a

High quality data (Gb) — Mapping ratio (%, against the reference genome)

b

Orphan reads
One End Anchor (OEA) reads

c

Depth coverage of missing gene embedded scaffolds by orphan reads

d

Coverage at least 1 × (%)
Coverage at least 2 × (%)
Coverage at least 3 × (%)
Coverage at least 4 × (%)
Coverage at least 10 × (%)

Erhualian
(*n* = 5)

Min
(*n* = 6)

Hetao
(*n* = 6)

Luchuan
(*n* = 6)

Chinese
wild boar
(*n* = 6)

Bamaxiang
(*n* = 6)

Laiwu
(*n* = 6)

Wuzhishan
(*n* = 6)

Duroc
(*n* = 20)

Large White
(*n* = 15)

Yucatan
(*n* = 12)

Korean wild boar
(*n* = 10)

Landrace
(*n* = 13)

Selective sweep screen
(*n* = 47)

Selected loci genotyping
(*n* = 70)

e

Ai et al. (2015) (n = 47)				Moon et al. (2015); Choi et al. (2015) (n = 70)				
SRS465717	SRS465764	SRS465773	SRS465709	SRS703313	SRS703266	SRS703324	SRS703290	SRS703302
SRS465718	SRS465767	SRS465770	SRS465710	SRS703308	SRS703279	SRS703326	SRS703287	SRS703303
SRS465716	SRS465761	SRS465771		SRS703315	SRS703261	SRS703319	SRS703283	SRS703304
SRS465719	SRS465760	SRS465768		SRS703314	SRS703267	SRS703317	SRS703291	SRS703295
SRS465721	SRS465758	SRS465769		SRS703316	SRS703272	SRS703327	SRS703284	SRS703305
SRS465720	SRS465757	SRS465725		SRS703307	SRS703257	SRS703321	SRS703282	SRS703300
SRS465774	SRS465756	SRS465726		SRS703311	SRS703260	SRS703325	SRS703281	SRS703294
SRS465776	SRS465759	SRS465724		SRS703312	SRS703265	SRS703320	SRS703293	SRS703301
SRS465775	SRS465753	SRS465723		SRS703309	SRS703273	SRS703323	SRS703292	SRS703298
SRS465714	SRS465750	SRS465727		SRS703310	SRS703274	SRS703322	SRS703289	SRS703299
SRS465715	SRS465754	SRS465722		SRS703264	SRS703262	SRS703334	SRS703288	
SRS465763	SRS465751	SRS465712		SRS703263	SRS703276	SRS703333	SRS703285	
SRS465765	SRS465752	SRS465711		SRS703278	SRS703271	SRS703332	SRS703286	
SRS465766	SRS465755	SRS465708		SRS703258	SRS703275	SRS703336	SRS703296	
SRS465762	SRS465772	SRS465713		SRS703259	SRS703277	SRS703331	SRS703306	

Supplemental Fig. S41. Retrieving orphan reads against the reference genome from 117 publicly available pig genome resequencing data[36-38]. Summary of mapping ratio **(a)** and unmapped reads **(b)** against the reference genome. For OEA reads, only one end was counted. Depth **(c)** and coverage **(d)** of the orphan reads against the intact scaffolds that harboured missing genes across ten assemblies (~636.38 Mb per assembly). **(e)** Accession numbers of 117 publicly available pig genomes. Of which, 6 wild boars and 41 domestic pigs in China (~27.29 × depth coverage of reference genome; ~3.91 Gb orphan reads per individual; ~14.43 × depth coverage of missing genes embedded scaffolds) were subjected to selective sweep screen. The rest of 70 individuals (including 10 Korean wild boars and 60 European/ North American domestic pigs) with the relatively lower depth coverage (~15.87 × depth coverage of reference genome; ~2.60 Gb orphan reads per individual; ~6.99 × depth coverage of missing gene embedded scaffolds) were used to investigate regional genotypic pattern at certain loci of interest.