***Animal* Journal - Supplymentary Materials**

**A genome scan for selection signatures in Taihu pig breeds using next-generation sequencing**

 Z. Wang1,2, H. Sun1,2, Q. Chen1,2, X. Zhang1,2, Q. Wang1,2 and Y. Pan1,2

*1**School of Agriculture and Biology, Department of Animal Science, Shanghai Jiao Tong University, Shanghai 200240, PR China*

*2Shanghai Key Laboratory of Veterinary Biotechnology, Shanghai 200240, PR China*

**Supplementary Figure S1** The distribution of the single nucleotide polymorphisms (SNPs) in each chromosome.



The densities of the SNPs in each chromosome, which were calculated as the number of SNPs per 100 kb.

**Supplementary Figure S2** The population structure based on the analysis of principal component analysis (PCA), Neighbor-joining (NJ) tree and STUCTURE.

****

(a) Population structures of the Taihu pigs and western pigs revealed by principal component analysis; (b) The neighbor-joining tree of the pigs based on the genome-wide SNPs; (c) Population structure of the Taihu pigs and western pigs revealed with the STRUCTURE software. MMS, Middle Meishan; SWT, Shawutou; EHL, Erhualian; M, Mi; FJ, Fengjing; JXB, Jiaxing Black; SMS, Small Meishan; YKS, Yorkshire; LR, Landrace; DRC, Duroc.

**Supplementary Figure S3** The distribution of genes under selection regions in the Taihu and Western pig populations.

****

T: Taihu population, W: Western population, REHH: Relative Extend Haplotype Homozygosity Test, XPEHH: Cross Population Extend Haplotype Homozygosity Test.

**Supplementary Table S1** *Sample sizes and summary statistics for the sequencing data.*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Population | Breed | Origin | Size | Average genome coverage (%) | Average sequencing depth1 | Average reads number (million) |
| Taihu | Meishan (Middle) | Jiading, Shanghai | 50 | 2.0 | 10.0 | 4.02 |
|  | Meishan (Small) | Jurong, Jiangsu (33)Taicang, Jiangsu (36) | 69 | 2.9 | 9.5 | 4.05 |
|  | Fengjing | Jinshan, Shanghai | 16 | 1.2 | 19.9 | 4.04 |
|  | Shawutou | Chongming, Shanghai | 21 | 1.8 | 18.5 | 4.43 |
|  | Erhualian | Changshu, Jiangsu | 31 | 1.7 | 21.9 | 2.83 |
|  | Mi | Jintan, Jiangsu | 36 | 2.7 | 7.9 | 3.85 |
|  | Jiaxing Black | Jiaxing, Zhejiang | 29 | 2.9 | 8.4 | 2.82 |
| Western | Yorkshire | Nanhui, Shanghai | 35 | 3.5 | 8.4 | 3.81 |
|  | Landrace | Nanhui, Shanghai | 37 | 4.0 | 9.3 | 5.10 |
|  | Duroc | Nanhui, Shanghai | 48 | 3.2 | 10.0 | 4.18 |
| Overall | 9 | - | 372 | - | - | - |
| Average | - | - | - | 2.7 | 10.9 | 3.95 |

1Sequencing data used for ultimate SNP (single nucleotide polymorphism) identification.

**Supplementary Table S2** *The number of quantitative trait locus for the five traits.*

|  |  |
| --- | --- |
| Traits | Number1 |
| Exterior | 269 |
| Reproduction | 575 |
| Production | 353 |
| Meat Quality & Carcass | 1 155 |
| Health | 241 |

1Some of the new defined quantitative trait loci might be related to multi traits.

**Supplementary Table S3** *Quantitative trait loci overlapped with the candidate selection regions (Relative Extend Haplotype Homozygosity Test).*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Chromosome | Start | End | *P* value | quantitative trait locus（ID） |
| T | 1 | 268556705 | 268561835 | 0.00250  | Drip loss (8001);Drip loss (8422);Drip loss (8546);Total number born alive (18061); |
|  | 2 | 143822206 | 143843513 | 0.00012  | average daily gain (22230); |
|  | 3 | 114736445 | 114756581 | 0.00020  | mummified pigs (18276);LDL cholesterol (7704); |
|  | 4 | 5518600 | 5621051 | 0.00018  | Feed conversion ratio (29557);Maternal infanticide (30993);Anal atresia (7235); |
|  | 6 | 77090305 | 77127881 | 0.00001  | Ejaculation duration (8689);Ejaculation times (8686); |
|  | 7 | 125046542 | 125077525 | 0.00011  | average daily gain (22246);average daily gain (birth-60 days) (716);backfat at mid-back (13250);Side fat thickness (13251); |
|  | 8 | 92696500 | 92790169 | 0.00019  | Muscle moisture percentage (9042); |
|  | 9 | 12427800 | 12430140 | 0.00009  | Corpus luteum number (577); |
|  | 11 | 77817839 | 77888171 | 0.00195  | CIE-b\* (4310);CIE-b\* (4311); |
|  | 12 | 7116095 | 7124680 | 0.00522  | Total number born alive (18091);Embryo survival (8833);Embryo weight (18352);Eosinophil number (5487);Eosinophil number (7512);Eosinophil number (7513);Feed conversion ratio (3903);HDL/LDL ratio (7723);Nonfunctional nipples (7465);Number of viable embryos (8832);Reproductive tract weight (18403);Spinal curvature (17689);uterine horn length (18401);uterine horn weight (18402); |
|  | 13 | 133343722 | 133461060 | 0.00034  | HDL/LDL ratio (7708);Stearic acid content (17744); |
|  | 14 | 145164688 | 145194143 | 0.00016  | Small intestine length (257); |
|  | 15 | 36876266 | 36901830 | 0.00020  | Number of stillborn (18135);Body weight (birth) (23016); |
|  | 17 | 38844752 | 39026345 | 0.00009  | Ratio of lifetime nonproductive days to herd life (16010); |
|  |  |  |  |  |  |
| W | 1 | 265215143 | 265322482 | 0.00357  | Adipocyte diameter (12818); |
|  | 2 | 2230966 | 2283431 | 0.00093  | hematocrit (17932);hematocrit (17933);hematocrit (17934);Hemoglobin (17929);Hemoglobin (17930);Hemoglobin (17931);Immunoglobulin G level (17939);Platelet count (17936);Platelet count (17937);Red cell distribution width (17935);White blood cell counts (17938); |
|  | 3 | 101324840 | 101329488 | 0.00023  | Corpus luteum number (31847);Average backfat thickness (7258); |
|  | 4 | 133835113 | 133920341 | 0.00136  | mummified pigs (18246); |
|  | 5 | 18111848 | 18119667 | 0.00551  | Backfat (average) thickness - ultrasound (31216);Backfat (average) thickness - ultrasound (31244);Backfat (average) thickness - ultrasound (31245); |
|  | 6 | 7770533 | 7897060 | 0.00037  | Intestinal fat percentage (728); |
|  | 7 | 106873365 | 106891339 | 0.00091  | Umbilical hernia (8757); |
|  | 8 | 34286910 | 34301822 | 0.00000  | Average backfat thickness (29569);average daily gain (55-80 kg) (3897);Heart weight (13278);Litter weight, piglets born alive (18515);Palmitic acid content (18595);Palmitoleic acid content (18594);Saturated fatty acid content (18592);Unsaturated fatty acid content (18593);Vaccenic acid to palmitoleic acid ratio (18622); |
|  | 9 | 129356633 | 129525370 | 0.00032  | Body weight (weaning) (29612); |
|  | 10 | 24668969 | 24690711 | 0.00869  | Inguinal hernia (8777);Maternal infanticide (17648); |
|  | 12 | 18217102 | 18228195 | 0.00004  | Backfat (average) thickness - ultrasound (31224);Backfat (average) thickness - ultrasound (31229);Backfat (average) thickness - ultrasound (31253);Backfat (average) thickness - ultrasound (31254);Backfat (average) thickness - ultrasound (31255);Backfat (average) thickness - ultrasound (31256);Haptoglobin concentration (9652); |
|  | 13 | 16886234 | 17003299 | 0.00121  | Number of stillborn (18134); |
|  | 14 | 107622749 | 107744197 | 0.00003  | Daily feed intake (22193); |
|  | 15 | 29307284 | 29524014 | 0.00113  | Insulin-like growth factor 1 level (16983);Body weight (birth) (23015); |
|  | 16 | 25248186 | 25252699 | 0.00711  | Loin muscle area (22311-22314); |
|  | 17 | 66507415 | 66555775 | 0.00015  | mummified pigs (18289);Percentage type I fibers (24114);Relative area of type IIa fibers (24115);Corpus luteum number (31908); |
|  | 18 | 10206588 | 10308654 | 0.00006  | Weight of ovary (18361); |

Note: T, Taihu population; W, Western population.

**Supplementary Table S4** *Quantitative trait loci overlapped with the candidate selection regions (the Cross Population Extend Haplotype Homozygosity Test).*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Chromosome | 1Start | 1End | Number of outlies | quantitative trait locus  |
| T | 1 | 163799063 | 163799080 | 2 | Total number born alive (22922); |
|  | 2 | 2728371 | 2728382 | 2 | Backfat at last lumbar (2933);Knuckle ham weight (3057);backfat at last rib (7303);Backfat thickness between 3rd and 4th rib (7301);Backfat thickness between 3rd and 4th rib (7302);Carcass weight (hot) (7304);Ham weight (7306);Ham weight (7307);Loin muscle area (7305);Shoulder weight (7308);Average backfat thickness (7299);Average Daily Gain (EBV) (11892);Average daily gain (RR) (11897);Backfat thickness (EBV) (11894);Backfat thickness (RR) (11899);Body weight (weaning) (13257);Cervical vertebra length (13311);Cervical vertebra length (9000);Feed conversion ratio (EBV) (11896);Feed conversion ratio (RR) (11901);Ham weight (EBV) (11895);Ham weight (RR) (11900);Lean meat percentage (7300);Loin and neck weight (EBV) (11893);Loin and neck weight (RR) (11898);Number weaned (13255);Number weaned (13256);Total number born (13254);Total number born alive (12707);Total number born alive (13253); |
|  | 14 | 12857870 | 12857870 | 1 | Total number born (18209); |
|  |  |  |  |  |  |
| W | 1 | 9312200 | 9312200 | 1 | Drip loss (8053);Drip loss (8338);Drip loss (8598); |
|  | 3 | 119205261 | 119205261 | 1 | Average backfat thickness (22292); |
|  | 7 | 11854647 | 11854647 | 1 | Carcass weight (hot) (16868);backfat at last rib (3764); |
|  | 12 | 41100378 | 41123787 | 2 | average daily gain (22256);Palmitoleic acid content (7678); |

Note: 1Start/End physical location of outliers; T, Taihu; W, western.

**Supplementary Table S5** *Candidate positions detected by FST tests between Taihu and Western pigs.*

|  |  |  |  |
| --- | --- | --- | --- |
| Chromosome | position | *FST* | gene |
| 1 | 93538788 | 0.8980847 |  *UBE3D* |
| 1 | 110152007 | 0.9020333 |  *MAPK4* |
| 1 | 115139853 | 0.8882554 |  *TCF4* |
| 1 | 148232206 | 0.8898912 |  *RASGRP1* |
| 1 | 153674683 | 0.9173455 |  *IGF1R* |
| 1 | 159419706 | 0.9258942 |  *KLF13* |
| 1 | 160197539 | 0.9074204 |  *APBA2* |
| 1 | 179958084 | 0.9374512 |  *NEDD4L* |
| 1 | 182425728 | 0.8631921 |  *SMAD6* |
| 1 | 207286501 | 0.98085 |  *SLC35F4* |
| 1 | 213094631 | 0.9348586 |  *NTRK3* |
| 1 | 223991374 | 0.9082625 |  *CDKN2A* |
| 1 | 226767984 | 0.9318407 |  *SLC24A2* |
| 1 | 257258050 | 0.8890089 |  *GNA14* |
| 1 | 263869338 | 0.9296339 |  *UNC13B* |
| 1 | 264077289 | 0.9388087 |  *CD72* |
| 1 | 264150455 | 0.8811628 |  *TLN1* |
| 1 | 264151137 | 0.9383382 |  *TLN1* |
| 1 | 266439511 | 0.8586763 |  *FRMPD1* |
| 1 | 266439514 | 0.8586763 |  *FRMPD1* |
| 1 | 267256943 | 0.9584537 |  *CCDC180* |
| 1 | 304493874 | 0.8882584 |  *ASS1* |
| 1 | 304493886 | 0.882777 |  *ASS1* |
| 1 | 304507922 | 0.9209009 |  *ASS1* |
| 1 | 305614329 | 0.8787544 |  *RAPGEF1* |
| 1 | 306234503 | 0.8668961 |  *TTF1* |
| 1 | 306234511 | 0.8668961 |  *TTF1* |
| 1 | 306487764 | 0.8981263 |  *GTF3C4* |
| 1 | 306789129 | 0.9091878 |  *GTF3C5* |
| 1 | 307412986 | 0.9288721 |  *VAV2* |
| 1 | 307423295 | 0.8769482 |  *VAV2* |
| 1 | 307502957 | 0.9120352 |  *BRD3* |
| 1 | 308665275 | 0.9012343 |  *BLG* |
| 2 | 3451921 | 0.9246261 |  *CHKA* |
| 2 | 5516769 | 0.8730668 |  *C11orf68* |
| 2 | 6565620 | 0.9494839 |  *RASGRP2* |
| 2 | 8353061 | 0.9465457 |  *POLR2G* |
| 2 | 17963008 | 0.9360367 |  *GYLTL1B* |
| 2 | 76016739 | 0.8918024 |  *CELF5* |
| 2 | 136371628 | 0.8832035 |  *SLC12A2* |
| 2 | 136386084 | 0.8791627 |  *SLC12A2* |
| 2 | 147204465 | 0.9251905 |  *DNAJC18* |
| 3 | 4290810 | 0.877662 |  *AP5Z1* |
| 3 | 4290821 | 0.8723878 |  *AP5Z1* |
| 3 | 7947481 | 0.8707127 |  *TFR2* |
| 3 | 17850888 | 0.8888481 |  *STX1B* |
| 3 | 18375404 | 0.879412 |  *SEPT1* |
| 3 | 18375436 | 0.8698787 |  *SEPT1* |
| 3 | 38470594 | 0.8596465 |  *PPL* |
| 3 | 38470623 | 0.8888802 |  *PPL* |
| 3 | 41415077 | 0.9234396 |  *METRN* |
| 3 | 41728146 | 0.961132 |  *CRAMP1L* |
| 3 | 42826007 | 0.9753472 |  *PRSS22* |
| 3 | 43380738 | 0.9329697 |  *CENPP* |
| 3 | 48895905 | 0.8572862 |  *NEURL3* |
| 3 | 51397222 | 0.9318472 |  *NCK2* |
| 3 | 55723012 | 0.8768524 |  *RPL31* |
| 3 | 59197354 | 0.9103476 |  *ZAP70* |
| 3 | 59197404 | 0.9159111 |  *ZAP70* |
| 3 | 61601587 | 0.8758836 |  *POLR1A* |
| 3 | 72173302 | 0.8684083 |  *TET3* |
| 3 | 76095169 | 0.9320905 |  *ANXA4* |
| 3 | 76706728 | 0.9193505 |  *ANTXR1* |
| 3 | 76758644 | 0.857653 |  *ANTXR1* |
| 3 | 85313712 | 0.9042594 |  *BCL11A* |
| 3 | 100073671 | 0.9325673 |  *RHOQ* |
| 3 | 102755689 | 0.8872803 |  *ABCG8* |
| 3 | 114756581 | 0.8648343 |  *XDH* |
| 3 | 115411121 | 0.8730668 |  *LCLAT1* |
| 3 | 117198965 | 0.9077202 |  *TRMT61B* |
| 4 | 2236433 | 0.8616609 |  *PTK2* |
| 4 | 2826133 | 0.880693 |  *TRAPPC9* |
| 4 | 6165807 | 0.859592 |  *CU151851.1* |
| 4 | 6967896 | 0.87492 |  *CU571095.1* |
| 4 | 7743979 | 0.8886331 |  *ST3GAL1* |
| 4 | 7743981 | 0.891792 |  *ST3GAL1* |
| 4 | 7743990 | 0.9106045 |  *ST3GAL1* |
| 4 | 38251263 | 0.8921189 |  *NCALD* |
| 4 | 38338014 | 0.8734996 |  *GRHL2* |
| 4 | 73554844 | 0.8791137 |  *ARFGEF1* |
| 4 | 89146424 | 0.9214293 |  *SLC19A2* |
| 4 | 103794313 | 0.8811628 |  *KCNN3* |
| 4 | 117850198 | 0.8693791 |  *RHOC* |
| 5 | 4305796 | 0.9437823 |  *DESI1* |
| 5 | 4378871 | 0.9227388 |  *POLR3H* |
| 5 | 4378910 | 0.9227388 |  *POLR3H* |
| 5 | 7215939 | 0.8741343 |  *PICK1* |
| 5 | 16005060 | 0.8755855 |  *PRPF40B* |
| 5 | 17908501 | 0.8764388 |  *ACVR1B* |
| 5 | 39285927 | 0.9428222 |  *TRH-DE* |
| 5 | 60770140 | 0.9320905 |  *RERG* |
| 5 | 66788349 | 0.9010014 |  *TNFRSF1A* |
| 5 | 77361413 | 0.8758546 |  *ADAMTS20* |
| 5 | 77478660 | 0.8765739 |  *ADAMTS20* |
| 5 | 99156416 | 0.8732725 |  *CEP290* |
| 5 | 110873481 | 0.8745055 |  *TTLL8* |
| 6 | 123555 | 0.8729007 |  *DBNDD1* |
| 6 | 174589 | 0.882281 |  *DBNDD1* |
| 6 | 35034935 | 0.8927676 |  *POP4* |
| 6 | 49231171 | 0.8596465 |  *LIG1* |
| 6 | 68821519 | 0.9137033 |  *TMEM51* |
| 6 | 77958712 | 0.8598706 |  *SLC9A1* |
| 6 | 83115808 | 0.8735185 |  *YARS* |
| 6 | 85973469 | 0.925813 |  *GRIK3* |
| 6 | 86669568 | 0.9455134 |  *INPP5B* |
| 6 | 86669575 | 0.9509072 |  *INPP5B* |
| 6 | 86669596 | 0.9320955 |  *INPP5B* |
| 6 | 149295595 | 0.878498 |  *FAF1* |
| 7 | 1149719 | 0.9258811 |  *GMDS* |
| 7 | 1149727 | 0.9258811 |  *GMDS* |
| 7 | 42678059 | 0.8583305 |  *C6orf132* |
| 7 | 60250005 | 0.8753576 |  *APN* |
| 7 | 63547708 | 0.8732648 |  *EDC3* |
| 7 | 103678596 | 0.9671813 |  *LTBP2* |
| 7 | 103780689 | 0.9495473 |  *AREL1* |
| 7 | 106603923 | 0.9036118 |  *POMT2* |
| 7 | 110423688 | 0.8872636 |  *SEL1L* |
| 7 | 116665309 | 0.8825694 |  *KCNK10* |
| 7 | 117268243 | 0.9196754 |  *TTC8* |
| 7 | 117695689 | 0.8887427 |  *FOXN3* |
| 7 | 117695691 | 0.8887427 |  *FOXN3* |
| 7 | 119609001 | 0.9227149 |  *CCDC88C* |
| 7 | 121786737 | 0.9582335 |  *PRIMA1* |
| 7 | 123700454 | 0.8741343 |  *CLMN* |
| 7 | 123710012 | 0.8732648 |  *CLMN* |
| 7 | 123710429 | 0.8586738 |  *CLMN* |
| 7 | 124941092 | 0.8855426 |  *PAPOLA* |
| 8 | 39390392 | 0.9581546 |  *ATP10D* |
| 8 | 39390404 | 0.9552784 |  *ATP10D* |
| 8 | 39390437 | 0.9638805 |  *ATP10D* |
| 8 | 39390453 | 0.9638805 |  *ATP10D* |
| 8 | 39704961 | 0.9500193 |  *CORIN* |
| 8 | 41299704 | 0.9585387 |  *LRRC66* |
| 8 | 42477559 | 0.893402 |  *LNX1* |
| 8 | 50558558 | 0.9610219 |  *RAPGEF2* |
| 8 | 55589529 | 0.9526945 |  *MARCH1* |
| 8 | 59098122 | 0.8795159 |  *IGFBP7* |
| 8 | 59103842 | 0.9114633 |  *IGFBP7* |
| 8 | 76215748 | 0.9667407 |  *CCDC158* |
| 8 | 76215766 | 0.9410182 |  *CCDC158* |
| 8 | 78157356 | 0.9466025 |  *FRAS1* |
| 8 | 78157357 | 0.9260225 |  *FRAS1* |
| 8 | 78157393 | 0.9466025 |  *FRAS1* |
| 8 | 78654148 | 0.87492 |  *RBM46* |
| 8 | 78667916 | 0.893402 |  *RBM46* |
| 8 | 109613634 | 0.9257287 |  *ANXA5* |
| 8 | 122379865 | 0.9202503 |  *SGMS2* |
| 8 | 130948067 | 0.8661699 |  *TSPAN5* |
| 9 | 49687926 | 0.8662453 |  *RNF214* |
| 9 | 49710830 | 0.8693791 |  *RNF214* |
| 9 | 51169991 | 0.8723878 |  *CXCR5* |
| 9 | 51169997 | 0.8547633 |  *CXCR5* |
| 9 | 55078704 | 0.8890029 |  *UBASH3B* |
| 9 | 55078709 | 0.8820278 |  *UBASH3B* |
| 9 | 71423725 | 0.8766732 |  *PIK3C2B* |
| 9 | 71423735 | 0.8829522 |  *PIK3C2B* |
| 9 | 71423759 | 0.8970404 |  *PIK3C2B* |
| 9 | 73828734 | 0.9435967 |  *IL19* |
| 9 | 74871878 | 0.9083083 |  *ADAM22* |
| 9 | 103023986 | 0.8698787 |  *KIAA1324L* |
| 9 | 135361605 | 0.8561069 |  *CACNA1E* |
| 10 | 12996051 | 0.9200614 |  *DUSP10* |
| 10 | 49026713 | 0.8671785 |  *SLC39A12* |
| 10 | 50848207 | 0.8950085 |  *ITGA8* |
| 11 | 1932630 | 0.9006718 |  *TNFRSF19* |
| 11 | 5388880 | 0.95259 |  *FLT1* |
| 11 | 18984245 | 0.9022119 |  *FNDC3A* |
| 11 | 18993552 | 0.87847 |  *FNDC3A* |
| 11 | 84420343 | 0.8557066 |  *COL4A1* |
| 12 | 6137140 | 0.8891643 |  *ARMC7* |
| 12 | 6153749 | 0.8920462 |  *SLC16A5* |
| 12 | 17921731 | 0.9105348 |  *LYZL6* |
| 12 | 19503578 | 0.95259 |  *MPP2* |
| 12 | 20929294 | 0.8824365 |  *KAT2A* |
| 12 | 21090703 | 0.9172674 |  *ACLY* |
| 12 | 23124365 | 0.9078832 |  *PGAP3* |
| 13 | 623969 | 0.8732873 |  *CPNE4* |
| 13 | 2488068 | 0.8823333 |  *SH3BP5* |
| 13 | 4769659 | 0.9047852 |  *TBC1D5* |
| 13 | 38424065 | 0.8674897 |  *TKT* |
| 13 | 43925404 | 0.9554209 |  *ABHD6* |
| 13 | 44109725 | 0.9436846 |  *PXK* |
| 13 | 107851551 | 0.8535489 |  *IQCJ-SCHIP1* |
| 13 | 115167924 | 0.9043267 |  *SERPINI1* |
| 13 | 115416284 | 0.879412 |  *GOLIM4* |
| 13 | 139854005 | 0.8891911 |  *ATP13A5* |
| 13 | 141187247 | 0.9754913 |  *TMEM44* |
| 13 | 141242288 | 0.9615406 |  *LSG1* |
| 13 | 145343998 | 0.8802487 |  *KALRN* |
| 13 | 146650871 | 0.8828302 |  *ADCY5* |
| 13 | 153704801 | 0.8605558 |  *LSAMP* |
| 13 | 205246546 | 0.9211641 |  *TIAM1* |
| 13 | 206158643 | 0.9324658 |  *EVA1C* |
| 13 | 206158742 | 0.8760559 |  *EVA1C* |
| 13 | 213344261 | 0.9167182 |  *SH3BGR* |
| 13 | 215782076 | 0.9211641 |  *UMODL1* |
| 14 | 31329699 | 0.8815517 |  *CDK2AP1* |
| 14 | 37624487 | 0.9228046 |  *TESC* |
| 14 | 37638337 | 0.8562814 |  *TESC* |
| 14 | 125026361 | 0.8790648 |  *CFAP43* |
| 14 | 135779993 | 0.8823418 |  *AFAP1L2* |
| 14 | 146940059 | 0.8686805 |  *ADAM12* |
| 15 | 37743337 | 0.8564763 |  *DLGAP2* |
| 15 | 55559082 | 0.8839836 |  *EIF4EBP1* |
| 15 | 55559094 | 0.8941693 |  *EIF4EBP1* |
| 15 | 74227655 | 0.8999656 |  *PLA2R1* |
| 16 | 80563090 | 0.8862892 |  *ADCY2* |
| 17 | 47425361 | 0.8543731 |  *PPP1R16B* |
| 17 | 47456489 | 0.8587658 |  *PPP1R16B* |
| 17 | 49231604 | 0.9612356 |  *PLCG1* |
| 17 | 55184997 | 0.8615116 |  *ZMYND8* |
| 17 | 57845111 | 0.8595951 |  *TMEM189* |
| 17 | 59132622 | 0.8896144 |  *CH242-277I8.2* |
| 17 | 59132631 | 0.8896144 |  *CH242-277I8.2* |
| 17 | 64136670 | 0.8600415 |  *CASS4* |
| 17 | 65172873 | 0.8685312 |  *TMEPAI* |
| 17 | 65172914 | 0.8685312 |  *TMEPAI* |
| 18 | 11057467 | 0.9199569 |  *ZAP* |
| 18 | 11272828 | 0.9299165 |  *KIAA1549* |
| 18 | 16064400 | 0.9644593 |  *EXOC4* |
| 18 | 21637304 | 0.9436229 |  *SND1* |
| 18 | 21637324 | 0.8738055 |  *SND1* |
| 18 | 25997568 | 0.869392 |  *CADPS2* |
| 18 | 46433394 | 0.8605042 |  *GHRHR* |
| 18 | 47701062 | 0.8646825 |  *CHN2* |
| 18 | 51015495 | 0.9012081 |  *NFE2L3* |
| X | 11413191 | 0.9289891 |  *GPM6B* |
| X | 11422298 | 0.9696058 |  *GPM6B* |
| X | 11422311 | 0.9696058 |  *GPM6B* |
| X | 11422312 | 0.9696058 |  *GPM6B* |
| X | 11422320 | 0.9696058 |  *GPM6B* |
| X | 11422337 | 0.9667542 |  *GPM6B* |
| X | 15184680 | 0.9437823 |  *NHS* |
| X | 15292088 | 0.938111 |  *NHS* |
| X | 15480122 | 0.9465965 |  *CH242-297D10.1* |
| X | 15502384 | 0.9202503 |  *CH242-297D10.1* |
| X | 15502393 | 0.9202503 |  *CH242-297D10.1* |
| X | 16347724 | 0.9509072 |  *PPEF1* |
| X | 16347762 | 0.9506178 |  *PPEF1* |
| X | 16420489 | 0.9781085 |  *PPEF1* |
| X | 17341557 | 0.9379539 |  *SH3KBP1* |
| X | 17341569 | 0.9379539 |  *SH3KBP1* |
| X | 19525203 | 0.8738055 |  *PHEX* |
| X | 21189192 | 0.9127325 |  *PRDX4* |
| X | 40501115 | 0.9121857 |  *MED14* |
| X | 46059908 | 0.9291434 |  *CHST7* |
| X | 47957125 | 0.9891056 |  *TFE3* |
| X | 50890925 | 0.9945737 |  *MAGED4B* |
| X | 50890988 | 0.9945737 |  *MAGED4B* |
| X | 50891077 | 0.9945737 |  *MAGED4B* |
| X | 51534632 | 0.9808076 |  *IQSEC2* |
| X | 51561392 | 0.97278 |  *IQSEC2* |
| X | 63035496 | 0.9752656 |  *EDA* |
| X | 78798046 | 0.9945737 |  *CHM* |
| X | 79072087 | 0.9890984 |  *CHM* |
| X | 90392943 | 0.9752065 |  *CSTF2* |
| X | 97454475 | 0.9945737 |  *TCEAL2* |
| X | 97470939 | 0.991858 |  *TCEAL2* |
| X | 97688026 | 0.991858 |  *TCEAL2* |
| X | 99631010 | 0.9891248 |  *IL1RAPL2* |
| X | 99653778 | 0.9835901 |  *IL1RAPL2* |
| X | 99668901 | 0.9918401 |  *IL1RAPL2* |
| X | 99668905 | 0.9918401 |  *IL1RAPL2* |
| X | 100274631 | 0.9891056 |  *IL1RAPL2* |
| X | 100517374 | 0.991858 |  *IL1RAPL2* |
| X | 100517409 | 0.991858 |  *IL1RAPL2* |
| X | 100910375 | 0.9863484 |  *NRK* |
| X | 106223225 | 0.8984115 |  *TRPC5* |
| X | 113652275 | 0.8811198 |  *NKRF* |

**Supplementary Table S6** *Gene enrichment analyses under candidate selection regions.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Population(method) | Category | Term | Count | P Value |
| T (REHH） | KEGG\_PATHWAY | hsa05320:Autoimmune thyroid disease | 9 | 2.04E-03 |
|  | KEGG\_PATHWAY | hsa05330:Allograft rejection | 7 | 5.43E-03 |
|  | KEGG\_PATHWAY | hsa03010:Ribosome | 11 | 6.22E-03 |
|  | KEGG\_PATHWAY | hsa04672:Intestinal immune network for IgA production | 8 | 6.57E-03 |
|  | KEGG\_PATHWAY | hsa05332:Graft-versus-host disease | 7 | 8.11E-03 |
|  | KEGG\_PATHWAY | hsa05310:Asthma | 6 | 9.49E-03 |
|  | KEGG\_PATHWAY | hsa04940:Type I diabetes mellitus | 7 | 1.16E-02 |
|  | GOTERM\_MF\_2 | GO:0004857~enzyme inhibitor activity | 31 | 5.25E-06 |
|  | GOTERM\_BP\_2 | GO:0009790~embryonic development | 41 | 2.22E-03 |
|  | GOTERM\_MF\_2 | GO:0019207~kinase regulator activity | 11 | 9.26E-03 |
|  | GOTERM\_BP\_2 | GO:0001503~ossification | 12 | 1.23E-02 |
|  | GOTERM\_BP\_2 | GO:0044238~primary metabolic process | 331 | 1.87E-02 |
|  |  |  |  |  |
| W (REHH) | KEGG\_PATHWAY | hsa04912:GnRH signaling pathway | 14 | 5.62E-03 |
|  | KEGG\_PATHWAY | hsa00590:Arachidonic acid metabolism | 10 | 5.80E-03 |
|  | KEGG\_PATHWAY | hsa00650:Butanoate metabolism | 7 | 1.48E-02 |
|  | KEGG\_PATHWAY | hsa04270:Vascular smooth muscle contraction | 14 | 1.67E-02 |
|  | KEGG\_PATHWAY | hsa00565:Ether lipid metabolism | 7 | 1.69E-02 |
|  | KEGG\_PATHWAY | hsa00592:alpha-Linolenic acid metabolism | 5 | 2.03E-02 |
|  | GOTERM\_BP\_2 | GO:0009653~anatomical structure morphogenesis | 102 | 8.76E-05 |
|  | GOTERM\_BP\_2 | GO:0009790~embryonic development | 56 | 1.46E-04 |
|  | GOTERM\_MF\_2 | GO:0030280~structural constituent of epidermis | 6 | 1.48E-04 |
|  | GOTERM\_CC\_2 | GO:0044446~intracellular organelle part | 291 | 1.64E-03 |
|  | GOTERM\_CC\_2 | GO:0044422~organelle part | 291 | 2.37E-03 |
|  | GOTERM\_BP\_2 | GO:0050793~regulation of developmental process | 58 | 2.97E-03 |
|  | GOTERM\_BP\_2 | GO:0051094~positive regulation of developmental process | 28 | 6.54E-03 |
|  | GOTERM\_BP\_2 | GO:0006996~organelle organization | 100 | 6.63E-03 |
|  | GOTERM\_CC\_2 | GO:0044424~intracellular part | 664 | 7.46E-03 |
|  | GOTERM\_CC\_2 | GO:0005622~intracellular | 685 | 7.76E-03 |
|  | GOTERM\_BP\_2 | GO:0048856~anatomical structure development | 174 | 1.08E-02 |
|  | GOTERM\_CC\_2 | GO:0043234~protein complex | 180 | 1.26E-02 |
|  | GOTERM\_BP\_2 | GO:0007275~multicellular organismal development | 194 | 1.32E-02 |
|  | GOTERM\_BP\_2 | GO:0030030~cell projection organization | 33 | 1.55E-02 |
|  | GOTERM\_BP\_2 | GO:0032989~cellular component morphogenesis | 35 | 1.61E-02 |
|  | GOTERM\_BP\_2 | GO:0051093~negative regulation of developmental process | 25 | 1.70E-02 |
|  |  |  |  |  |
| T (XPEHH) | KEGG\_PATHWAY | hsa04960:Aldosterone-regulated sodium reabsorption | 5 | 2.09E-02 |
|  | GOTERM\_BP\_2 | GO:0007565~female pregnancy | 14 | 1.10E-05 |
|  | GOTERM\_BP\_2 | GO:0055085~transmembrane transport | 28 | 4.75E-03 |
|  | GOTERM\_BP\_2 | GO:0006950~response to stress | 64 | 8.17E-03 |
|  | GOTERM\_MF\_2 | GO:0004857~enzyme inhibitor activity | 16 | 8.68E-03 |
|  | GOTERM\_MF\_2 | GO:0008144~drug binding | 6 | 2.08E-02 |
|  | GOTERM\_CC\_2 | GO:0012505~endomembrane system | 32 | 2.66E-02 |
|  | GOTERM\_MF\_2 | GO:0008289~lipid binding | 21 | 2.70E-02 |
|  |  |  |  |  |
| W(XPEHH) | KEGG\_PATHWAY | hsa04740:Olfactory transduction | 28 | 1.73E-02 |
|  | KEGG\_PATHWAY | hsa03410:Base excision repair | 6 | 2.22E-02 |
|  | GOTERM\_CC\_2 | GO:0044424~intracellular part | 457 | 1.54E-03 |
|  | GOTERM\_CC\_2 | GO:0043233~organelle lumen | 97 | 2.25E-03 |
|  | GOTERM\_CC\_2 | GO:0005622~intracellular | 469 | 2.76E-03 |
|  | GOTERM\_MF\_2 | GO:0016874~ligase activity | 28 | 6.74E-03 |
|  | GOTERM\_BP\_2 | GO:0048522~positive regulation of cellular process | 97 | 8.12E-03 |
|  | GOTERM\_MF\_2 | GO:0019825~oxygen binding | 7 | 8.33E-03 |
|  | GOTERM\_BP\_2 | GO:0001659~temperature homeostasis | 5 | 9.67E-03 |
|  | GOTERM\_BP\_2 | GO:0009056~catabolic process | 69 | 1.04E-02 |
|  | GOTERM\_BP\_2 | GO:0065009~regulation of molecular function | 54 | 1.99E-02 |

Note: T, Taihu population; W, Western population. REHH: Relative Extend Haplotype Homozygosity Test, XPEHH: Cross Population Extend Haplotype Homozygosity Test.

**Supplementary Table S7** *Top ingenuity pathway analysis networks summary.*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population(method) | ID | Molecules in Network | Score | Focus Molecules | Top Diseases and Functions |
| Taihu(REHH) | 1 | ATXN7L3, B3GALT5, CCDC59, CDHR1, CLYBL, CTSZ, CUX1, EMX2, ENTPD3, EXOSC2, HNF1A, HNF4A, Insulin, LRRC6, MDFI, NFE2L3, PAFAH2, PANK1, PNLIPRP1, PRELID3B, Proinsulin, RAB37, SLC22A3, SLC35A1, SNX17, SNX19, SPO11, SQLE, ST6GALNAC1, SUPT7L, TDRKH, TMEM101, TRMT12, UBTF, UROS | 51 | 33 | Glomerular Injury, Metabolic Disease, Organismal Injury and Abnormalities |
| 2 | ALKBH2, ATP5L, BCCIP, BCL2, BYSL, C12orf43, CLGN, Ctbp, CYB5R1, FMNL1, FNDC4, GHITM, GSKIP, GZF1, HISTONE, histone deacetylase, KCTD10, KIF19, MAP3K14, MCOLN3, MRM1, MRPS5, OAT, OTUD4, RFX1, RPL4, RPL11, RPL13, RPL14, RPL27, RPL30, SMYD2, SRP72, TCF, ZNF512 | 46 | 31 | Hair and Skin Development and Function, Organ Morphology, DNA Replication, Recombination, and Repair |
| 3 | C1orf198, CC2D1A, CCDC121, CCDC130, CCDC138, CEP135, CLIC6, Creb, EXOC1, GLI2, GSE1, Guk, HAUS1, Hdac, MEOX1, MPP2, MPP3, MPP5, NFkB (family), NINL, NTF3, Pka, PLC gamma, POU4F1, RALB, RET, SLC39A12, SNPH, SPATA2L, TFIP11, TRPV1, TRPV3, TSSC1, TUFT1, ZNF572 | 41 | 29 | Cellular Development, Skeletal and Muscular System Development and Function, Nervous System Development and Function |
| 4 | ABCE1, ASF1B, BRCA1, CA4, CBX3, CDK10, DHX8, EML5, FAM175B, FAM84B, FBXL7, GPN1, Gsk3, H2AFY, Histone h3, Histone h4, Importin beta, IRF2BPL, JMJD6, KDM5B, LHX1, PAPD7, PNLIPRP2, RBM39, RNA polymerase II, RPA, SETD2, SLC16A12, SMARCA5, TBATA, TFEB, VRK1, WDR48, XRCC5, ZBTB7C | 41 | 29 | Dermatological Diseases and Conditions, Organ Morphology, Organismal Injury and Abnormalities |
| 5 | CASP3, caspase, CD3, Cg, CHMP1A, CRYBA4, CRYBB1, DOCK8, EIF1B, EIF2S1, EN1, FOXI1, G6PC3, GRB10, hemoglobin, HSP, Hsp70, Hsp90, IgG, KSR1, MAP2K1, Mek, PAICS, PANK2, PAPOLA, PPAT, RCAN3, RUNX1, SHROOM2, SLC4A1, SLC4A1AP, UNC5B, VPS4B, YWHAE, ZFP36L2 | 35 | 26 | Cellular Development, Cellular Growth and Proliferation, Embryonic Development |
| 6 | 20s proteasome, 26s Proteasome, Adaptor protein 2, Alp, ARRDC4, ATP6V1D, C/ebp, CYTH1, EIF4EBP2, estrogen receptor, FAM189A2, FKBP1A, Focal adhesion kinase, GRN, HERC3, LITAF, NEDD4L, PAQR7, Pdgfr, PDZD8, PSMA7, PSMB4, RHBDF2, SCN10A, SLC9A3R1, Smad, SMAD3, SMAD5, SMAD6, SNX27, SOST, TMTC4, TRIM63, Ubiquitin, VAT1 | 33 | 25 | Cardiovascular Disease, Connective Tissue Disorders, Developmental Disorder |
| 7 | ADAM33, aldo, Alpha catenin, BMP7, Cadherin, Caspase 3/7, CDH4, CDH15, Cyclin D, DUB, ETV4, FOXP4, GATA5, GCKR, Hedgehog, HHAT, HHIP, Jnk, MED20, MED28, MED30, mediator, PGC, PPM1G, PRKAA, SFRP2, SH3RF1, SNX9, SRD5A1, SRD5A2, transglutaminase, USP30, USP36, Wnt, WNT3 | 29 | 23 | Organ Morphology, Organismal Development, Reproductive System Development and Function |
| 8 | 14-3-3, Alpha tubulin, ATP synthase, ATP5A1, Calcineurin B, Calmodulin, CCK, CDC25B, Ck2, CST3, elastase, FUBP3, FXN, Gm-csf, HTT, LRPAP1, MRC1, NBR1, NUDT9, P38 MAPK, PCBD1, PFKFB2, phosphatase, PRSS46, PRSS50, PXYLP1, Rsk, STMN1, SYT1, SYT2, TUBB1, tubulin (complex), tubulin (family), UBE2O, VPS9D1 | 27 | 22 | Cell Death and Survival, Cellular Compromise, Neurological Disease |
| 9 | ACTA2, ADAMTS14, ANGEL1, ANGPT2, ASB18, ASS1, CD93, Collagen type I, Collagen type II, Collagen type III, Collagen type IV, Collagen(s), COX4I1, CYGB, DDAH1, DDR2, GOT, HID1, Hsp27, Laminin, NADPH oxidase, NELFCD, Notch, PRF1, Pro-inflammatory Cytokine, Secretase gamma, SERPINB5, SERPINB7, SGPL1, SIGLEC1, Tgf beta, TGFBI, TIMP2, VASH1, Vegf | 25 | 21 | Cell-mediated Immune Response, Inflammatory Response, Cell-To-Cell Signaling and Interaction |
| 10 | BCL10, BCR (complex), Calcineurin A, CD300C, CD300LB, CD300LF, CH25H, CST7, EDAR, FCMR, HEXIM1, HEXIM2, HGFAC, HLA-DR, Iga, Ige, IgG1, Igg3, IgG2a, IgG2b, Igm, Ikb, Immunoglobulin, MALT1, MARCO, NFAT (complex), NFkB (complex), NIPAL3, P-TEFb, SCLY, SH2B2, SRSF2, ST6GALNAC2, TNFRSF17, UNG | 23 | 20 | Humoral Immune Response, Protein Synthesis, Hematological System Development and Function |
| 11 | CD55, ERK, GORASP1, HES6, IFI35, IFIT1, IFIT2, IFIT3, IFIT5, Ifn, IFN alpha/beta, IFN Beta, IFN type 1, Ifnar, IFNLR1, IL12 (complex), IL27RA, Interferon alpha, Interferon-α Induced, JAK, MAL, MAVS, MHC CLASS I (family), MHC Class II (complex), Mir122a, b, NSFL1C, NXT1, Oas, OASL, RNASEL, SLA, STAT5a/b, TAP1, Tlr, UBE4A | 21 | 19 | Antimicrobial Response, Inflammatory Response, Cell Signaling |
| 12 | ANAPC10, APC (complex), BUB3, Cbp/p300, CCND3, Cdc2, Cdk, CGA, chemokine receptor, COX7A2, Cyclin A, DUSP3, E2f, EDN3, FDXR, FSH, GINS2, IL1R2, KIT, Lh, LIN28A, Mapk, p70 S6k, Pka catalytic subunit, PPY, PTPase, PTPN21, PYY, Rb, RGS12, SCAND1, Smad2/3, TG, THRB, TSH | 21 | 19 | Developmental Disorder, Endocrine System Disorders, Neurological Disease |
| 13 | ACSS1, ADRB, Ap1, COL6A3, cytochrome C, cytochrome-c oxidase, FAS, HSD17B, HSD17B7, HSD17B11, HSD17B13, Ifn gamma, IL1, LBH, MAP4K4, Nfat (family), NOS2, PARP, PI3K (family), PI4KB, PLEK2, RAB11A, Rac, RAE1, Ras, Rnr, RPS21, Sapk, Sos, SPSB4, Tnf (family), Tnf receptor, ZIC2, ZP3, ZRANB1 | 20 | 18 | Small Molecule Biochemistry, Gastrointestinal Disease, Hepatic System Disease |
| 14 | AAGAB, ACAC, ACACB, Aconitase, ACSL1, ADIPOR1, AMPK, amylase, Ap1 gamma, Ap2 alpha, CAMKK1, DPEP1, EDRF1, Eif4g, GRHL3, Growth hormone, HDL, HDL-cholesterol, HMG CoA synthase, IBSP, IL23, LDL, LDL-cholesterol, LDLRAP1, LIPA, MMAB, MVK, Nos, NPC1, NSUN2, Pkc(s), SAA, Srebp, TRAPPC12, XDH | 18 | 17 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry |
| 15 | ABCA2, ACADS, ADH6, ANKFY1, ARL4D, C11orf57, CAMSAP3, CDR2L, CNKSR1, FAM110A, FAM196B, FHIT, GABRA3, miR-1275 (and other miRNAs w/seed UGGGGGA), MTCL1, MYO9B, NCMAP, NEUROG2, OTOR, PECR, POGZ, PRKCSH, PRPF38A, PTMS, RHOD, RHOF, RHPN1, RND2, RPUSD1, SAMHD1, SDCBP2, SEC22C, SEZ6L, TTYH2, ZNF831 | 18 | 17 | Infectious Diseases, Developmental Disorder, Hereditary Disorder |
| 16 | B3GNT6, BORA, C5orf58, CNR2, CYTH1, FAM3B, FGFR1, FGFR4, GGNBP2, GJB7, GRB7, KAZN, KLB, LARP7, LCTL, LEPROT, LTBP2, MASP1, miR-150-5p (and other miRNAs w/seed CUCCCAA), MTCH2, MUC4, PDP1, PIK3AP1, PROSER2, R3HDML, RASA3, RNF219, RTP1, S1PR3, SIRPB2, SLA, UBE3B, ZDHHC22, ZER1, ZNF621 | 18 | 17 | Cellular Movement, Hematological System Development and Function, Humoral Immune Response |
| 17 | AK7, ARHGAP27, ARL6IP4, C19orf53, C1orf158, CD300LG, CNPY3, CPEB2, CPXM2, GTPase, HSPB11, IFT27, IFT46, IFT52, IFT172, KLHL18, miR-4640-5p (and other miRNAs w/seed GGGCCAG), NDPK, NFS1, NME3, NR1D1, NR1D2, OTOP3, RGS8, RGS16, RGS18, RHBDD2, SMPDL3B, TBC1D2, TBC1D10B, TLR4, TMEM169, TTC30B, Vnn3, ZC3H14 | 18 | 17 | Cell Signaling, Cellular Assembly and Organization, Cellular Function and Maintenance |
| 18 | ADCYAP1R1, ADORA1, ADRA1A, C19orf25, C19orf57, C1orf111, CHST3, CMTM5, EGR3, ESPNL, GAST, GDAP1L1, GGACT, GLTP, GPAT2, GRK6, HS3ST2, HS6ST1, KRTAP10-9, LINGO4, LRRC46, MGLL, miR-762 (and other miRNAs w/seed GGGCUGG), MRI1, NPY, OPRL1, P2RY2, PDZRN3, PLCB3, PLCD3, PRDM12, RBBP8NL, ROMO1, TRH, ZNF594 | 17 | 16 | Carbohydrate Metabolism, Small Molecule Biochemistry, Molecular Transport |
| 19 | ACSF3, COLEC11, CTNS, FAM53B, FBXL18, GADD45G, KLHL30, KRTCAP3, LRIT2, MAPK6, miR-134-3p (and other miRNAs w/seed UGUGGGC), miR-1538 (and other miRNAs w/seed GGCCCGG), miR-290b-3p (and other miRNAs w/seed AGUGCCC), miR-296-5p (miRNAs w/seed GGGCCCC), miR-3192-5p (miRNAs w/seed CUGGGAG), miR-3195 (miRNAs w/seed GCGCCGG), miR-3605-3p (miRNAs w/seed CUCCGUG), miR-3661 (and other miRNAs w/seed GACCUGG), miR-3675-5p (miRNAs w/seed AUGGGGC), miR-4456 (and other miRNAs w/seed CUGGUGG), miR-4479 (miRNAs w/seed GCGCGGC), miR-4674 (miRNAs w/seed UGGGCUC), miR-4740-3p (miRNAs w/seed CCCGAGA), miR-4746-3p (miRNAs w/seed GCGGUGC), miR-491-5p (and other miRNAs w/seed GUGGGGA), miR-555 (miRNAs w/seed GGGUAAG), NAT9, PLEKHM1, PODNL1, RSPO4, SIRPB1, SPEF1, TMEM104, TMEM132B, TMEM63C | 17 | 16 | Connective Tissue Disorders, Developmental Disorder, Hereditary Disorder |
| 20 | ACBD4, BTNL3, C11orf42, C2orf81, C6orf141, CCDC88C, CXCL14, CYB5D2, DRC3, EXTL1, FAM71D, FLRT1, FOXD4L1, GALNT18, HMX2, IRX1, KDM4E, KLHL17, miR-1237-5p (and other miRNAs w/seed GGGGGCG), miR-4690-5p (miRNAs w/seed AGCAGGC), miR-625-5p (and other miRNAs w/seed GGGGGAA), NANOS3, OAZ3, PNPLA7, REL, SH3BP1, SIRPD, SLC52A3, TBX10, TMEM125, TTC21A, UPK2, UPK3B, WDR63, ZDHHC24 | 17 | 16 | Auditory and Vestibular System Development and Function, Cellular Growth and Proliferation, Embryonic Development |
| 21 | Akt, Alpha 1 antitrypsin, BTNL2, C4BP, C4BPA, C4BPB, Ciap, CNKSR1, Collagen Alpha1, death receptor, DHRS3, DMP1, DNAJ, DSPP, ENaC, HTATIP2, JINK1/2, Kallikrein, Laminin2, LHPP, N-cor, Nr1h, PEPCK, PLG, Rar, RBM38, RIDA, Rxr, SCNN1G, SERCA, SERPINA5, SERPINA12, thyroid hormone receptor, TMSB4, trypsin | 15 | 15 | Tissue Morphology, Auditory Disease, Dental Disease |
| 22 | ADGRB1, AP5B1, AP5S1, BRS3, CCR9, DHX32, FADS6, FAM122A, FAM196A, FAM89A, FZD6, FZD10, GHSR, GPR63, GPR88, GPR153, GPR171, GPR180, GRM7, GRPR, HCAR2, HCAR3, HTR2A, KDSR, KRT20, LYZL4, MARCH4, miR-16-5p (and other miRNAs w/seed AGCAGCA), MTFR1L, RASGEF1B, STOX2, SYDE2, SYNDIG1, TEDDM1, TPPP3 | 15 | 15 | Cardiovascular Disease, Hematological Disease, Metabolic Disease |
| 23 | ADAMTS15, AK1, ANKRD29, ARCN1, ARL9, BCAP31, BTBD17, CASC3, CCDC155, CELF3, CHST5, CHST15, ECHDC3, EIF5A, GGA3, HK1, HS6ST1, HS6ST3, MEGF11, MFSD11, miR-4755-3p (miRNAs w/seed GCCAGGC), miR-4798-5p (miRNAs w/seed UCGGUAU), PRCD, SFMBT2, SLC30A2, SLC35E1, SMIM8, SULT1C2, SULT1E1, TAF7L, TBX19, TCF21, TJAP1, TTPAL, WSB1 | 15 | 15 | Post-Translational Modification, Carbohydrate Metabolism, Small Molecule Biochemistry |
| 24 | ALLC, BCL2L12, CABLES2, Cops2, CSRNP1, CUEDC2, DCLRE1A, DNAI2, EPO, FILIP1, GLTSCR2, GRXCR1, HMX3, HSPA12A, KLHL12, LRIT1, METTL23, mir-486, MRPL41, P4HTM, PHF20L1, PHKG1, PPP1CA, Rps3a1, RPS4Y1, SHP, STAMBPL1, THG1L, Top2, TP53, TTC36, UBC, Ube3, YOD1, ZNHIT1 | 15 | 15 | Cell Death and Survival, Cellular Function and Maintenance, Embryonic Development |
| 25 | Actn3, C20orf202, C2orf16, CASQ1, CATSPER4, COL21A1, DCAF15, DMD, DND1, EMC3, EMC4, EMC6, EMC7, EMC8, FAM188B, LRFN4, LYZL6, MIEN1, miR-1913 (and other miRNAs w/seed CUGCCCC), miR-4443 (miRNAs w/seed UGGAGGC), MMAA, MRPL9, MRPL53, MYH8, NAPB, PSTPIP2, RB1, RPRML, SNX10, SPATA32, SYNE3, TOMM6, Troponin t, UMODL1, YDJC | 15 | 15 | Cellular Compromise, Organismal Injury and Abnormalities, Skeletal and Muscular Disorders |
|  |  |  |  |  |  |
| Taihu(XPEHH) | 1 | Actin, CD79B, CHRM1, Cyclin A, ERK1/2, ERN1, FADD, FSH, FTSJ3, GH1, GNL3, GPC1, HDL, Igm, Immunoglobulin, Insulin, Iti, ITIH1, ITIH3, ITIH4, LDL, Lh, Mek, P3H1, PDGF BB, Pkc(s), PLC, PLCH2, PPIH, PRKCD, Sapk, SLC22A8, STK25, STX5, WDR48 | 39 | 19 | Connective Tissue Disorders, Developmental Disorder, Hereditary Disorder |
| 2 | 26s Proteasome, Akt, BSCL2, CACNG2, CCR8, CD3, CX3CR1, cytochrome C, DDX42, ERK, estrogen receptor, Focal adhesion kinase, GORASP1, Gpcr, Histone h3, Hsp90, ICAM2, INTS5, Jnk, Mapk, MYH9, NFkB (complex), P38 MAPK, PI3K (complex), Pka, POLR2B, POLR2G, PSMC5, SNRPC, SPDEF, TAF6L, TCR, TXN2, UBXN1, Vegf | 34 | 17 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking |
| 3 | AP5Z1, CALML6, CAV1, CCL27, CLDN19, CONNEXIN, DUSP28, FAM186B, FAM213B, FOXK1, HPD, HRAS, Intersectin, JUNB, LIMD2, MAPK3, miR-1343-5p (and other miRNAs w/seed GGGGAGC), miR-675-5p (and other miRNAs w/seed GGUGCGG), miR-762 (and other miRNAs w/seed GGGCUGG), MMD2, NEK4, OXSM, PANK4, Pcmt1, PYDC1, RADIL, Rasgrf, RGL4, SCN4A, SMARCD2, TMEM52, TMEM86B, TPTE2, TTC9C, WDR74 | 31 | 16 | Cell Cycle, Connective Tissue Development and Function, Dermatological Diseases and Conditions |
| 4 | ACYP1, APP, APPBP2, ATRAID, C1orf50, C5orf15, CCDC30, CSRNP1, CYP2C19, GUCA2A, Hrk, Ifi47, IL1B, KLHL35, METTL12, miR-1245a (and other miRNAs w/seed AGUGAUC), miR-381-3p (and other miRNAs w/seed AUACAAG), MMEL1, NR3C1, P2rx7, PACSIN1, PIGG, RPS10, SDHAF3, SLC22A6, SLC25A38, SNX9, TCEAL2, TEX2, Tgtp1/Tgtp2, UGGT2, Uox, ZBTB3, ZMYND12, ZSCAN16 | 28 | 15 | Small Molecule Biochemistry, Gene Expression, Connective Tissue Disorders |
| 5 | ANKMY1, C19orf38, CCNI, CMC1, COX14, DKC1, EIF3D, FLAD1, FN1, FOXRED2, GANAB, GPN2, HIST1H4E, HIST1H4L, MIEN1, miR-125b-5p (and other miRNAs w/seed CCCUGAG), miR-4456 (and other miRNAs w/seed CUGGUGG), NXF1, OGFR, OR13A1, PAPOLB, REL, RIMKLA, SEPT2, SH2D3A, SMIM20, SNORA62, SRRD, SSR2, SURF1, TMEM223, TSTA3, TTC21A, UQCC3, VDAC1 | 24 | 13 | Developmental Disorder, Hereditary Disorder, Metabolic Disease |
| 6 | AOC1, C11orf52, CCDC47, CYP3A7, FCAMR, FUZ, FXYD7, GLT8D1, GNB1L, GNGT2, HNF4A, LBHD1, miR-1972 (miRNAs w/seed CAGGCCA), miR-637 (and other miRNAs w/seed CUGGGGG), MRPS12, PMEL, PRMT7, RBM42, REM1, RNPEPL1, SFMBT1, SLC17A2, SLC25A18, SLC43A1, SMIM24, SPCS1, THOC3, TMEM187, TRMT61B, UBL7, UGT1A1, UGT1A4, UGT1A5, UGT1A6, XIRP1 | 9 | 6 | Amino Acid Metabolism, Drug Metabolism, Endocrine System Development and Function |
|  |  |  |  |  |  |
| Western(REHH) | 1 | ADAM8, ADCK1, BAG2, C1D, CCDC138, CEP131, COPRS, CSNK1E, EXOSC2, EXOSC10, HEATR1, HNRNPM, IFT27, KDM6B, KIAA0753, LDLRAD4, MAP3K14, MINOS1, NDRG1, NOS2, PNO1, PTBP1, RPL3, RTFDC1, SEC24C, SFXN1, SPACA1, SRSF2, SS18L2, ST6GALNAC1, STAU1, TUBGCP2, UBE2O, UBXN10, VCP | 53 | 35 | RNA Post-Transcriptional Modification, Cellular Assembly and Organization, Developmental Disorder |
| 2 | ACSM3, ANAPC16, ANKRD40, BCL9, CCDC25, CD3, CDR2L, CHST3, CHST10, DAZAP2, DCUN1D3, DHCR24, DIP2B, ELAVL1, FAM46C, FAS, GSDMC, HAO2, IL10RA, JOSD1, LMNB1, MESDC1, MEX3D, NKTR, ORAOV1, PAPD4, PRELID3B, REEP5, sulfotransferase, SULT1C2, SULT1C3, SULT1C4, TSPAN14, VPS37C, ZNF281 | 47 | 33 | Drug Metabolism, Endocrine System Development and Function, Lipid Metabolism |
| 3 | AATK, ACIN1, ARID4B, BCAS3, CHMP6, ERMAP, EVX1, FAM49A, FKBP4, FXR2, Histone h3, HOXA1, HOXA2, HOXA11, JMJD6, LRRC8A, LRRC8C, MED8, MED31, mediator, MTR, NR3C1, PDCL3, RNA polymerase II, SIX2, SNAI2, TADA2B, TARBP1, TEPSIN, TFAP2C, TP53BP2, USP54, ZFYVE28, ZNF451, ZNF503 | 44 | 32 | Digestive System Development and Function, Neurological Disease, Cellular Development |
| 4 | BACE1, CACNA1G, Dishevelled, DLL1, ELP2, ETNK2, GRIK3, GRIK4, Histone h4, HK1, IGFBP1, KCNA5, MAFF, NEURL1, Notch, NUP98, NUP188, PADI3, PCSK7, PITPNM3, proprotein convertase, PSAP, PTF1A, PTK2B, Rab11, RAB11B, RAB11FIP4, RANBP2, RANBP9, RNF4, SEH1L, TAGLN, TBC1D14, TDG, UBE2I | 40 | 30 | Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance, Nervous System Development and Function |
| 5 | 26s Proteasome, ANKRA2, ARHGAP25, ATF4, BCL2L1, CCL20, CEBPG, CRAT, Creb, DDX17, DPYSL4, FAM120B, FMNL1, GJA5, GLI2, Hdac, HERC3, Hsp70, IFT140, KCNA6, METTL23, MPDU1, NOXO1, PDIA6, PHAX, PPM1D, SPTLC2, STOML2, TAB1, TBPL1, TBX2, TBX4, TCF, TULP3, XRCC6 | 40 | 30 | Embryonic Development, Organismal Development, Skeletal and Muscular System Development and Function |
| 6 | ALLC, ANXA8/ANXA8L1, ASL, C1q, C1QA, C1QB, C1QC, CD93, Ctbp, ECHS1, ERCC3, FDXR, FIGNL1, HISTONE, IFN type 1, KANK3, MFAP2, Mir122a, b, NTHL1, PADI4, Pias, PMM1, PVALB, RBM34, Rnr, RPS19BP1, SLC25A47, TAF1B, TBXAS1, TIMM44, TOMM7, TOMM20, TOMM22, TP53, WRAP53 | 35 | 28 | Developmental Disorder, Hereditary Disorder, Immunological Disease |
| 7 | APC, AURKA, BTF3, Calcineurin A, CCK, CEP76, CEP192, Ck2, CNGB1, CNTROB, CSNK2A2, EPHX2, GDAP2, Gsk3, HEXIM1, L3MBTL2, MBD3, MIER2, MYBBP1A, NMDA Receptor, NT5C, Pdgf (complex), phosphatase, PP1 protein complex group, PP1-C, PPP1R15B, PTPA, PTPN2, RPS28, SLC9A3R1, SLC9A3R2, TELO2, WARS, WNT2B, ZSWIM8 | 33 | 27 | Cell Cycle, Cellular Movement, Cellular Assembly and Organization |
| 8 | ADIPOR2, AIFM2, Alp, APLN, Cg, DBI, E2f, EIF4A1, FGF1, FGF19, HSD3B1, Insulin, KCNT2, KSR1, LAMTOR1, Lh, MAP2K1/2, MARCH2, MARCH3, NAPB, NLGN2, PRKCE, Proinsulin, SETSIP, SHH, SIDT2, SLC5A7, Sod, SQLE, SRM, STX6, SYT1, TBC1D7, TCF3, TMEM132A | 33 | 27 | Cellular Development, Endocrine System Development and Function, Tissue Morphology |
| 9 | AP-3, APLF, BMP, BMP10, CHD1L, CHRNA2, CHRNA10, Cytokeratin, DAD1, Gli, H2AFY, HEXIM2, ID1, KCNJ4, KRT10, KRT12, KRT13, KRT19, KRT20, KRT23, MICU1, NFkB (complex), nicotinic acetylcholine receptor, NOP14, Nuclear factor 1, P-TEFb, PKN3, RWDD3, SLC2A12, Smad, ST18, TCF21, TMPRSS6, UMOD, WDR34 | 31 | 26 | Cancer, Endocrine System Disorders, Gastrointestinal Disease |
| 10 | APC (complex), ARMC7, Cbp/p300, CCDC185, Cdc2, CDC20, Cyclin B, CYTH4, GAN, Gi-coupled receptor, INA, Keratin, KIFC3, KRT15, KRT27, KRT31, KRT32, KRT35, KRT36, KRT82, KRT84, KRT85, Mapk, NEFL, NEFM, OXA1L, PPBP, Rab5, RHNO1, SLC15A3, SYCE1, Tenascin, TFIP11, TNR, ZNF572 | 31 | 26 | Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Nervous System Development and Function |
|  |  |  |  |  |  |
| Western(XPEHH) | 1 | 14-3-3, AANAT, ADAM17, ADRB, AEBP1, Calcineurin protein(s), CaMKII, caspase, CDT1, CHI3L1, Collagen Alpha1, Cr3, CYGB, DDX56, ERK1/2, FGF18, FURIN, HMGB1, Ifn gamma, IL23, ITGB1BP1, MAP2K1/2, Mlc, MYBPH, MYL7, MYOG, Notch, P38 MAPK, PCNA, POLD2, POLM, PP2A, Pro-inflammatory Cytokine, Rb, RHBDF2 | 33 | 18 | Gene Expression, DNA Replication, Recombination, and Repair, Cellular Movement |
| 2 | ACSF3, ALPK2, ASAP2, BCL2L1, C2orf40, Ca2 ATPase, calpain, CAPN7, CDH26, CDS2, CTNNB1, EAF1, IRX4, ITGB1, LDH (family), LDHB, LMNA, METTL23, MFSD11, mir-361, miR-3083-5p (and other miRNAs w/seed GGCUGGG), miR-30c-5p (and other miRNAs w/seed GUAAACA), miR-330-3p (and other miRNAs w/seed CAAAGCA), miR-361-3p (miRNAs w/seed CCCCCAG), Nucleoporin, PRCD, PTRH1, RCCD1, ROMO1, ST6GALNAC1, TMEM230, TRIL, UBTD2, UROC1, YKT6 | 33 | 18 | Cancer, Hematological Disease, Immunological Disease |
| 3 | ADCY, ADORA1, AMPK, CBFA2T3, CDH15, CDH22, Cg, Creb, DIRAS3, DRD2, Focal adhesion kinase, FSH, G protein alphai, Gi-coupled receptor, GLIS1, GNAI3, Gpcr, Gsk3, GSTM3, Histone h3, Histone h4, JMJD6, Mapk, NCAM1, NFkB (complex), PI3K (complex), Pka, Pkc(s), PROKR2, Ras homolog, SLC12A5, TLX3, USPL1, WLS, Wnt | 28 | 16 | Behavior, Nervous System Development and Function, Skeletal and Muscular System Development and Function |
| 4 | APP, ATXN7L2, CFAP100, CLEC3A, CYB561D1, DENND6B, DEPDC7, DPH7, FAM110D, GPR15, GPR61, GPR78, GTF3C6, LINGO2, LRRC42, MAN2A2, MAN2B1, miR-2115-5p (miRNAs w/seed GCUUCCA), miR-3202 (miRNAs w/seed GGAAGGG), miR-4667-3p (miRNAs w/seed CCCUCCU), MRPL36, MT-ND2, MT-ND3, NCOA5, NDUFB1, NDUFS6, NXF1, OC90, Sec23, SNX14, TEX26, TM6SF2, TMED4, ZNF574, ZXDC | 19 | 12 | Developmental Disorder, Hereditary Disorder, Metabolic Disease |
| 5 | 26s Proteasome, ADAM23, ADAMTS13, AMIGO1, Atf, BOLA2/BOLA2B, BTBD3, CD3, Ck2, CTSA, CTSW, ELMO2, ERK, HIST1H2BC, Il12 receptor, KEL, LRP8, MAGOH, Metalloprotease, MT1G, MYL3, NEDD4L, NPM1, p38 Sapk, Pde4, Presenilin, RNA polymerase II, SERBP1, SIGLEC7, Sos, SRSF2, TFIIF, Vegf, WASP (family), YWHAQ | 17 | 11 | Cancer, Hematological Disease, Organismal Injury and Abnormalities |
| 6 | AFM, APP, ARHGAP9, BUD31, C4, C19orf43, CARS, CD36, DMRTB1, EPS8L3, FAM50A, HDDC3, Hspg, Iga, IL26, MEDAG, METTL6, miR-4711-5p (miRNAs w/seed GCAUCAG), MSMB, NAT6, NNMT, OARD1, PCIF1, plasminogen activator, RAD51C, SH3BP5, SLC41A3, SPATA4, ST6GALNAC2, STARD10, TGFB1, TMEM183A, TRAPPC2L, WNK1, ZNF839 | 17 | 11 | Cellular Movement, Nervous System Development and Function, Cardiovascular System Development and Function |
|  | AHR, ALDH3A1, C1orf123, CCDC138, CDKN1A, CEBPB, CHIT1, COLQ, CPB2, CPVL, Fc receptor, FCAR, Foxo, Gamma tubulin, GH2, GSTA1, GSTA5, IDH3B, IFITM3, Igh (family), Lpa receptor, NUDCD3, PCM1, PDGF-AA, PI3K (complex), PLB1, RPF2, SH3PXD2B, SHOX, SLC35C2, SPP1, TTC12, TTLL5, UGT1A6, UNC45A | 15 | 10 | Cellular Development, Connective Tissue Development and Function, Cellular Growth and Proliferation |
| 7 | Akt, ALOX5AP, Ap1, BLVRA, CD40, chemokine, Collagen(s), CPT2, FES, GCK, Growth hormone, Hsp70, IFN Beta, Ige, IgG, IgG1, IL1, IL12 (complex), IL12 (family), Immunoglobulin, Interferon alpha, JAK, Jnk, LDL, Mek, Mmp, MMP9, NADPH oxidase, NFkB (family), NPC1L1, Nr1h, p85 (pik3r), Tgf beta, Tlr, ZNF335 | 13 | 9 | Cardiovascular Disease, Cell Morphology, Gastrointestinal Disease |
| 8 | NF2, OR4X1 | 2 | 1 | Cancer, Cell Morphology, Cellular Growth and Proliferation |

REHH: Relative Extend Haplotype Homozygosity Test, XPEHH: Cross Population Extend Haplotype Homozygosity Test.

**Supplementary Table S8** *The frequency distribution of single nucleotide polymorphisms with the p values (Top 5).*

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| pop | method | Chr | position | ref | alle | A1 | a1 | AA1 | Aa1 | aa1 | A2 | a2 | AA2 | Aa2 | aa2 | p.value3 | p.value4 | gene |
| T | REHH | chr12 | 51598140 | T | C | 219 | 21 | 101 | 17 | 2 | 221 | 283 | 53 | 115 | 84 | 2.64E-30 | 2.58E-34 | *CTNS* |
| T | REHH | chr12 | 51598146 | C | A | 217 | 23 | 100 | 17 | 3 | 223 | 281 | 54 | 115 | 83 | 4.57E-29 | 1.24E-32 | *CTNS* |
| T | REHH | chr6 | 77099521 | G | A | 196 | 44 | 76 | 44 | 0 | 504 | 0 | 252 | 0 | 0 | NA | 1.96E-22 | *EXTL1* |
| T | REHH | chr6 | 77099635 | T | C | 197 | 43 | 77 | 43 | 0 | 504 | 0 | 252 | 0 | 0 | NA | 6.48E-22 | *EXTL1* |
| T | REHH | chr5 | 106969622 | A | T | 86 | 154 | 0 | 86 | 34 | 463 | 41 | 211 | 41 | 0 | 6.46E-54 | 1.02E-58 | *SYT1* |
| T | REHH | chr5 | 106972787 | G | A | 208 | 32 | 88 | 32 | 0 | 142 | 362 | 4 | 134 | 114 | 4.92E-52 | 5.65E-50 | *SYT1* |
| T | REHH | chr5 | 106972819 | C | A | 208 | 32 | 88 | 32 | 0 | 138 | 366 | 9 | 120 | 123 | 2.75E-48 | 2.29E-51 | *SYT1* |
| T | REHH | chr5 | 106972821 | A | G | 209 | 31 | 89 | 31 | 0 | 139 | 365 | 9 | 121 | 122 | 7.34E-49 | 1.07E-51 | *SYT1* |
| W | REHH | chr14 | 107997625 | G | A | 189 | 51 | 69 | 51 | 0 | 469 | 35 | 217 | 35 | 0 | NA | 2.37E-08 | *SGMS1* |
| W | REHH | chr14 | 107997766 | T | A | 172 | 68 | 53 | 66 | 1 | 410 | 94 | 158 | 94 | 0 | 1.55E-03 | 3.77E-03 | *SGMS1* |
| W | REHH | chr14 | 108040953 | T | C | 239 | 1 | 119 | 1 | 0 | 444 | 60 | 192 | 60 | 0 | NA | 2.03E-07 | *SGMS1* |
| W | REHH | chr14 | 108513282 | T | G | 240 | 0 | 120 | 0 | 0 | 450 | 54 | 199 | 52 | 1 | 4.07E-07 | 3.15E-07 | *MINPP1* |
| W | REHH | chr14 | 12214589 | C | A | 83 | 157 | 35 | 13 | 72 | 17 | 487 | 0 | 17 | 235 | 2.04E-19 | 7.20E-31 | *TRIM35* |
| W | REHH | chr14 | 12215246 | G | A | 240 | 0 | 120 | 0 | 0 | 455 | 49 | 203 | 49 | 0 | NA | 1.30E-06 | *TRIM35* |
| W | REHH | chr14 | 12218136 | G | A | 240 | 0 | 120 | 0 | 0 | 356 | 148 | 112 | 132 | 8 | 6.13E-24 | 1.67E-20 | *TRIM35* |
| T | XPEHH | chr12 | 15019656 | A | G | 74 | 166 | 9 | 56 | 55 | 1 | 503 | 0 | 1 | 251 | 1.07E-35 | 9.30E-38 | *SCN4A* |
| T | XPEHH | chr12 | 15019594 | T | C | 77 | 163 | 11 | 55 | 54 | 2 | 502 | 0 | 2 | 250 | 1.85E-35 | 1.44E-38 | *SCN4A* |
| W | XPEHH | chr17 | 53996117 | C | T | 240 | 0 | 120 | 0 | 0 | 319 | 185 | 82 | 155 | 15 | 4.24E-33 | 6.79E-27 | *CDH22* |

Note: T, Taihu population; W, Western population; ref or A, the reference allele; alle or a, the alternative allele; 1the allele or genotype counts in Taihu population; 2the allele or genotype counts in Western population; 3Chi-square test for Taihu and western pig population in the genotype frequency; 4Chi-square test for Taihu and western pig population in the allele frequency; NA, one of the genotype is not exiting in both population leading to the p value cannot be calculated.

**Supplementary Table S9** *The frequency distribution of single nucleotide polymorphism locating in the genes of Asthma pathway.*

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chromosome | position | ref | alle | A1 | a1 | AA1 | Aa1 | aa1 | A2 | a2 | AA2 | Aa2 | aa2 | p.value3 | p.value4 | gene |
| chr2 | 140441497 | G | A | 240 | 0 | 120 | 0 | 0 | 460 | 44 | 208 | 44 | 0 | NA | 5.29E-06 | *IL13* |
| chr4 | 97100197 | G | A | 208 | 32 | 88 | 32 | 0 | 294 | 210 | 76 | 142 | 34 | 4.96E-15 | 2.39E-14 | *FCER1G* |
| chr4 | 99072632 | G | A | 239 | 1 | 119 | 1 | 0 | 303 | 201 | 75 | 153 | 24 | 8.40E-35 | 3.03E-29 | *FCER1A* |
| chr7 | 27552245 | C | T | 240 | 0 | 120 | 0 | 0 | 453 | 51 | 202 | 49 | 1 | 1.06E-06 | 7.38E-07 | *TNFA* |
| chr7 | 27552276 | C | T | 240 | 0 | 120 | 0 | 0 | 440 | 64 | 196 | 48 | 8 | 1.52E-07 | 1.75E-08 | *TNFA* |
| chr7 | 29114579 | C | T | 240 | 0 | 120 | 0 | 0 | 459 | 45 | 207 | 45 | 0 | NA | 4.00E-06 | *SLA-DRB* |
| chr7 | 29114676 | A | G | 204 | 36 | 84 | 36 | 0 | 371 | 133 | 120 | 131 | 1 | 2.42E-04 | 7.46E-04 | *SLA-DRB* |
| chr7 | 29169235 | C | T | 63 | 177 | 2 | 59 | 59 | 39 | 465 | 0 | 39 | 213 | 2.91E-12 | 1.49E-11 | *SLA-DQA* |
| chr7 | 29182717 | T | C | 4 | 236 | 0 | 4 | 116 | 74 | 430 | 6 | 62 | 184 | 4.51E-07 | 1.23E-07 | *SLA-DQB1* |
| chr7 | 29183895 | C | G | 230 | 10 | 110 | 10 | 0 | 471 | 33 | 219 | 33 | 0 | NA | 2.57E-01 | *SLA-DQB1* |
| chr7 | 29187591 | G | A | 221 | 19 | 101 | 19 | 0 | 472 | 32 | 220 | 32 | 0 | NA | 5.25E-01 | *SLA-DQB1* |
| chr12 | 36319633 | A | T | 132 | 108 | 14 | 104 | 2 | 13 | 491 | 0 | 13 | 239 | 4.73E-68 | 3.73E-63 | *EPX* |
| chr12 | 36321984 | T | C | 177 | 63 | 59 | 59 | 2 | 89 | 415 | 4 | 81 | 167 | 6.74E-42 | 7.97E-50 | *EPX* |
| chr12 | 36325021 | G | A | 208 | 32 | 88 | 32 | 0 | 454 | 50 | 202 | 50 | 0 | NA | 2.06E-01 | *EPX* |
| chr17 | 53934614 | A | G | 29 | 211 | 0 | 29 | 91 | 41 | 463 | 0 | 41 | 211 | NA | 1.12E-01 | *CD40* |
| chr17 | 53934624 | G | A | 29 | 211 | 0 | 29 | 91 | 41 | 463 | 0 | 41 | 211 | NA | 1.12E-01 | *CD40* |

Note: T, Taihu population; W, Western population; ref or A, the reference allele; alle or a, the alternative allele; 1the allele or genotype counts in Taihu population; 2the allele or genotype counts in Western population; 3Chi-square test for Taihu and western pig population in the genotype frequency; 4Chi-square test for Taihu and western pig population in the allele frequency; NA, one of the genotype is not exiting in both population leading to the p value cannot be calculated.