	NJ	Male	Chinese	Asian	0.981	27.2	13.4	/	Zhu,et al., 2017, Genomic evolution and selection
38	Neijiang	CB25-2	NJ	Male	Chinese	Asian	0.981	27.2	14.0	Scanned	Zhu,et al., 2017, Genomic evolution and selection
39	Neijiang	CB25-3	NJ	Female	Chinese	/	0.978	27.6	/	/	Zhu,et al., 2017, Genomic evolution and selection
40	Neijiang	CB25-4	NJ	Male	Chinese	Asian	0.980	24.5	13.0	Scanned	Zhu,et al., 2017, Genomic evolution and selection

41	Neijiang	CB25-5	NJ	Male	Chinese	Asian	0.981	24.9	13.0	Scanned	Zhu,et al., 2017, Genomic evolution and selection
42	Neijiang	CB25-6	NJ	Male	Chinese	Asian	0.980	26.2	13.1	/	Zhu,et al., 2017, Genomic evolution and selection
43	Tibetan (Yunnan)	CB22-1	YNT	Male	Chinese	Asian	0.981	25.6	13.0	Scanned	This study
44	Tibetan (Yunnan)	CB22-2	YNT	Male	Chinese	European	0.982	29.2	16.0	Scanned	This study
45	Tibetan (Yunnan)	CB22-3	YNT	Male	Chinese	Asian	0.981	26.3	13.2	/	This study
46	Tibetan (Yunnan)	CB22-4	YNT	Male	Chinese	Asian	0.981	25.6	12.9	Scanned	This study
47	Tibetan (Yunnan)	CB22-5	YNT	Male	Chinese	Asian	0.981	25.0	12.4	/	This study
48	Tibetan (Yunnan)	CB22-6	YNT	Male	Chinese	Asian	0.981	25.3	12.9	Scanned	This study
49	Tibetan (Yunnan)	CB3-1	YNT	Male	Chinese	Asian	0.982	27.7	13.6	/	Ai, et al., 2015, Nature genetics
50	Tibetan (Yunnan)	CB3-2	YNT	Male	Chinese	Asian	0.980	28.6	14.4	Scanned	Ai, et al., 2015, Nature genetics
51	Tibetan (Yunnan)	CB3-3	YNT	Male	Chinese	Asian	0.981	28.1	13.7	Scanned	Ai, et al., 2015, Nature genetics
52	Tibetan (Yunnan)	CB3-4	YNT	Male	Chinese	Asian	0.982	26.8	12.6	Scanned	Ai, et al., 2015, Nature genetics
53	Tibetan (Yunnan)	CB3-5	YNT	Male	Chinese	Asian	0.982	26.6	13.4	Scanned	Ai, et al., 2015, Nature genetics
54	Tibetan (Yunnan)	CB3-6	YNT	Male	Chinese	Asian	0.981	22.1	12.7	Scanned	Ai, et al., 2015, Nature genetics
55	Tibetan (Sichuan)	CB23-1	SCT	Male	Chinese	Asian	0.981	25.8	12.8	Scanned	This study
56	Tibetan (Sichuan)	CB23-2	SCT	Male	Chinese	Asian	0.981	28.9	15.4	Scanned	This study
57	Tibetan (Sichuan)	CB23-3	SCT	Male	Chinese	Asian	0.980	25.5	13.2	Scanned	This study
58	Tibetan (Sichuan)	CB23-4	SCT	Male	Chinese	Asian	0.981	28.2	14.6	Scanned	This study
59	Tibetan (Sichuan)	CB23-5	SCT	Male	Chinese	Asian	0.981	25.0	13.1	Scanned	This study
60	Tibetan (Sichuan)	CB23-6	SCT	Male	Chinese	Asian	0.980	26.2	13.1	Scanned	This study
61	Tibetan (Sichuan)	CB4-1	SCT	Female	Chinese	/	0.976	27.1	/	Scanned	Ai, et al., 2015, Nature genetics
62	Tibetan (Sichuan)	CB4-2	SCT	Female	Chinese	/	0.976	26.2	/	Scanned	Ai, et al., 2015, Nature genetics
63	Tibetan (Sichuan)	CB4-3	SCT	Male	Chinese	Asian	0.980	26.3	13.5	Scanned	Ai, et al., 2015, Nature genetics
64	Tibetan (Sichuan)	CB4-4	SCT	Male	Chinese	Asian	0.980	26.8	13.9	Scanned	Ai, et al., 2015, Nature genetics

65	Tibetan (Sichuan)	CB4-5	SCT	Male	Chinese	Asian	0.980	28.3	14.6	Scanned	Ai, et al., 2015, Nature genetics
66	Tibetan (Sichuan)	CB4-6	SCT	Male	Chinese	Asian	0.979	27.0	13.5	Scanned	Ai, et al., 2015, Nature genetics
67	Tibetan (Sichuan)	SRS387327	SCT	Female	Chinese	/	0.978	34.3	/	/	Li, et al., 2013, Nature genetics
68	Jinhua	CB20-1	JH	Female	Chinese	/	0.977	24.8	/	Scanned	Zhu,et al., 2017, Genomic evolution and selection
69	Jinhua	CB20-2	JH	Female	Chinese	/	0.977	29.5	/	Scanned	Zhu,et al., 2017, Genomic evolution and selection
70	Jinhua	CB20-3	JH	Male	Chinese	Asian	0.981	25.3	13.0	Scanned	Zhu,et al., 2017, Genomic evolution and selection
71	Jinhua	CB20-4	JH	Male	Chinese	Asian	0.980	27.0	14.2	Scanned	Zhu,et al., 2017, Genomic evolution and selection
72	Jinhua	CB20-5	JH	Female	Chinese	/	0.977	24.4	/	Scanned	Zhu,et al., 2017, Genomic evolution and selection
73	Jinhua	CB20-6	JH	Male	Chinese	Aisan	0.981	26.4	13.7	/	Zhu,et al., 2017, Genomic evolution and selection
74	Erhualian	CB10-1	EHL	Female	Chinese	/	0.976	27.6	/	Scanned	Ai, et al., 2015, Nature genetics
75	Erhualian	CB10-2	EHL	Female	Chinese	/	0.976	26.9	/	Scanned	Ai, et al., 2015, Nature genetics
76	Erhualian	F0-1190	EHL	Female	Chinese	/	0.977	25.8	/	Scanned	This study
77	Erhualian	F0-126	EHL	Female	Chinese	/	0.977	26.2	/	/	This study
78	Erhualian	F0-142	EHL	Female	Chinese	/	0.977	25.9	/	Scanned	This study
79	Erhualian	F0-146	EHL	Female	Chinese	/	0.977	25.5	/	Scanned	This study
80	Erhualian	F0-174	EHL	Female	Chinese	/	0.977	26.1	/	Scanned	This study
81	Erhualian	F0-196	EHL	Female	Chinese	/	0.977	26.0	/	Scanned	This study
82	Erhualian	F0-292	EHL	Female	Chinese	/	0.977	25.7	/	Scanned	This study
83	Erhualian	F0-38	EHL	Female	Chinese	/	0.977	24.6	/	Scanned	This study
84	Erhualian	F0-52	EHL	Female	Chinese	/	0.977	25.9	/	Scanned	This study
85	Erhualian	F0-54	EHL	Female	Chinese	/	0.977	25.5	/	Scanned	This study
86	Erhualian	F0-58	EHL	Female	Chinese	/	0.977	26.3	/	Scanned	This study

87	Erhualian	F0-68	EHL	Female	Chinese	/	0.977	25.9	/	Scanned	This study
88	Erhualian	F0-74	EHL	Female	Chinese	/	0.977	26.6	/	Scanned	This study
89	Erhualian	F0-124	EHL	Female	Chinese	/	0.978	37.2	/	Scanned	This study
90	Erhualian	F0-202	EHL	Female	Chinese	/	0.979	37.0	/	Scanned	Ai, et al., 2015, Nature genetics
91	Erhualian	F0-90	EHL	Female	Chinese	/	0.978	35.9	/	Scanned	Ai, et al., 2015, Nature genetics
92	Erhualian	F0-94	EHL	Female	Chinese	/	0.979	36.6	/	Scanned	Ai, et al., 2015, Nature genetics
93	Erhualian	CB10-3	EHL	Male	Chinese	Asian	0.980	25.9	12.5	/	This study
94	Erhualian	CB10-4	EHL	Male	Chinese	Asian	0.981	27.1	12.7	/	This study
95	Erhualian	CB10-5	EHL	Male	Chinese	Asian	0.981	27.7	12.3	Scanned	This study
96	Erhualian	CB10-6	EHL	Female	Chinese	/	0.977	32.9	/	/	This study
97	Erhualian	CB10-7	EHL	Female	Chinese	/	0.977	30.9	/	/	This study
98	Erhualian	CB10-8	EHL	Female	Chinese	/	0.978	27.8	/	/	This study
99	Erhualian	CB10-9	EHL	Female	Chinese	/	0.977	25.4	/	/	This study
100	Erhualian	CB10-10	EHL	Male	Chinese	Asian	0.980	25.1	12.4	/	This study
101	Laiwu	CB9-1	LWU	Male	Chinese	Asian	0.979	25.5	12.4	Scanned	Ai, et al., 2015, Nature genetics
102	Laiwu	CB9-2	LWU	Male	Chinese	Asian	0.979	24.0	11.7	Scanned	Ai, et al., 2015, Nature genetics
103	Laiwu	CB9-3	LWU	Male	Chinese	Asian	0.980	27.7	13.1	Scanned	Ai, et al., 2015, Nature genetics
104	Laiwu	CB9-4	LWU	Male	Chinese	Asian	0.980	26.7	12.9	Scanned	Ai, et al., 2015, Nature genetics
105	Laiwu	CB9-5	LWU	Male	Chinese	Asian	0.980	26.7	13.8	Scanned	Ai, et al., 2015, Nature genetics
106	Laiwu	CB9-6	LWU	Male	Chinese	Asian	0.980	26.3	13.3	Scanned	Ai, et al., 2015, Nature genetics
107	Laiwu	CB9-7	LWU	Female	Chinese	/	0.977	25.4	/	/	This study
108	Laiwu	CB9-8	LWU	Female	Chinese	/	0.977	27.0	/	/	This study
109	Laiwu	CB9-9	LWU	Female	Chinese	/	0.977	24.3	/	/	This study
110	Laiwu	CB9-10	LWU	Female	Chinese	/	0.976	30.4	/	/	This study
111	Laiwu	CB9-11	LWU	Male	Chinese	Asian	0.981	32.2	13.2	/	This study

112	Laiwu	CB9-12	LWU	Male	Chinese	Asian	0.980	25.6	12.6	/	This study
113	Laiwu	CB9-13	LWU	Male	Chinese	Asian	0.980	28.5	13.1	/	This study
114	Laiwu	CB9-14	LWU	Male	Chinese	Asian	0.980	33.2	16.1	/	This study
115	Laiwu	CB9-15	LWU	Male	Chinese	Asian	0.980	28.7	13.4	/	This study
116	Bamei	CB26-1	BAM	Male	Chinese	Asian	0.979	23.3	12.1	Scanned	Zhu,et al., 2017, Genomic evolution and selection
117	Bamei	CB26-2	BAM	Male	Chinese	Asian	0.981	23.3	11.5	Scanned	Zhu,et al., 2017, Genomic evolution and selection
118	Bamei	CB26-3	BAM	Male	Chinese	Asian	0.981	28.2	13.6	Scanned	Zhu,et al., 2017, Genomic evolution and selection
119	Bamei	CB26-4	BAM	Male	Chinese	Asian	0.980	23.8	12.0	Scanned	Zhu,et al., 2017, Genomic evolution and selection
120	Bamei	CB26-5	BAM	Male	Chinese	Asian	0.980	26.3	13.7	Scanned	Zhu,et al., 2017, Genomic evolution and selection
121	Bamei	CB26-6	BAM	Male	Chinese	Asian	0.981	24.3	12.3	Scanned	Zhu,et al., 2017, Genomic evolution and selection
122	Hetao	CB6-1	HT	Female	Chinese	/	0.975	26.0	/	Scanned	Ai, et al., 2015, Nature genetics
123	Hetao	CB6-2	HT	Female	Chinese	/	0.975	25.1	/	Scanned	Ai, et al., 2015, Nature genetics
124	Hetao	CB6-3	HT	Male	Chinese	European	0.971	20.4	11.3	Scanned	Ai, et al., 2015, Nature genetics
125	Hetao	CB6-4	HT	Male	Chinese	Asian	0.979	24.5	12.0	Scanned	Ai, et al., 2015, Nature genetics
126	Hetao	CB6-5	HT	Female	Chinese	/	0.976	25.5	/	Scanned	Ai, et al., 2015, Nature genetics
127	Hetao	CB6-6	HT	Female	Chinese	/	0.973	24.8	/	Scanned	Ai, et al., 2015, Nature genetics
128	Min	CB7-1	MIN	Female	Chinese	/	0.975	26.0	/	Scanned	Ai, et al., 2015, Nature genetics
129	Min	CB7-2	MIN	Male	Chinese	European	0.979	25.6	13.3	Scanned	Ai, et al., 2015, Nature genetics
130	Min	CB7-3	MIN	Male	Chinese	European	0.981	26.5	13.8	Scanned	Ai, et al., 2015, Nature genetics
131	Min	CB7-4	MIN	Male	Chinese	European	0.978	26.1	14.1	Scanned	Ai, et al., 2015, Nature genetics
132	Min	CB7-5	MIN	Male	Chinese	European	0.977	23.5	12.8	Scanned	Ai, et al., 2015, Nature genetics
133	Min	CB7-6	MIN	Male	Chinese	European	0.979	27.0	14.6	Scanned	Ai, et al., 2015, Nature genetics

European pigs

134	White Duroc	F0-73	WDU	Male	European	European	0.983	36.1	21.4	Scanned	This study
135	White Duroc	F0-75	WDU	Male	European	European	0.983	37.5	19.9	Scanned	This study
136	White Duroc	EB4-1	WDU	Male	Chinese	European	0.983	32.7	16.9	/	This study
137	White Duroc	EB4-2	WDU	Male	Chinese	European	0.982	31.0	14.5	/	This study
138	White Duroc	EB4-3	WDU	Female	European	/	0.978	26.7	/	/	This study
139	White Duroc	EB4-4	WDU	Male	Chinese	European	0.983	33.0	15.1	/	This study
140	White Duroc	EB4-5	WDU	Female	Chinese	/	0.979	28.6	/	/	This study
141	White Duroc	EB4-6	WDU	Male	European	European	0.982	28.0	14.2	/	This study
142	White Duroc	EB4-7	WDU	Female	Chinese	/	0.978	24.4	/	/	This study
143	White Duroc	EB4-8	WDU	Female	European	/	0.979	33.4	/	/	This study
144	Iberian	SRR1513307	Ib	Male	European	European	0.969	13.8	6.2	/	Ramírez, et al., 2014, Heredity
145	Creole	SRR1513309	Cr	Female	European	/	0.968	13.9	/	/	Ramírez, et al., 2014, Heredity
146	Duroc	DRC1729	DU	Female	European	/	0.979	15.2	/	/	Kim, et al., 2015, Plos one
147	Duroc	DRC1735	DU	Female	European	/	0.979	17.3	/	/	Kim, et al., 2015, Plos one
148	Duroc	DRC1795	DU	Female	European	/	0.981	17.1	/	/	Kim, et al., 2015, Plos one
149	Duroc	DRC25-24	DU	Female	European	/	0.979	16.6	/	/	Kim, et al., 2015, Plos one
150	Duroc	DRC25-78	DU	Female	European	/	0.978	14.9	/	/	Kim, et al., 2015, Plos one
151	Duroc	DRC26-23	DU	Female	European	/	0.979	16.9	/	/	Kim, et al., 2015, Plos one
152	Duroc	DRC26-66	DU	Female	European	/	0.978	15.1	/	/	Kim, et al., 2015, Plos one
153	Duroc	DRC27-20	DU	Female	European	/	0.979	17.6	/	/	Kim, et al., 2015, Plos one
154	Duroc	DRC27-81	DU	Female	European	/	0.978	15.7	/	/	Kim, et al., 2015, Plos one
155	Duroc	DRCDA973	DU	Female	European	/	0.978	16.4	/	/	Kim, et al., 2015, Plos one

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156	Duroc	DRCDA973	DU	Female	European	/	0.978	15.2	/	/	Kim, et al., 2015, Plos one
		8									
157	Landrace	EB1-1	LR	Male	European	European	0.981	26.5	12.6	/	This study
158	Landrace	EB1-2	LR	Male	European	European	0.981	31.7	11.3	/	This study
159	Landrace	EB1-3	LR	Female	European	/	0.978	25.0	/	/	This study
160	Landrace	EB1-4	LR	Female	European	/	0.979	37.9	/	/	This study
161	Landrace	EB1-5	LR	Male	European	European	0.982	26.4	12.9	/	This study
162	Landrace	EB1-6	LR	Female	Chinese	/	0.979	34.3	/	/	This study
163	Landrace	EB1-7	LR	Female	Chinese	/	0.979	31.2	/	/	This study
164	Landrace	EB1-8	LR	Female	European	/	0.979	29.1	/	/	This study
165	Landrace	LRS_10	LR	Female	European	/	0.967	14.1	/	/	Kim, et al., 2015, Plos one
166	Landrace	LRS_11	LR	Female	European	/	0.967	14.5	/	/	Kim, et al., 2015, Plos one
167	Landrace	LRS_14	LR	Female	European	/	0.971	13.7	/	/	Kim, et al., 2015, Plos one
168	Large White	EB2-1	LW	Male	Chinese	European	0.982	24.9	13.0	/	This study
169	Large White	EB2-2	LW	Female	Chinese	/	0.978	33.9	/	/	This study
170	Large White	EB2-3	LW	Female	Chinese	/	0.978	28.6	/	/	This study
171	Large White	EB2-4	LW	Female	Chinese	/	0.978	27.0	/	/	This study
172	Large White	EB2-5	LW	Female	Chinese	/	0.978	27.5	/	/	This study
173	Large White	EB2-6	LW	Male	Chinese	European	0.981	23.5	12.4	/	This study
174	Large White	EB2-7	LW	Male	European	European	0.982	28.7	13.7	/	This study
175	Large White	YorkshireKL1	LW	Male	Chinese	European	0.979	17.0	6.9	/	Kim, et al., 2015, Plos one
176	Large White	YorkshireKL2	LW	Male	Chinese	European	0.979	16.8	7.4	/	Kim, et al., 2015, Plos one
177	Large White	YorkshireKL3	LW	Male	Chinese	European	0.981	16.4	6.5	/	Kim, et al., 2015, Plos one
178	Large White	YorkshireKL4	LW	Male	Chinese	European	0.979	16.3	6.3	/	Kim, et al., 2015, Plos one
179	Large White	YorkshireKL6	LW	Female	Chinese	/	0.977	16.9	/	/	Kim, et al., 2015, Plos one
180	Large White	YorkshireKL7	LW	Female	Chinese	/	0.978	26.1	/	/	Kim, et al., 2015, Plos one

181	Pietrain	EB3-1	PT	Male	European	European	0.982	28.9	15.0	/	This study
182	Pietrain	EB3-2	PT	Male	European	European	0.981	27.2	14.2	/	This study
183	Pietrain	EB3-3	PT	Male	European	European	0.983	35.4	18.3	/	This study
184	Pietrain	EB3-4	PT	Female	Chinese	/	0.978	24.8	/	/	This study
185	Pietrain	EB3-5	PT	Female	European	/	0.978	27.9	/	/	This study
186	Pietrain	EB3-6	PT	Male	European	European	0.983	33.8	15.7	/	This study
187	Mangalica	SRR1178916	MG	Male	European	European	0.980	16.1	8.0	/	Molnár, et al., 2014, BMC Genomics
188	Mangalica	SRR1178923	MG	Male	European	European	0.970	11.5	4.8	/	Molnár, et al., 2014, BMC Genomics
189	Mangalica	SRR1178925	MG	Male	European	European	0.980	16.5	8.5	/	Molnár, et al., 2014, BMC Genomics
190	European Wild Boar	WB25U11	EUW	Male	European	European	0.974	11.3	6.8	/	Frantz, et al., 2015, Nature Genetics
191	European Wild Boar	WB28M39	EUW	Male	European	European	0.975	13.4	6.6	/	Frantz, et al., 2015, Nature Genetics
192	European Wild Boar	SRR1513306	EUW	Male	European	European	0.982	14.9	7.5	/	Ramírez, et al., 2014, Heredity
193	European Wild Boar	WB21F04	EUW	Female	European	/	0.978	16.7	/	/	Frantz, et al., 2015, Nature Genetics
194	European Wild Boar	WB21M05	EUW	Male	European	European	0.983	23.4	8.9	/	Frantz, et al., 2015, Nature Genetics
195	European Wild Boar	WB22M03	EUW	Male	European	European	0.980	15.1	7.0	/	Frantz, et al., 2015, Nature Genetics
196	European Wild Boar	WB33U04	EUW	Male	European	European	0.981	13.3	6.7	/	Frantz, et al., 2015, Nature Genetics
197	European Wild Boar	WB42M09	EUW	Female	European	/	0.978	14.7	/	/	Frantz, et al., 2015, Nature Genetics
198	European Wild Boar	WB44U06	EUW	Female	European	/	0.978	14.1	/	/	Frantz, et al., 2015, Nature Genetics
199	European Wild Boar	WB44U07	EUW	Female	European	/	0.977	12.7	/	/	Frantz, et al., 2015, Nature Genetics
200	European Wild Boar	WB21M03	EUW	Male	European	European	0.980	15.1	6.7	/	Frantz, et al., 2015, Nature Genetics
Sumatran wild boars											
201	Sumatran Wild Boar	ERR173176	SWB	Female	/	/	0.802	11.3	/	/	Groenen, et al., 2012, Nature
202	Sumatran Wild Boar	ERR173178	SWB	Male	/	/	0.799	11.0	3.5	/	Groenen, et al., 2012, Nature
Outgroups											
										/	

203	African Common Warthog	ERR173203	AWP	Female	/	/	0.780	13.1	/	/	Groenen, et al., 2012, Nature
204	Java Warty Pig	ERR977084	JWP	Male	/	/	0.980	45.7	19.4	/	Frantz, et al., 2015, Nature Genetics
205	Celebes Wild Boar	ERR173210	CWP	Female	/	/	0.819	23.9	/	/	Groenen, et al., 2012, Nature

a, The 4 genome sequence data downloaded from the NCBI SRA database, denoted with blue float number here, were extracted from their alignment files; their genome coverages were all smaller than 0.82.

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466 **Supplementary Table S3.** SNPs statistics of 200 Eurasian pigs along the whole genome.

Chromosome	SNPs of our data^a	SNPs in dbSNP^b	Common SNPs between our data and dbSNP	Proportion of common SNPs	Novel SNPs in our data compared to dbSNP	Proportion of novel SNPs
chr1	3564719	6343241	2884835	80.9%	679884	19.1%
chr2	2321609	4101086	1892176	81.5%	429433	18.5%
chr3	2213970	3699676	1786700	80.7%	427270	19.3%
chr4	2123108	3731799	1785100	84.1%	338008	15.9%
chr5	1790803	2901033	1380722	77.1%	410081	22.9%
chr6	2638342	4046647	1973616	74.8%	664726	25.2%
chr7	2088205	3575023	1730578	82.9%	357627	17.1%
chr8	2198478	3865719	1813779	82.5%	384699	17.5%
chr9	2326329	4057285	1950839	83.9%	375490	16.1%
chr10	1506527	2574859	1267666	84.1%	238861	15.9%
chr11	1502467	2564529	1236119	82.3%	266348	17.7%
chr12	1180906	1855147	922166	78.1%	258740	21.9%
chr13	2782549	4932653	2240889	80.5%	541660	19.5%
chr14	2193738	3898861	1839568	83.9%	354170	16.1%
chr15	2135572	3647251	1732300	81.1%	403272	18.9%
chr16	1430666	2458662	1195541	83.6%	235125	16.4%
chr17	1239531	2038315	1010548	81.5%	228983	18.5%
chr18	1094923	1825643	911530	83.3%	183393	16.7%
chrX	1167598	1742989	934505	80.0%	233093	20.0%
chrY	42288	21025	1642	3.9%	40646	96.1%
chrM	524	335	200	38.2%	324	61.8%

a, Except chrY and chrM, SNPs on the other chromosomes were called using 200 Eurassian pigs; SNPs on the chrY and chrM were called using all male pigs, including 101 Eurasian pigs, one Sumatran wild boar and one Java Warty pig.

b, Build 151 of the *Sus scrofa* dbSNP dataset from the NCBI database.

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468 **Supplementary Table S4.** D-statistics test for the phylogenetic relationships among
 469 pig populations from different geographic regions.

Migration		Pop1 (W)	Pop2 (X)	Pop3 (Y)	Pop4 (Outgroup)	D-statistics	se.	Z score
EHL <-> HT		HT	BAM	EHL	AWP	0.020	0.0019	10.371
		EHL	JH	HT	AWP	0.019	0.0020	9.826
EHL <-> MIN		MIN	BAM	EHL	AWP	0.005	0.0020	2.617
		EHL	JH	MIN	AWP	0.015	0.0019	7.971
HT <-> MIN		HT	BAM	MIN	AWP	0.018	0.0021	8.767
HT <-> LWU		HT	BAM	LWU	AWP	0.011	0.0020	5.292
HT <-> BAM		HT	MIN	BAM	AWP	0.016	0.0020	7.813
		HT	LWU	BAM	AWP	0.013	0.0021	5.821
European -> Asian	MG -> MIN	MIN	HT	MG	AWP	0.030	0.0037	8.154
		MG	EWB	MIN	AWP	0.021	0.0023	8.996
		DU	EWB	MIN	AWP	0.023	0.0029	7.772
		LW	EWB	MIN	AWP	0.024	0.0027	8.815
		DU	MG	MIN	AWP	0.005	0.0031	1.658
		LW	MG	MIN	AWP	0.007	0.0029	2.325
		DU	MG	HT	AWP	0.013	0.0029	4.630
		DU	MG	BS	AWP	0.031	0.0025	12.525
		DU	MG	YNT	AWP	0.022	0.0024	9.197
		DU	MG	WZS	AWP	0.041	0.0030	13.683
		LW	MG	HT	AWP	0.014	0.0024	5.820
		LW	MG	BS	AWP	0.026	0.0022	11.700
		LW	MG	YNT	AWP	0.029	0.0021	14.196
		LW	MG	WZS	AWP	0.050	0.0026	18.917
	Europe -> HT	LW	DU	HT	AWP	0.001	0.0025	0.468
		HT	BAM	DU	AWP	0.014	0.0028	5.141
		HT	BAM	LW	AWP	0.005	0.0027	1.691
	Europe -> YNT	LW	DU	YNT	AWP	0.008	0.0021	3.683
		YNT	LUC	DU	AWP	0.006	0.0020	3.091
		YNT	LUC	LW	AWP	0.006	0.0020	2.835
	Europe -> WZS	LW	DU	WZS	AWP	0.010	0.0026	3.583
		WZS	LUC	DU	AWP	0.013	0.0019	6.515
		WZS	LUC	LW	AWP	0.013	0.0019	7.106
	recent DU -> BS	DU	LW	BS	AWP	0.011	0.0021	5.209
		BS	YNT	EWB	AWP	0.003	0.0019	1.519
		BS	YNT	DU	AWP	0.012	0.0021	5.390
		BS	YNT	LW	AWP	0.001	0.0017	0.845
	Cr -> LWU	LWU	WZS	Cr	AWP	0.067	0.0034	19.664
		LWU	EHL	Cr	AWP	0.039	0.0030	13.046

		LWU	YNT	Cr	AWP	0.069	0.0029	24.024
Asia -> Europe	BMX -> Europe	BMX	LUC	LW	AWP	0.008	0.0019	4.040
		BMX	LUC	DU	AWP	0.004	0.0019	2.137
		BMX	LUC	WDU	AWP	0.007	0.0018	3.790
		BMX	LUC	PT	AWP	0.008	0.0019	4.371
	EHL -> Europe	EHL	JH	LW	AWP	0.019	0.0019	9.527
		EHL	JH	DU	AWP	0.019	0.0020	9.702
		EHL	JH	WDU	AWP	0.019	0.0019	10.147
		EHL	JH	PT	AWP	0.019	0.0020	9.701
SWB -> Asia	WZS	MIN	SWB	AWP	0.018	0.0021	8.796	
	LUC	MIN	SWB	AWP	0.018	0.0023	7.974	
	BMX	MIN	SWB	AWP	0.017	0.0022	7.681	
	BS	MIN	SWB	AWP	0.013	0.0020	6.345	
	YNT	MIN	SWB	AWP	0.013	0.0018	7.321	
	SCT	MIN	SWB	AWP	0.014	0.0020	7.117	
JWP <- SWB -> SCW	HT	DU	JWP	AWP	0.017	0.0027	6.027	
	MIN	DU	JWP	AWP	0.018	0.0031	5.843	
	BAM	DU	JWP	AWP	0.023	0.0030	7.705	
	LWU	DU	JWP	AWP	0.015	0.0031	4.819	
	EHL	DU	JWP	AWP	0.020	0.0028	7.196	
	JH	DU	JWP	AWP	0.018	0.0031	5.828	
	BS	DU	JWP	AWP	0.024	0.0029	8.399	
	NJ	DU	JWP	AWP	0.025	0.0029	8.653	
	SCT	DU	JWP	AWP	0.026	0.0029	9.043	
	YNT	DU	JWP	AWP	0.025	0.0026	9.650	
	LUC	DU	JWP	AWP	0.025	0.0031	8.139	
	WZS	DU	JWP	AWP	0.024	0.0028	8.351	
	BMX	DU	JWP	AWP	0.023	0.0028	8.226	
	SCW	DU	JWP	AWP	0.024	0.0028	8.474	
	HT	EWB	JWP	AWP	0.019	0.0029	6.807	
	MIN	EWB	JWP	AWP	0.021	0.0031	6.820	
	BAM	EWB	JWP	AWP	0.026	0.0029	8.989	
	LWU	EWB	JWP	AWP	0.018	0.0032	5.695	
	EHL	EWB	JWP	AWP	0.023	0.0028	8.150	
	JH	EWB	JWP	AWP	0.021	0.0032	6.615	
	BS	EWB	JWP	AWP	0.027	0.0029	9.154	
	NJ	EWB	JWP	AWP	0.028	0.0030	9.374	
	SCT	EWB	JWP	AWP	0.029	0.0028	10.298	
	YNT	EWB	JWP	AWP	0.028	0.0027	10.543	
	LUC	EWB	JWP	AWP	0.028	0.0032	8.526	
	WZS	EWB	JWP	AWP	0.026	0.0029	8.923	
	BMX	EWB	JWP	AWP	0.026	0.0029	8.749	

	SCW	EWB	JWP	AWP	0.026	0.0028	9.552
	HT	MG	JWP	AWP	0.016	0.0030	5.383
	MIN	MG	JWP	AWP	0.018	0.0031	5.645
	BAM	MG	JWP	AWP	0.022	0.0030	7.438
	LWU	MG	JWP	AWP	0.015	0.0032	4.536
	EHL	MG	JWP	AWP	0.019	0.0029	6.747
	JH	MG	JWP	AWP	0.018	0.0032	5.417
	BS	MG	JWP	AWP	0.023	0.0030	7.710
	NJ	MG	JWP	AWP	0.025	0.0030	8.034
	SCT	MG	JWP	AWP	0.025	0.0029	8.653
	YNT	MG	JWP	AWP	0.025	0.0028	8.898
	LUC	MG	JWP	AWP	0.024	0.0032	7.506
	WZS	MG	JWP	AWP	0.022	0.0030	7.529
	BMX	MG	JWP	AWP	0.022	0.0031	7.272
	SCW	MG	JWP	AWP	0.023	0.0029	7.788

NOTE.—See supplementary table S1 for the full names of the population codes.

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473 **Supplementary Table S5.** Comparison of nucleotide diversity on autosomes and in the

474 MSY region.

	Pi (Chinese pigs with Asian haplotypes)	Pi (Chinese pigs with European haplotypes)	Pi (European pigs with European haplotypes)
Autosome	3.67×10^{-3}	3.66×10^{-3}	2.36×10^{-3}
MSY	1.18×10^{-4}	2.97×10^{-5}	5.00×10^{-5}
MSY:Autosome	1:31	1:123	1:47

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477 **Supplementary Table S6.** Higher than expected frequency of European Y
 478 chromosomes in Asian pig populations. P values are calculated using a binomial test
 479 over the range of expected Y chromosome frequencies. Even when all contributions
 480 from Europe are male, HT&MIN, WZS, and BS have higher than expected European
 481 Y chromosome frequencies. In contrast, the lack of European mitochondria is consistent
 482 with expectations.

Population	Mean X-chromosomal ancestry	Mean autosomal ancestry	<i>p</i> value range, mtDNA (number of European haplotypes/sample size)	<i>p</i> value range, Y chr (number of European haplotypes/sample size)
HT&MIN	0.16	0.20	0.002-1 (0/12)	0-0.022 (6/7)
WZS	0.043	0.078	0.35-1 (0/6)	0-0.026 (2/2)
YNT	0.021	0.045	0.32-1 (0/12)	0-0.68 (1/12)
BS	0.025	0.074	0.38-1 (0/6)	0-0.0034 (3/3)

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485 **Supplementary Table S7.** The parameters of the best-fitted demographic models of
 486 the target pairs of European and Chinese pig populations.

population pairs	s1	t1	nu11	nu12	m1_12	m1_21	t2	nu21	nu22	m2_12	m2_21	Nanc	Log likelihood
MIN&HT_ LW&MG	3.51E-01	5.13E-01	7.28E-01	1.78E-01	3.49E-01	2.60E+00	3.62E-02	2.67E-02	6.75E-02	6.75E+00	3.28E+00	91137.07	-1220.06
BS_WDU	9.48E-01	2.52E-01	5.66E-01	1.69E-01	2.70E-13	1.71E+00	1.90E-02	3.92E-01	1.82E-02	2.45E+00	3.19E+00	180007.45	-543.77
WZS_LW	5.02E-01	6.08E-01	9.47E-01	1.66E-01	2.25E-01	1.16E+00	1.30E-01	3.29E-01	6.56E-02	8.93E-01	5.21E+00	86643.27	-681.80
YNT_LW	3.74E-01	6.60E-01	1.21E+00	2.31E-01	2.90E-04	1.95E+00	1.13E-01	2.18E-01	7.65E-02	1.61E+00	3.52E+00	84721.51	1223.32

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491 **Supplementary Table S8.** The possibility of the simulated European Y frequency in
 492 Chinese pigs that match observed frequency in Chinese pigs.

population pairs	number of simulation repeats	number of simulations that match the observed data	<i>p</i> -value
MIN&HT_LW&MG	1000	38	0.038
BS_WDU	1000	3	0.003
WZS_LW	1000	209	0.209
YNT_LW	1000	89	0.089

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494 **Supplementary Table S9.** The geographical distribution of the two haplogroups in a large panel of 426 male pigs from around the globe.

Full_breed_name	Abbreviation	WildorDomesticType	Country	Location	Longitude	Latitude	Number	Asian haplogroup	European haplogroup	Sumatran haplotype
Hanjianghei	HJH	Domestic	China	Shanxi_Hanzhong	106.66	33.24	1	1	0	0
Ningxiang	NX	Domestic	China	Hunan_Ningxiang	112.36	28.13	1	1	0	0
Yushanhei	YSH	Domestic	China	Jiangxi_Yushan	118.17	28.76	1	1	0	0
Mi	MI	Domestic	China	Jiangsu_Changzhou	119.52	31.72	2	2	0	0
Lepinghua	LPH	Domestic	China	Jiangxi_Leping	117.15	28.98	3	3	0	0
Jinhua	JH	Domestic	China	Zhejiang_Jinhua	119.65	29.09	3	3	0	0
TibetTibetan1	TT1	Domestic	China	Tibet_Gongbujiangda	93.24	30.03	4	4	0	0
Tongcheng	TC	Domestic	China	Hubei_Xianning	113.8	29.23	5	5	0	0
Bamei	BAM	Domestic	China	Gansu_Longdong	107.63	35.75	6	6	0	0
Meishan	MS	Domestic	China	China_Jiading	121.27	31.38	6	6	0	0
Shaziling	SZL	Domestic	China	Hunan_Xiangtan	112.91	27.87	7	7	0	0
Neijiang	NJ	Domestic	China	Sichuan_Neijiang	104.85	29.81	8	8	0	0
Rongchang	RC	Domestic	China	Chongqing_Rongchang	106.21	29.62	8	8	0	0
Ganxi	GX	Domestic	China	Jiangxi_Shanggao	114.86	28.2	8	8	0	0
SichuanTibetan	SCT	Domestic	China	Sichuan_Litang	100.28	30	10	10	0	0
Congjiangxiang	CJX	Domestic	China	Guizhou_Congjiang	108.54	25.35	11	11	0	0
Laiwu	LWU	Domestic	China	Shandong_Laiwu	117.67	36.22	11	11	0	0
Diannan	DN	Domestic	China	Yunan_Xishuangbanna	101	21.5	14	14	0	0
Dongshan	DS	Domestic	China	Guangxi_Quanzhou	111.08	25.94	14	14	0	0
Daweizi	DWZ	Domestic	China	Hunan_Changsha	113.22	28.32	15	15	0	0
Erhualian	EHL	Domestic	China	Jiangsu_Jiaoxi	119.93	31.72	15	15	0	0
Bamaxiang	BMX	Domestic	China	Guangxi_Bama	107.25	24.15	15	15	0	0

SouthChineseWildBoar	SCWB	WildBoar	China	China_Shangyou	114.55	25.8	1	1	0	0
SouthChineseWildBoar	SCWB	WildBoar	China	China_Wuyishan	117	27.93	1	1	0	0
CenterChineseWildBoar	CCWB	WildBoar	China	China_Funiushan	111.82	33.87	1	1	0	0
NorthChineseWildBoar	NCWB	WildBoar	China	China_North	128.07	44.36	1	1	0	0
ChineseWildboar	CWB	WildBoar	China	China	114.35	37.35	1	1	0	0
SouthChineseWildBoar	SCWB	WildBoar	China	China_Xiangshan	119.73	29.48	2	2	0	0
SouthChineseWildBoar	SCWB	WildBoar	China	China_Nanchang	115.89	28.85	7	7	0	0
KoreanWildBoar	KWB	WildBoar	Korea	Korea	128.52	37.94	6	6	0	0
Khabarovsk	KBR	WildBoar	Russia	Russia_Khabarovsk	135.07	48.51	1	1	0	0
PrimoskyWildBoar	RPWB	WildBoar	Russia	Russia_Primosky	135	48.72	8	8	0	0
Qingping	QP	Domestic	China	Hubei_Dangyang	112.41	31.21	2	1	1	0
Hetao	HT	Domestic	China	Inner_Mongolia_Hetao	107.42	40.75	3	2	1	0
TibetTibetan2	TT2	Domestic	China	Tibet_Milin	94.22	29.22	5	4	1	0
YunnanTibetan	YNT	Domestic	China	Yunan_Diqing	99.71	27.83	12	11	1	0
GansuTibetan	GST	Domestic	China	Gansu_Hezuo	102.91	35	6	1	5	0
Dahe	DH	Domestic	China	Yunan_Fuyuan	104.37	25.47	7	4	3	0
Mingguang	MG	Domestic	China	Yunan_Tengchong	98.5	25.02	15	8	7	0
Xiangxihei	XXH	Domestic	China	Hunan_Luxi	110.22	28.22	14	4	10	0
Putianhei	PTH	Domestic	China	Fujian_Putian	118.94	25.5	1	0	1	0
Tunchang	TUN	Domestic	China	Hainan_Tunchang	110.06	19.35	1	0	1	0
Xu	XU	Domestic	China	Anhui_Nanling	118.29	30.9	1	0	1	0
Huai	HUAI	Domestic	China	Jiangsu_Donghai	118.79	34.56	2	0	2	0
Dahuabai	DHB	Domestic	China	Guangdong_Zhongshan	113.42	22.55	8	0	8	0
Wuzhishan	WZS	Domestic	China	Hainan_Wuzhishan	109.52	18.78	8	0	8	0
Min	MIN	Domestic	China	Northeast_China	126.28	46.27	9	0	9	0

Mashen	MAS	Domestic	China	Shanxi_Datong	113.29	40.11	13	0	13	0
Iberian	IB	Domestic	Europe	Spain_IberianPeninsula	-4.09	40.49	1	0	1	0
Semirechensk	SEM	Domestic	Kazakhstan	Kazakhstan_Southeast	66.92	48.02	1	0	1	0
Hampshire	HPS	Domestic	America	America_Kentucky	-84.27	37.85	2	0	2	0
Ukrainian white-steppe	UWS	Domestic	Ukraine	Ukraine_AskainaNova	32.31	48.23	2	0	2	0
Minisib	MSB	Domestic	Russia	Russia_Novosibirsk	82.94	55.01	2	0	2	0
Mangalica	MGL	Domestic	Europe	Hungary	19.5	47.16	3	0	3	0
Ukrainian spotted steppe	USS	Domestic	Ukraine	Ukraine_AskainaNova	32.31	48.23	3	0	3	0
Belorussian pork swine	BPS	Domestic	Belorussia	Belorussia	27.95	53.71	5	0	5	0
WhiteDuroc	WD	Domestic	America	America_Southburn	-86.61	36.33	6	0	6	0
Pietrain	PI	Domestic	Europe	Belgium_Piétrain	4.92	50.72	7	0	7	0
Red White Belted	RWB	Domestic	Ukraine	Ukraine_Nikolaev	32.39	49.44	7	0	7	0
Yorkshire	LW	Domestic	Europe	England_Yorkshire	-1.76	53.81	15	0	15	0
Landrace	LR	Domestic	Europe	Denmark	9.5	56.26	18	0	18	0
Duroc	DRC	Domestic	America	America_NewEngland	-70.78	44.1	18	0	18	0
EuropeanWildboar	EWB	WildBoar	Greece	Greece_Samos	26.98	37.76	1	0	1	0
EuropeanWildboar	EWB	WildBoar	Spain	Spain_Northeast	16.97	45.63	1	0	1	0
EuropeanWildboar	EWB	WildBoar	France	France	2.21	46.23	1	0	1	0
EuropeanWildboar	EWB	WildBoar	Switzerland	Switzerland_Malcantone	10.09	47.82	1	0	1	0
Ivanovo	IVA	WildBoar	Russia	Russia_Ivanovo	40.98	57.01	1	0	1	0
Kirov	KIR	WildBoar	Russia	Russia_Kirov	49.67	58.61	1	0	1	0
Krasnodar	KSD	WildBoar	Russia	Russia_Krasnodar	38.99	45.04	1	0	1	0
Leningrad	LNG	WildBoar	Russia	Russia_Leningrad	30.34	59.94	1	0	1	0
Omsk	OMSK	WildBoar	Russia	Russia_Omsk	73.32	54.99	1	0	1	0
Saratov	SRT	WildBoar	Russia	Russia_Saratov	45.96	51.6	1	0	1	0

Tver	TVER	WildBoar	Russia	Russia_Tver	35.92	56.86	1	0	1	0
Vladimir	VDM	WildBoar	Russia	Russia_Vladimir	40.42	56.15	1	0	1	0
EuropeanWildboar	EWB	WildBoar	Netherlands	Netherlands_Veluwe	5.83	52.24	2	0	2	0
Cheliabinsk	CLB	WildBoar	Russia	Russia_Cheliabinsk	61.44	55.17	2	0	2	0
Kharkov	KK	WildBoar	Ukraine	Ukraine_Kharkov	36.23	50	2	0	2	0
Tumen	TUM	WildBoar	Russia	Russia_Tumen	65.53	57.17	2	0	2	0
Volgograd	VGG	WildBoar	Russia	Russia_Volgograd	44.51	48.71	2	0	2	0
Arhangelsk	ARH	WildBoar	Russia	Russia_Arhangelsk	40.56	64.55	3	0	3	0
Kurgan	KGN	WildBoar	Russia	Russia_Kurgan	65.31	55.47	3	0	3	0
Smolensk	SML	WildBoar	Russia	Russia_Smolensk	32.05	54.79	3	0	3	0
SumatranWildBoar	SWB	WildBoar	Indonesia	Indonesia_Sumatra	101.34	-0.58	1	0	0	1

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Supplementary Table S10. 44 Models tested by jModeltest for the build 11.1 Y

chromosome.

Model	-lnL	K	AIC	delta	weight	cumWeight
TVM	21735.9018	211	43893.8036	0.0000	0.4295	0.4295
GTR	21735.9015	212	43895.8030	1.9994	0.1581	0.5876
TVM+G	21735.9035	212	43895.8071	2.0034	0.1577	0.7453
GTR+G	21735.9033	213	43897.8065	4.0029	0.0580	0.9090
TVMef	21742.8090	208	43901.6181	7.8144	8.63E-03	0.9565
TPM1uf	21741.8178	209	43901.6356	7.8319	8.56E-03	0.9651
TPM3uf	21742.3804	209	43902.7608	8.9571	4.88E-03	0.9700
SYM	21742.6264	209	43903.2527	9.4491	3.81E-03	0.9738
TVMef+G	21742.8108	209	43903.6215	9.8179	3.17E-03	0.9769
TIM1	21741.8178	210	43903.6356	9.8319	3.15E-03	0.9801
TPM1uf+G	21741.8195	210	43903.6389	9.8353	3.14E-03	0.9832
TIM3	21742.3798	210	43904.7597	10.9560	1.79E-03	0.9893
TPM3uf+G	21742.3821	210	43904.7642	10.9606	1.79E-03	0.9910
SYM+G	21742.6281	210	43905.2563	11.4526	1.40E-03	0.9924
TIM1+G	21741.8195	211	43905.6389	11.8353	1.16E-03	0.9948
TIM3+G	21742.3815	211	43906.7630	12.9593	6.59E-04	0.9972
TPM1	21747.5650	206	43907.1301	13.3264	5.48E-04	0.9977
TPM3	21748.2092	206	43908.4183	14.6147	2.88E-04	0.9985
TIM1ef	21747.3814	207	43908.7628	14.9592	2.42E-04	0.9987
TPM1+G	21747.5668	207	43909.1335	15.3299	2.01E-04	0.9989
TIM3ef	21748.0285	207	43910.0569	16.2533	1.27E-04	0.9992
TPM2uf	21746.1517	209	43910.3033	16.4997	1.12E-04	0.9993
TPM3+G	21748.2109	207	43910.4218	16.6182	1.06E-04	0.9994
TIM1ef+G	21747.3831	208	43910.7662	16.9626	8.90E-05	0.9995
HKY	21747.5741	208	43911.1482	17.3445	7.36E-05	0.9995
TIM3ef+G	21748.0302	208	43912.0604	18.2568	4.66E-05	0.9997
TIM2	21746.1517	210	43912.3034	18.4998	4.13E-05	0.9998
TPM2uf+G	21746.1534	210	43912.3068	18.5032	4.12E-05	0.9998
TrN	21747.5741	209	43913.1482	19.3446	2.71E-05	0.9999
HKY+G	21747.5758	209	43913.1516	19.3479	2.70E-05	0.9999
TIM2+G	21746.1534	211	43914.3068	20.5031	1.52E-05	0.9999
TrN+G	21747.5758	210	43915.1515	21.3479	9.94E-06	1.0000
K80	21752.9698	205	43915.9396	22.1359	6.70E-06	1.0000
TPM2	21752.4640	206	43916.9280	23.1244	4.09E-06	1.0000
TrNef	21752.7853	206	43917.5706	23.7669	2.97E-06	1.0000
K80+G	21752.9715	206	43917.9429	24.1393	2.46E-06	1.0000
TIM2ef	21752.2754	207	43918.5508	24.7472	1.82E-06	1.0000
TPM2+G	21752.4657	207	43918.9314	25.1278	1.50E-06	1.0000
TrNef+G	21752.7870	207	43919.5740	25.7704	1.09E-06	1.0000
TIM2ef+G	21752.2772	208	43920.5544	26.7508	6.67E-07	1.0000
JC	22597.8019	204	45603.6037	1709.8001	0.00E+00	1.0000

F81	22595.3073	207	45604.6146	1710.8109	0.00E+00	1.0000
JC+G	22597.8024	205	45605.6048	1711.8012	0.00E+00	1.0000
F81+G	22595.3079	208	45606.6157	1712.8121	0.00E+00	1.0000

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497

498 **Supplementary Table S11.** Estimates of the TMRCA of phylogenetic nodes of

499 particular interest using the MSY sequence via BEAST when divergence time estimates

500 of *Sus verucosus* (JVWP) and *Sus scrofa* was set as 4.2 million years ago.

Node	Estimate of T _{MRC} A (Thousand years)	95% highest posterior density (HPD) interval
All <i>Sus scrofa</i>	1253	1220-1287
Sumatran wild boars and Chinese pigs with Asian haplotype	703	633-767
All pigs with Asian haplotypes	133	128-139
All pigs with European haplotypes	113	108-120
Chinese pigs with European haplotypes	25	23-27
Hetao pig and Large White	1.1	0.7-1.6
Min pig and SwallowBelly Manglica	0.9	0.6-1.3
Yunnan Tibetan pig and Large White	0.6	0.3-0.9
Wuzhishan pig and Large White	0.5	0.3-0.8
Baoshan pig and White Duroc	0.3	0.1-0.4

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504 **Supplementary Table S12.** Estimates of the TMRCA of phylogenetic nodes of
 505 particular interest using the MSY sequence via BEAST when divergence time estimates
 506 of *Sus verucosus* (JVWP) and *Sus scrofa* was set as 1.36 million years ago.

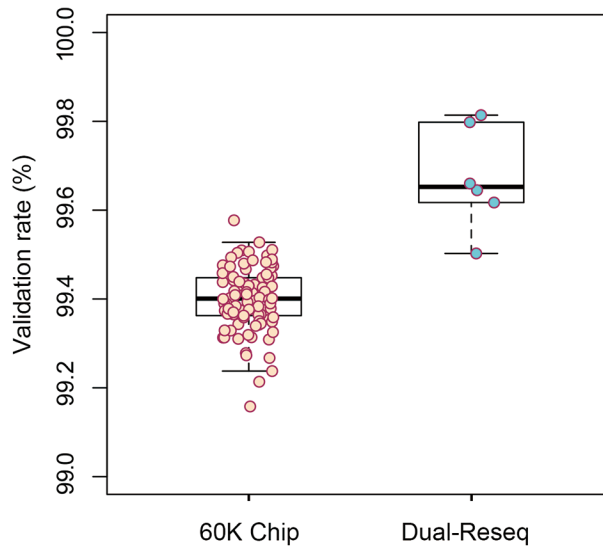
Node	Estimate of T_{MRCA} (Million years)	95% highest posterior density (HPD) interval
All <i>Sus scrofa</i>	0.225	0.192-0.231
Sumatran wild boars and Chinese pigs with Asian haplotype	0.216	0.189-0.223
All pigs with Asian haplotypes	0.025	0.024-0.027
All pigs with European haplotypes	0.022	0.020-0.023
Chinese pigs with European haplotypes	0.007	0.006-0.008

507

508 **Supplementary Table S13.** Filter standard set as default options in the variant calling
 509 of Platypus.

Label	Meaning	Filter
HapScore	The calling window has multiple haplotypes	> 4
strandBias	Variant fails strand-bias filter	< 0.001
alleleBias	Variant fails allele-bias filter	< 0.001
badReads	Variant is supported only by low-quality reads	> 15
Q20	Variant call has low posterior Phred score	< 20
MQ	Variant call has low root mean square of mapping qualities of reads at the variant position	< 40
QD	Ratio of variant quality to number of supporting reads is low	< 10
SC	Sequence context surrounding variant has low complexity	> 0.95
PASS	Variant passes all filters	

510 **4. Supplementary Figures**



511

512 **Supplementary Figure S1. SNPs accuracy validation by the data of 60K chip array**
513 **and dual-resequencing.** The boxplot labelled by 60K Chip means that 53,908
514 polymorphic loci with same positions to the 60K chip array were extracted from our
515 SNPs set of the 98 pigs with resequencing data and 60K chip array data simultaneously,
516 and 99.4% of informative SNPs were consistent to the SNP genotypes from the 60K
517 chip arrays. The boxplot labelled by Dual-Reseq means that six pigs were re-sequenced
518 twice and called SNPs using Platypus, and 99.6% were consistent with the SNPs of
519 their duplicate individuals.

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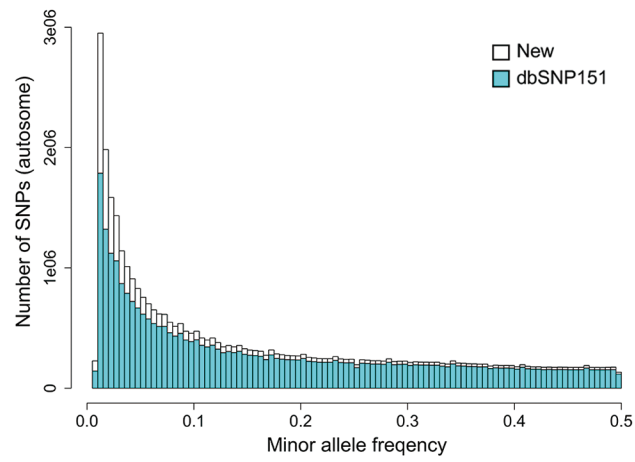
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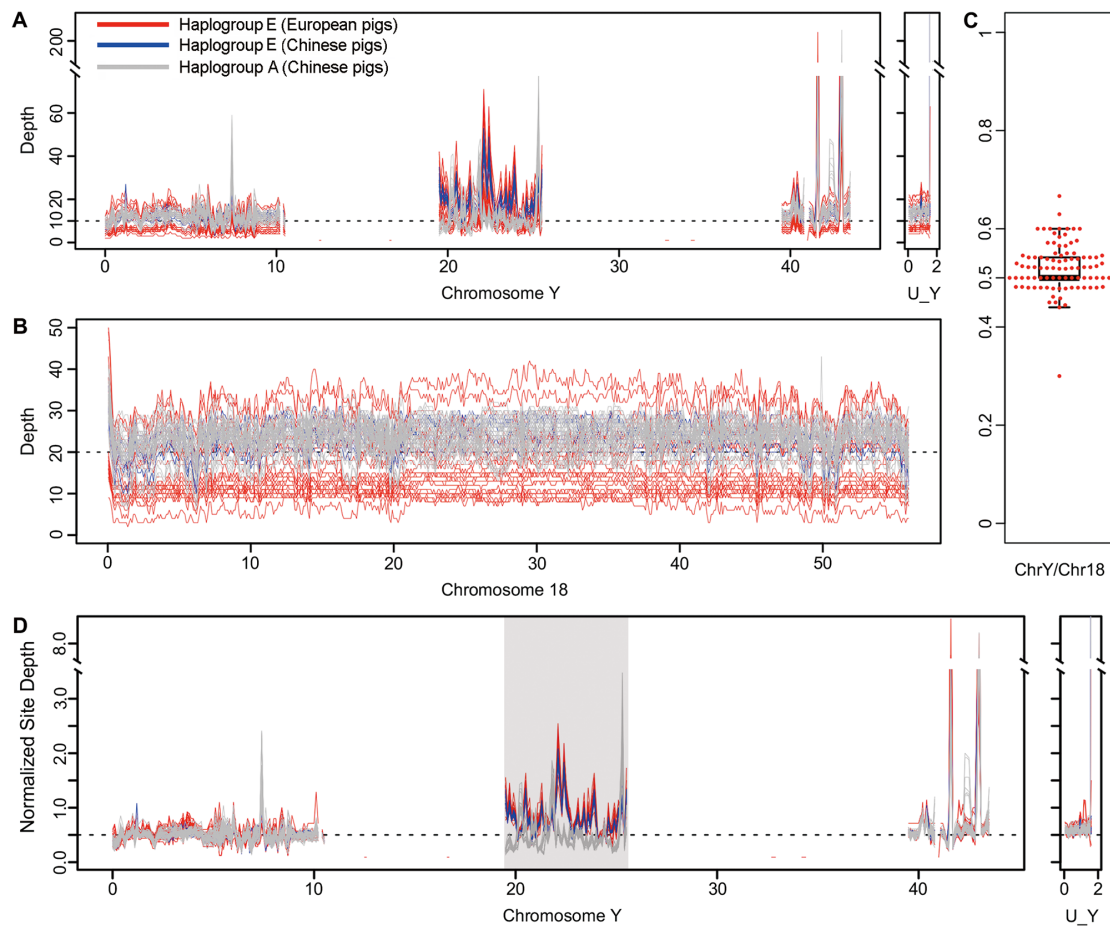
529 **Supplementary Figure S2. Autosomal SNP distribution of 200 Eurasian pigs.** Cyan

530 histogram indicates the distribution of SNPs shared with Build 151 of the *Sus scrofa*

531 dbSNP on the NCBI GenBank database. Blank parts indicate the novel SNPs identified

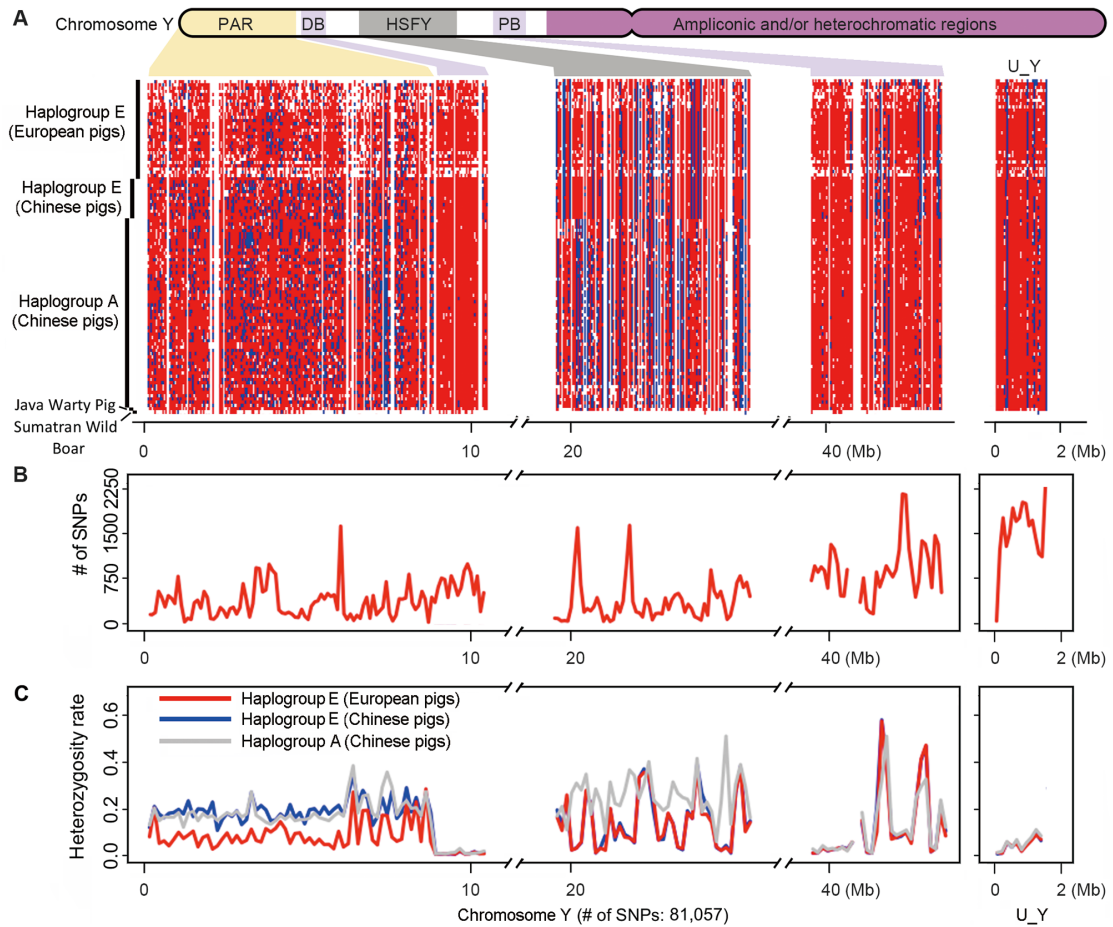
532 in this study.

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534

535 **Supplementary Figure S3. Depth distribution along the effective regions on the Y**
 536 **chromosome and chromosome 18 of Eurasian pigs based on Build 11.1 reference**
 537 **genome in a window size of 100 Kb with a step size of 50 Kb.** (A) The distribution
 538 of depth along the effective regions on the Y. (B) The distribution of depth along
 539 chromosome 18. (C) Boxplot of the ratio of (median) average depths of the Y and
 540 chromosome 18 among Eurasian pigs. (D) The distribution of normalized depth along
 541 the effective regions on the Y. The depth in each window of each individual is divided
 542 by the average depth of whole chromosome 18 of that individual. Haplogroup E
 543 (European pigs), Haplogroup E (Chinese pigs) and Haplogroup A (Chinese pigs) are
 544 indicated by red, blue and grey, respectively. The grey background in **supplementary**
 545 **fig. S3D** marks abnormally high depth in the PB interval (19.5Mb-25.5Mb) of
 546 Haplogroup E.



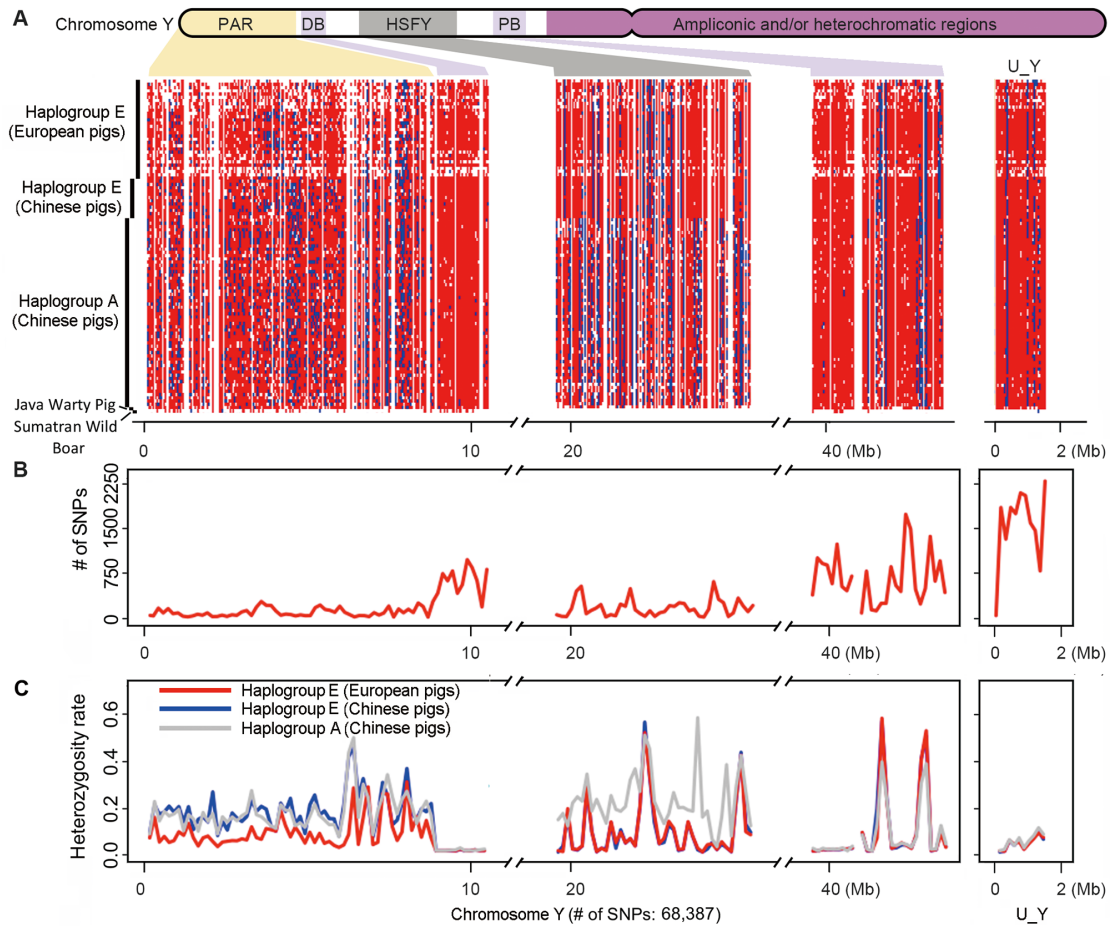
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548 **Supplementary Figure S4. The pattern of heterozygous position distribution on**
 549 **the Y chromosome derived from the initial called 81,057 SNPs among all male**
 550 **individuals. (A) The distribution of heterozygous sites along the Y chromosome.**
 551 **Alleles that are homozygous or heterozygous are indicated by red or blue, respectively.**
 552 **(B) The pattern of SNPs distribution in a window size of 150 Kb along the Y**
 553 **chromosome. (C) The distribution of heterozygosity rate in a window size of 150 Kb**
 554 **along the Y chromosome among Eurasian pigs.**

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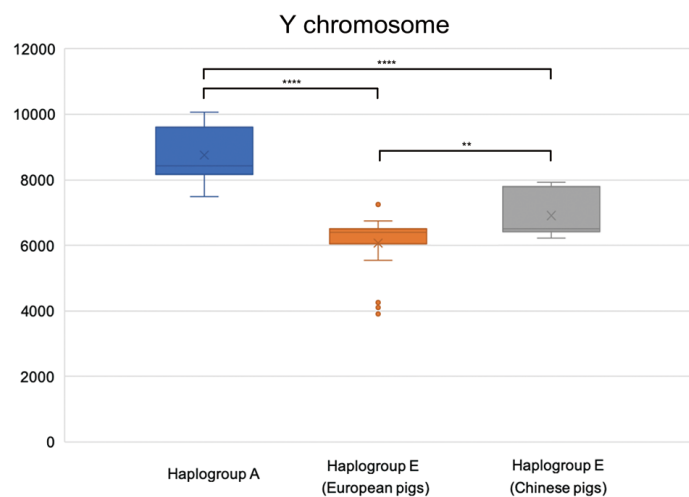


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559 **Supplementary Figure S5. The pattern of heterozygous position distribution on**
 560 **the Y chromosome derived from 68,387 SNPs after removing SNPs same as the**
 561 **SNPs called by the reads of female individuals misaligned to Y chromosome**
 562 **reference sequence among all male individuals. (A) The distribution of heterozygous**
 563 **sites along the Y chromosome. Alleles that are homozygous or heterozygous are**
 564 **indicated by red or blue, respectively. (B) The pattern of SNPs distribution in a window**
 565 **size of 150 Kb along the Y chromosome. (C) The distribution of heterozygosity rate in**
 566 **a window size of 150 Kb along the Y chromosome among Eurasian pigs.**

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570 **Supplementary Figure S6. The comparison of heterozygous sites distribution on**
 571 **the Y chromosome derived from 68,387 SNPs after removing SNPs same as the**
 572 **SNPs called by the reads of female individuals misaligned to Y chromosome**
 573 **reference sequence among Haplogroup A, Haplogroup E (European pigs) and**
 574 **Haplogroup E (Chinese pigs).**

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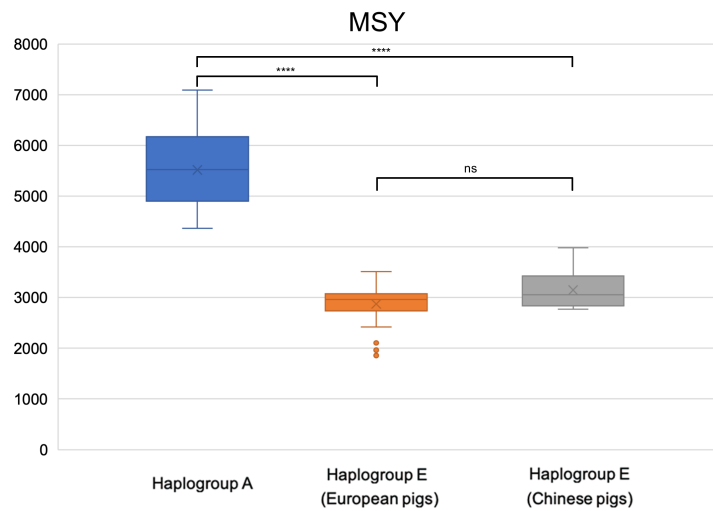
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582 **Supplementary Figure S7. The comparison of heterozygous sites distribution on**
 583 **the MSY among Haplogroup A, Haplogroup E (European pigs) and Haplogroup**
 584 **E (Chinese pigs).**

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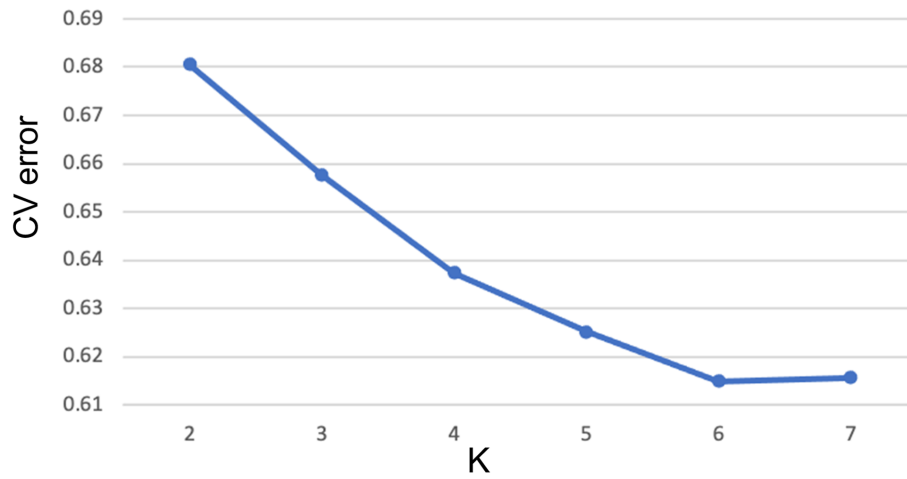
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599 **Supplementary Figure S8.** The CV error for the ADMIXTURE analysis at K values
600 ranging from 2 to 7.

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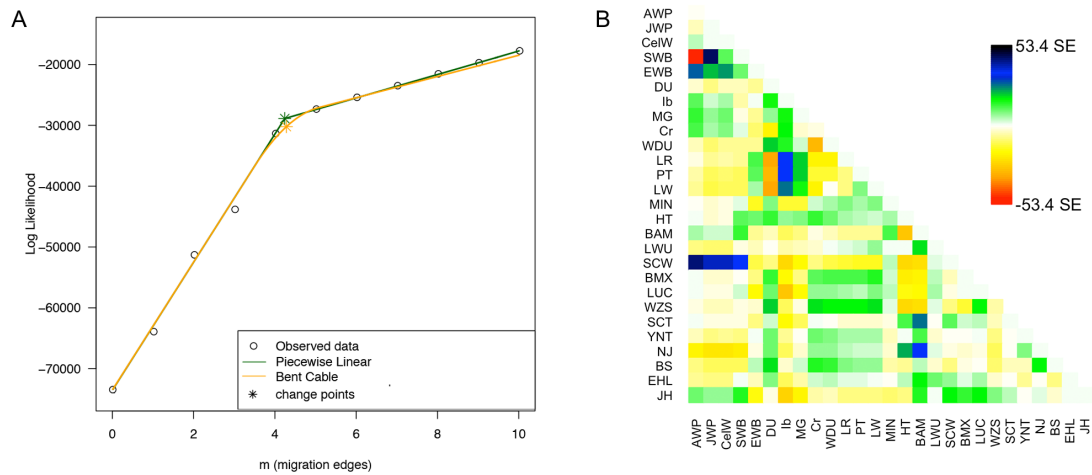
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614 **Supplementary Figure S9. Determination of the migration edge number in the**

615 **TreeMix model and residual heatmap with 4 migration events. (A) Observed Log**

616 **likelihood values are plotted against the number of migration edges tested from 0 to 10,**

617 **and two models are fitted to the data. Both the piecewise and the Bent Cable fitting**

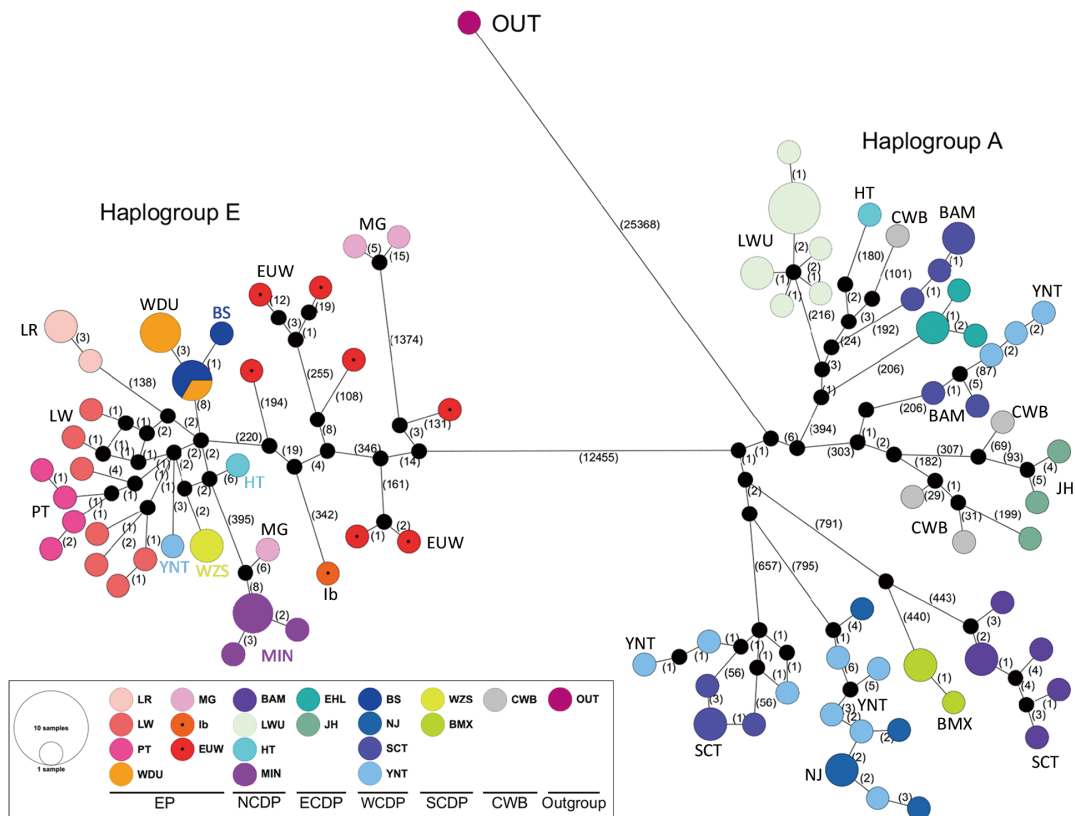
618 **delivered an optimal value of 4 for the number of migration edges (change points). (B)**

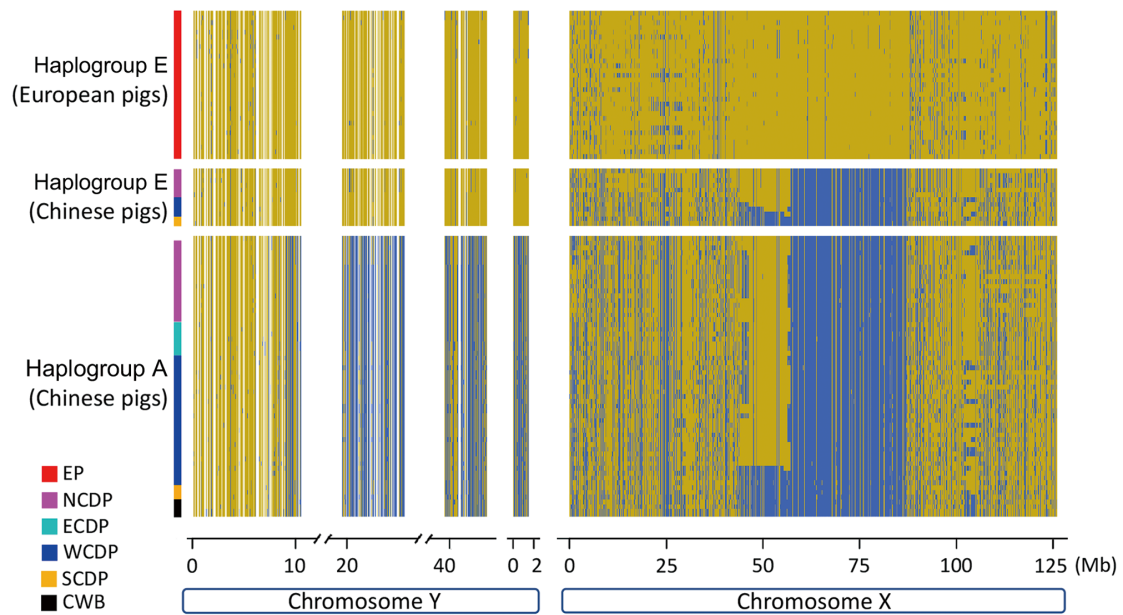
619 **Residual fit from the maximum likelihood tree with four migration edges. The**

620 **abbreviations EP, NCDP, ECDP, WCDP, SCDP, and CWB are as in Figure 1; Full**

621 **names of the pig breeds are detailed in Supplementary Table S1. B.**

622





630

631 **Supplementary Figure S11. The different haplotype patterns between the Y**

632 **chromosome and the X chromosome in Eurasian pigs.** This plot includes all 101

633 Eurasian male pigs, which are divided into three groups: European pigs in MSY

634 Haplogroup E, Chinese pigs in MSY Haplogroup E and Chinese pigs in MSY

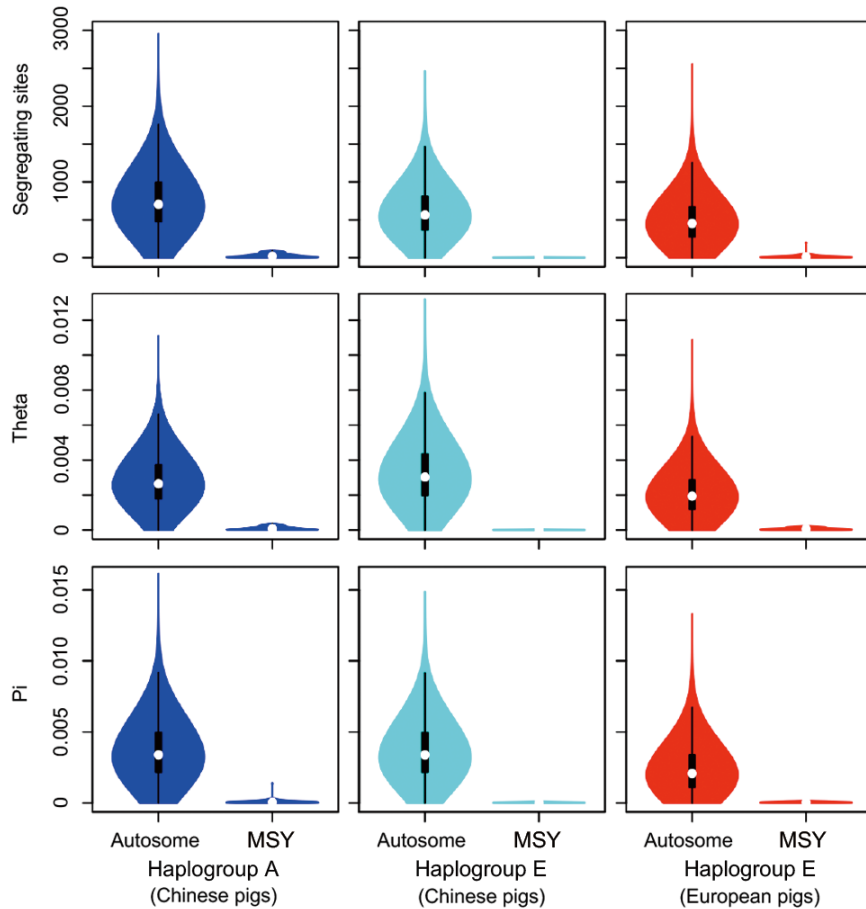
635 Haplogroup A. The haplotypes are constructed for each individual using all qualified

636 SNPs on Y and X chromosome. Alleles that are identical and different from the ones in

637 the Duroc reference genome are indicated by orange and blue, respectively. The

638 abbreviations EP, NCDP, ECDP, WCDP, SCDP and CWB are as in **Figure 1**.

639



640

641 **Supplementary Figure S12. Comparison of nucleotide variability within the**
 642 **proximal and distal regions of the Y chromosome and on autosomes.** There are two
 643 different haplogroups on the proximal and distal regions of the Y chromosome (MSY)
 644 in all tested Eurasian pigs. Haplogroup A consists of Chinese pigs with Asian-origin
 645 MSY; Haplogroup E contains European pigs and some Chinese pigs with European-
 646 origin MSY. Statistics of segregation sites, theta, Pi values were calculated in a window
 647 size of 50 kb for European pigs in Haplogroup E, Chinese pigs in Haplogroup E, and
 648 Chinese pigs in Haplogroup A, respectively. Pi, nucleotide diversity referred to Tajima's
 649 Pi; theta, nucleotide diversity referred to Watterson's theta.

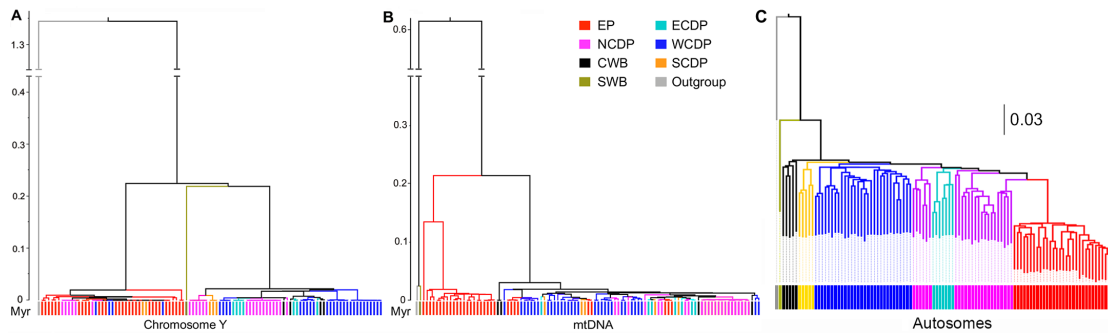
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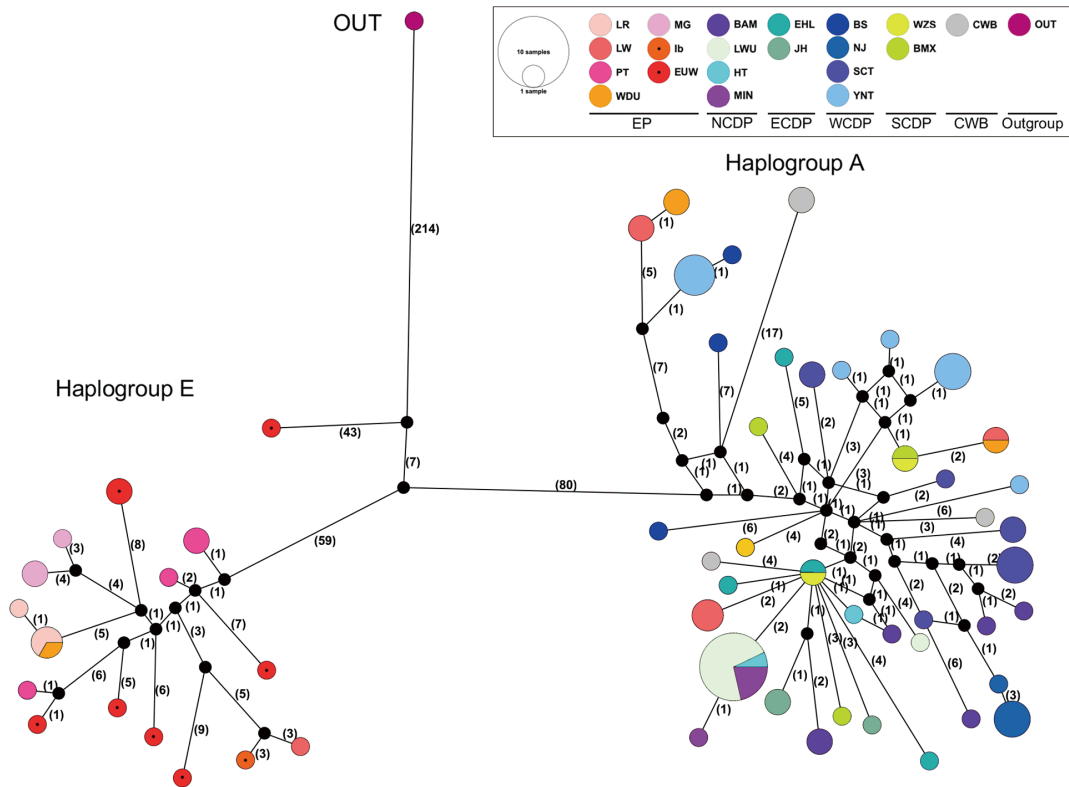
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Supplementary Figure S13. Different phylogenetic relationships of *Sus* revealed by Y chromosome, mtDNA and autosomes. (A) Phylogenetic relationships among the 103 male Eurasian pigs constructed using the MSY sequence of the Build 11.1 Y chromosome. Inferred divergence time is shown on the Y-axis of the Bayesian tree. (B) Phylogenetic relationships among the 103 male Eurasian pigs constructed using the Build 11.1 chrM sequences via BEAST. Divergence time estimate of EUW (WB21M05) and CWB (CB11-2), 0.219 million years (Zhang et al. 2021), was used as softbound priors. (C) Neighbor-joining tree of these pigs based on autosomal data. The abbreviations EP, ECDP, NCDP, WCDP, CWB, SCDP and SWB are described in figure 1. *S. verrucosus* (Java warty pig) was set as the outgroup.



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672 **Supplementary Figure S14. Median joining haplotype network of chrM sequences**

673 **(n = 102).** The circles represent different haplotypes with size proportional to the

674 number of individuals represented. Lines connect each haplotype to its most similar

675 relative and the number on the lines indicate mutation steps. **Haplogroup E here**

676 **includes chrM haplotypes present only in Europe and haplogroup A includes chrM**

677 **haplotypes fixed in Asia but present in some European breeds.** Colors correspond with

678 the different pig breeds. Full names of the pig breeds are detailed in **supplementary**

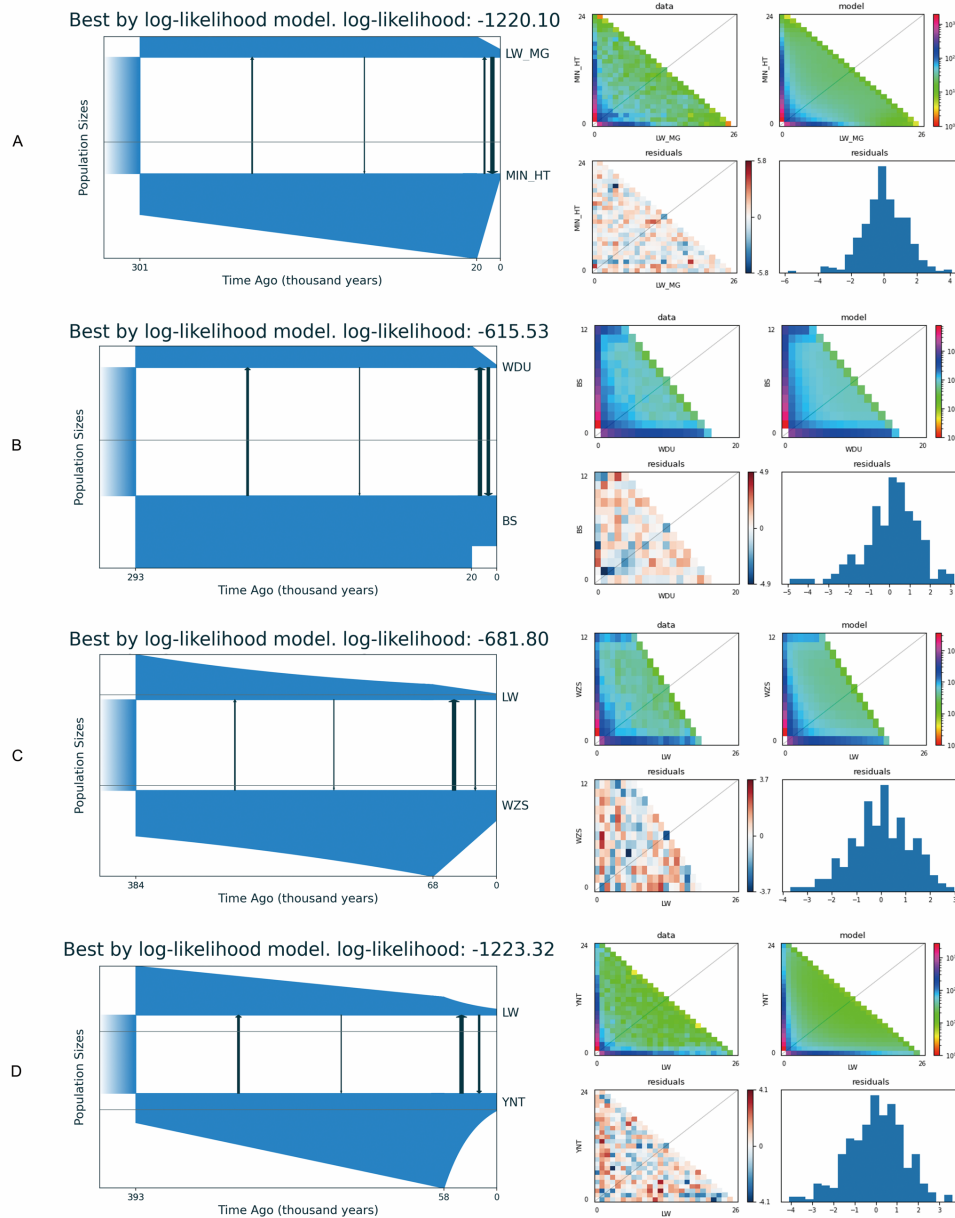
679 **table S1.**

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685 **Supplementary Figure S15. Comparisons of allele frequency spectra (AFS)**

686 **between the modelled and real data of four pairs of European and Chinese pig**

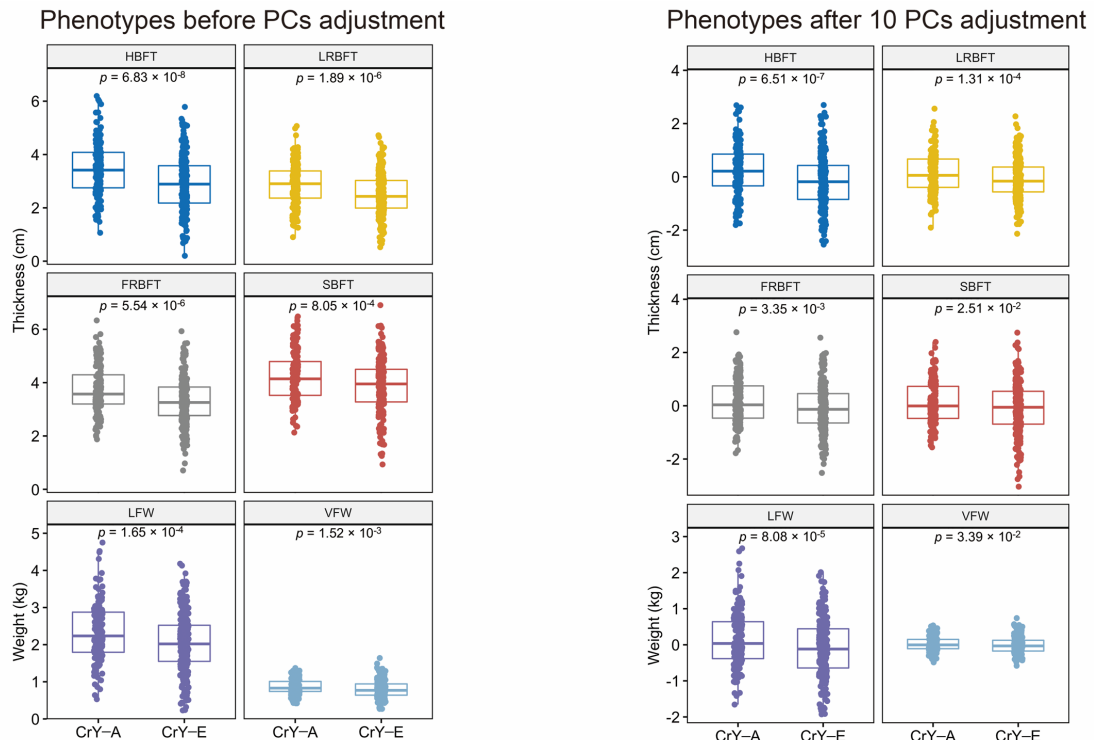
687 **populations using $\partial a \partial i$: (A) LW&MG and MIN&HT; (B)WDU and BS; (C) LW and**

688 **WZS; (D) LW and YNT. In every panel, there are five plots, which are: the best-fitted**

689 **demographic model; marginal AFS of the real data for each pair of populations; AFS**

690 **of the maximum-likelihood model simulation based on the real data; The residuals**

691 **between the modelled and real data are shown in heat maps and bar graphs.**



#N	eigenvalue	difference	twstat	p-value	effect. n
1	11.1367	NA	1.924	0.0118162	125.93
2	9.88512	-1.25158	1.464	0.0246142	143.474
3	9.38544	-0.49968	2.664	0.00322227	161.564
4	8.35373	-1.03171	2.395	0.00524606	191.574
5	7.68496	-0.66877	2.885	0.00212799	225.944
6	6.86444	-0.82052	2.43	0.00492809	273.987
7	6.09358	-0.77086	1.233	0.0348088	327.99
8	5.7178	-0.37578	1.392	0.027443	376.408
9	5.26814	-0.44966	0.784	0.0105222	438.039
10	4.99697	-0.27117	1.001	0.0652097	500.879
11	4.81715	-0.17982	1.993	0.0505362	582.871
12	4.35609	-0.46106	0.328	0.115895	720.843
13	4.19474	-0.16135	0.758	0.0674937	827.679
14	3.8763	-0.31844	-0.898	0.385593	981.569
15	3.76082	-0.11548	-0.734	0.338299	1079.798

692

693 **Supplementary Figure S16. Comparison of fatness traits between the male pigs**

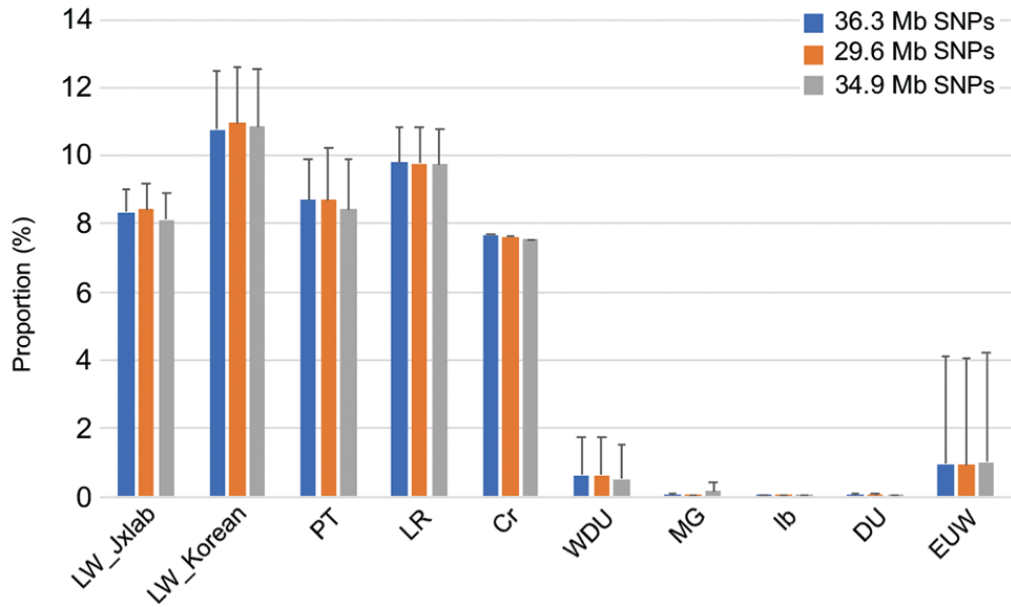
694 **with Chinese chromosome Y and with European chromosome Y. (A) Phenotypes**

695 **before PCs adjustment. (B) the number of statistically significant principal components**

696 **using twstats method. (C) Phenotypes After PCs adjustment.**

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700 **Supplementary Figure S17. Estimated percentage of the Asian component of**

701 **European pigs from an unsupervised ADMIXTURE analysis with K = 2.** Blue bars

702 show the results of 36.3M SNPs used in our present study; red bars show the results of

703 29.6 M SNPs shared with Build 151 of the *Sus scrofa* dbSNP database; gray bars show

704 the results of 34.9M SNPs called using the variance of Build 151 of the *Sus scrofa*

705 dbSNP as known variants in the 200 Eurasian pigs. LW_Jxlab, Large White our group

706 sequenced; LW_Korean, Large White submitted by a Korean group; PT, Pietran; LR,

707 Landrace; Cr, Creole; WDU, White Duroc; MG, Mangalica; Ib, Iberian; DU, Duroc;

708 EUW, European wild boar. All the SNPs dataset were filtered with LD of $r^2 = 0.4$.

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