

Supplementary Material of “Porcine Y-chromosome variation is consistent with the occurrence of paternal gene flow from non-Asian to Asian populations”

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Supplementary Figures

Figure S1. Distributions and confidence intervals (CI) for the Y chromosome variability to divergence ratio obtained by bootstrap analysis. (A) Distributions of the ratios considering i) all wild boars together, Asian wild boars and Non-Asian wild boars (from left to right). Red vertical lines are indicating the percentiles 2.5 and 97.5 of the distribution and vertical blue line is indicating the mean of the ratio (B) On top, distributions of the ratios for the Non-Asian (left) and Asian wild boars (right). Distribution of the difference of the Non-Asian from the Asian ratios (bottom).

Figure S2.

A Matrix representing the sequence variation of samples of each group. On the top, the name of each locus where the variants are located and the position number in the concatenated fragment of 9903 bp. Bold values indicate that the position is already genotyped. On the right and with different colours, the code number for the sequenced samples in each group. Gray lines inside the matrix mean missing data.

Figure S3. The effect of different evolutionary processes on the Y/A ratio. (A) Subdivision process. (C) Population decline process. (B, D) The same Subdivision and Population decline processes as in A and C but adding an arbitrary reduction of 22x in the levels of variability at Y-chromosome, mimicking the effect of selective linkage event. The time of split is indicated in the x-axis, while the effective population size of the second population is indicated in the y-axis. The orange arrow indicates the range of values of the observed Y/A ratio. The black arrow indicates the expected range of values under the SNM with an equal females vs males ratio.

Figure S4. Validation of the ABC analysis: (A) Cross-validation analysis using pseudo-observed data (PODs). In black, the percentage of cases where the true model was correctly identified. (B) Comparison of the empirical and posterior probabilities obtained from PODs assuming the model IM as the true model.

Figure S5. Posterior predictive simulations for the model IM. The figure shows where each observed summary statistic (red vertical line) fall within the distribution of summary statistics obtained from simulated data (black curve). Their respective probabilities are indicated on the

top.

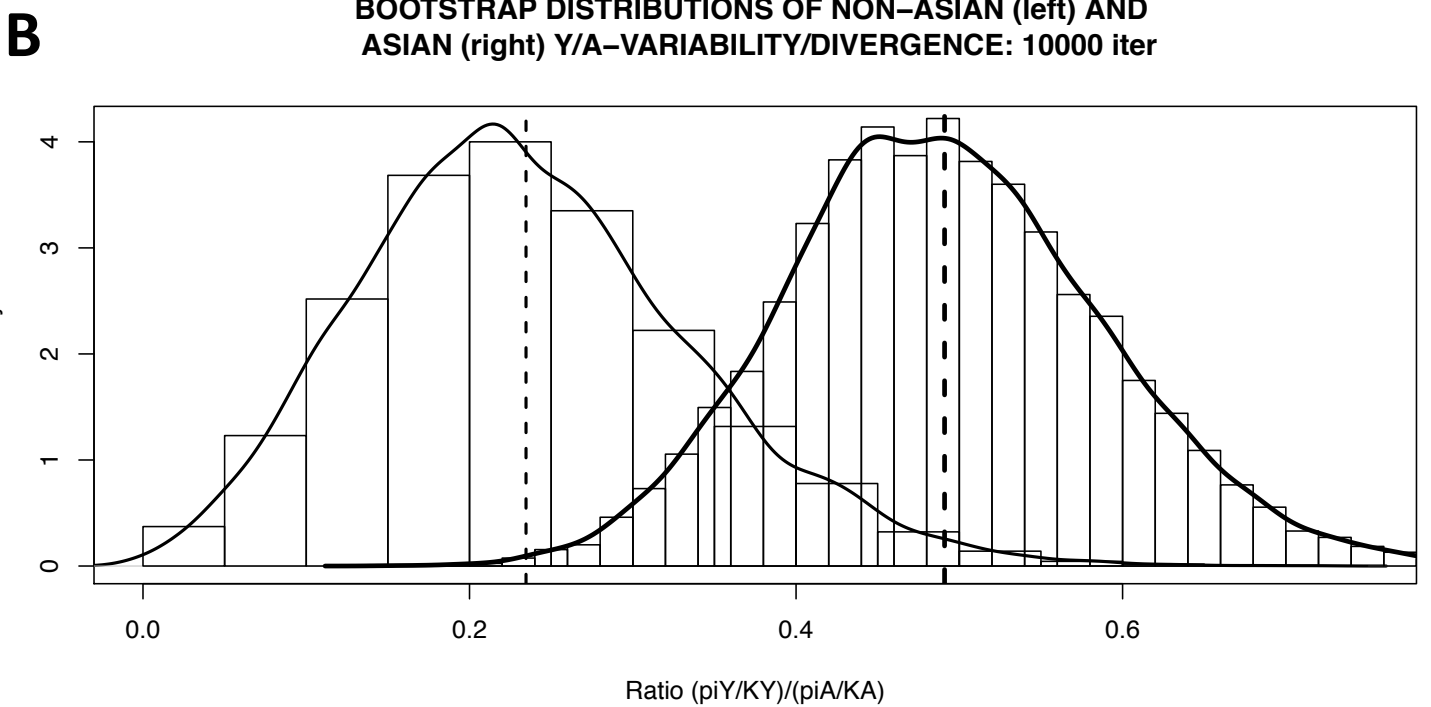
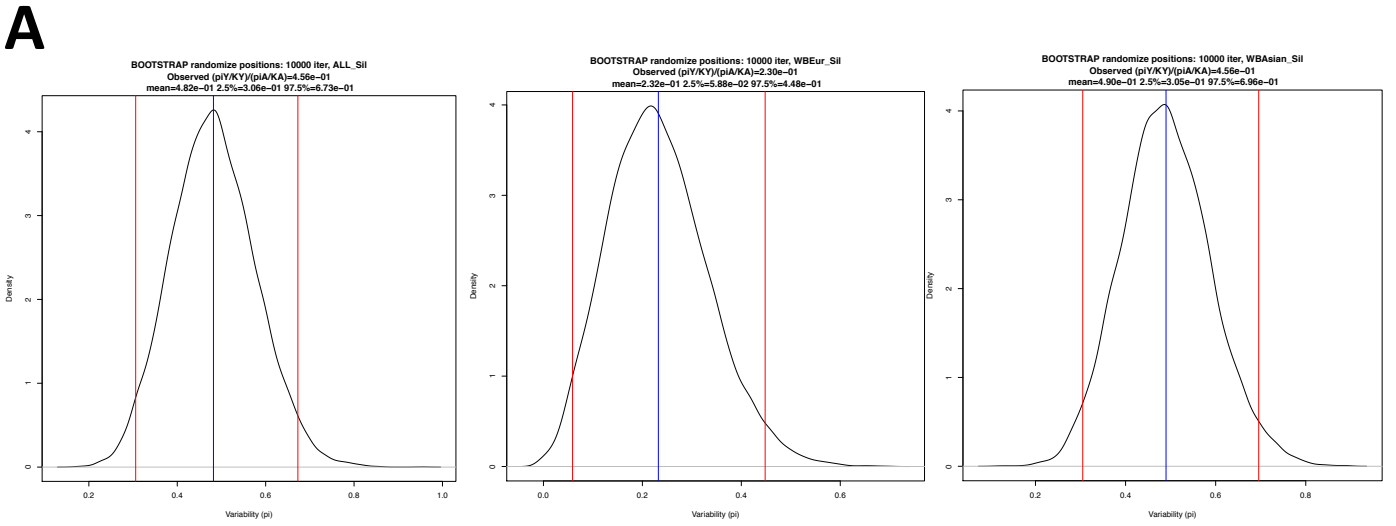
Figure S6. Posterior quantile distributions of model parameters. Simulations of 1,000 PODs were used. The Kolmogorov-Smirnov test for uniformity probabilities are indicated above each parameter.

Figure S7. Heat Map of the expected estimates of variability and linkage disequilibrium as a function of Time of migration (T_{mig}) and the ratio of Recombination versus θ . Coalescent simulations were performed considering an arbitrary sample of $n=20$ divided into two populations (Asian and non-Asian) of 10 individuals each and a single locus of 1000 sites for both, Y chromosome and an Autosome. The population mutation parameter was set to $\theta=0.05$ per site. The chrom-Y linked locus does not suffer of recombination, while the Autosomal locus has a population recombination parameter $R=4N_e r$, where r is the recombination rate per generation. The demographic history was modeled considering that the current size of the second population (Asian) is five times that of the first population (non-Asian). The simulated historical events (see also Figure 2, model IM), described from present to past, were: 1) A migration event ($M=4N_e m$, where m is the migration rate per generation) from first (non-Asian) to second (Asian) population that started at time T_{mig} and lasted for $0.01 \times 4N_e$ generations. 2) An isolation period until the two populations merge in an ancestral population of the same size as the first population at $2.5 \times 4N_e$ generations after present. We consider that only males migrate from non-Asian to Asian population, therefore the value of migration parameter for Autosomal loci was set to half the value of the migration parameter for Y-linked loci. The ranges of Migration, Time of migration and Recombination values were drawn from a log 10-uniform distribution ranging from: i) 10 to 1000 for Migration (M), except for figure S2 A, where M was set to zero; ii) 0.005 to $0.5 \times 4N_e$ generations for Time of migration (T_{mig}); iii) from 0.01 to 0.25 for Recombination (R). One million iterations were performed in all cases.

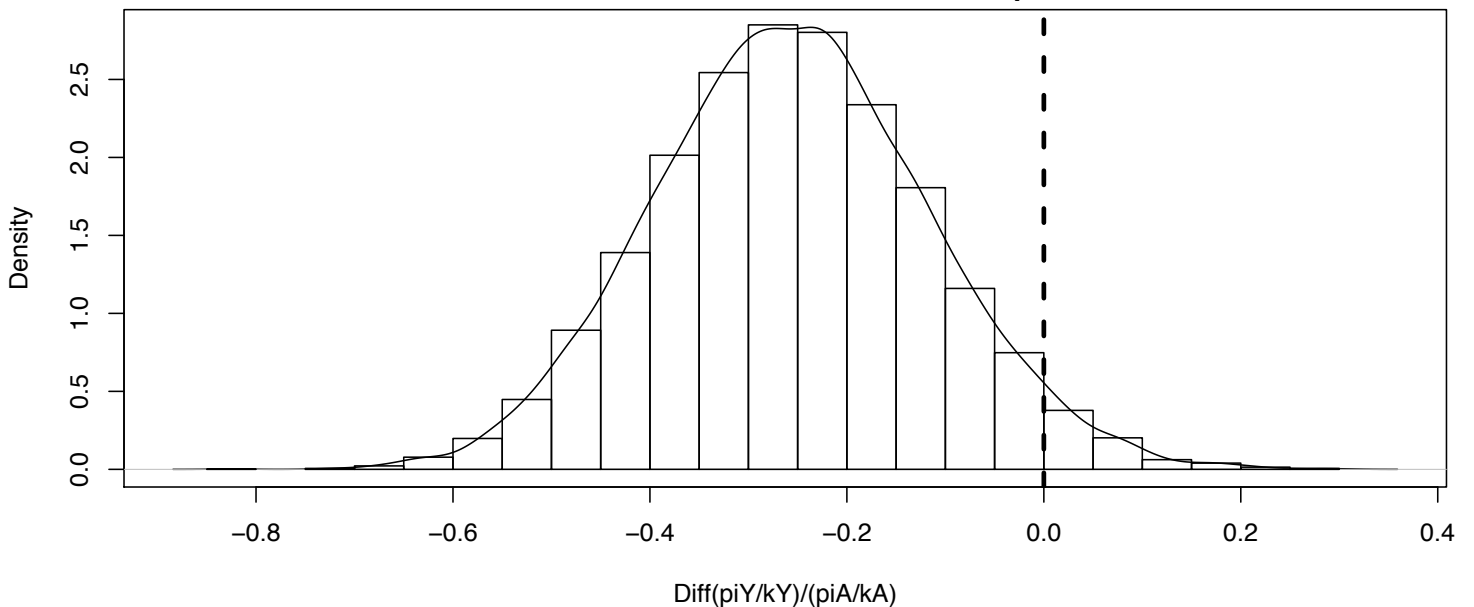
For each section/panel of Figure S2 (A-F): On the left, the ratio of estimates of chrom-Y versus autosomal locus only for Asian populations. On the right, the ratio of estimated of non-Asian versus Asian Autosomal locus. On the top, population mutation parameter estimates (θ_Y/θ_{Aut} and θ_{noA}/θ_A). On the bottom, linkage disequilibrium estimates (Zns_Y/Zns_{Aut} and Zns_{noA}/Zns_A). (A) Migration values from population one (non-Asian) to population 2 (Asian) equal to zero. (B-F) Migration values from population one (non-Asian) to population

2 (Asian) drawn from a log10-uniform distribution. In all cases, the time of migration was $0.01 \times 4N_e$ generations. The values of the distribution were ranging logarithmically, from: (B) $M=10$ to $M=25.1$. (C) $M=25.1$ to $M=63.1$. (D) $M=63.1$ to $M=158.5$ during. (E) $M=158.5$ to $M=398.1$. (F) $M=398.1$ to $M=1000$.

Figure S8. Geographical distribution of the Non-Asian and Asian haplogroups of the Asian Local Pigs (ALP) and Asian Wild boars (AWB). Pie symbols are proportional to the pig sample size.



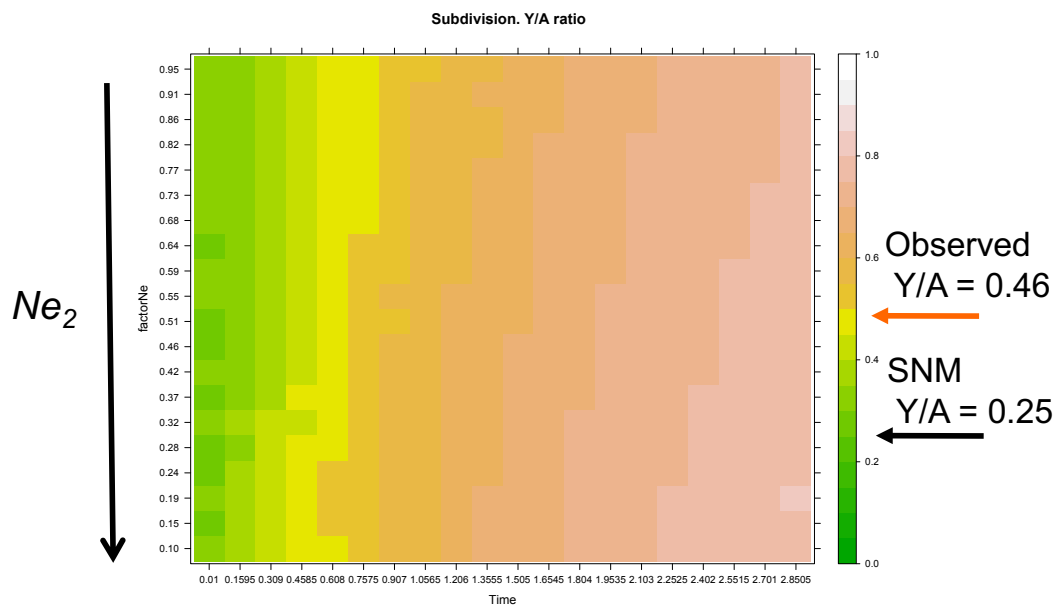
TESTING DIFFERENCE (piY/kY)/(piA/kA) BETWEEN NON-ASIAN AND ASIAN: 10000 iter
 Observed=-2.26e-01
 mean=-2.56e-01 2.5%=-5.23e-01 97.5%=2.22e-02 p-value= 3.51e-02



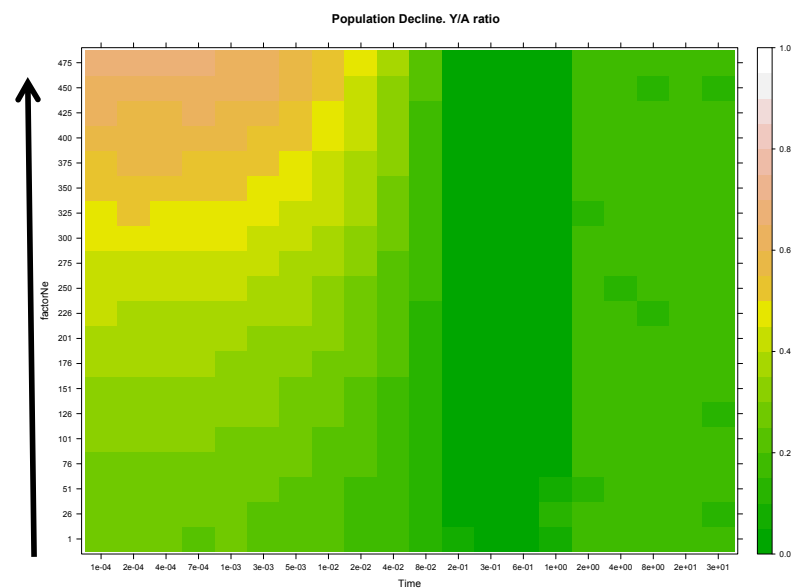
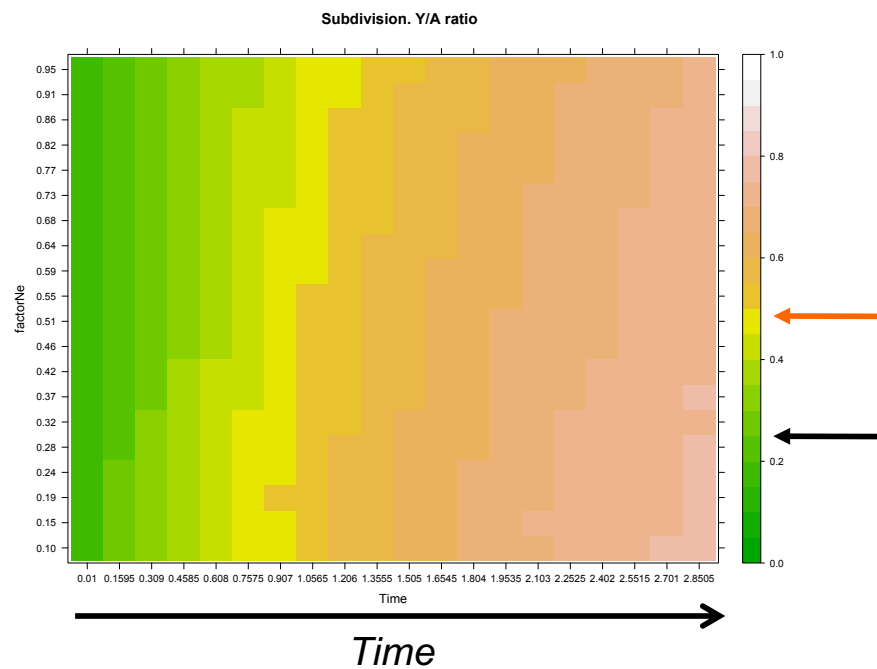
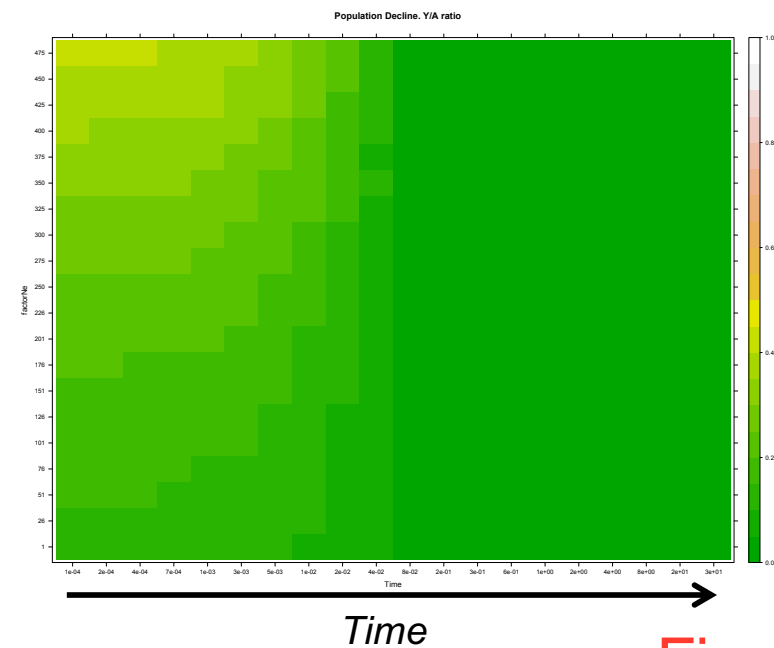
		SRY	AMELY	USP9Y	DBY	DDX3Y	UTY		
		527 SRYpro2_3_1 644 672 1119 SRYpro4 1493 SRYpro5 1652 2409 2754 SRYpro6 3331 4250 SRY_1 4367 4675 SRY_3 4719 4861 SRY_5 4918	5186 AmelY_ProF#1 5220 AmelY_ProF#2 5858 AmelY_i2F2_1 6041 AmelY_i2F2_2	6368	6744 DBYin1_A#1 6789 DBYin1_A#2 7169 7227 DBYin1_B_2	7574 7575 DBYin5_1#2 7772 DBYin5_2 7892 DBYin5_3	8059 UTYin1_1 8152 UTYin1_2 8205 UTYin1_3 8397 UTYin7#2 8399 UTYin7#2b 8581 9573		
EUROPE	EWB	WBES0103 WBBE0256	G T A T C G T C A C C G G G A A	G C T G A	T	A G G C	C G C G	G T C T T T C	
	MEDLP	IBES0106 IBES0475 IBES0541 PNES0155 IBES0002 IBES0247 IBES0073	. .	A A A C G C G C G C G C G C G C G . . .	
	ANGLP	TWGB0371 TWGB0372 C C A . . C . G T A . T C . . C C A	C C	G A C A G A C A	T A T A T A T A	C C G G C C G G	
	INTP	LWES0284 LWES0477 LWGB0345 PIES0459 PIGB0478 LDES0423 LWES0509 PTES0501 PTES0505 PTES0506 DUES0188 DUGB0353 LRES0400 LRGB0338	. .	A A A A A A A A A A A A A A A C G C G C G C G C G C G C G C G C G C G C G C G C G C G C G . . .	
		AFWB	WBTN0226 WBTN0228 WBTN0229 WBTN0230 WBTN0231	. .	A A A A A C C G C G C G C G C G . . .	
		AFP	NABE0024 NABE0025 NAKE0131 MUZW0725 MUZW0175 C C A T . C G T C A T C C C G A C A G A C A T A T A T A T A C G C G C C G . . . G C C G . . . G C C G . . . G
NEAR EAST		WBIR0189 WBTQ0122 WBTQ0119 WBAM0001 WBAM0002 T T	A A A A A		
AMERICA		SCAP	HLMX0146 HLMX0950	
ASIA		AWB	WBCN0695 WBJP0491 WBKR0446	. C . G T . . T C A A C . G C T C A	C C C	G A C A C G A C A	T A T A T A T A T A T A	C C G G C C G G
		ALP	MSUS0621 MICN0681 MSCN0405 MSES0283 MSUS0620 VTES0307	. C . G T . . T C G . . . C G C G C G C G C G C T C A T C A T C A T C A A	C C C C C C	G A C A G A C A G A C A G A C A G A C A	T A T A T A T A T A T A T A T A T A T A	C C G G C G C C G G C C G G C C G G
		OUTG	BBES0280 BAGB0335	. C . G . . . T C C T T C	G . C A G . C A	. . . T T .	. C C

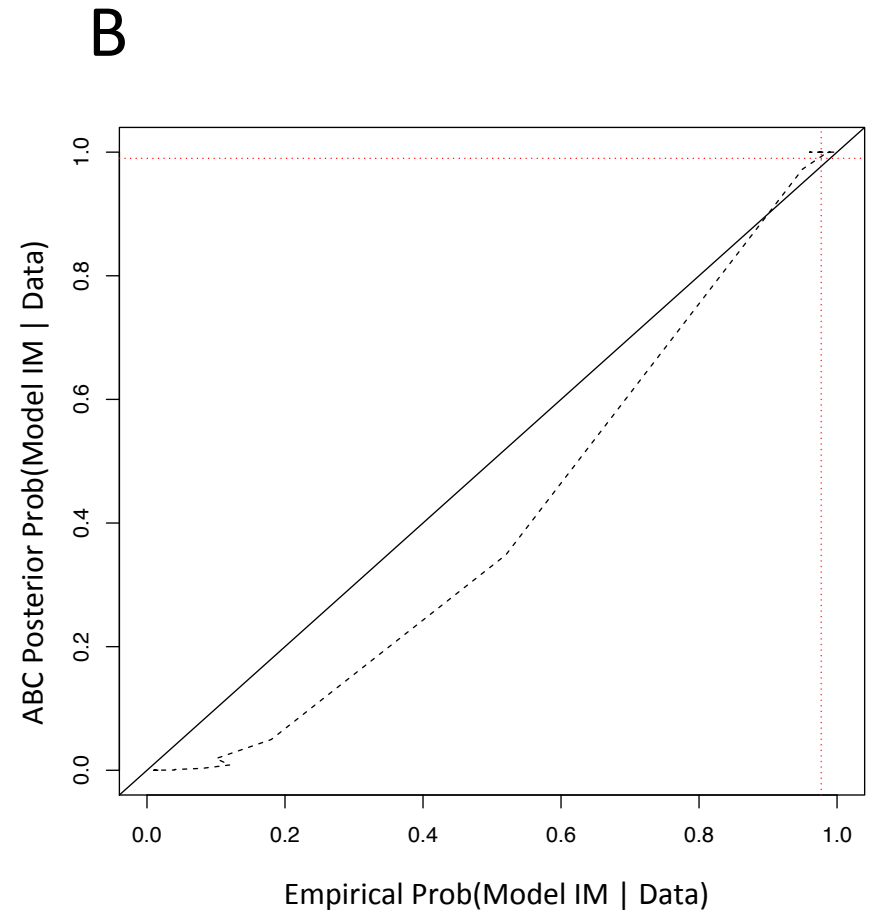
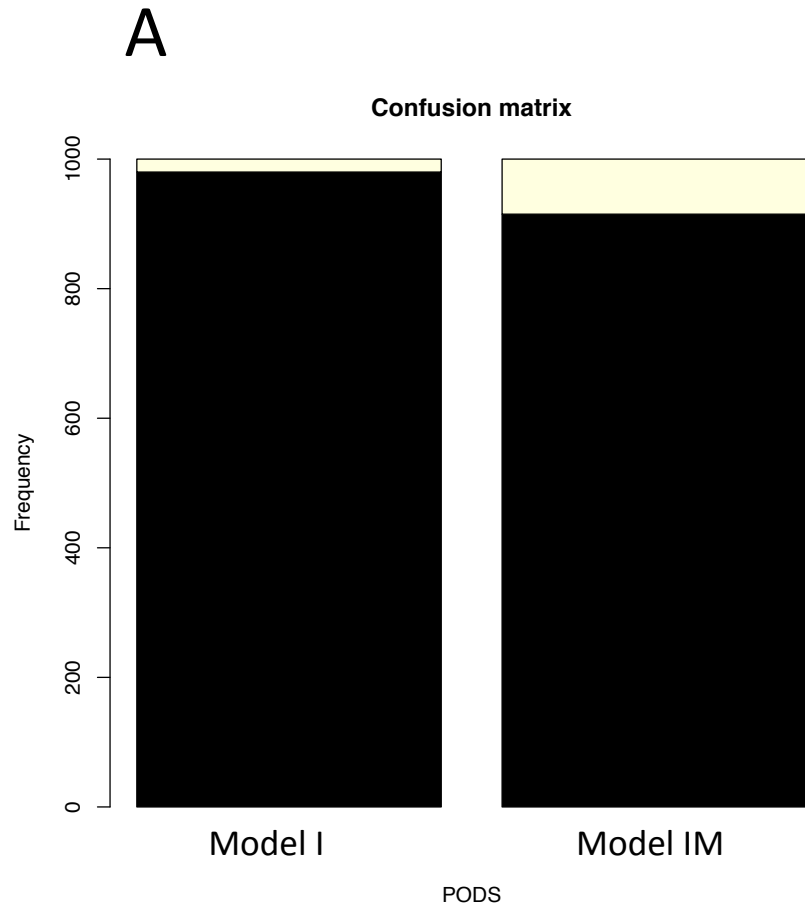
A

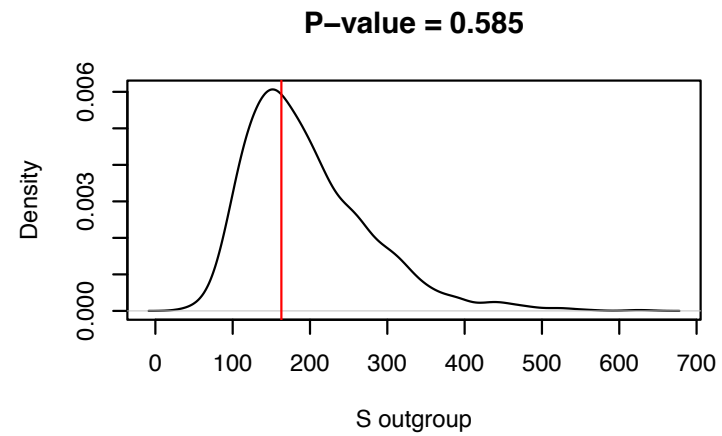
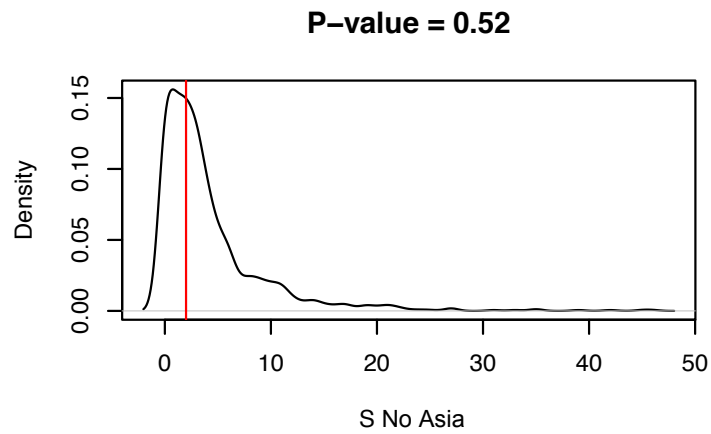
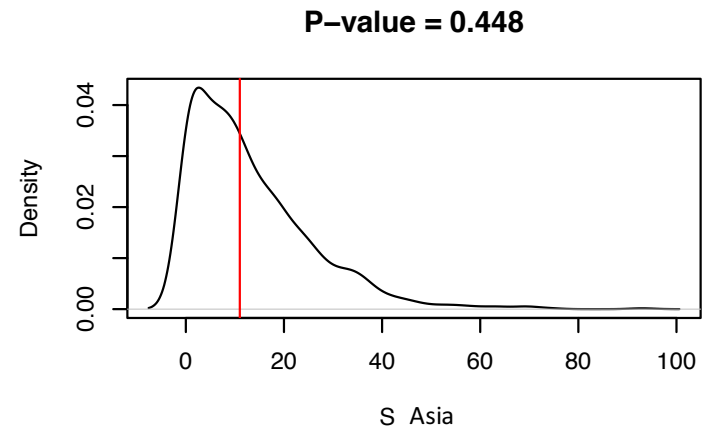
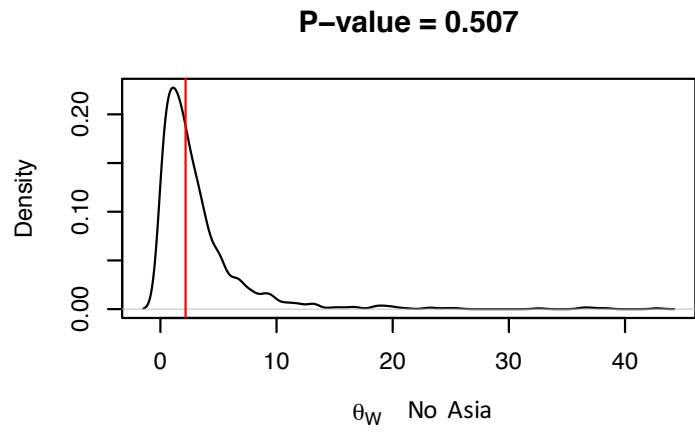
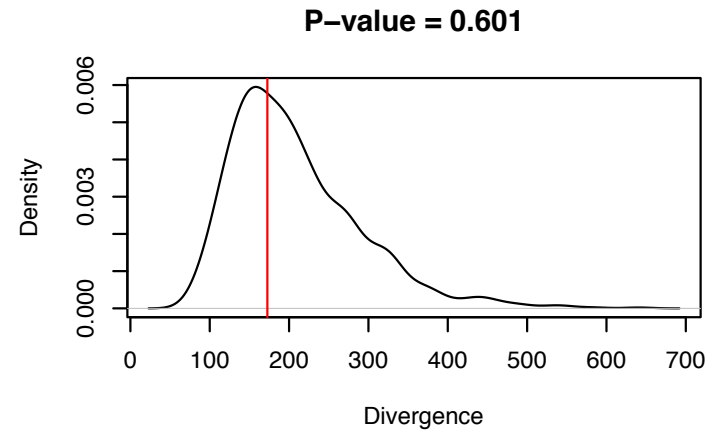
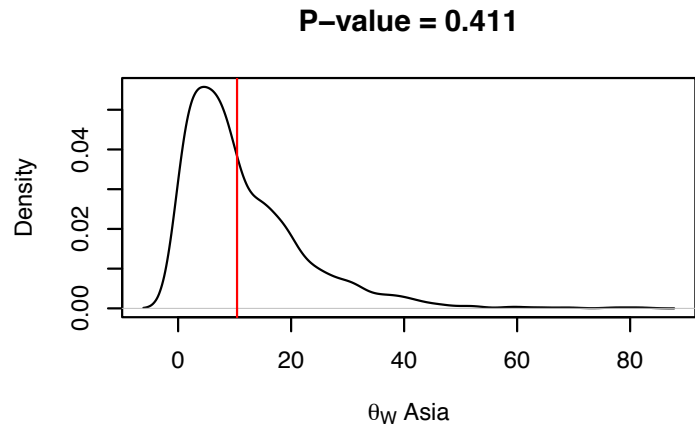
Subdivision (2 pops, one constant in size. Split at time T)

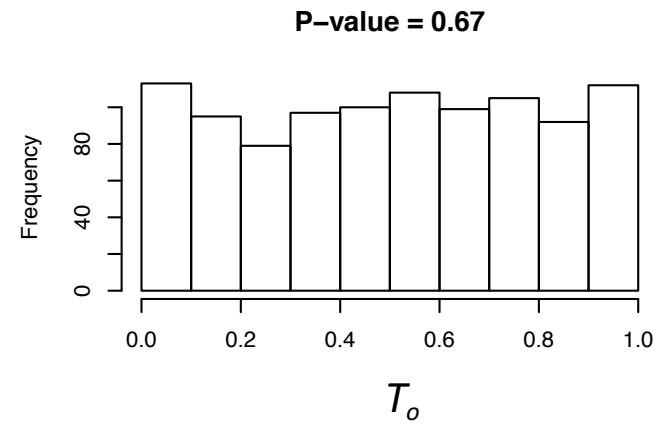
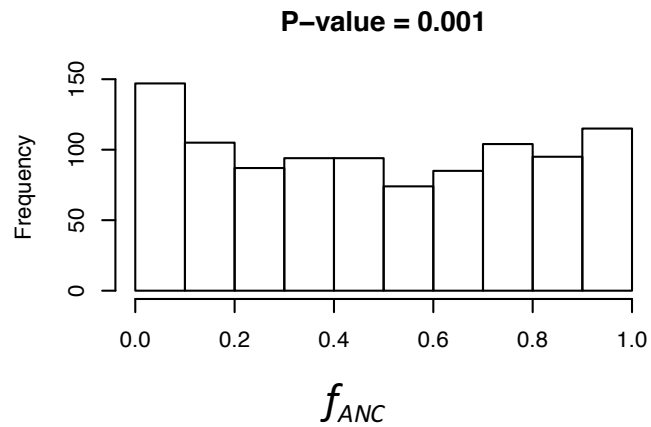
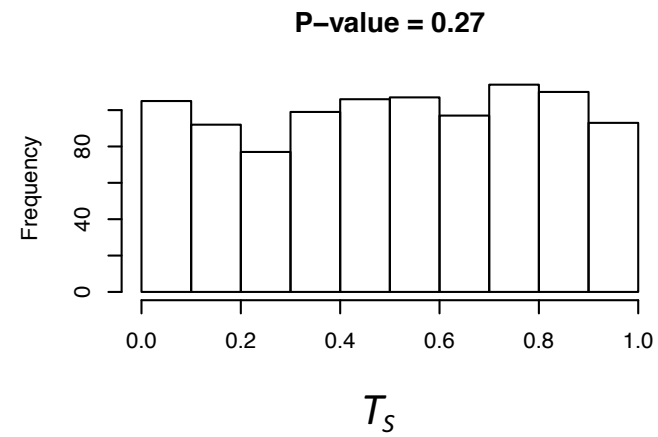
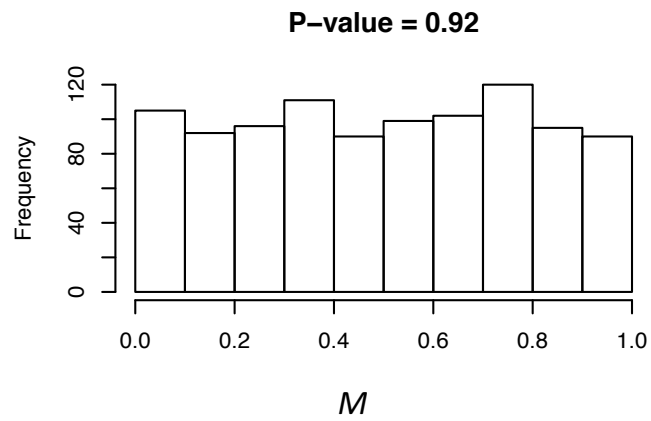
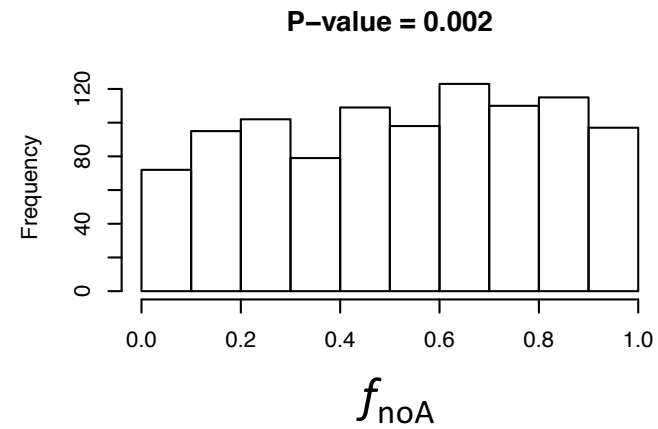
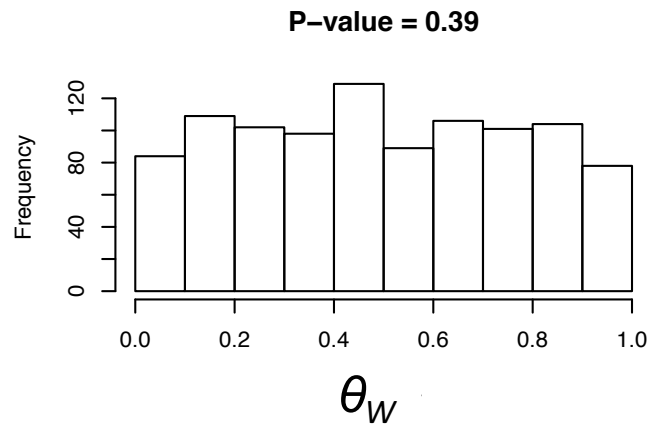
**C**

Population Decline (Ne of the Ancestral pop. Split at time T)

**B****D**







A

Pop2 (Asian): Chrom Y / Autosome

Autosome: Pop1(non-Asian) / Pop2 (Asian)

Subdivision and Migration. Theta ratio Y/A.
No Migration

Time mig

0.3974
0.3158
0.2510
0.1993
0.1576
0.1251
0.0995
0.0790
0.0628
0.0500
0.0397
0.0315
0.0250
0.0198
0.0158
0.0125
0.0100
0.0079
0.0063
0.0050

0.2 0.235 0.276 0.324 0.381 0.447 0.526 0.618 0.725 0.852 1.003 1.178 1.384 1.627 1.91 2.244 2.634 3.092 3.634 4.262

ratio R/theta

Subdivision and Migration. LD ratio Y/A.
No Migration

0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15

Subdivision and Migration. Theta ratio Autosome non-mixed vs mixed.
No Migration

Time mig

0.3974
0.3158
0.2510
0.1993
0.1576
0.1251
0.0995
0.0790
0.0628
0.0500
0.0397
0.0315
0.0250
0.0198
0.0158
0.0125
0.0100
0.0079
0.0063
0.0050

0.2 0.235 0.276 0.324 0.381 0.447 0.526 0.618 0.725 0.852 1.003 1.178 1.384 1.627 1.91 2.244 2.634 3.092 3.634 4.262

ratio R/theta

Subdivision and Migration. LD ratio Autosome non-mixed vs mixed.
No Migration

0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10

Linkage
Disequilibrium

Time mig

0.3974
0.3158
0.2510
0.1993
0.1576
0.1251
0.0995
0.0790
0.0628
0.0500
0.0397
0.0315
0.0250
0.0198
0.0158
0.0125
0.0100
0.0079
0.0063
0.0050

0.2 0.235 0.276 0.324 0.381 0.447 0.526 0.618 0.725 0.852 1.003 1.178 1.384 1.627 1.91 2.244 2.634 3.092 3.634 4.262

ratio R/theta

Subdivision and Migration. LD ratio Autosome non-mixed vs mixed.
No Migration

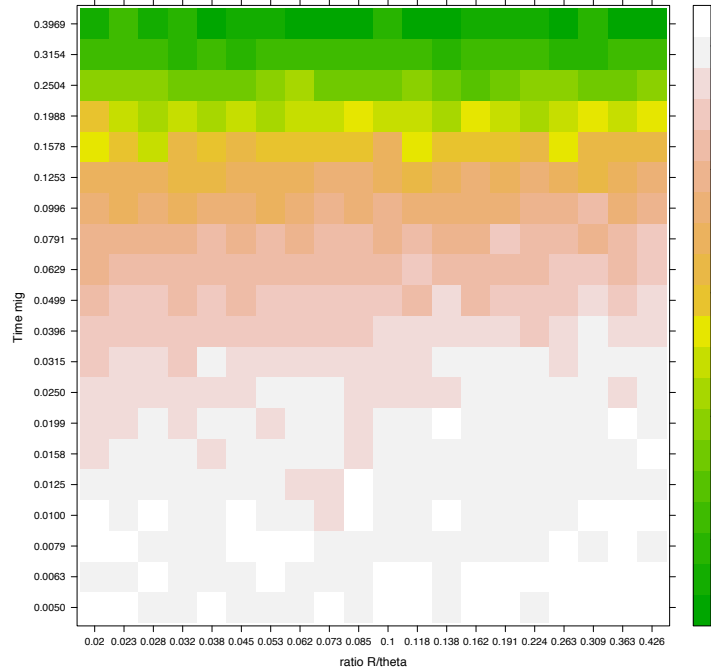
2.8
2.6
2.4
2.2
2.0

$O = W$

B

Pop2 (Asian): Chrom Y / Autosome

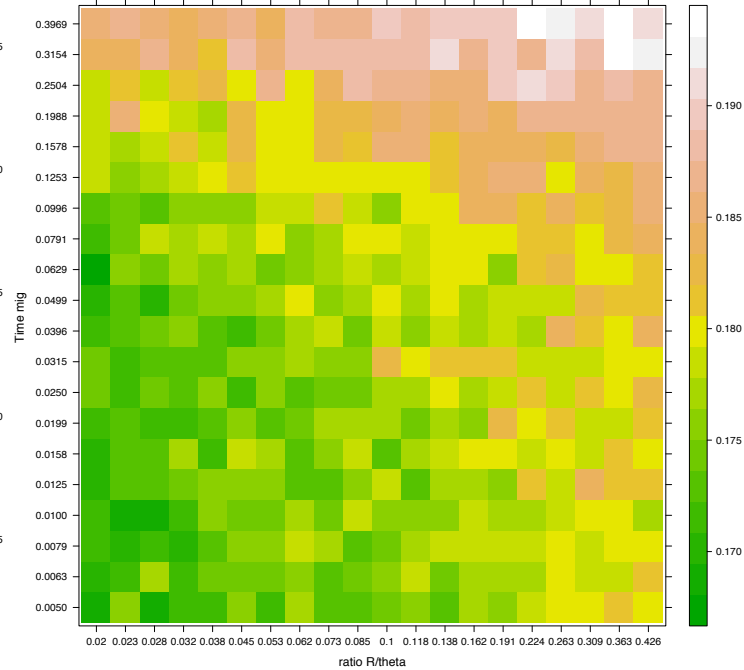
Subdivision and Migration. Theta ratio Y/A.
Total Migration: 1.00 2.51



Variability

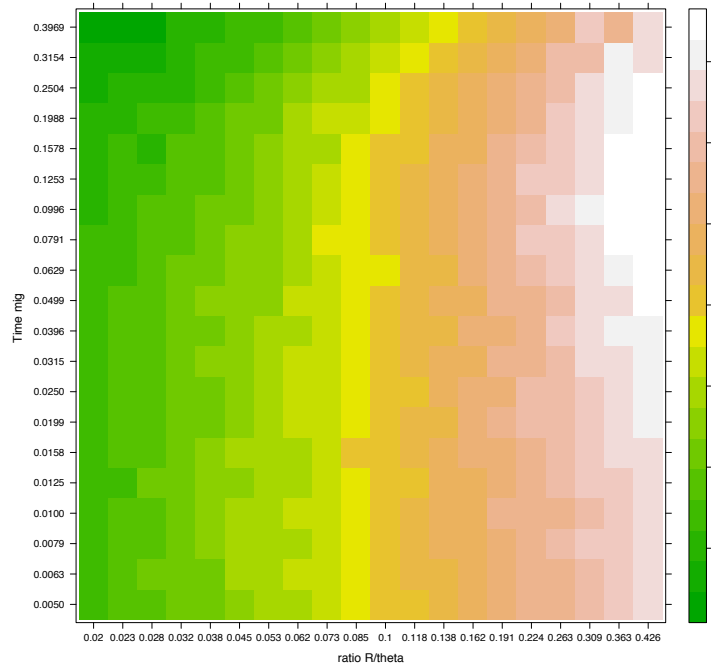
Autosome: Pop1(non-Asian) / Pop2 (Asian)

Subdivision and Migration. Theta ratio Autosome non-mixed vs mixed.
Total Migration: 1.00 2.51



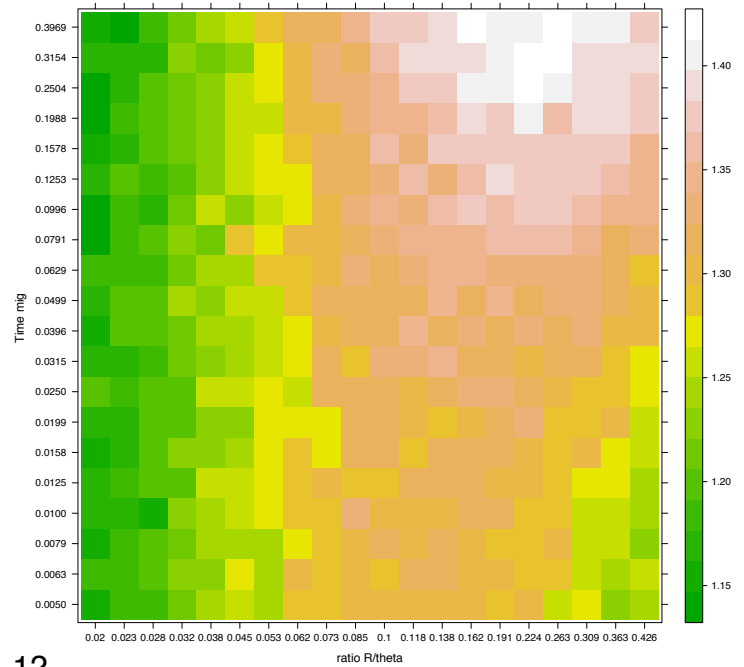
$M = \text{range}(10 : 25.1)$

Subdivision and Migration. LD ratio Y/A.
Total Migration: 1.00 2.51



Linkage
Disequilibrium

Subdivision and Migration. LD ratio Autosome non-mixed vs mixed.
Total Migration: 1.00 2.51

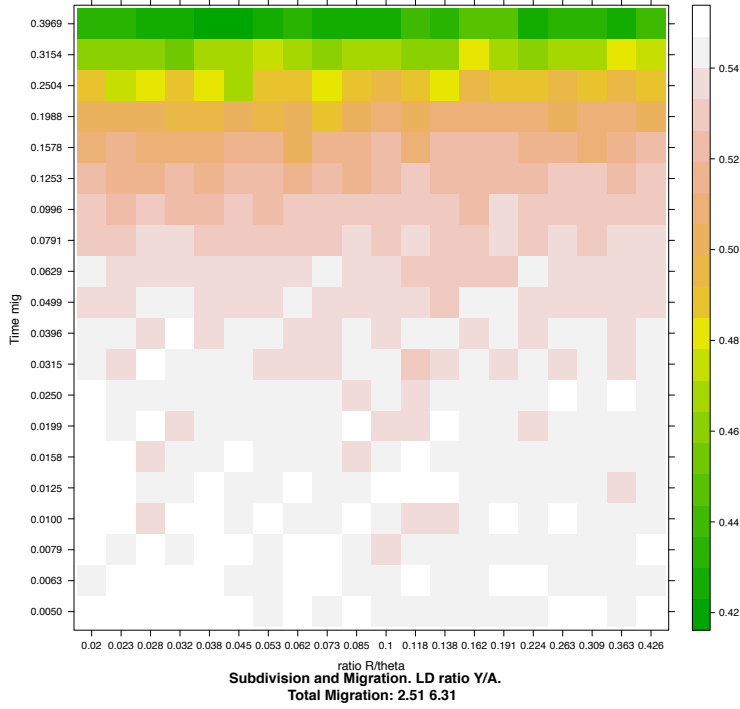


C

Pop2 (Asian): Chrom Y / Autosome

Subdivision and Migration. Theta ratio Y/A.
Total Migration: 2.51 6.31

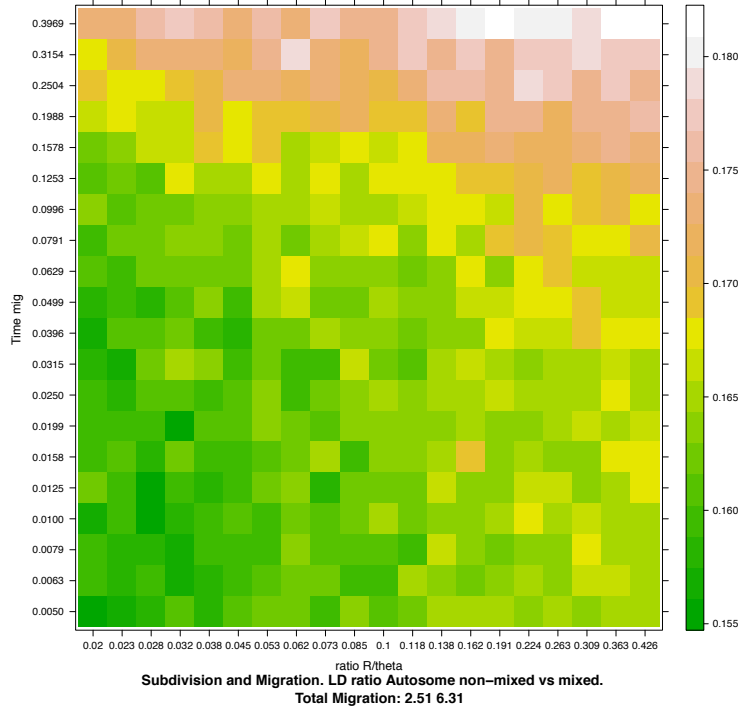
Variability



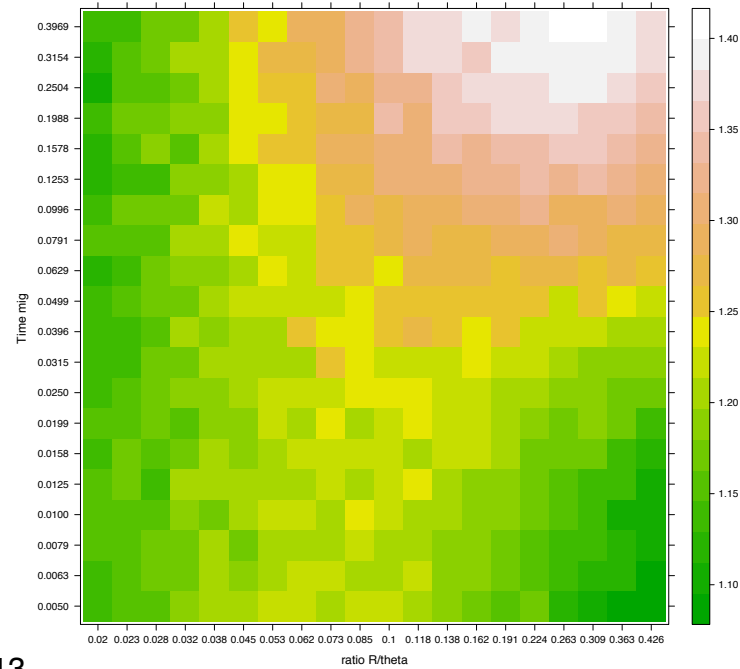
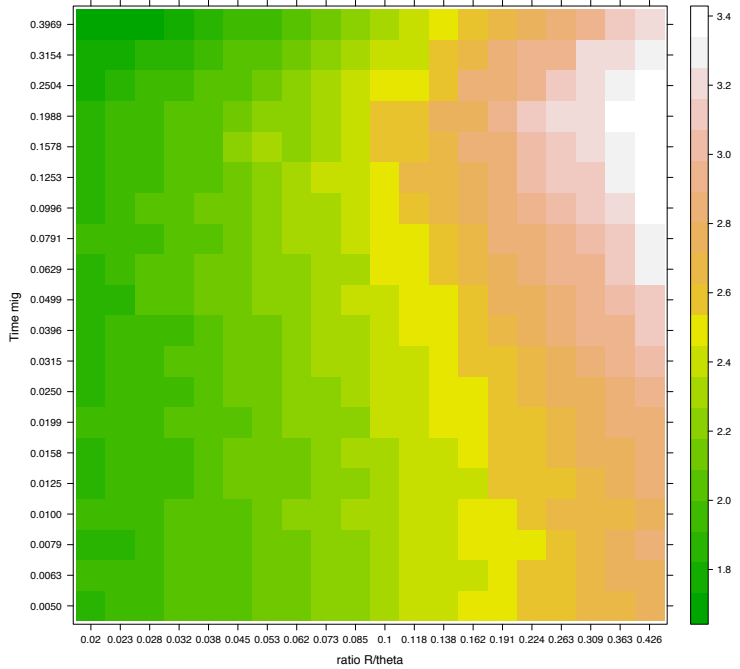
Autosome: Pop1(non-Asian) / Pop2 (Asian)

Subdivision and Migration. Theta ratio Autosome non- mixed vs mixed.
Total Migration: 2.51 6.31

M = range(25.1 : 63.1)



Linkage Disequilibrium

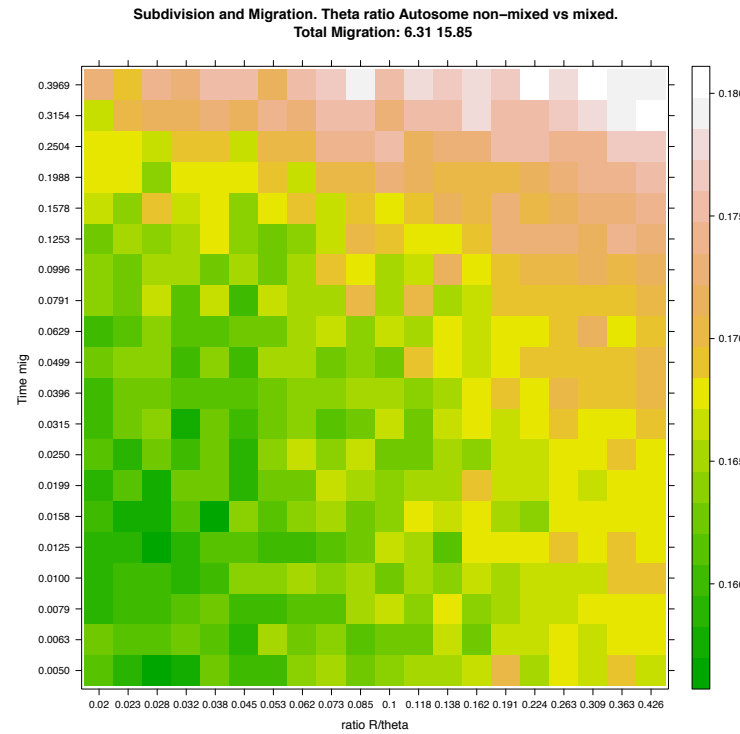
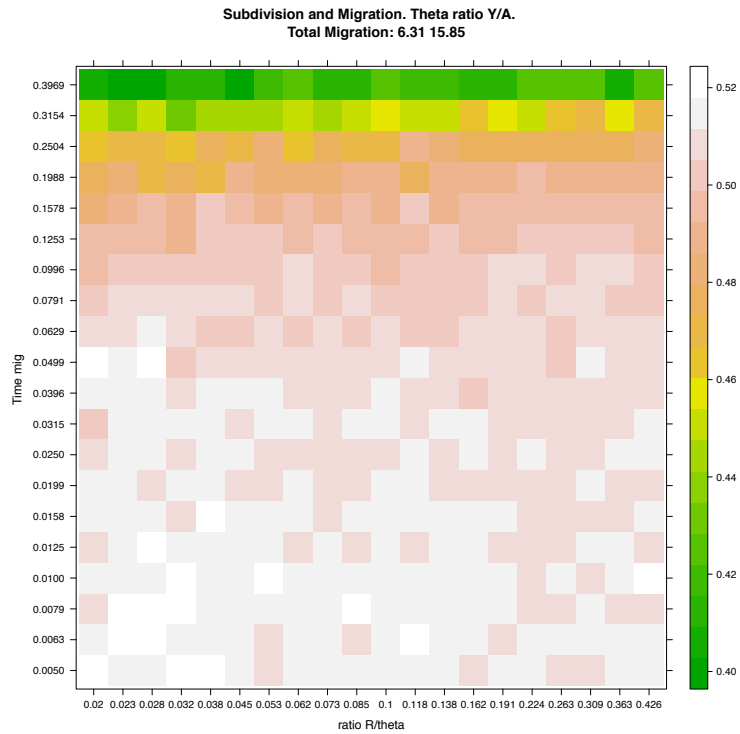


D

Pop2 (Asian): Chrom Y / Autosome

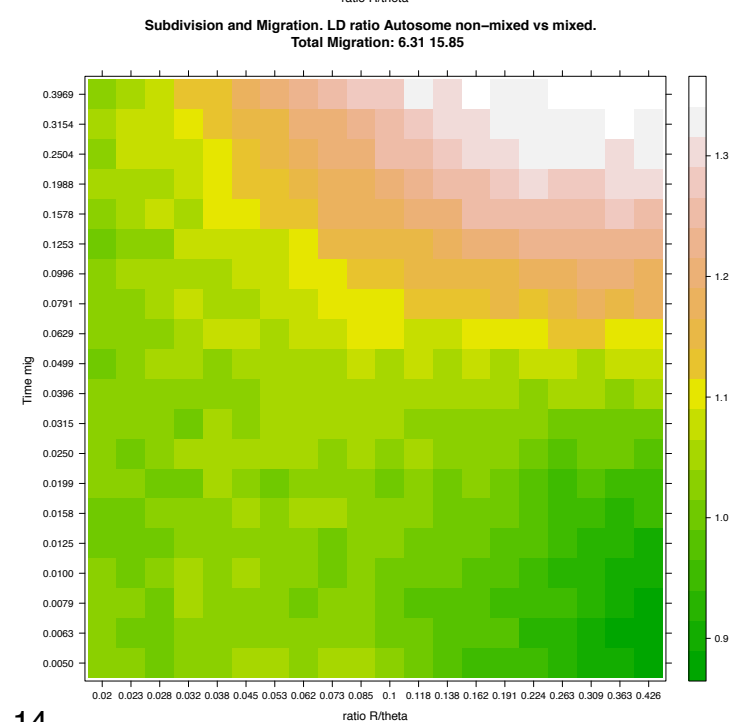
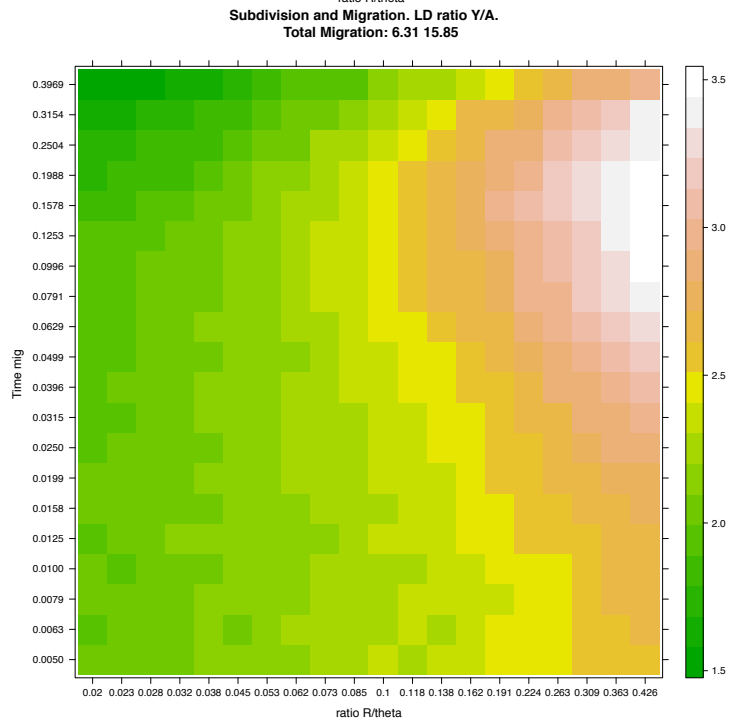
Autosome: Pop1(non-Asian) / Pop2 (Asian)

Variability



$M = \text{range}(63.1 : 158.5)$

Linkage Disequilibrium

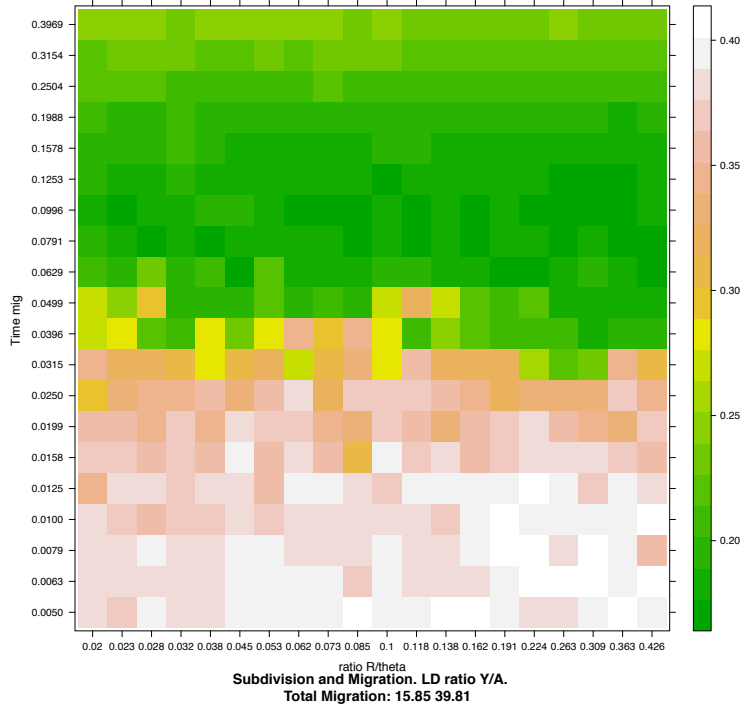




Pop2 (Asian): Chrom Y / Autosome

Subdivision and Migration. Theta ratio Y/A.
Total Migration: 15.85 39.81

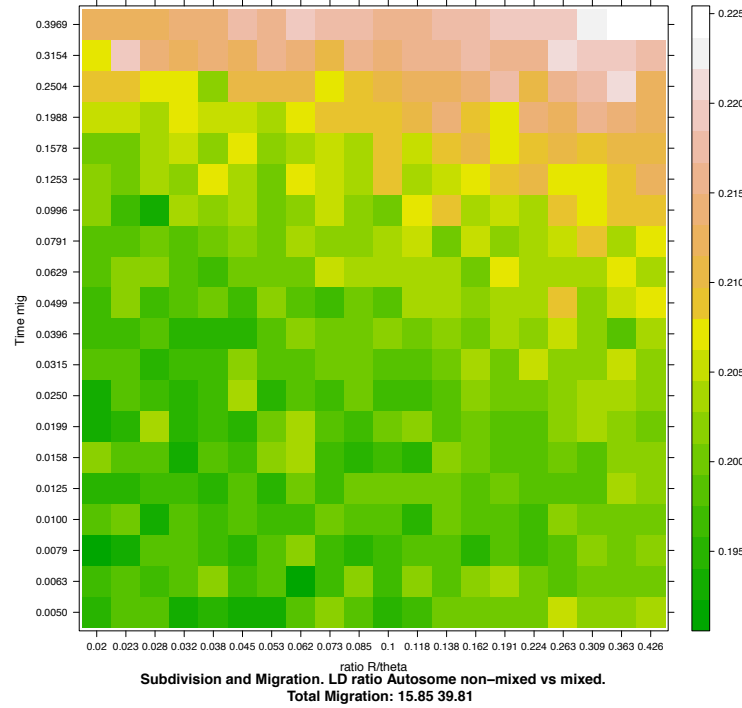
Variability



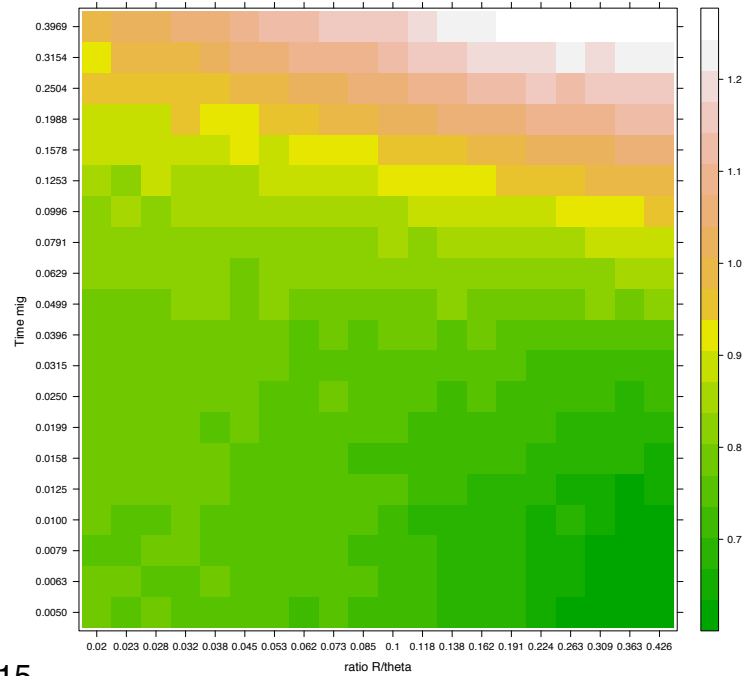
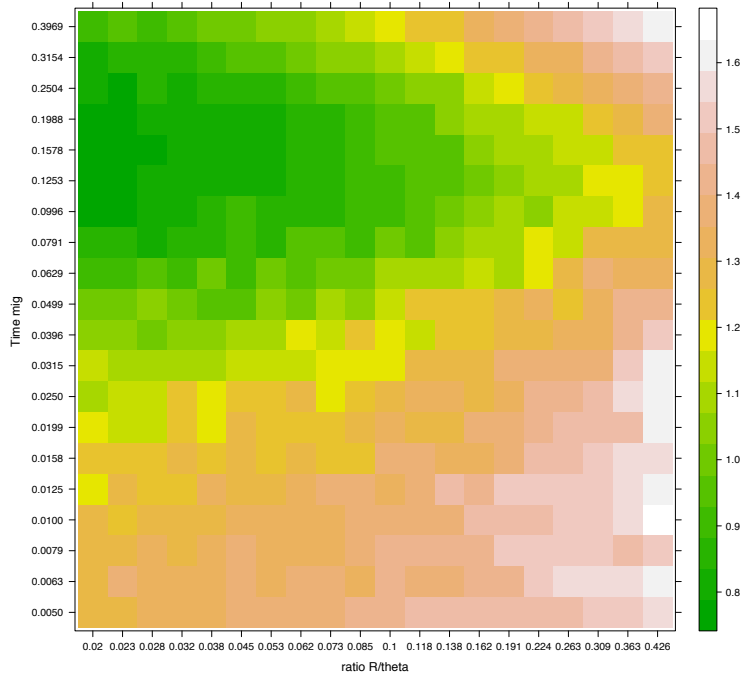
Autosome: Pop1(non-Asian) / Pop2 (Asian)

Subdivision and Migration. Theta ratio Autosome non-mixed vs mixed.
Total Migration: 15.85 39.81

M = range(158.5 : 398.1)



Linkage Disequilibrium

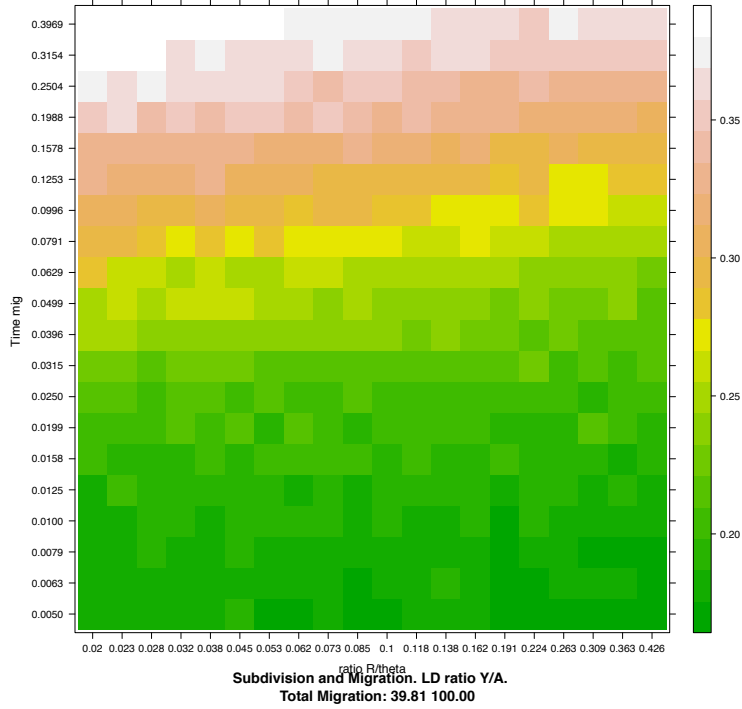




Pop2 (Asian): Chrom Y / Autosome

Subdivision and Migration. Theta ratio Y/A.
Total Migration: 39.81 100.00

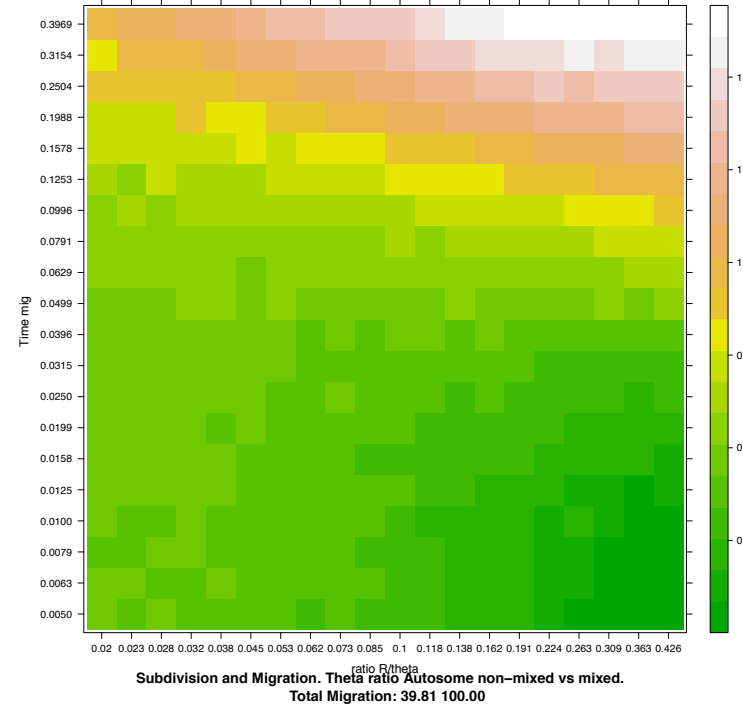
Variability



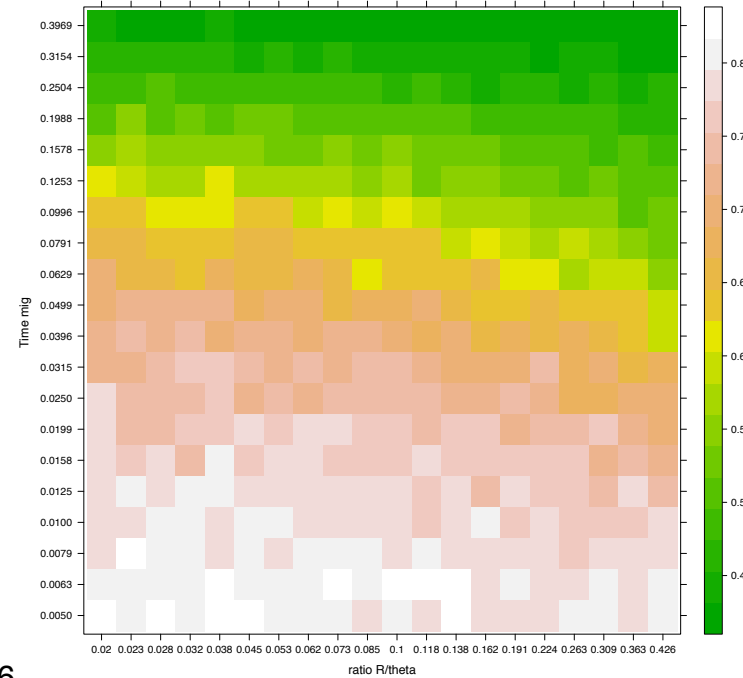
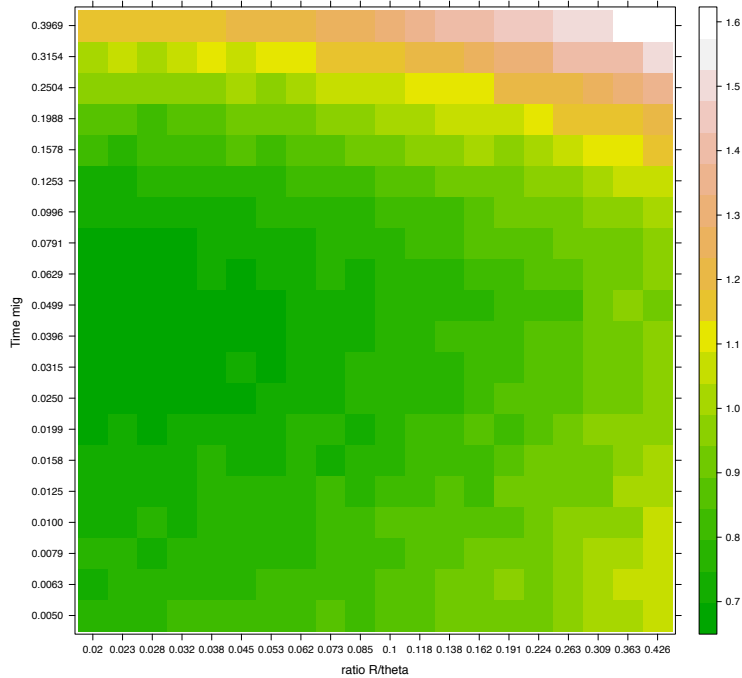
Autosome: Pop1(non-Asian) / Pop2 (Asian)

Subdivision and Migration. LD ratio Autosome non-mixed vs mixed.
Total Migration: 15.85 39.81

$M = \text{range}(398.1 : 1000)$



Linkage Disequilibrium



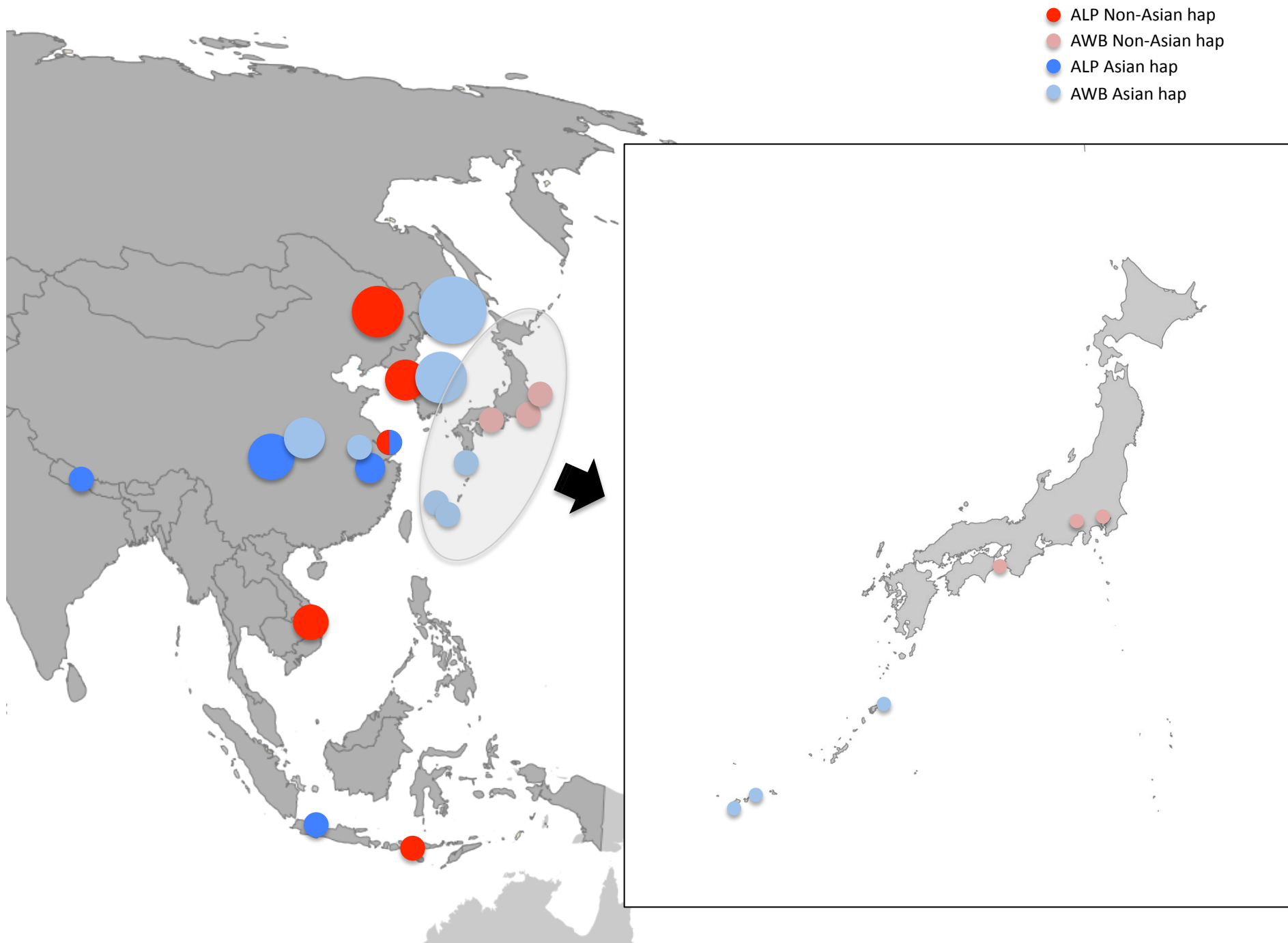


Figure S8

Supplementary table S1. Number of genotyped and sequenced samples for each group

Group	Number of samples	
	Genotyped	Sequenced
European Wild Boar (EWB)	39	2
Mediterranean Local Pig (MEDLP)	20	7
Commercial Pig (INTP)	62	14
Anglo-Saxon Local Pig (ANGLP)	29	2
African Wild Boar (AFWB)	5	5
African Pig (AFP)	22	5
Near-East Wild Boar (NEWB)	2	5
South and Central American Pig (SCAP)	17	2
Asian Wild Boar (AWB)	22	6
Asian Local Pig (ALP)	18	3
OUTGROUPS	2	2
TOTAL	238	53

#NAME	Species	Origin	Breed	Population	Genotyped	Sequenced
EWB_WBCZ0233	<i>Sus scrofa</i>	Czech Republic	Wild boar	EWB	Yes	No
EWB_WBCZ1045	<i>Sus scrofa</i>	Czech Republic	Wild boar	EWB	Yes	No
EWB_WBCZ1048	<i>Sus scrofa</i>	Czech Republic	Wild boar	EWB	Yes	No
EWB_WBES0001	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0005	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0018	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0103	<i>Sus scrofa</i>	Spain	Wild boar	EWB	No	Yes
EWB_WBES0256	<i>Sus scrofa</i>	Spain	Wild boar	EWB	No	Yes
EWB_WBES0494	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0500	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0502	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0504	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0507	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBES0509	<i>Sus scrofa</i>	Spain	Wild boar	EWB	Yes	No
EWB_WBFI0313	<i>Sus scrofa</i>	Finland	Wild boar	EWB	Yes	No
EWB_WBFR0511	<i>Sus scrofa</i>	France	Wild boar	EWB	Yes	No
EWB_WBIT0077	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0078	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0080	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0239	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0240	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0526	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0770	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0771	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0775	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0776	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0780	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0781	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0783	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT0786	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT1038	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBIT1269	<i>Sus scrofa</i>	Italy	Wild boar	EWB	Yes	No
EWB_WBBE0263	<i>Sus scrofa</i>	Belgium	Wild boar	EWB	Yes	No
EWB_WBTN0960	<i>Sus scrofa</i>	Tunisia	Wild boar	EWB	Yes	No
EWB_WBTN0961	<i>Sus scrofa</i>	Tunisia	Wild boar	EWB	Yes	No
EWB_WBPO0374	<i>Sus scrofa</i>	Poland	Wild boar	EWB	Yes	No
EWB_WBPO0377	<i>Sus scrofa</i>	Poland	Wild boar	EWB	Yes	No
EWB_WBPO0989	<i>Sus scrofa</i>	Poland	Wild boar	EWB	Yes	No
EWB_WBPO0992	<i>Sus scrofa</i>	Poland	Wild boar	EWB	Yes	No
EWB_WBPT0438	<i>Sus scrofa</i>	Portugal	Wild boar	EWB	Yes	No
EWB_WBRU0279	<i>Sus scrofa</i>	Russia	Wild boar	EWB	Yes	No
MEDLP_IBES0002	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	No	Yes
MEDLP_IBES0073	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	No	Yes
MEDLP_IBES0106	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	Yes
MEDLP_IBES0109	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0113	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0161	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0163	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0247	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	No	Yes
MEDLP_IBES0273	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0323	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0325	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0475	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	Yes
MEDLP_IBES0521	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0539	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES0541	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	No	Yes
MEDLP_IBES0787	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_IBES1192	<i>Sus scrofa</i>	Spain	Iberian	MEDLP	Yes	No
MEDLP_COFR0332	<i>Sus scrofa</i>	France	Corsican	MEDLP	Yes	No
MEDLP_COFR0334	<i>Sus scrofa</i>	France	Corsican	MEDLP	Yes	No
MEDLP_MGHU0093	<i>Sus scrofa</i>	Hungary	Mangalitza	MEDLP	Yes	No
MEDLP_MGHU0095	<i>Sus scrofa</i>	Hungary	Mangalitza	MEDLP	Yes	No
MEDLP_MGHU0098	<i>Sus scrofa</i>	Hungary	Mangalitza	MEDLP	Yes	No
MEDLP_PAPT0434	<i>Sus scrofa</i>	Portugal	Alentejan Black Pig	MEDLP	Yes	No
MEDLP_SIT1029	<i>Sus scrofa</i>	Italy	Sicilian Black Swine	MEDLP	Yes	No
MEDLP_PNES0147	<i>Sus scrofa</i>	Spain	Majorcan Black	MEDLP	Yes	No
MEDLP_PNES0155	<i>Sus scrofa</i>	Spain	Majorcan Black	MEDLP	No	Yes
ANGLP_BKGB0366	<i>Sus scrofa</i>	Great Britain	Berkshire	ANGLP	Yes	No
ANGLP_BKGB0367	<i>Sus scrofa</i>	Great Britain	Berkshire	ANGLP	Yes	No
ANGLP_BKGB0752	<i>Sus scrofa</i>	Great Britain	Berkshire	ANGLP	Yes	No
ANGLP_BKUS0622	<i>Sus scrofa</i>	United States	Berkshire	ANGLP	Yes	No
ANGLP_BKUS0624	<i>Sus scrofa</i>	United States	Berkshire	ANGLP	Yes	No
ANGLP_BKUS0626	<i>Sus scrofa</i>	United States	Berkshire	ANGLP	Yes	No
ANGLP_BLGB0373	<i>Sus scrofa</i>	Great Britain	British Lop	ANGLP	Yes	No

ANGLP_CWUS0640	<i>Sus scrofa</i>	United States	Chester White	ANGLP	Yes	No
ANGLP_CWUS0641	<i>Sus scrofa</i>	United States	Chester White	ANGLP	Yes	No
ANGLP_LBGB0361	<i>Sus scrofa</i>	Great Britain	Large Black	ANGLP	Yes	No
ANGLP_LBGB0362	<i>Sus scrofa</i>	Great Britain	Large Black	ANGLP	Yes	No
ANGLP_LBGB0619	<i>Sus scrofa</i>	Great Britain	Large Black	ANGLP	Yes	No
ANGLP_LBGB0744	<i>Sus scrofa</i>	Great Britain	Large Black	ANGLP	Yes	No
ANGLP_MWGB0359	<i>Sus scrofa</i>	Great Britain	Middle White	ANGLP	Yes	No
ANGLP_MWGB0360	<i>Sus scrofa</i>	Great Britain	Middle White	ANGLP	Yes	No
ANGLP_MWGB0743	<i>Sus scrofa</i>	Great Britain	Middle White	ANGLP	Yes	No
ANGLP_OSGB0368	<i>Sus scrofa</i>	Great Britain	Old Spot	ANGLP	Yes	No
ANGLP_OSGB0369	<i>Sus scrofa</i>	Great Britain	Old Spot	ANGLP	Yes	No
ANGLP_OSGB0740	<i>Sus scrofa</i>	Great Britain	Old Spot	ANGLP	Yes	No
ANGLP_OSGB0985	<i>Sus scrofa</i>	Great Britain	Old Spot	ANGLP	Yes	No
ANGLP_PLUS0638	<i>Sus scrofa</i>	United States	Poland China	ANGLP	Yes	No
ANGLP_PLUS0639	<i>Sus scrofa</i>	United States	Poland China	ANGLP	Yes	No
ANGLP_SBGB0363	<i>Sus scrofa</i>	Great Britain	Saddleback	ANGLP	Yes	No
ANGLP_SBGB0364	<i>Sus scrofa</i>	Great Britain	Saddleback	ANGLP	Yes	No
ANGLP_WEGB0746	<i>Sus scrofa</i>	Great Britain	Welsh	ANGLP	Yes	No
ANGLP_SBGB0756	<i>Sus scrofa</i>	Great Britain	Saddleback	ANGLP	Yes	No
ANGLP_TWGB0371	<i>Sus scrofa</i>	Great Britain	Tamworth	ANGLP	Yes	Yes
ANGLP_TWGB0372	<i>Sus scrofa</i>	Great Britain	Tamworth	ANGLP	Yes	Yes
ANGLP_TWGB0748	<i>Sus scrofa</i>	Great Britain	Tamworth	ANGLP	Yes	No
INTP_DUDK0474	<i>Sus scrofa</i>	Denmark	Duroc	INTP	Yes	No
INTP_DUES0169	<i>Sus scrofa</i>	Spain	Duroc	INTP	Yes	No
INTP_DUES0188	<i>Sus scrofa</i>	Spain	Duroc	INTP	No	Yes
INTP_DUES0194	<i>Sus scrofa</i>	Spain	Duroc	INTP	Yes	No
INTP_DUES0277	<i>Sus scrofa</i>	Spain	Duroc	INTP	Yes	No
INTP_DUES0460	<i>Sus scrofa</i>	Spain	Duroc	INTP	Yes	No
INTP_DUES0538	<i>Sus scrofa</i>	Spain	Duroc	INTP	Yes	No
INTP_DUGB0353	<i>Sus scrofa</i>	Great Britain	Duroc	INTP	Yes	Yes
INTP_DUGB0355	<i>Sus scrofa</i>	Great Britain	Duroc	INTP	Yes	No
INTP_DUGB0356	<i>Sus scrofa</i>	Great Britain	Duroc	INTP	Yes	No
INTP_DUGB0357	<i>Sus scrofa</i>	Great Britain	Duroc	INTP	Yes	No
INTP_DUHU0199	<i>Sus scrofa</i>	Hungary	Duroc	INTP	Yes	No
INTP_DUHU0202	<i>Sus scrofa</i>	Hungary	Duroc	INTP	Yes	No
INTP_DUNO0087	<i>Sus scrofa</i>	Norway	Duroc	INTP	Yes	No
INTP_DUNO0088	<i>Sus scrofa</i>	Norway	Duroc	INTP	Yes	No
INTP_DUUS0458	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_DUUS0602	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_DUUS0603	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_DUUS0604	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_DUUS0605	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_DUUS0613	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_HSGB0977	<i>Sus scrofa</i>	Great Britain	Duroc	INTP	Yes	No
INTP_HSUS0614	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_HSUS0615	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_HSUS0616	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_HSUS0618	<i>Sus scrofa</i>	United States	Duroc	INTP	Yes	No
INTP_LDES0423	<i>Sus scrofa</i>	Spain	Landrace	INTP	No	Yes
INTP_LRES0285	<i>Sus scrofa</i>	Spain	Landrace	INTP	Yes	No
INTP_LRES0400	<i>Sus scrofa</i>	Spain	Landrace	INTP	No	Yes
INTP_LRES0465	<i>Sus scrofa</i>	Spain	Landrace	INTP	Yes	No
INTP_LRGB0336	<i>Sus scrofa</i>	Great Britain	Landrace	INTP	Yes	No
INTP_LRGB0338	<i>Sus scrofa</i>	Great Britain	Landrace	INTP	Yes	Yes
INTP_LRGB0339	<i>Sus scrofa</i>	Great Britain	Landrace	INTP	Yes	No
INTP_LRGB0341	<i>Sus scrofa</i>	Great Britain	Landrace	INTP	Yes	No
INTP_LRGB0342	<i>Sus scrofa</i>	Great Britain	Landrace	INTP	Yes	No
INTP_LRGB0967	<i>Sus scrofa</i>	Great Britain	Landrace	INTP	Yes	No
INTP_LRUS0633	<i>Sus scrofa</i>	United States	Landrace	INTP	Yes	No
INTP_LRUS0635	<i>Sus scrofa</i>	United States	Landrace	INTP	Yes	No
INTP_LRUS0637	<i>Sus scrofa</i>	United States	Landrace	INTP	Yes	No
INTP_LWDK0473	<i>Sus scrofa</i>	Denmark	Large White	INTP	Yes	No
INTP_LWES0284	<i>Sus scrofa</i>	Spain	Large White	INTP	Yes	Yes
INTP_LWES0477	<i>Sus scrofa</i>	Spain	Large White	INTP	Yes	Yes
INTP_LWES0509	<i>Sus scrofa</i>	Spain	Large White	INTP	No	Yes
INTP_LWFI0343	<i>Sus scrofa</i>	Finland	Large White	INTP	Yes	No
INTP_LWFR0351	<i>Sus scrofa</i>	France	Large White	INTP	Yes	No
INTP_LWFR0352	<i>Sus scrofa</i>	France	Large White	INTP	Yes	No
INTP_LWGB0344	<i>Sus scrofa</i>	Great Britain	Large White	INTP	Yes	No
INTP_LWGB0345	<i>Sus scrofa</i>	Great Britain	Large White	INTP	Yes	Yes
INTP_LWGB0348	<i>Sus scrofa</i>	Great Britain	Large White	INTP	Yes	No
INTP_LWGB0349	<i>Sus scrofa</i>	Great Britain	Large White	INTP	Yes	No
INTP_LWGB0350	<i>Sus scrofa</i>	Great Britain	Large White	INTP	Yes	No
INTP_LWGB0987	<i>Sus scrofa</i>	Great Britain	Large White	INTP	Yes	No
INTP_PIDE0463	<i>Sus scrofa</i>	Germany	Pietrain	INTP	Yes	No
INTP_PIDE0478	<i>Sus scrofa</i>	Germany	Pietrain	INTP	Yes	No

INTP_PIES0464	<i>Sus scrofa</i>	Spain	Pietrain	INTP	Yes	No
INTP_PIES0470	<i>Sus scrofa</i>	Spain	Pietrain	INTP	Yes	No
INTP_PIES0459	<i>Sus scrofa</i>	Spain	Pietrain	INTP	No	Yes
INTP_PIFR0479	<i>Sus scrofa</i>	France	Pietrain	INTP	Yes	No
INTP_PTES0501	<i>Sus scrofa</i>	Spain	Pietrain	INTP	No	Yes
INTP_PTES0505	<i>Sus scrofa</i>	Spain	Pietrain	INTP	No	Yes
INTP_PTES0506	<i>Sus scrofa</i>	Spain	Pietrain	INTP	No	Yes
INTP_PIGB0478	<i>Sus scrofa</i>	Great Britain	Pietrain	INTP	No	Yes
INTP_PIGB0747	<i>Sus scrofa</i>	Great Britain	Pietrain	INTP	Yes	No
INTP_SYES0472	<i>Sus scrofa</i>	Spain	Synthetic	INTP	Yes	No
INTP_YKUS0627	<i>Sus scrofa</i>	United States	Yucatan	INTP	Yes	No
INTP_YKUS0628	<i>Sus scrofa</i>	United States	Yucatan	INTP	Yes	No
INTP_YKUS0631	<i>Sus scrofa</i>	United States	Yucatan	INTP	Yes	No
INT_MPES0758	<i>Sus scrofa</i>	Spain	Minipig	INTP	Yes	No
INT_MPES0759	<i>Sus scrofa</i>	Spain	Minipig	INTP	Yes	No
INT_MPES0760	<i>Sus scrofa</i>	Spain	Minipig	INTP	Yes	No
INT_MPKD0728	<i>Sus scrofa</i>	Denmark	Minipig	INTP	Yes	No
INT_MPKD1034	<i>Sus scrofa</i>	Denmark	Minipig	INTP	Yes	No
AFWB_WBTN0226	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	No	Yes
AFWB_WBTN0228	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	No	Yes
AFWB_WBTN0229	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	No	Yes
AFWB_WBTN0230	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	No	Yes
AFWB_WBTN0231	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	No	Yes
AFWB_WBTN0962	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	Yes	No
AFWB_WBTN0963	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	Yes	No
AFWB_WBTN0964	<i>Sus scrofa</i>	Tunisia	Wild boar	AFWB	Yes	No
AFWB_NEWB0517	<i>Sus scrofa</i>	Turkey	Wild boar	AFWB	Yes	No
AFWB_NEWB1271	<i>Sus scrofa</i>	Turkey	Wild boar	AFWB	Yes	No
AFP_NABE0024	<i>Sus scrofa</i>	Benin	native pig	AFP	No	Yes
AFP_NABE0025	<i>Sus scrofa</i>	Benin	native pig	AFP	No	Yes
AFP_NABF0913	<i>Sus scrofa</i>	Burkina Faso	native pig	AFP	Yes	No
AFP_NABF0922	<i>Sus scrofa</i>	Burkina Faso	native pig	AFP	Yes	No
AFP_NABF0923	<i>Sus scrofa</i>	Burkina Faso	native pig	AFP	Yes	No
AFP_NABF0927	<i>Sus scrofa</i>	Burkina Faso	native pig	AFP	Yes	No
AFP_NACI0911	<i>Sus scrofa</i>	Ivory Coast	native pig	AFP	Yes	No
AFP_NAKE0131	<i>Sus scrofa</i>	Kenia	native pig	AFP	No	Yes
AFP_NAKE0852	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0854	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0855	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0860	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0861	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0866	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0871	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0875	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0887	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NAKE0890	<i>Sus scrofa</i>	Kenia	native pig	AFP	Yes	No
AFP_NATZ0895	<i>Sus scrofa</i>	Tanzania	native pig	AFP	Yes	No
AFP_NATZ0897	<i>Sus scrofa</i>	Tanzania	native pig	AFP	Yes	No
AFP_NATZ0900	<i>Sus scrofa</i>	Tanzania	native pig	AFP	Yes	No
AFP_NATZ0903	<i>Sus scrofa</i>	Tanzania	native pig	AFP	Yes	No
AFP_NATZ0906	<i>Sus scrofa</i>	Tanzania	native pig	AFP	Yes	No
AFP-NABF0912	<i>Sus scrofa</i>	Burkina Faso	native pig	AFP	Yes	No
AFP-NABF0926	<i>Sus scrofa</i>	Burkina Faso	native pig	AFP	Yes	No
AFP-MUZW0725	<i>Sus scrofa</i>	Zimbabwe	Mukota	AFP	No	Yes
AFP-MUZW0725	<i>Sus scrofa</i>	Zimbabwe	Mukota	AFP	No	Yes
NEWB_WBIR0189	<i>Sus scrofa</i>	Iran	Wild boar	NEWB	No	Yes
NEWB_WBTQ0122	<i>Sus scrofa</i>	Turkey	Wild boar	NEWB	No	Yes
NEWB_WBTQ0119	<i>Sus scrofa</i>	Turkey	Wild boar	NEWB	No	Yes
NEWB_WBAM0001	<i>Sus scrofa</i>	Armenia	Wild boar	NEWB	No	Yes
NEWB_WBAM0002	<i>Sus scrofa</i>	Armenia	Wild boar	NEWB	No	Yes
NEWB_AM1281	<i>Sus scrofa</i>	Armenia	Wild boar	NEWB	Yes	No
NEWB_WBIR1270	<i>Sus scrofa</i>	Iran	Wild boar	NEWB	Yes	No
SCAP_BOBO0644	<i>Sus scrofa</i>	Bolivia	Criollo	SCAP	Yes	No
SCAP_BOBO0647	<i>Sus scrofa</i>	Bolivia	Criollo	SCAP	Yes	No
SCAP_BOBO0657	<i>Sus scrofa</i>	Bolivia	Criollo	SCAP	Yes	No
SCAP_CRRCR0566	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No
SCAP_CRRCR0570	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No
SCAP_CRRCR0572	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No
SCAP_CRRCR0579	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No
SCAP_CRRCR0583	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No
SCAP_CRRCR0593	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No
SCAP_CRRCR0599	<i>Sus scrofa</i>	Costa Rica	Criollo	SCAP	Yes	No

SCAP_CRCU1115	<i>Sus scrofa</i>	Cuba	Criollo	SCAP	Yes	No
SCAP_CRCU1126	<i>Sus scrofa</i>	Cuba	Criollo	SCAP	Yes	No
SCAP_CRCU1149	<i>Sus scrofa</i>	Cuba	Criollo	SCAP	Yes	No
SCAP_CRCU1150	<i>Sus scrofa</i>	Cuba	Criollo	SCAP	Yes	No
SCAP_CRCU1163	<i>Sus scrofa</i>	Cuba	Criollo	SCAP	Yes	No
SCAP_CRCU1169	<i>Sus scrofa</i>	Cuba	Criollo	SCAP	Yes	No
SCAP_HLMX0146	<i>Sus scrofa</i>	Mexico	Hairless	SCAP	No	Yes
SCAP_HLMX0950	<i>Sus scrofa</i>	Mexico	Hairless	SCAP	No	Yes
SCAP_HLMX0956	<i>Sus scrofa</i>	Mexico	Hairless	SCAP	Yes	No
AP_MICN0529	<i>Sus scrofa</i>	China	Minzhu	ALP	Yes	No
AP_MICN0677	<i>Sus scrofa</i>	China	Minzhu	ALP	Yes	No
AP_MICN0679	<i>Sus scrofa</i>	China	Minzhu	ALP	Yes	No
AP_MICN0680	<i>Sus scrofa</i>	China	Minzhu	ALP	Yes	No
AP_MICN0681	<i>Sus scrofa</i>	China	Minzhu	ALP	No	Yes
AP_MICN0682	<i>Sus scrofa</i>	China	Minzhu	ALP	Yes	No
AP_NPKR0794	<i>Sus scrofa</i>	Korea	native pig	ALP	Yes	No
AP_NPKR0796	<i>Sus scrofa</i>	Korea	native pig	ALP	Yes	No
AP_NPKR0798	<i>Sus scrofa</i>	Korea	native pig	ALP	Yes	No
AP_VTES0104	<i>Sus scrofa</i>	Vietnam (Marid zoo)	vietnamite	ALP	Yes	No
AP_VTES0307	<i>Sus scrofa</i>	Vietnam (Catalonia)	vietnamite	ALP	Yes	Yes
AP_NAID1272	<i>Sus scrofa</i>	Indonesia	native pig	ALP	Yes	No
AP_NAID1276	<i>Sus scrofa</i>	Indonesia	native pig	ALP	Yes	No
AP_FGCN0527	<i>Sus scrofa</i>	China	Fengjing	ALP	Yes	No
AP_JHCN0686	<i>Sus scrofa</i>	China	Jinhua	ALP	Yes	No
AP_JHCN0688	<i>Sus scrofa</i>	China	Jinhua	ALP	Yes	No
AP_MSCN0405	<i>Sus scrofa</i>	China	Meishan	ALP	Yes	Yes
AP_MSES0283	<i>Sus scrofa</i>	China	Meishan	ALP	No	Yes
AP_MSUS0620	<i>Sus scrofa</i>	United States (China)	Meishan	ALP	Yes	Yes
AP_MSUS0621	<i>Sus scrofa</i>	United States (China)	Meishan	ALP	No	Yes
AP_NANP1274	<i>Sus scrofa</i>	Nepal	native pig	ALP	Yes	No
AWB_WBJP0491	<i>Sus scrofa</i>	Japan	Wild boar	AWB	Yes	Yes
AWB_WBJP1001	<i>Sus scrofa</i>	Japan	Wild boar	AWB	Yes	No
AWB_WBJP1007	<i>Sus scrofa</i>	Japan	Wild boar	AWB	Yes	No
AWB_WBCN0695	<i>Sus scrofa</i>	China	Wild boar	AWB	Yes	Yes
AWB_WBCN0696	<i>Sus scrofa</i>	China	Wild boar	AWB	Yes	No
AWB_WBCN0698	<i>Sus scrofa</i>	China	Wild boar	AWB	Yes	No
AWB_WBCN0699	<i>Sus scrofa</i>	China	Wild boar	AWB	Yes	No
AWB_WBRU1089	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBKR0446	<i>Sus scrofa</i>	Korea	Wild boar	AWB	No	Yes
AWB_WBKR0829	<i>Sus scrofa</i>	Korea	Wild boar	AWB	Yes	No
AWB_WBRU1098	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBRU1102	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBJP1003	<i>Sus scrofa</i>	Japan	Wild boar	AWB	Yes	No
AWB_WBJP1010	<i>Sus scrofa</i>	Japan	Wild boar	AWB	Yes	No
AWB_WBJP1011	<i>Sus scrofa</i>	Japan	Wild boar	AWB	Yes	No
AWB_WBKR0827	<i>Sus scrofa</i>	Korea	Wild boar	AWB	Yes	No
AWB_WBKR0828	<i>Sus scrofa</i>	Korea	Wild boar	AWB	Yes	No
AWB_WBKR0831	<i>Sus scrofa</i>	Korea	Wild boar	AWB	Yes	No
AWB_WBRU1064	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBRU1070	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBRU1079	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBRU1097	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
AWB_WBRU1100	<i>Sus scrofa</i>	Russia	Wild boar	AWB	Yes	No
OUTG_SLID1275	<i>Sus celebensis</i>	Indonesia	Wild	-	Yes	No
OUTG_SCPH1280	<i>Sus cebifrons</i>	Philippines	Wild	-	Yes	No
OUTG_BBES0280	<i>Babyrusa babyrussa</i>	Madrid Zoo	Wild	-	No	Yes
OUTG_BAGB0335	<i>Sus barbatus</i>	London Zoo	Wild	-	No	Yes

Supplementary table S3. Primers used for the amplification of the Y-chromosome 7 loci

LOCUS	PCR	PRIMERS	SEQUENCE	Tm ¹ (°C)	Reference
UTY	1	UTY _{exo1} F	AGCTGTTTTTCGGTGATGAGG	65	Ramírez et al. 2009
		UTY _{exo2} R	TGCCCAACAGAGTTTTAGTCC		
	2	UTY _{in7} F	CATTTTCAGTTAGCTTTGATTGACTC	65	Ramírez et al. 2009
		UTY _{in7R4}	TCCTGAAGGACAATCATATAATCAA		
3	UTY _{in7F5}	GTACATTCAGAGCATTGTGTTT			
	UTY _{in7R5}	CAACTGGGCAATATGAAACTGA			
4	UTY _{in9F3}	GGCCTTACCCAAGGCATGTAG	65	Ramírez et al. 2009	
	UTY _{in9R2}	CCCTCCAAAGCTGTGTGTATATCTC			
USP9Y	5	USP9Y _{in24} F USP9Y _{exo25} R	GGACTGGTTCCTAATCAGGGTAATTTA TAGCACCCTGCTTGATCATGAG	65	Ramírez et al. 2009
DBY	6	DBY _{in1F2} DBY _{in1R2}	CTAAACAGAGTGTGCTGTTTGACA TCATAATCATTCCTGCCACGA	60	
DDX3Y	7	DBY _{in5F} DBY _{in5R}	CTGTCCTCGACATATTGAAAGTG CCATCTCAACATCGCTGAAC	67	
EIF2s3Y	8	EIF2s3YF EIF2s3YR	TCCTACTTAGACGGCTTCTTGG AGCCCACAGCAGGAGAACT	65	Ramírez et al. 2009
SRY	9	SRY1F	TCTATAACATCCGCCGCCTG	60	
		SRY1R	ATCCTCTCCTCTACGCGCAC		
	10	SRY2F	GGCTCCTCACTATTTCCGACG		
		SRY2R	ATTCTGCATGCTCCCCAG		
		SRY3F	AGCTTGGGAAATCTGTTCA		
11	SRY3R	ACCCAATTCCTTTCCTTTCG			
AMELY	12	AmelY _{proFW} AmelY _{E1Rv}	GCGTTACATGCATATTGCCTTG TCAAGGATGCTGGAGCTTTT	55	Ramírez et al. 2009
		I2FW2	TGTCCTCCAAATTACAGTGCTC		
	13	I2RV3	CATGATGGGTGTAGTAAAGTGGA		

Supplementary table S4. Functional annotations for the sequenced regions

Locus	Feature	Start	End
SRY-1	PROMOTER	1	3879
SRY-2	P5UTR	1	236
SRY-2	CDS	237	434
SRY-3	CDS	1	395
SRY-3	3UTR	396	635
AMELY-1	noncoding	1	535
AMELY-1	5UTR	536	543
AMELY-2	intron	1	710
USP9Y	intron	1	404
USP9Y	CDS	405	427
DBY	intron	1	679
DBY	CDS	680	695
DDX3Y	unknown	1	16
DDX3Y	intron	17	618
DDX3Y	unknown	619	626
UTY-1	CDS	1	97
UTY-1	intron	98	289
UTY-1	CDS	290	325
UTY-1	CDS	326	330
UTY-2	CDS	1	42
UTY-2	intron	43	596
UTY-3	intron	1	491
UTY-4	intron	1	353
eifs3y	unknown	1	7
eifs3y	CDS	8	49
eifs3y	unknown	50	184

Supplementary table S5. Genotyped regions for the seven loci of Chromosome-Y

Position	Ancestral Allele	Alleles	5' seq
367	gtag	gtag/----	CTTTTCATTTATTTG
527	g	g/a	CATGTGAGTGCACCTTAG
1119	g	g/t	GTAGGACTTACTCCCACCTTTGCTT
1493	c	c/t	TGGGGGTTCAATT
2754	t	t/c	TACAGTCATTACTCCCATT
4250	c	c/g	CACTATTTCCGACGGACAATCATAGCTCAAA
4675	g	g/c	GCTCACTTCTGCAACAGGAGGATC
4861	g	g/a	CTGTTATTTACCTGTGACTTA
5186	g	g/a	AAAATGGTAACTCCCTCAAATAC
5220	t	t/c	CATAACATGTTCTTAAAAGTAAACTTGAA
5858	NA	t/c	CCCCAAGAGGTCTGCA
6041	NA	g/a	GCTCACTGTCTGA
6744	g	g/a	GTCACAGTCATTGCACAAGCATAAAA
6789	g	g/a	CTTAGTATCTGGCTAGTCCAGTATTGTTTT
7227	a	a/c	CTTGTGACAAGAAATTTTCATT
7575	g	g/a	CCTGCATCCTCATGGATACTAGTCTGATTY
7772	t	t/c	TGTTAGATTAGACTCAGAAGTCCAT
7892	g	g/a	AAAACATTTTAGGAGAAAATGGATTTCTCGTTAT
8059	g	g/c	TTAGCGGAATGGACAGGTACGGACCGCT
8152	c	c/t	TCGTCCAAGTGGT
8205	c	c/g	CCGTCAAGTGGCTTTACTTA
8397	t	t/c	TTTCAAATAATGAC
8399	t	t/g	TTTCAAATAATGACYA

Supplementary table S6. Prior parameter ranges of the demographic models.

Prior parameters	Range of values	Distribution
θ_W Asia	5E-04 – 1E-02	log uniform
f_{noA}	5E-02 – 1E01	log uniform
M	1E02 – 1E04	log uniform
T_s	5E-01 – 1E01	log uniform
f_{ANC}	5E-02 – 1E01	log uniform
T_0	1E01 – 5E02	log uniform
T_M	1E-03	Fixed

θ_W Asia, Asian current population mutation parameter. f_{noA} , a fraction of the non-Asian current population size. M , unidirectional population migration from the non-Asian to the Asian population. T_s , time of split between the Asian and the non-Asian population. f_{ANC} , fraction of the ancestral population size. T_0 , time of split between the ancestral population of these populations and the outgroup. T_M , time of the onset of migration. Times and population migration parameter are given in N units.

ANGLP_PLUS0638 C G G . .
 ANGLP_PLUS0639 C G G . .
 ANGLP_SGB0363 C G
 ANGLP_SGB0364 C G
 ANGLP_WGB0746 C G G . .
 ANGLP_SGB0756 C G
 ANGLP_TWGB0371 . . G T T . C A G T C A G A A A T A C C G . . G C A A G T G T A C
 ANGLP_TWGB0372 . . G T T . C A G T C A G A A A T A C C G . . G C A A G T G T . A C
 ANGLP_TWGB0748 . . G T T . C A G T C A G A A A T A C C G . . G C A A G T G T . A C

INTP

INTP_DUDK0474 C G
 INTP_DUES0169 C G
 INTP_DUES0194 C G
 INTP_DUES0277 C G
 INTP_DUES0460 C G
 INTP_DUES0538 C G
 INTP_DUGB0353 C G
 INTP_DUGB0355 C G
 INTP_DUGB0356 C G
 INTP_DUGB0357 C G
 INTP_DUHU0199 C G
 INTP_DUHU0202 C G
 INTP_DUNO0087 C G
 INTP_DUNO0088 C G
 INTP_DUUS0458 C G
 INTP_DUUS0602 C G
 INTP_DUUS0603 C G
 INTP_DUUS0604 C G
 INTP_DUUS0605 C G
 INTP_DUUS0613 C G
 INTP_HSGB0977 C G
 INTP_HSUS0614 C G
 INTP_HSUS0615 C G
 INTP_HSUS0616 C G
 INTP_HSUS0618 C G
 INTP_LRES0285 C G
 INTP_LRES0465 C G
 INTP_LRGB0336 C G
 INTP_LRGB0338 C G
 INTP_LRGB0339 C G
 INTP_LRGB0341 C G
 INTP_LRGB0342 C G
 INTP_LRGB0967 C G
 INTP_LRUS0633 C G
 INTP_LRUS0635 C G
 INTP_LRUS0637 C G
 INTP_LWDK0473 C G
 INTP_LWES0284 C G
 INTP_LWFI0343 C G
 INTP_LWFR0351 C G
 INTP_LWFR0352 C G
 INTP_LWGB0344 C G
 INTP_LWGB0345 C G
 INTP_LWGB0348 C G
 INTP_LWGB0349 C G
 INTP_LWGB0350 C G
 INTP_LWGB0987 C G
 INTP_PIDE0463 C G
 INTP_PIDE0478 C G
 INTP_PIES0464 C G
 INTP_PIES0470 C G
 INTP_PIFR0479 C G
 INTP_PIGB0747 C G
 INTP_SYES0472 C G
 INTP_YKUS0627 C G
 INTP_YKUS0628 C G
 INTP_YKUS0631 C G
 INT_MPES0758 C G
 INT_MPES0759 C G
 INT_MPES0760 C G
 INT_MPDK0728 C G
 INT_MPDK1034 C G
 . . G T T G T C A G A A A T A C C G . . G C A A G T G T G T . C

AFWB

AFWB_WBTN0962 G
 AFWB_WBTN0963 G
 AFWB_WBTN0964 G
 AFWB_NEWB0517 G
 AFWB_NEWB1271 G

AFRICA

AFP_NABF0913 C G
 AFP_NABF0922 C G
 AFP_NABF0923 C G
 AFP_NABF0927 C G
 AFP_NACI0911 C G
 AFP_NAKE0852 C G
 AFP_NAKE0854 C G
 AFP_NAKE0855 C G
 AFP_NAKE0860 C G
 AFP_NAKE0861 C G
 AFP_NAKE0866 C G

Supplementary table S8. Population differentiation between Asian and non-Asian groups

	Sequencing		Genotyping	
	<i>Fst</i>	<i>P-value</i>	<i>Fst</i>	<i>P-value</i>
Asia vs Non-Asia	0.5036	<1e ⁻³ *	0.5843	<1e ⁻³ *

* Significant for multiple test with Bonferroni correction ($\epsilon=0.05$)

Supplementary table S9. Population differentiation between each group and the rest **(A)** and between all pairwise comparisons **(B)** for genotype data

A.

Group	nsam	<i>Fst</i>	<i>P</i>-value
EWB	39	0.274	<1E-3
MEDLP	20	0.138	0.004
INTP	62	0.160	<1E-3
ANGLP	29	0.027	0.134
AFWB	5	0.194	0.031
AFP	22	0.141	<1E-3
NEWB	2	0.358	0.019
SCAP	17	0.197	<1E-3
ALP	18	0.117	0.016
AWB	22	0.757	<1E-3

B.

<i>Fst</i>/<i>P</i>-value	EWB	MEDLP	INTP	ANGLP	AFWB	AFP	NEWB	SCAP	ALP	AWB
EWB		0.017	<1E-3	<1E-3	0.989	<1E-3	0.108	<1E-3	<1E-3	<1E-3
MEDLP	0.119		<1E-3	<1E-3	0.311	<1E-3	0.130	<1E-3	<1E-3	<1E-3
INTP	0.600	0.384		0.168	<1E-3	0.634	0.002	0.312	<1E-3	<1E-3
ANGLP	0.348	0.193	0.027		0.001	0.165	0.006	0.067	0.032	<1E-3
AFWB	-0.123	0.024	0.539	0.309		0.001	0.436	0.001	0.060	<1E-3
AFP	0.667	0.419	-0.017	0.060	0.590		0.011	0.497	0.002	<1E-3
NEWB	0.645	0.603	0.759	0.490	0.353	0.841		0.005	0.099	0.014
SCAP	0.792	0.582	0.005	0.101	0.719	-0.022	0.926		0.002	<1E-3
ALP	0.336	0.296	0.266	0.141	0.316	0.304	0.382	0.330		<1E-3
AWB	0.830	0.820	0.813	0.714	0.818	0.837	0.838	0.851	0.378	

Supplementary table S10. Marginal densities and Posterior distributions of the demographic models

Model	Marginal density	<i>P</i>-value	Posterior probability
Model <i>I_{old}</i>	4.08E-07	5E-03	2.28E-12
Model <i>IM</i>	1.78E-05	9.77E-01	>9.99E-01

Model *I_{old}*, Isolation model. Model *IM*, isolation with unidirectional admixture.