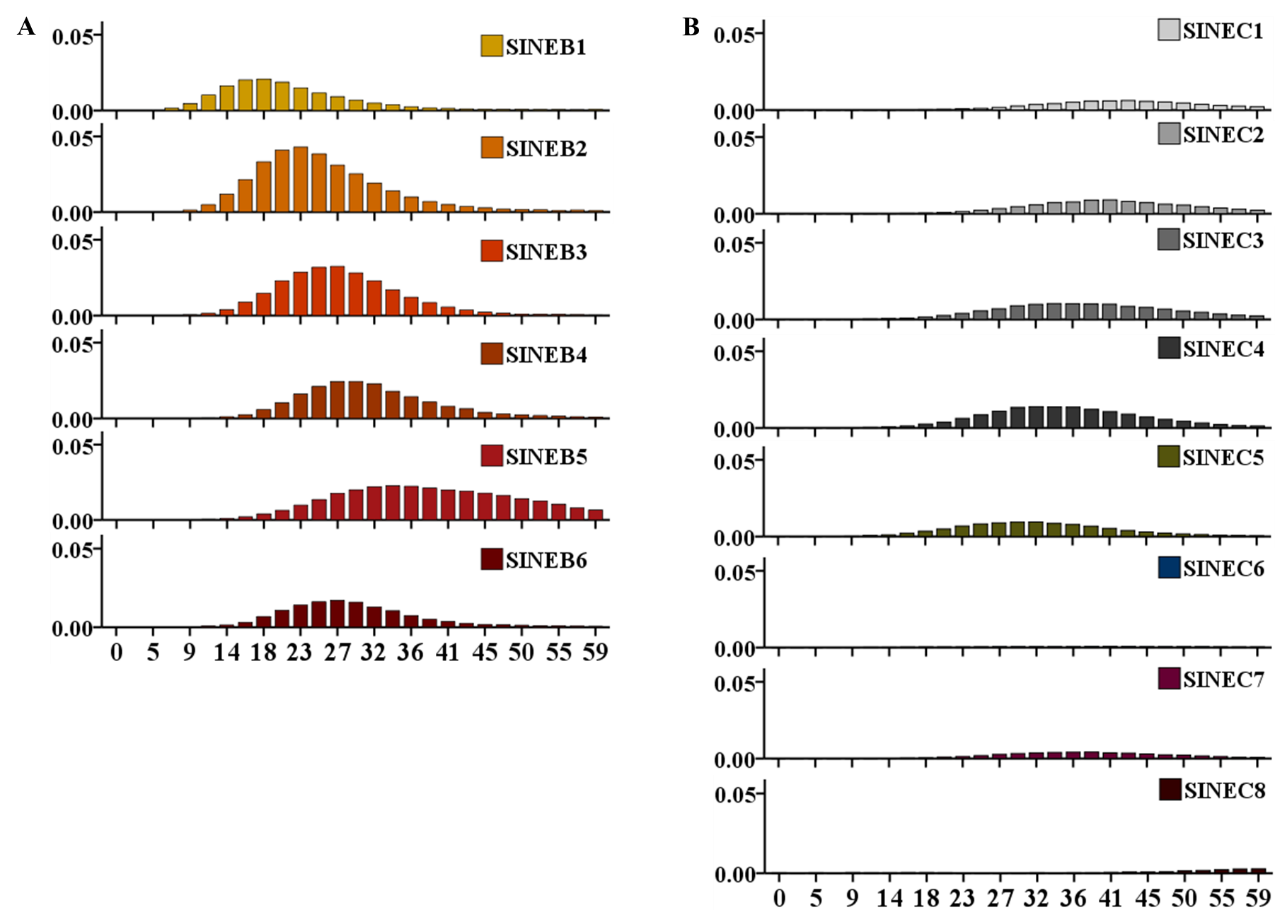
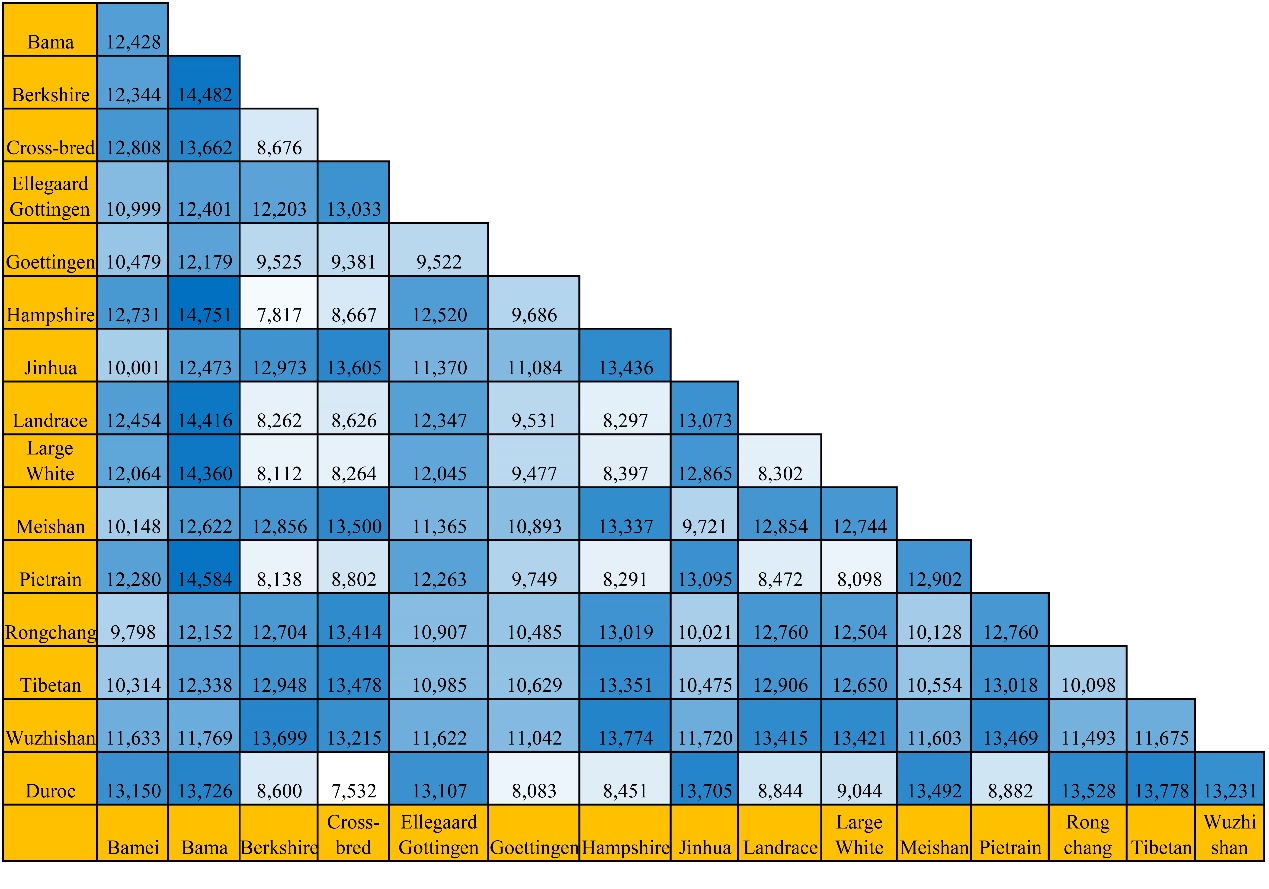


**Fig. S1.** Alignment of the sequences of SINEA1-A11 subfamilies.



**Fig. S2.** Insertion ages of SINEB and SINEC families.



**Fig. S3.** Distribution of the differential SINE RIP alleles between each pair of genomes.

**Table S1.** Predicted polymorphic ratio of SINE insertions from different subfamilies located in intergenic and intragenic regions.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Name of SINE subfamily (age) | Intragenic SINE insertions | | | |  | Intergenic SINE insertions | | |
| No. of blast insertions | No. of predicted  polymorphic insertions | | The ratio of polymorphisms |  | No. of blast insertions | No. of predicted  polymorphic insertions | The ratio of polymorphisms |
| SINEA1 （2Ma） | 200 | 45 | 22.5 | |  | 200 | 53 | 26.5 |
| SINEA2 （5Ma） | 200 | 18 | 9.0 | |  | 200 | 21 | 10.5 |
| SINEA3 （5Ma） | 200 | 10 | 5.0 | |  | 200 | 25 | 12.5 |
| SINEA4 （11Ma） | 200 | 4 | 2.0 | |  | 200 | 1 | 0.5 |
| SINEB2 （23Ma） | 200 | 0 | 0.0 | |  | 200 | 0 | 0.0 |
| SINEB6 （27Ma） | 200 | 0 | 0.0 | |  | 200 | 1 | 0.5 |
| SINEC4 （32Ma） | 200 | 0 | 0.0 | |  | 200 | 0 | 0.0 |

**Table S2.** Polymorphic ratio of randomly selected polymorphic and non-polymorphic SINE insertions following PCR verification.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| SINE type | No. of randomly selected polymorphic or non-polymorphic insertions | | | | |
| Predicted polymorphic by Blast | Confirmed polymorphic by PCR |  | Predicted non-polymorphic by Blast | Confirmed polymorphic by PCR | |
| SINEA1-A3 | 18 | 16 (83.33%) |  | 5 | 2 (40.00%) | |
| SINEA4-A11 | 4 | 4 (75.00%) |  | 9 | 2 (22.22%) | |
| SINEB | 1 | 1 (100.00%) |  | 2 | 0 (0.00%) | |
| SINEC | 2 | 1 (100.00%) |  | 9 | 0 (0.00%) | |
| Total | 25 | 22 (88.00%) |  | 25 | 4 (16.00%) | |

**Table S3.** Summary of the number of SINE insertions in the protocol used for annotating SINE RIPs.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genome | No. of SINE insertions | | | | |
| Repeatmasker result1 | Successfully mapped | Differential between genomes | Verified by Blast | Finally remained |
| Bama | 104260 | 100074 | 17641 | 6714 | 6603 |
| Bamei | 89114 | 86939 | 13555 | 4306 | 4306 |
| Berkshire | 92230 | 90415 | 9746 | 2856 | 2856 |
| Cross-bred | 102103 | 98412 | 9388 | 3054 | 2995 |
| Ellegaard Gottingen minipig | 81923 | 80073 | 13588 | 4222 | 4215 |
| Goettingen | 71314 | 68595 | 6395 | 736 | 736 |
| Hampshire | 93288 | 91538 | 9965 | 2994 | 2993 |
| Jinhua | 90567 | 88377 | 14522 | 4916 | 4915 |
| Landrace | 92016 | 90259 | 9991 | 2962 | 2961 |
| Large White | 91345 | 89580 | 10008 | 2893 | 2893 |
| Meishan | 88877 | 86708 | 14108 | 4714 | 4714 |
| Pietrain | 92023 | 90267 | 9984 | 2990 | 2990 |
| Rongchang | 88655 | 86424 | 13713 | 4426 | 4423 |
| Tibetan | 90277 | 87734 | 14916 | 4567 | 4536 |
| Wuzhishan | 91357 | 88602 | 15815 | 5272 | 5260 |
| Duroc | 103065 | 103065 | 80502 | 36452 | 13223 |
| Total | 1462414 | 1427062 | 263837 | 94074 | 70619 |

1: **Repeatmasker result**filtered with (1) SINEA1-3, (2) score≥1000, (3) length:100-330.

**Table S4.** Positive ratios of SINE RIPs obtained by PCR verification for rare SINE RIPs.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Rare SINE RIPs type | No. of genome | No. of SINE RIPs be verified | No. of polymorphic sites | No. of Non- polymorphic sites | Positive ratio |
| Deletion | 2 | 28 | 9 | 19 | 32.14% |
|  | 3 | 32 | 12 | 20 | 37.50% |
|  | 4 | 32 | 26 | 6 | 81.25% |
| Insertion | 1 | 30 | 24 | 6 | 80.00% |
|  | 2 | 30 | 25 | 5 | 83.33% |
|  | 14 | 18 | 15 | 3 | 83.33% |
|  | 15 | 3 | 3 | 0 | 100.00% |

**Table S5.** Positive ratios of the 36,284 SINE RIPs obtained by PCR verification with limited samples.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Source of SINE RIPs | Total No. of SINE RIPs | No. of SINE RIPs show polymorphic | Positive ratio | No. of uncertain SINE RIPs | No. of SINE RIPs show non-polymorphic |
| Meishan to Duroc | 27 | 24 | 88.89% | 2 | 1 |
| Duroc to Meishan | 28 | 22 | 78.57% | 4 | 2 |
| Landrace to Duroc | 30 | 24 | 80.00% | 4 | 2 |
| Duroc to Landrace | 28 | 23 | 82.14% | 3 | 2 |
| Large White to Duroc | 30 | 28 | 93.33% | 0 | 2 |
| Duroc to Large White | 30 | 18 | 60.00% | 9 | 3 |
| Duroc to Bama | 28 | 26 | 92.86% | 1 | 1 |
| Bama to Duroc | 29 | 20 | 68.97% | 7 | 2 |
| Total | 230 | 185 | 80.43% | 30 | 15 |

**Table S6.** Density of SINE RIPs in each chromosome.

|  |  |  |
| --- | --- | --- |
| Chr | No. of SINE RIPs | Density(/1Mb) |
| Chr1 | 3095 | 11.28 |
| Chr2 | 2139 | 14.08 |
| Chr3 | 1925 | 14.49 |
| Chr4 | 1902 | 14.53 |
| Chr5 | 1805 | 17.27 |
| Chr6 | 2247 | 13.15 |
| Chr7 | 2014 | 16.53 |
| Chr8 | 2076 | 14.94 |
| Chr9 | 2291 | 16.42 |
| Chr10 | 1500 | 21.63 |
| Chr11 | 1449 | 18.30 |
| Chr12 | 1195 | 19.40 |
| Chr13 | 2416 | 11.60 |
| Chr14 | 1972 | 13.91 |
| Chr15 | 1826 | 13.00 |
| Chr16 | 1169 | 14.62 |
| Chr17 | 1158 | 18.24 |
| Chr18 | 1047 | 18.70 |
| ChrX | 1610 | 12.78 |
| Others | 1448 | 13.14 |
| Total | 36284 | 14.50 |

**Table S7.** Characterization of 16 SINE RIPs analysed in 23 pig populations.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus | Chr | Genotype frequency | | | Ne | Obs\_Het | Exp\_Heta | PIC | FIS | FST | No. of populations not comply with the Hardy–Weinberg equilibrium |
| +/+ | +/- | -/- |
| ESA1-98 | chr1 | 0.115 | 0.238 | 0.648 | 1.557 | 0.238 | 0.358 | 0.294 | 0.013 | 0.311 | 9 |
| REF-11172 | chr2 | 0.186 | 0.349 | 0.465 | 1.856 | 0.349 | 0.461 | 0.355 | 0.013 | 0.209 | 2 |
| REF-14902 | chr4 | 0.051 | 0.392 | 0.557 | 1.592 | 0.392 | 0.372 | 0.303 | -0.178 | 0.117 | 5 |
| DR-68328 | chr5 | 0.186 | 0.166 | 0.648 | 1.649 | 0.166 | 0.394 | 0.316 | 0.328 | 0.339 | 20 |
| REF-16266 | chr6 | 0.648 | 0.253 | 0.099 | 1.537 | 0.253 | 0.350 | 0.288 | -0.028 | 0.270 | 6 |
| REF-17668 | chr7 | 0.087 | 0.417 | 0.496 | 1.714 | 0.417 | 0.417 | 0.330 | -0.254 | 0.203 | 5 |
| ESA2-58 | chr8 | 0.487 | 0.395 | 0.118 | 1.760 | 0.395 | 0.432 | 0.339 | -0.195 | 0.221 | 4 |
| DR-93949 | chr9 | 0.113 | 0.327 | 0.561 | 1.666 | 0.327 | 0.400 | 0.320 | -0.177 | 0.284 | 4 |
| ESA1-16 | chr11 | 0.287 | 0.436 | 0.277 | 2.000 | 0.436 | 0.500 | 0.375 | -0.315 | 0.336 | 7 |
| REF-3992 | chr12 | 0.299 | 0.468 | 0.233 | 1.991 | 0.468 | 0.498 | 0.374 | -0.248 | 0.254 | 9 |
| ESA1-25 | chr13 | 0.530 | 0.332 | 0.139 | 1.734 | 0.332 | 0.423 | 0.334 | -0.049 | 0.241 | 6 |
| ESA2-18 | chr14 | 0.268 | 0.433 | 0.299 | 1.998 | 0.433 | 0.500 | 0.375 | -0.167 | 0.256 | 3 |
| ESA1-33 | chr15 | 0.149 | 0.268 | 0.583 | 1.683 | 0.268 | 0.406 | 0.323 | -0.037 | 0.369 | 3 |
| REF-9432 | chr16 | 0.192 | 0.448 | 0.361 | 1.944 | 0.448 | 0.486 | 0.368 | -0.057 | 0.128 | 6 |
| ESA1-42 | chr17 | 0.246 | 0.422 | 0.332 | 1.986 | 0.422 | 0.496 | 0.373 | -0.158 | 0.259 | 5 |
| ESA1-43 | chr18 | 0.079 | 0.323 | 0.598 | 1.575 | 0.323 | 0.365 | 0.298 | -0.183 | 0.242 | 6 |
| Mean |  | 0.245 | 0.354 | 0.401 | 1.765 | 0.354 | 0.429 | 0.335 | -0.106 | 0.252 | 6.250 |
| St. Dev |  | 0.173 | 0.088 | 0.193 | 0.172 | 0.088 | 0.055 | 0.031 | 0.153 | 0.069 | 4.155 |

a Nei's (1973) expected heterozygosity

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table S8. The pig genomes used for the SINE RIP screen protocol.** | | | | | | | | | | | |
| Genome Name | WGS Name | Size (Mb) | Scaffolds | Rele-ase Date | Level | Sequence depth | Sequence technology | Assembly method | Sex | Submitter | Website |
| Duroc （susScr11.1） | AEMK02 | 2501.91 | 706 | 2017-2-7 | Chromosome | 65.0x | PacBio | Falcon v. OCT-2015 | female | The Swine Genome Sequencing Consortium (SGSC) | https://www.ncbi.nlm.nih.gov/assembly/GCA\_000003025.6 |
| Cross-bred(Yorkshire\_Landrace\_Duroc) | NPJO01 | 2755.44 | 14157 | 2017-12-20 | Chromosome | 65.0x | PacBio; Illumina NextSeq 500 | Celera Assembler v. 8.3rc2 | male | USDA ARS | https://www.ncbi.nlm.nih.gov/assembly/GCA\_002844635.1 |
| Goettingen | LIDP01 | 2611.36 | 5206 | 2015-9-16 | Scaffold | 20.0x | 454; SOLiD | GMAP v. DEC-2012; BioScope v. 1.2; Newbler v. 2.7 | female | F. Hoffmann - La Roche AG | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001292865.1 |
| Wuzhishan | AJKK01 | 2508.91 | 137577 | 2015-3-18 | Scaffold | 120x | Illumina HiSeq2000 | SOAPdenovo v. 2.03 | male | BGI-shenzhen | https://www.ncbi.nlm.nih.gov/assembly/GCA\_000325925.2 |
| Ellegaard Gottingen minipig | AOCR01 | 2358.02 | 231585 | 2013-1-10 | Contig | 79.0x | Illumina HiSeq | SOAPdenovo v. September 2011 | female | GlaxoSmithKline | https://www.ncbi.nlm.nih.gov/assembly/GCA\_000331475.1 |
| Tibetan | AORO02 | 2437.74 | 72068 | 2016-8-8 | Scaffold | 131.0x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_000472085.2 |
| Large White | LUXX01 | 2457.91 | 102342 | 2016-8-5 | Scaffold | 95.48x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700135.1 |
| Rongchang | LUXR01 | 2459.03 | 120246 | 2016-8-5 | Scaffold | 93.54x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700155.1 |
| Hampshire | LUXS01 | 2437.11 | 82206 | 2016-8-5 | Scaffold | 100.88x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700165.1 |
| Meishan | LUXQ01 | 2467.5 | 133833 | 2016-8-5 | Scaffold | 111.13x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700195.1 |
| Landrace | LUXT01 | 2440.98 | 94659 | 2016-8-5 | Scaffold | 91.23x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700215.1 |
| Bamei | LUXV01 | 2460.76 | 129335 | 2016-8-5 | Scaffold | 88.72x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700235.1 |
| Bama | SIDA01 | 2491.05 | 6610 | 2019-8-1 | Chromosome | 361x | Illumina; PacBio; Oxford Nanopore MinION; 10x Genomics; Hi-C | supernovo v. Dec-2016; SOAPdenovo v. Jan-2017; PBJelly v. Feb-2017; LACHESIS v. Feb-2017 | male | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_007644095.1 |
| Pietrain | LUXU01 | 2438.32 | 88436 | 2016-8-5 | Scaffold | 96.22x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700255.1 |
| Jinhua | LUXY01 | 2453.7 | 115554 | 2016-8-5 | Scaffold | 109.05x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700295.1 |
| Berkshire | LUXW01 | 2434.71 | 94468 | 2016-8-5 | Scaffold | 113.47x | Illumina HiSeq | SOAPdenovo v. 2.0 | female | Novogene | https://www.ncbi.nlm.nih.gov/assembly/GCA\_001700575.1 |