Supplementary Materials

Cultural variation impacts paternal and maternal genetic lineages of the Hmong-Mien and Sino-Tibetan groups from Thailand

Wibhu Kutanan[1,2,*], Rasmi Shoocongdej[3], Metawee Srikummool[4], Alexander Hübner[2], Thanatip Suttipai[1], Suparat Srithawong[1], Jatupol Kampuansai[5,6], and Mark Stoneking[2,*]

There are 10 Supplementary Figures and 10 Supplementary Tables in this manuscript.

Supplementary Figures

Fig. S1 Bar plots of the distribution of major haplogroups for (A) MSYand (B) mtDNA. The new populations are placed at the left of the figure.

Fig. S2 Bayesian maximum clade credibility (MCC) tree of MSY sequences belonging to: (A) haplogroup C*; (B) haplogroup F; (C) haplogroup O2a2a*.

Fig. S3 Bayesian maximum clade credibility (MCC) trees of mtDNA sequences belonging to: (A) haplogroup A; (B) haplogroup B4; (C) haplogroup B5a1c1a; (D) haplogroup B6; (E) haplogroup C; (F) haplogroup D; (G) haplogroup F1g; (H) haplogroup G; and (I) haplogroup R9.

Fig. S4 The MDS plot for 73 Thai/Lao populations based on the MSY Φ_{st} distances for (A) dimension 1 vs. 2; (B) dimension 1 vs. 3; (C) dimension 2 vs. 3 and based on mtDNA Φ_{st} distances for (D) dimension 1 vs. 2; (E) dimension 1 vs. 3; (F) dimension 2 vs. 3.

Fig. S5 The heat plot of the five-dimensional MDS for the 73 Thai/Lao populations. (A) MSY; (B) mtDNA.

Fig. S6 Correspondence Analysis based on MSY haplogroup frequencies for (A) dimension 1 vs. 2; (B) dimension 1 vs. 3; (C) dimension 1 vs. 4; (D) dimension 2 vs. 3; (E) dimension 2 vs. 4; (F) dimension 3 vs. 4.

Fig. S7 Correspondence Analysis based on mtDNAhaplogroup frequencies for (A) dimension 1 vs. 2; (B) dimension 1 vs. 3; (C) dimension 1 vs. 4; (D) dimension 2 vs. 3; (E) dimension 2 vs. 4; (F) dimension 3 vs. 4.

Fig. S8 The BSPs based on the MSY and mtDNA for 14 populations. Solid lines are the median estimated effective population size (y axis) through time from the present in years (x axis). The 95% highest posterior density limits are indicated by dotted lines.

Fig. S9 Bar plots of (A) haplotype diversity and (B) mean number of pairwise differences for patrilocal (blue) and matrilocal (orange) populations. Population abbreviations are in Table S1.

Fig. S10 Genetic variation among populations within groups, defined by ethnicity, language and cultural practice.

Supplementary Tables

Table S1 General information concerning the studied populations and genetic diversity values.

Table S2 Sequencing coverage and MSY haplogroup of each individual.

Table S3 Sequencing coverage and mtDNA haplogroup of each individual.

Table S4 Details for populations included in the MSY and mtDNA comparisons.

Table S5 Frequency of MSY/mtDNA lineages of Northeast Asian (NEA) and Southeast Asian (SEA) origin in Hmong-Mien and Sino-Tibetan speaking populations from China and Vietnam.

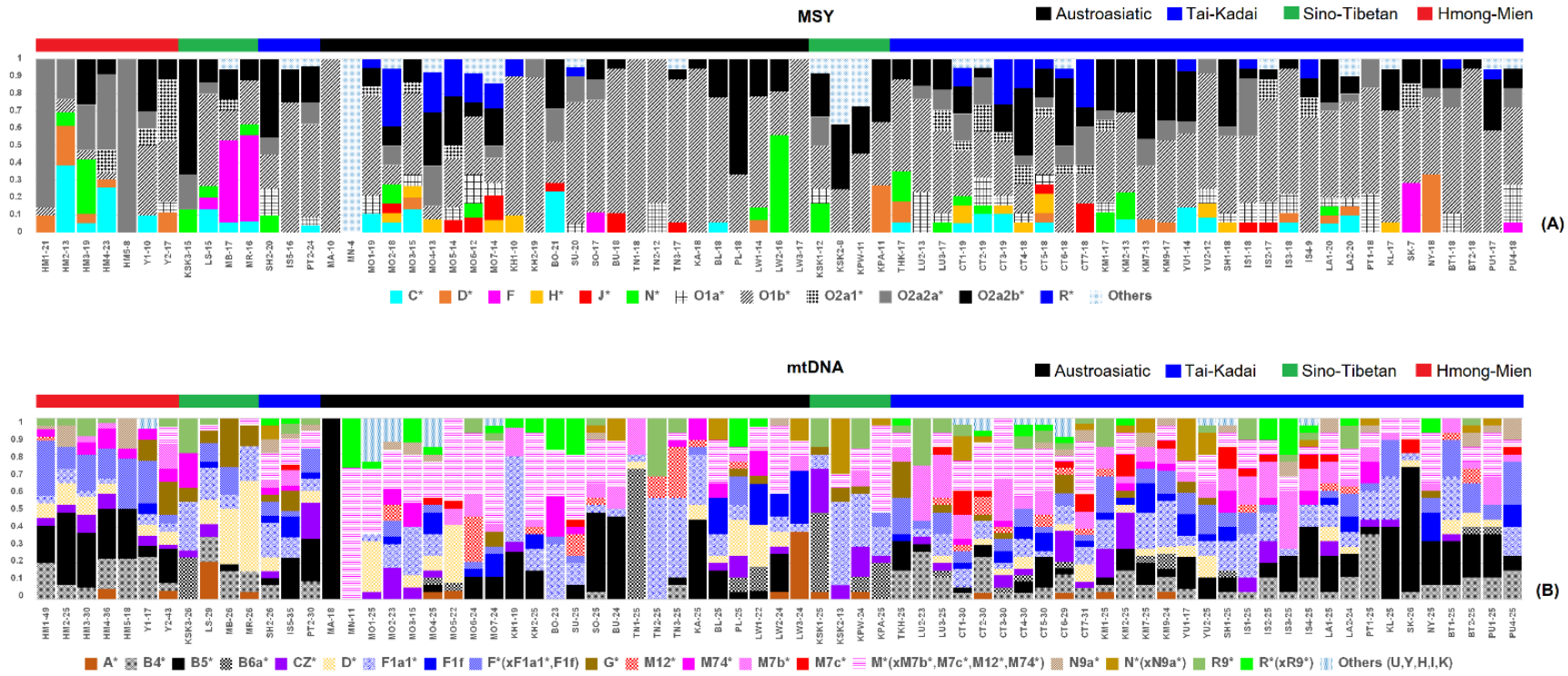
Table S6 Details on BEAST analyses.

Table S7 MSY haplolgroup frequencies. The populations sequenced in this study are on the left side of the table, and newly-reported haplogroups are in red font.

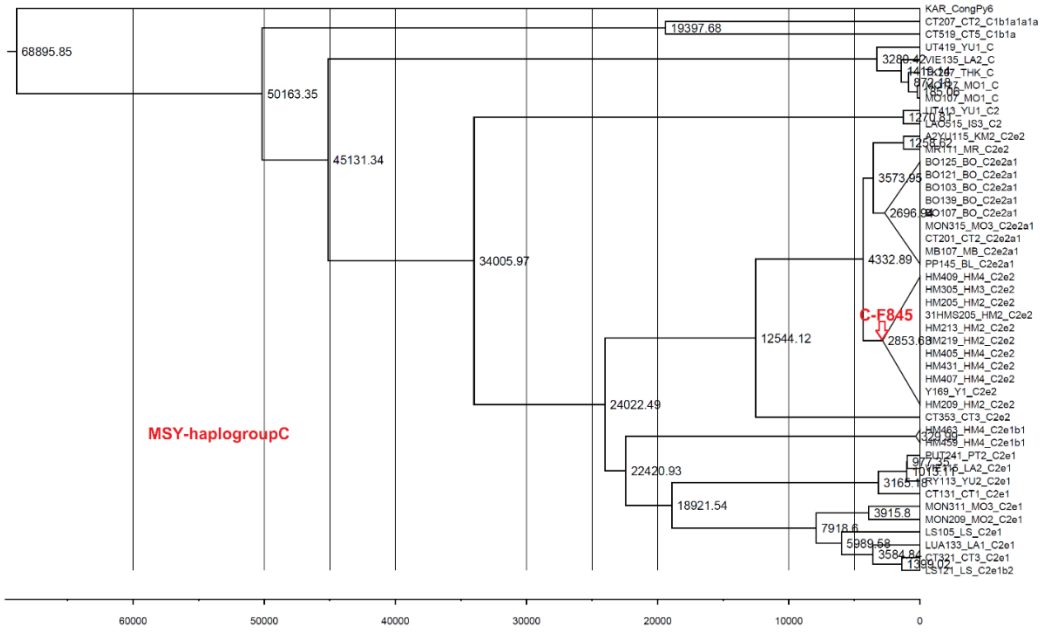
Table S8 MtDNA haplolgroup frequencies. The populations sequenced in this study are on the left side of the table, and newly-reported haplogroups are in red font.

Table S9 Mann-Whitney U test results for comparing genetic diversity values between different language families and residence patterns.

Table S10 Haplotype sharing between populations of the same patrilocal or matrilocal group, for groups with at least two different populations sampled.



Supplementary Fig. S1 Bar plots of the distribution of major haplogroups for (A) MSYand (B) mtDNA. The new populations are placed at the left of the figure.



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VIE135_LA2_C
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UT413_YU1_C2
LAO515_IS3_C2
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MR111_MR_C2e2
BO125_BO_C2e2a1
BO121_BO_C2e2a1
BO103_BO_C2e2a1
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RY113_YU2_C2e1
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MON311_MO3_C2e1
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CT321_CT3_C2e1
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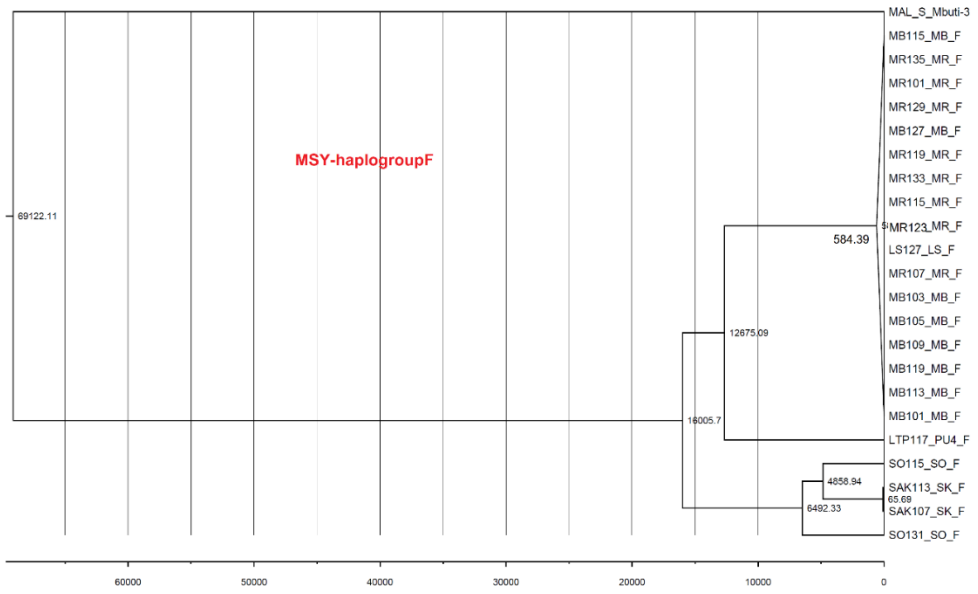

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MR101_MR_F
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MB127_MB_F
MR119_MR_F
MR133_MR_F
MR115_MR_F
MR123_MR_F
LS127_LS_F
MR107_MR_F
MB103_MB_F
MB105_MB_F
MB109_MB_F
MB119_MB_F
MB113_MB_F
MB101_MB_F
LTP117_PU4_F
SO115_SO_F
SAK113_SK_F
SAK107_SK_F
SO131_SO_F
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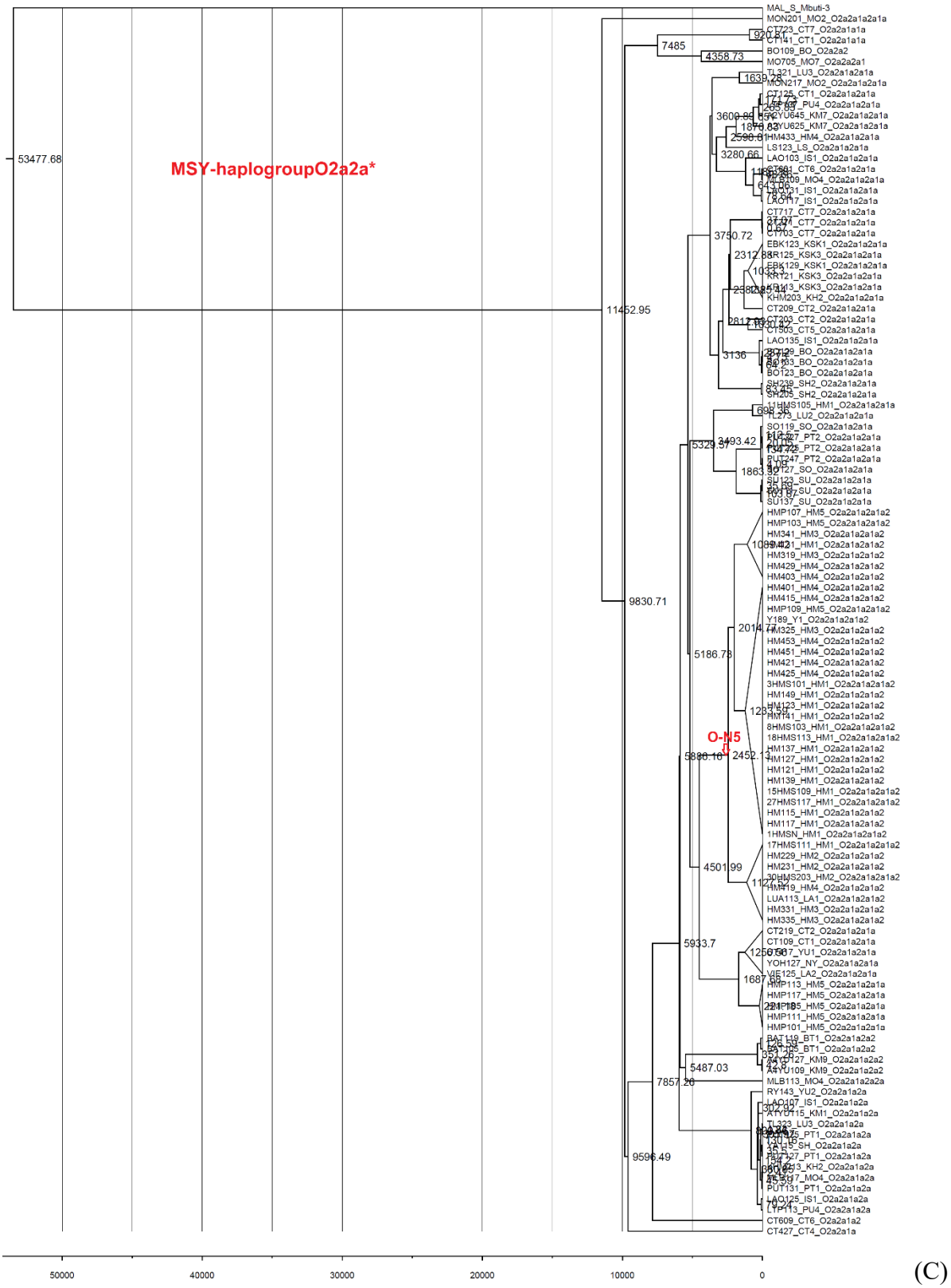
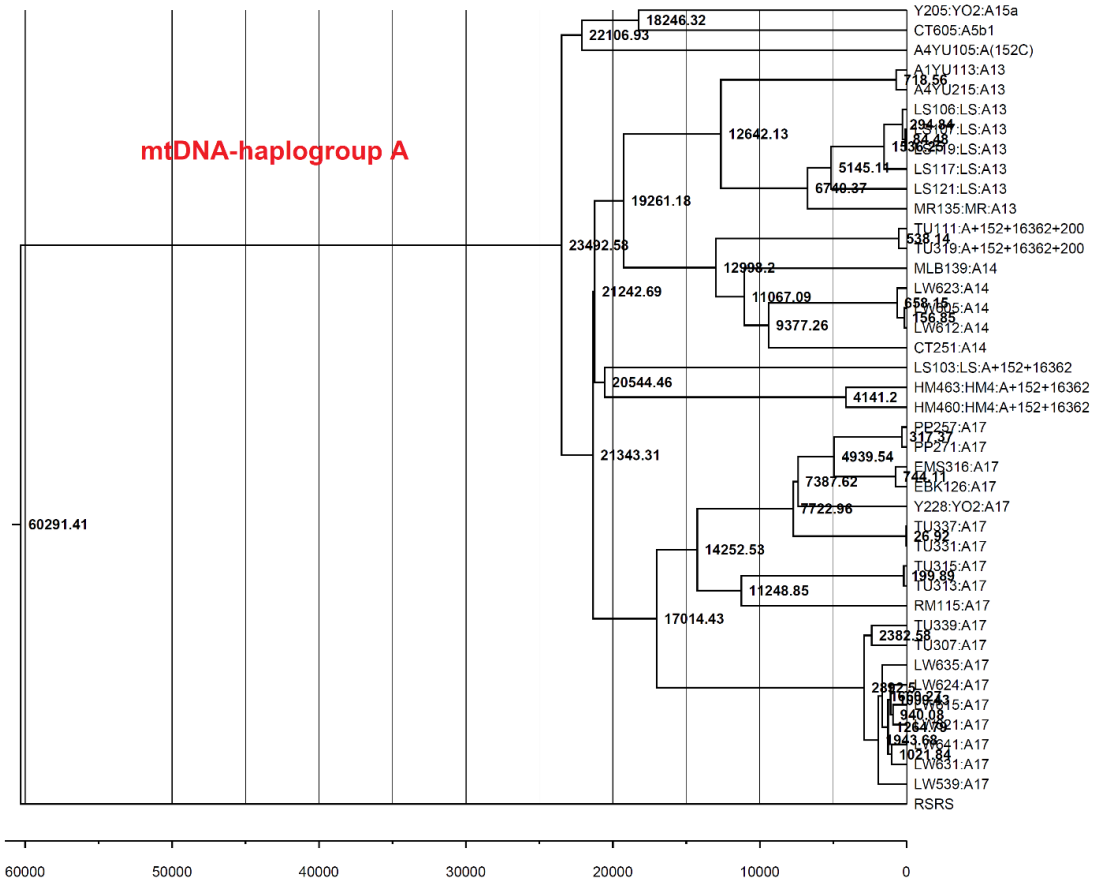
(B)



(C)

Supplementary Fig. S2 Bayesian maximum clade credibility (MCC) tree of MSY sequences belonging to: (A) haplogroup C*; (B) haplogroup F; (C) haplogroup O2a2a*.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LS106:LS:A13
LS117:LS:A13
LS121:LS:A13
MR135:MR:A13
TU111:A+152+16362+200
TU319:A+152+16362+200
MLB139:A14
LW623:A14
LW612:A14
CT251:A14
LS103:LS:A+152+16362
HM463:HM4:A+152+16362
HM460:HM4:A+152+16362
PP257:A17
PP271:A17
EMS316:A17
EBK126:A17
Y228:YO2:A17
TU337:A17
TU331:A17
TU315:A17
TU313:A17
RM115:A17
TU339:A17
TU307:A17
LW635:A17
LW631:A17
LW539:A17
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6740.37
12998.2
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9377.26
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7722.96
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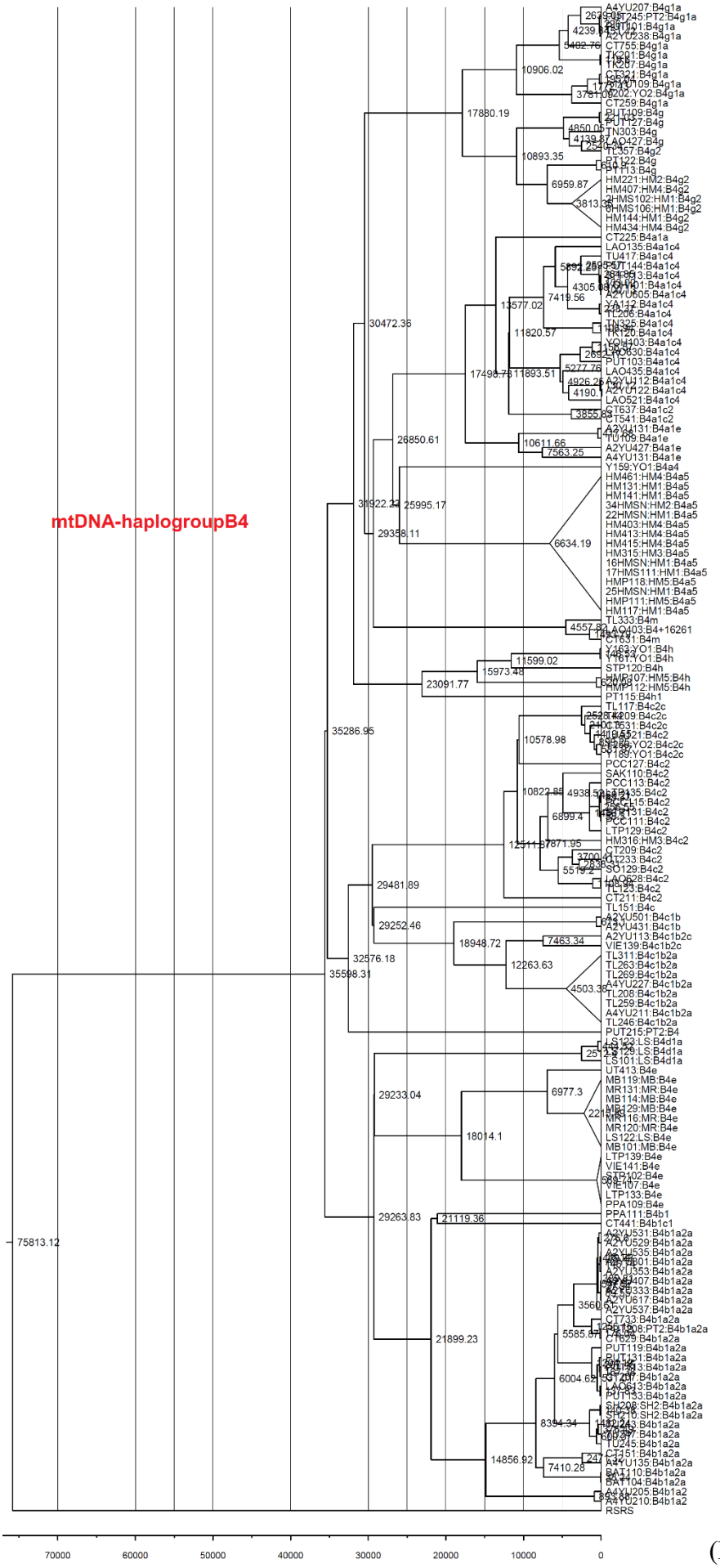
(A)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CT202:YO2:B4g1a
CT259:B4g1a
PUT109:B4g
PUT127:B4g
TN303:B4g
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HM407:HM4:B4g2
HMS102:HM1:B4g2
HMS106:HM1:B4g2
HM144:HM1:B4g2
HM434:HM4:B4g2
CT225:B4a1a
LAO135:B4a1c4
TU417:B4a1c4
PUT144:B4a1c4
A2YU605:B4a1c4
TC206:B4a1c4
TN325:B4a1c4
TK120:B4a1c4
LAO630:B4a1c4
PUT103:B4a1c4
LAO435:B4a1c4
A2YU112:B4a1c4
A2YU122:B4a1c4
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CT637:B4a1c2
CT541:B4a1c2
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TU109:B4a1e
A2YU427:B4a1e
A4YU131:B4a1e
Y159:YO1:B4a4
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HM131:HM1:B4a5
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HM413:HM4:B4a5
HM415:HM4:B4a5
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HM117:HM1:B4a5
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Y161:YO1:B4h
STP120:B4h
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PT115:B4h1
TL117:B4c2c
SO209:B4c2c
SO189:YO1:B4c2c
PCC127:B4c2
SAK110:B4c2
PCC113:B4c2
PCC111:B4c2
LTP129:B4c2
HM316:HM3:B4c2
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SO129:B4c2
LAO628:B4c2
TL123:B4c2
CT211:B4c2
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A4YU211:B4c1b2a
TL246:B4c1b2a
PUT215:PT2:B4
LS123:LS:B4d1a
LS129:LS:B4d1a
LS101:LS:B4d1a
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MB119:MB:B4e
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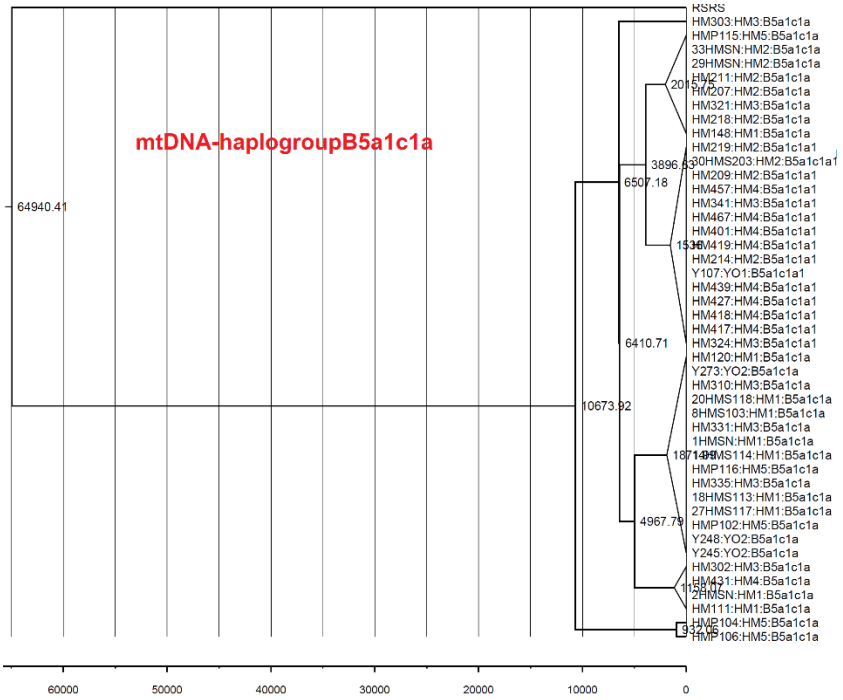
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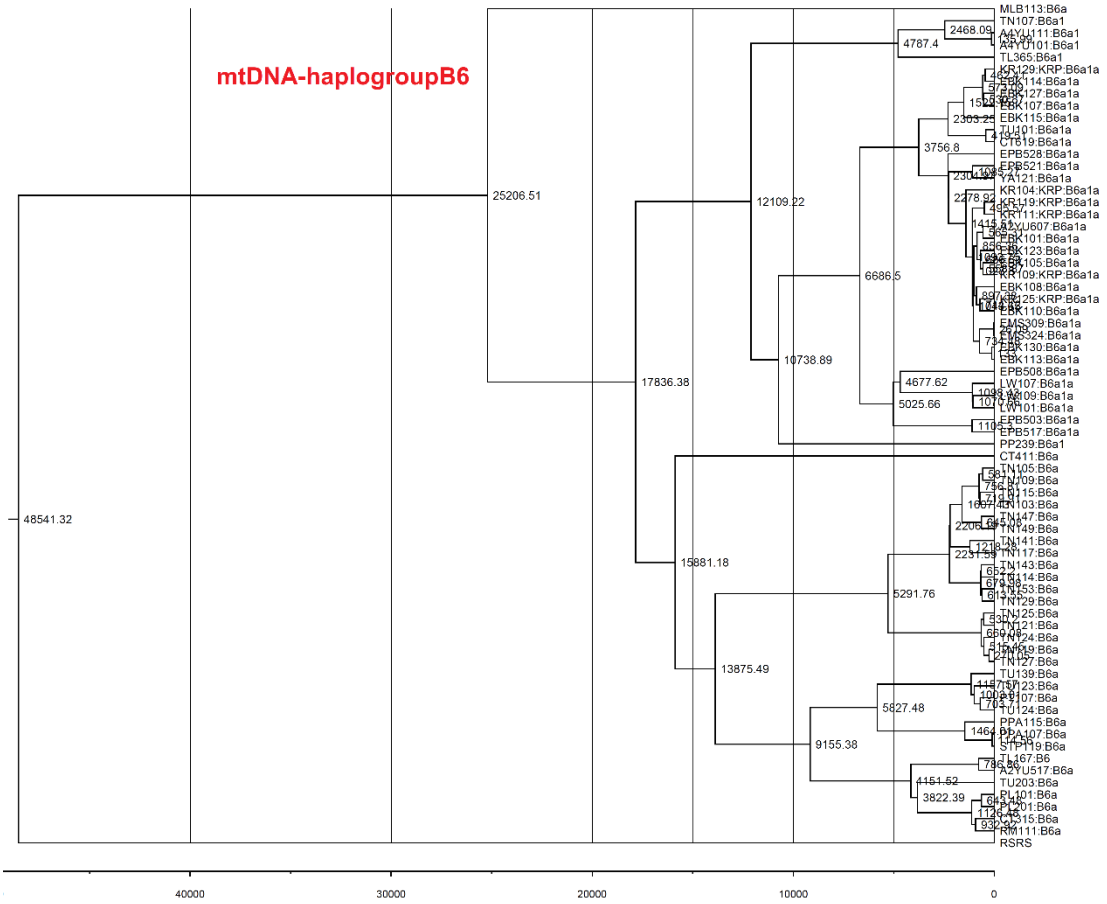
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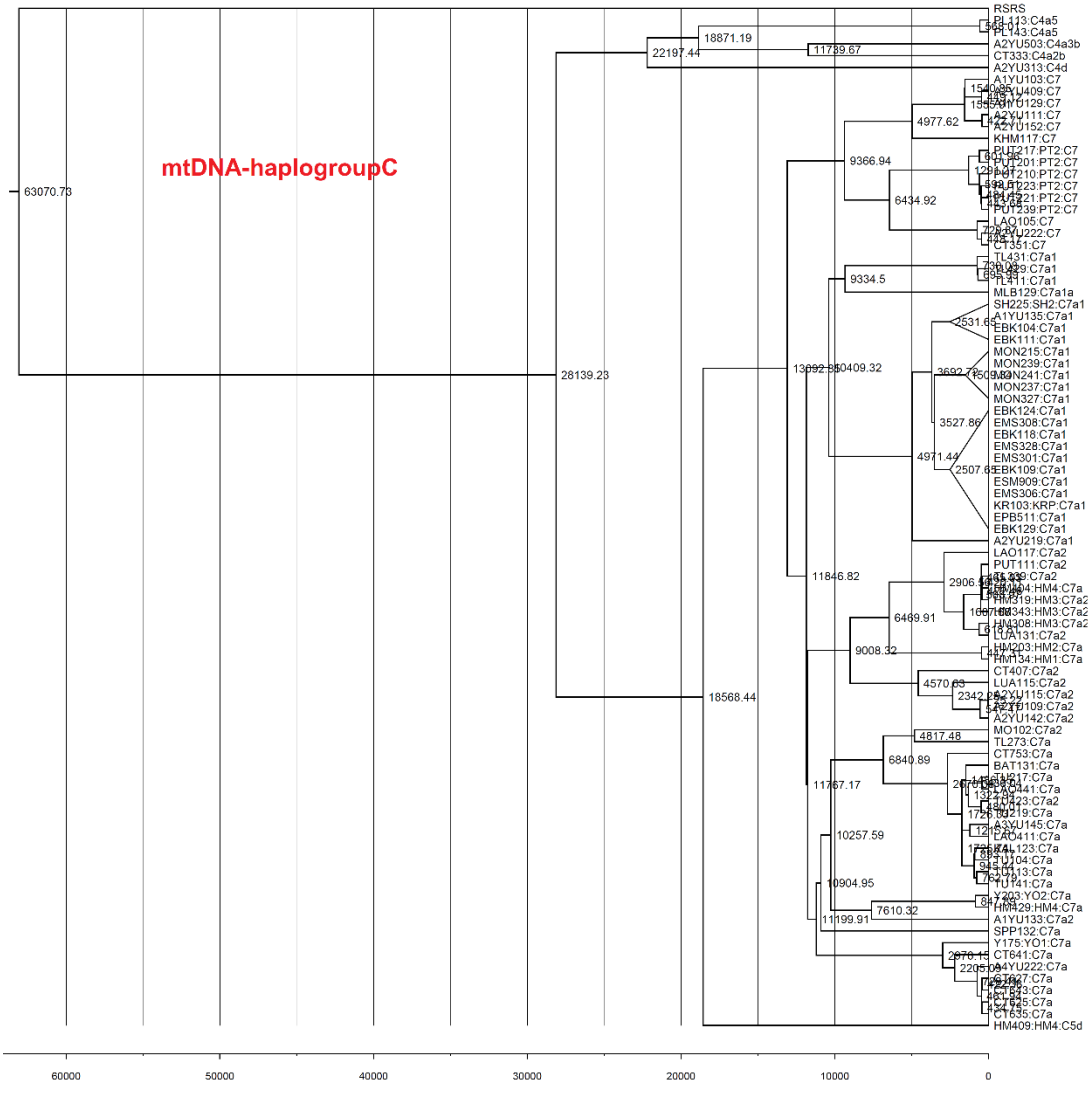
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A2YU222:C7
CT351:C7
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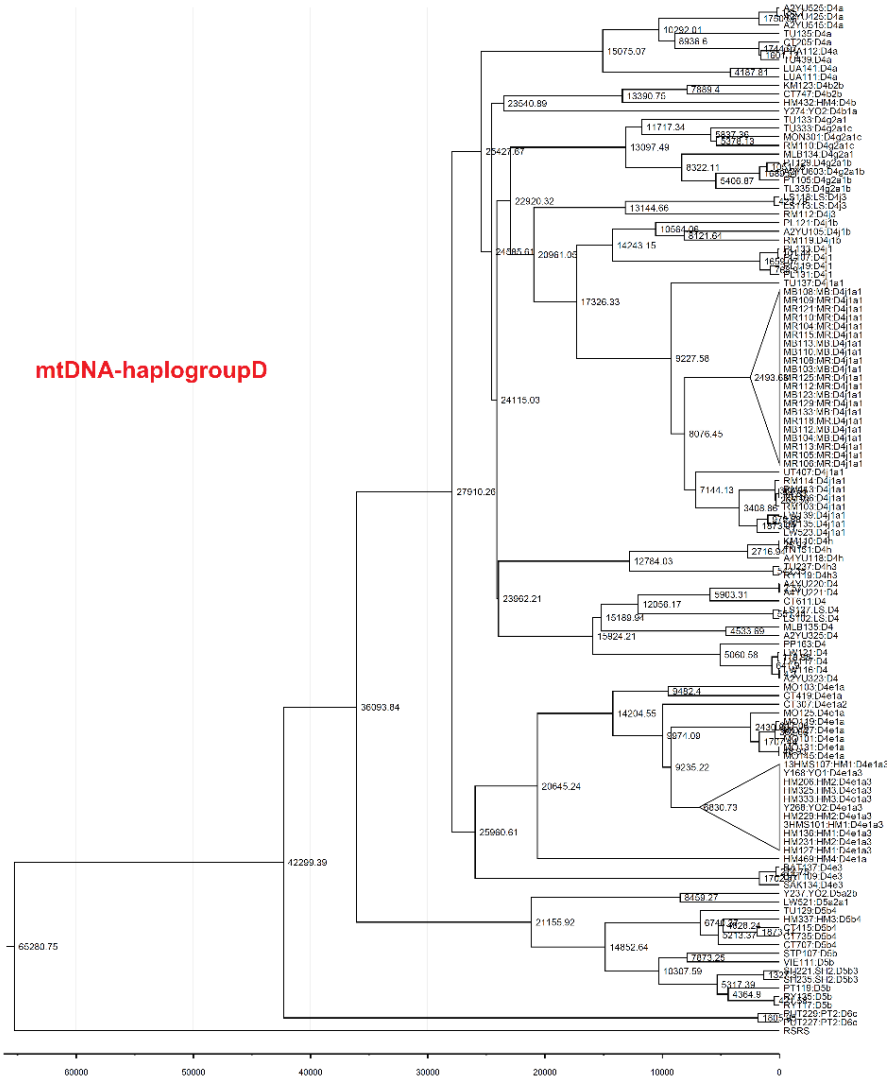
(E)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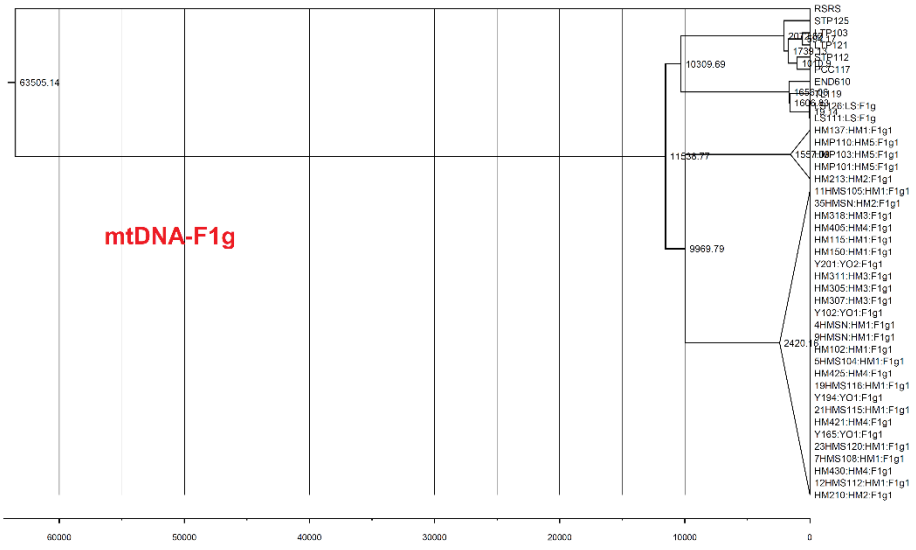
50000
40000
30000
20000
10000
0

(F)


mtDNA-F1g
RSRS
STP125
STP103
STP121
STP112
PCC117
END610
LS111:LS:F1g
HM137:HM1:F1g1
HMP110:HM5:F1g1
HMP103:HM5:F1g1
HMP101:HM5:F1g1
HM213:HM2:F1g1
11HMS105:HM1:F1g1
35HMSN:HM2:F1g1
HM318:HM3:F1g1
HM405:HM4:F1g1
HM115:HM1:F1g1
HM150:HM1:F1g1
Y201:YO2:F1g1
HM311:HM3:F1g1
HM305:HM3:F1g1
HM307:HM3:F1g1
Y102:YO1:F1g1
4HMSN:HM1:F1g1
9HMSN:HM1:F1g1
HM102:HM1:F1g1
5HMS104:HM1:F1g1
HM425:HM4:F1g1
19HMS116:HM1:F1g1
Y194:YO1:F1g1
21HMS115:HM1:F1g1
HM421:HM4:F1g1
Y165:YO1:F1g1
23HMS120:HM1:F1g1
7HMS108:HM1:F1g1
HM430:HM4:F1g1
12HMS112:HM1:F1g1
HM210:HM2:F1g1
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10309.69
11538.77
9969.79
60000
50000
40000
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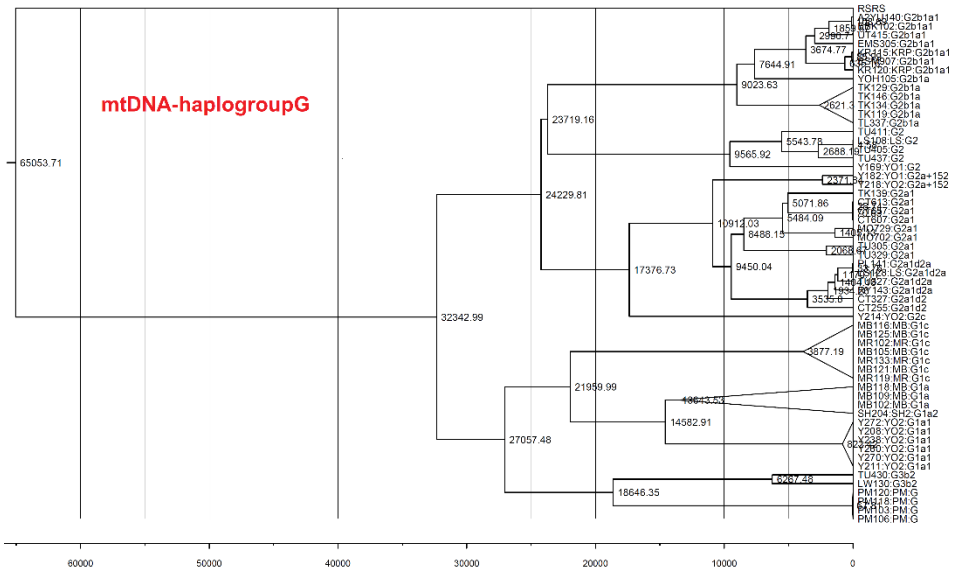
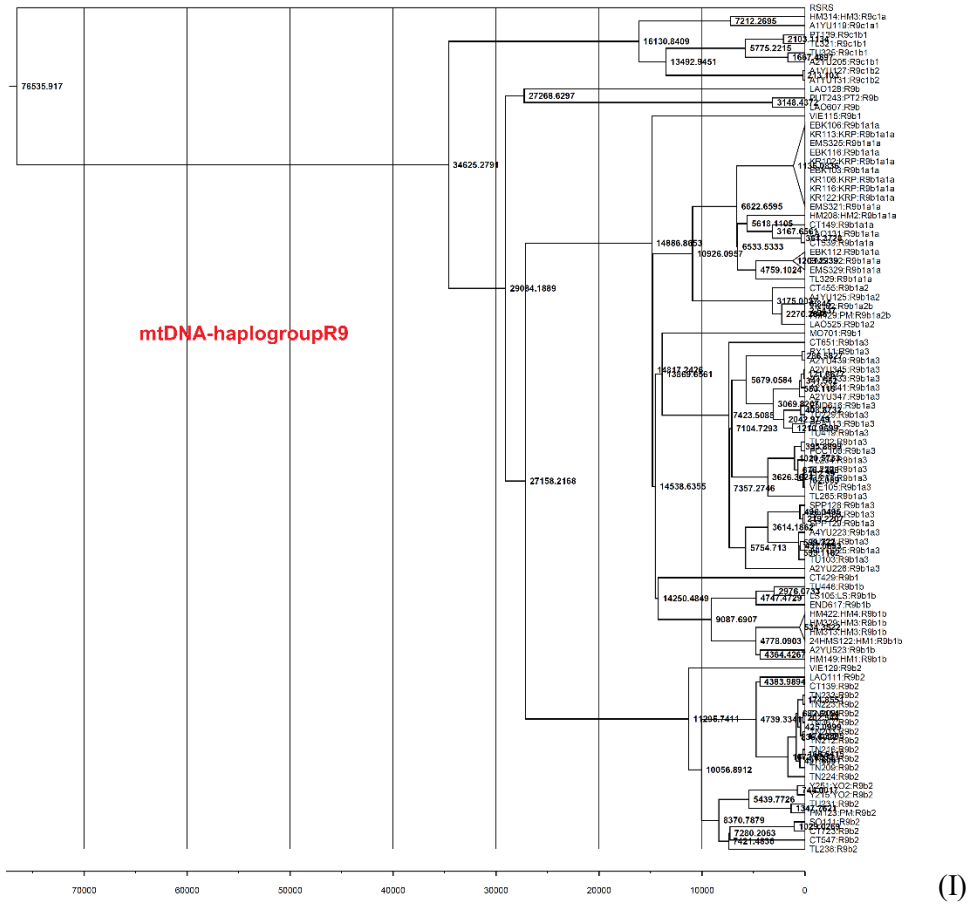
20000
10000
0

(G)

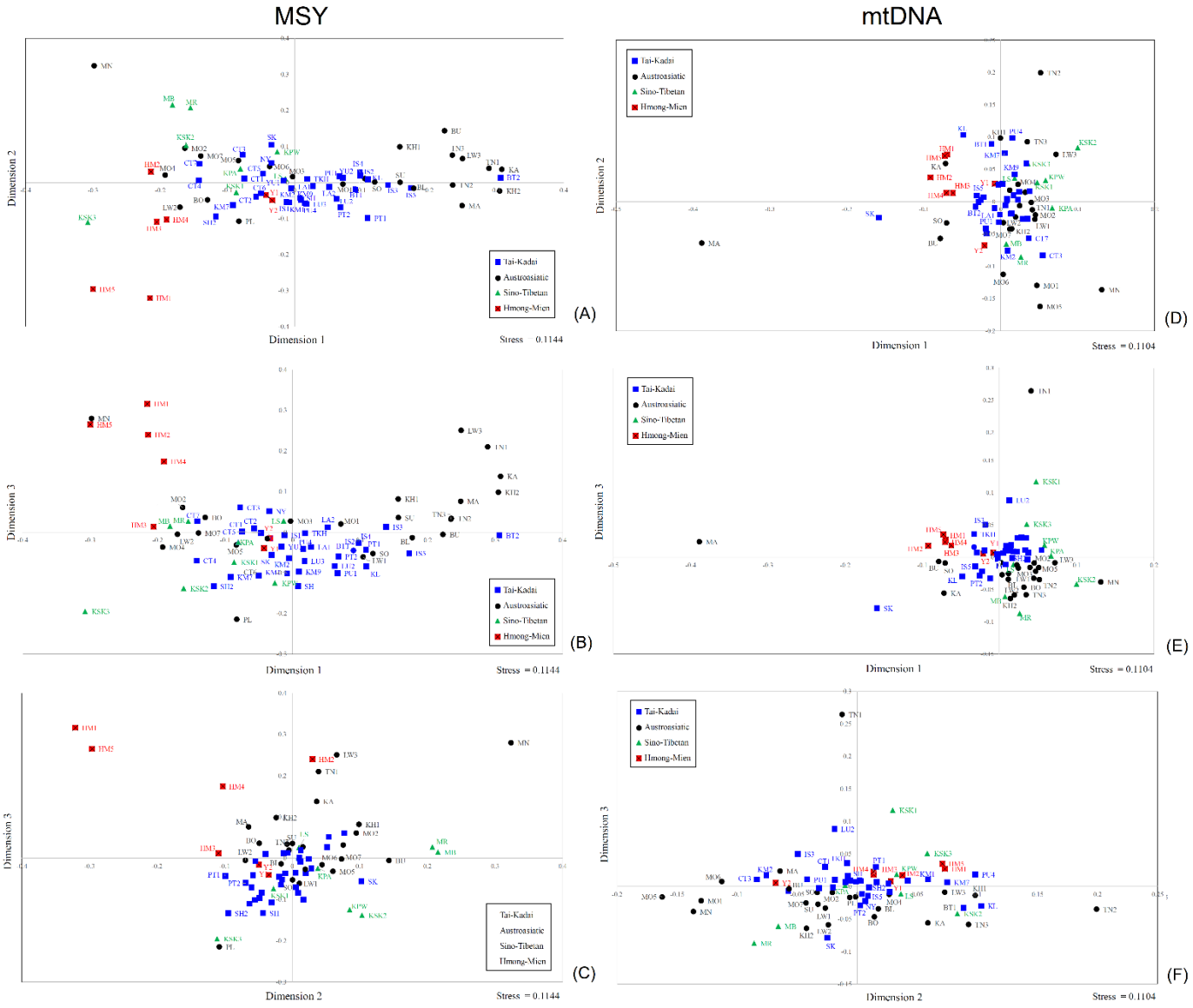


(H)

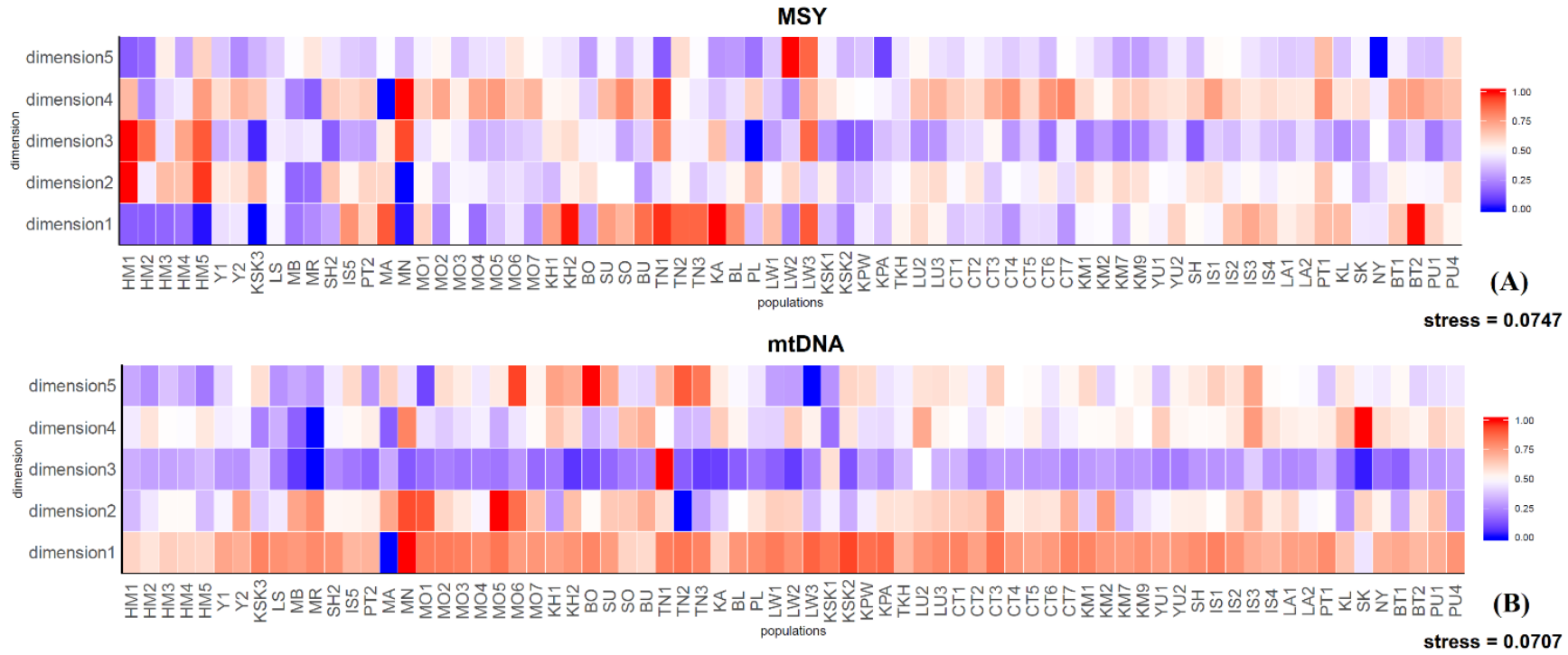


(I)

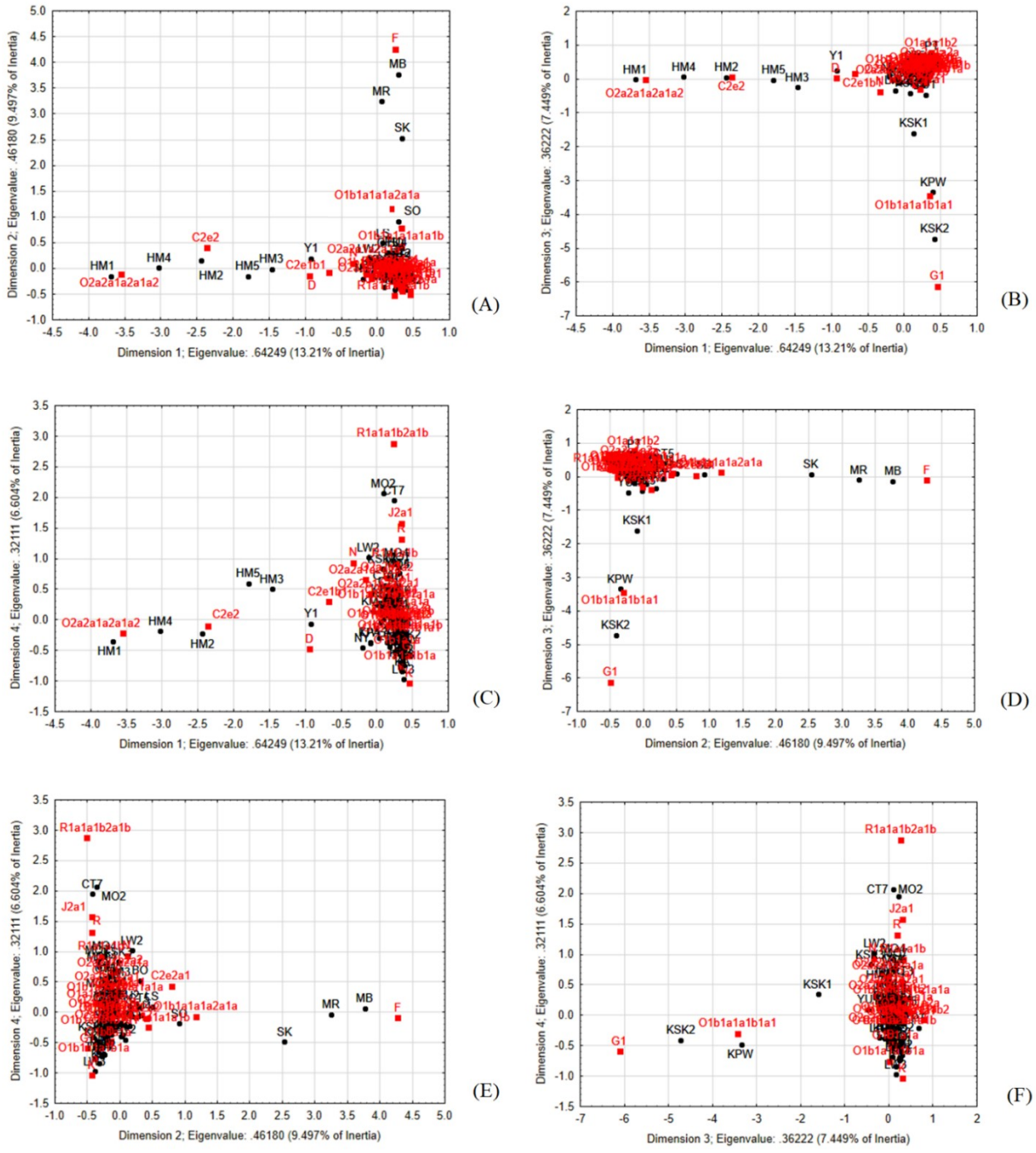
Supplementary Fig. S3 Bayesian maximum clade credibility (MCC) trees of mtDNA sequences belonging to: (A) haplogroup A; (B) haplogroup B4; (C) haplogroup B5a1c1a; (D) haplogroup B6; (E) haplogroup C; (F) haplogroup D; (G) haplogroup F1g; (H) haplogroup G; and (I) haplogroup R9.



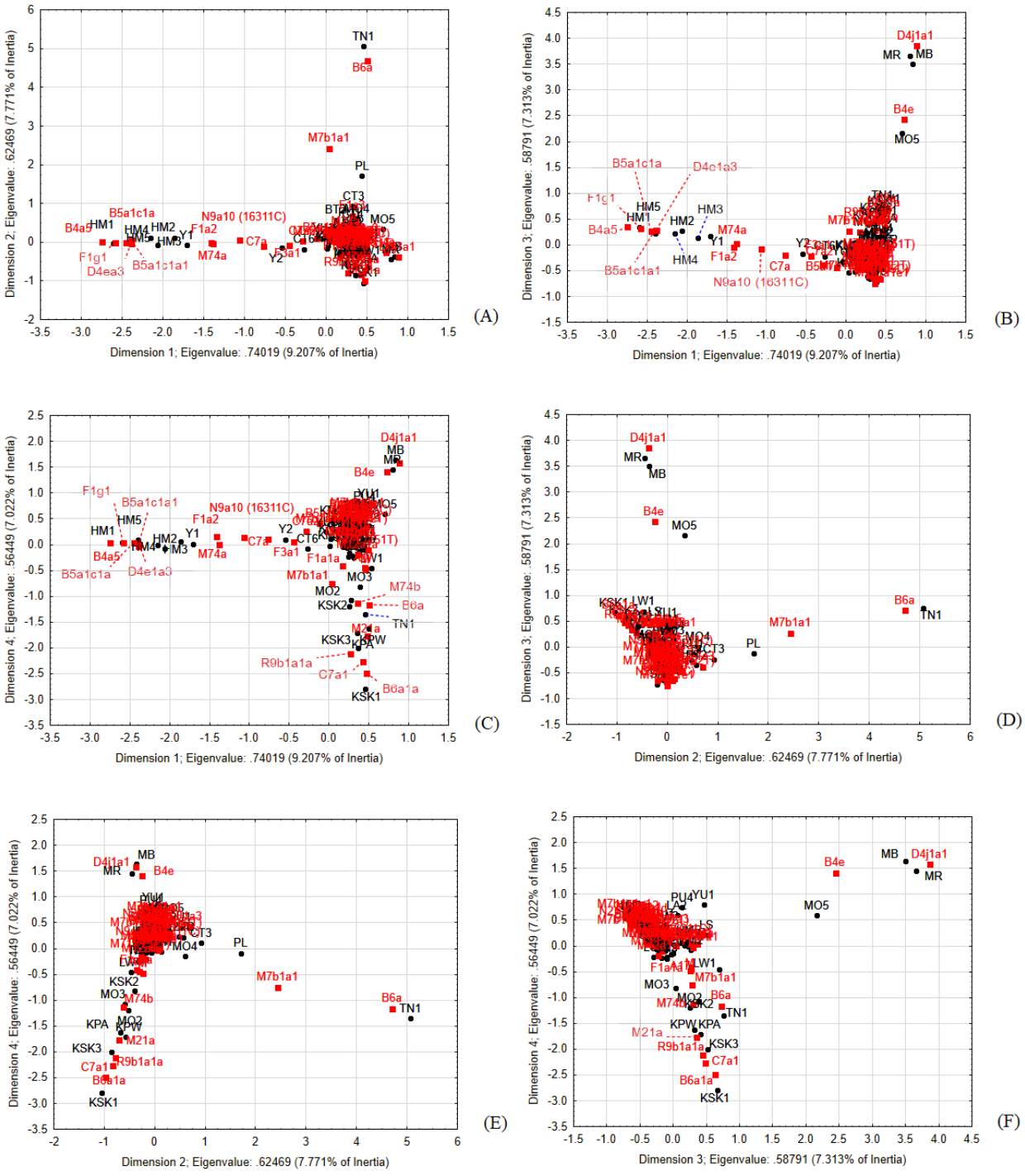
Supplementary Fig. S4 The MDS plot for 73 Thai/Lao populations based on the MSY Φ_{st} distances for (A) dimension 1 vs. 2; (B) dimension 1 vs. 3; (C) dimension 2 vs. 3 and based on mtDNA Φ_{st} distances for (D) dimension 1 vs. 2; (E) dimension 1 vs. 3; (F) dimension 2 vs. 3.



Supplementary Fig. S5 The heat plot of the five-dimensional MDS for the 73 Thai/Lao populations. (A) MSY; (B) mtDNA.

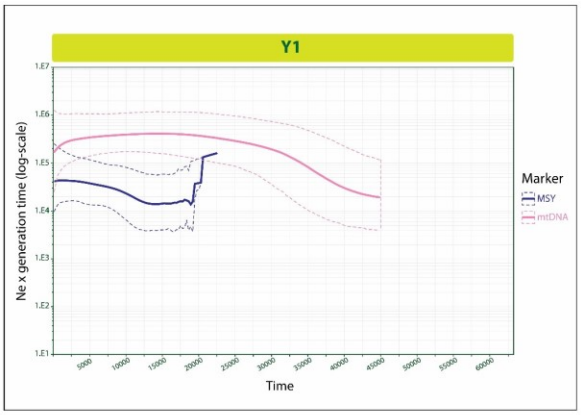


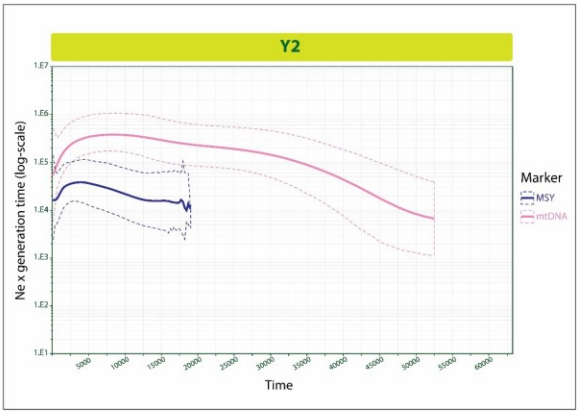
Supplementary Fig. S6 Correspondence Analysis based on MSY haplogroup frequencies for (A) dimension 1 vs. 2; (B) dimension 1 vs. 3; (C) dimension 1 vs. 4; (D) dimension 2 vs. 3; (E) dimension 2 vs. 4; (F) dimension 3 vs. 4.

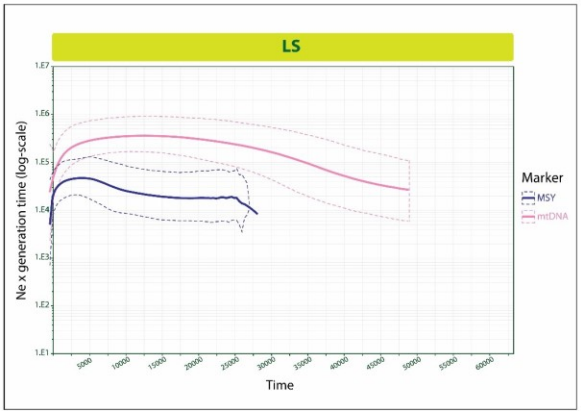


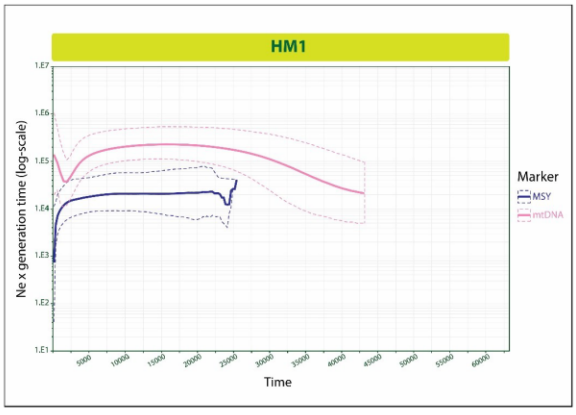
Supplementary Fig. S7 Correspondence Analysis based on mtDNAhaplogroup frequencies for (A) dimension 1 vs. 2; (B) dimension 1 vs. 3; (C) dimension 1 vs. 4; (D) dimension 2 vs. 3; (E) dimension 2 vs. 4; (F) dimension 3 vs. 4.

HM5
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA

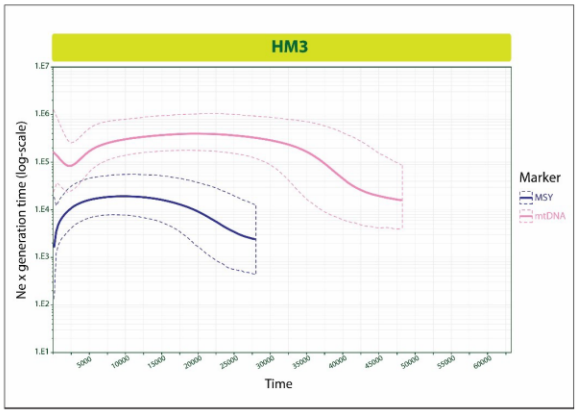

Y1
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA

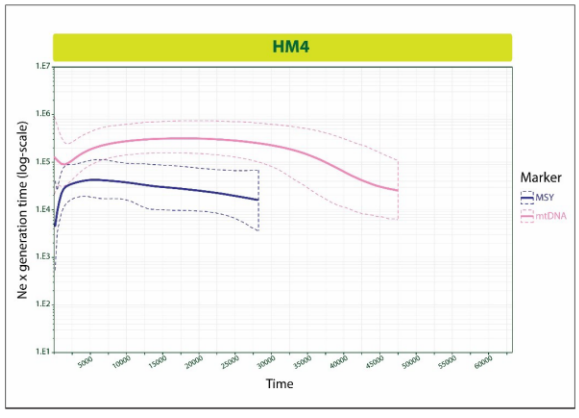

Y2
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA

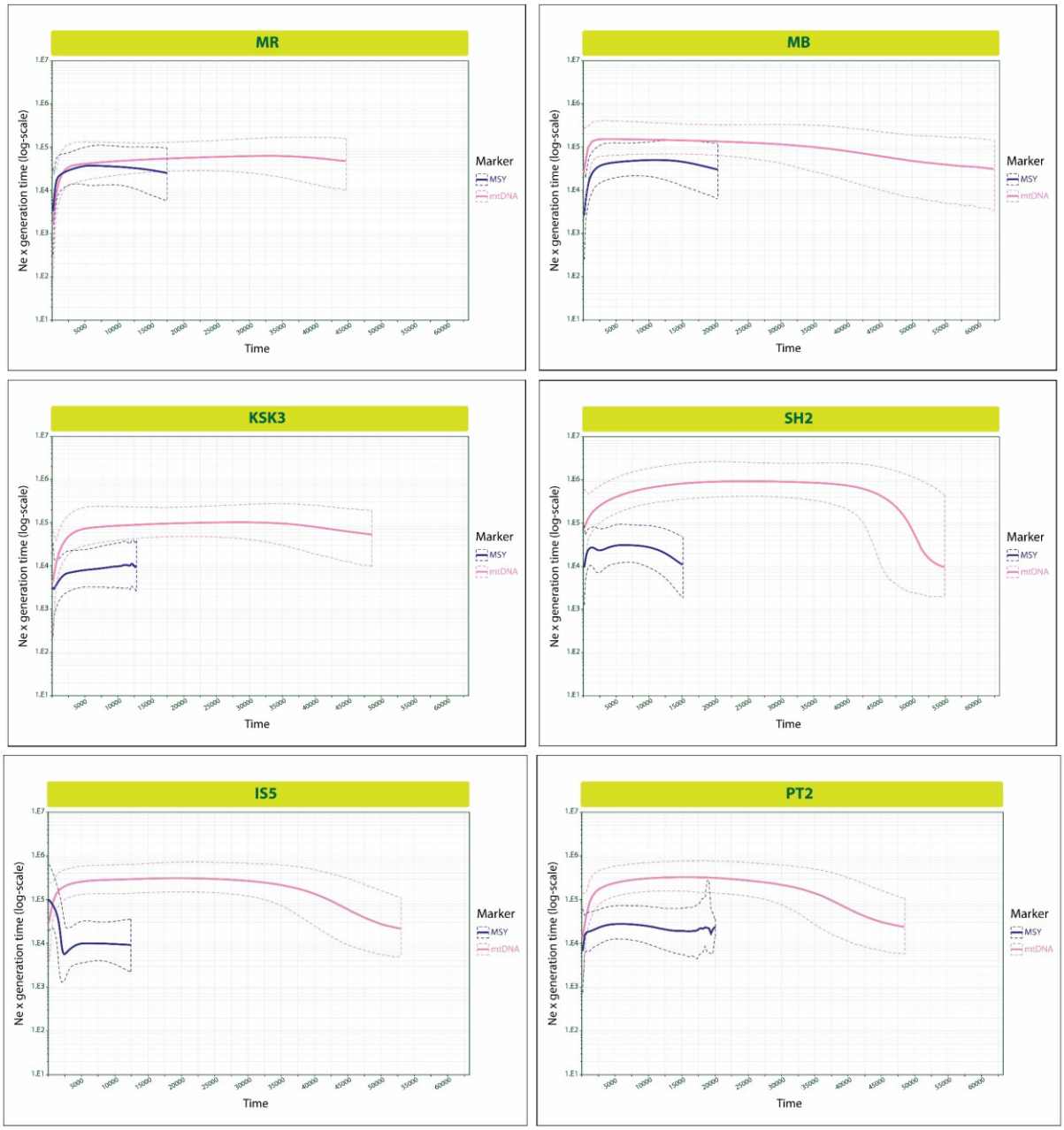

LS
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA


HM1
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA

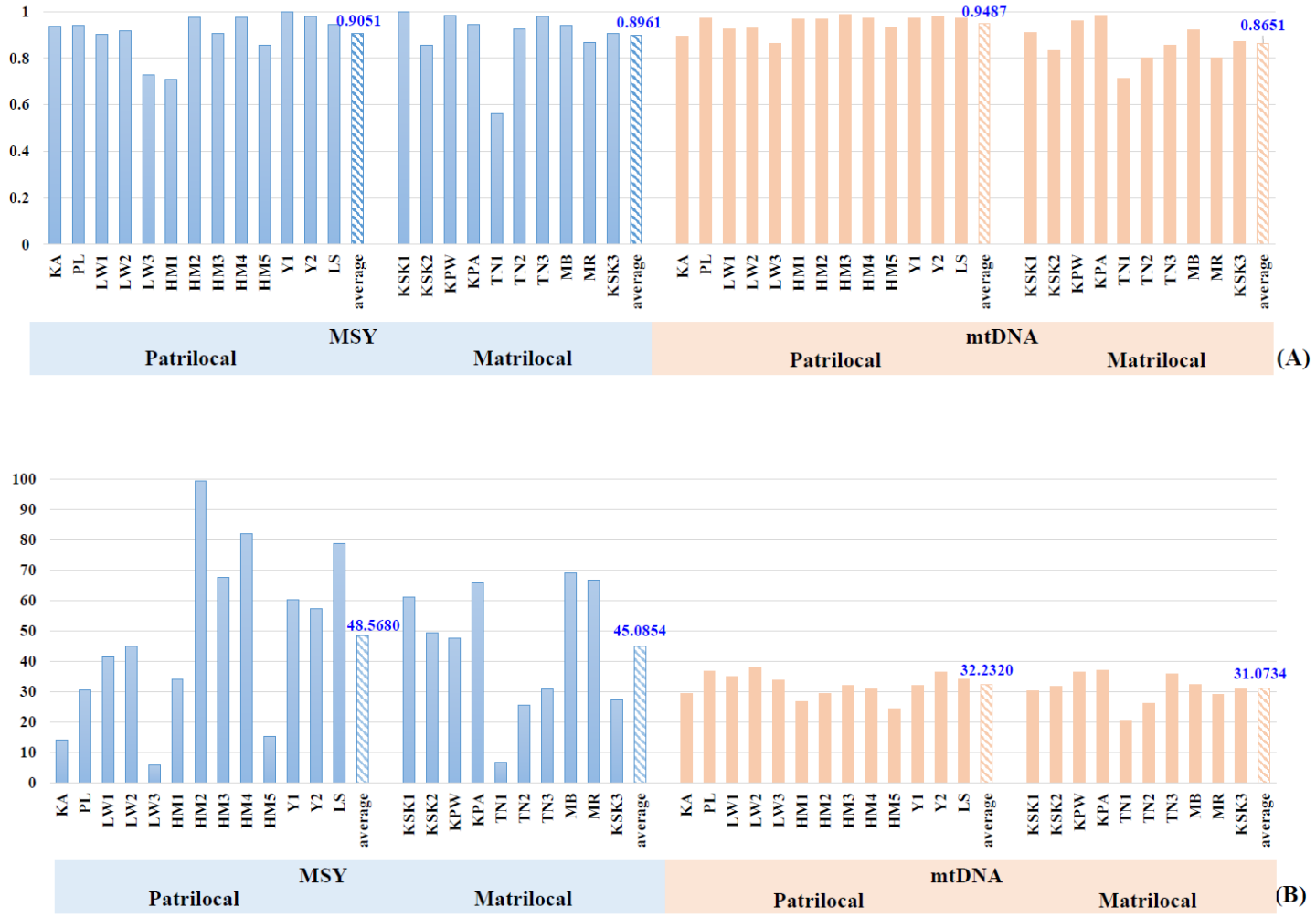
HM2
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA


HM3
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA

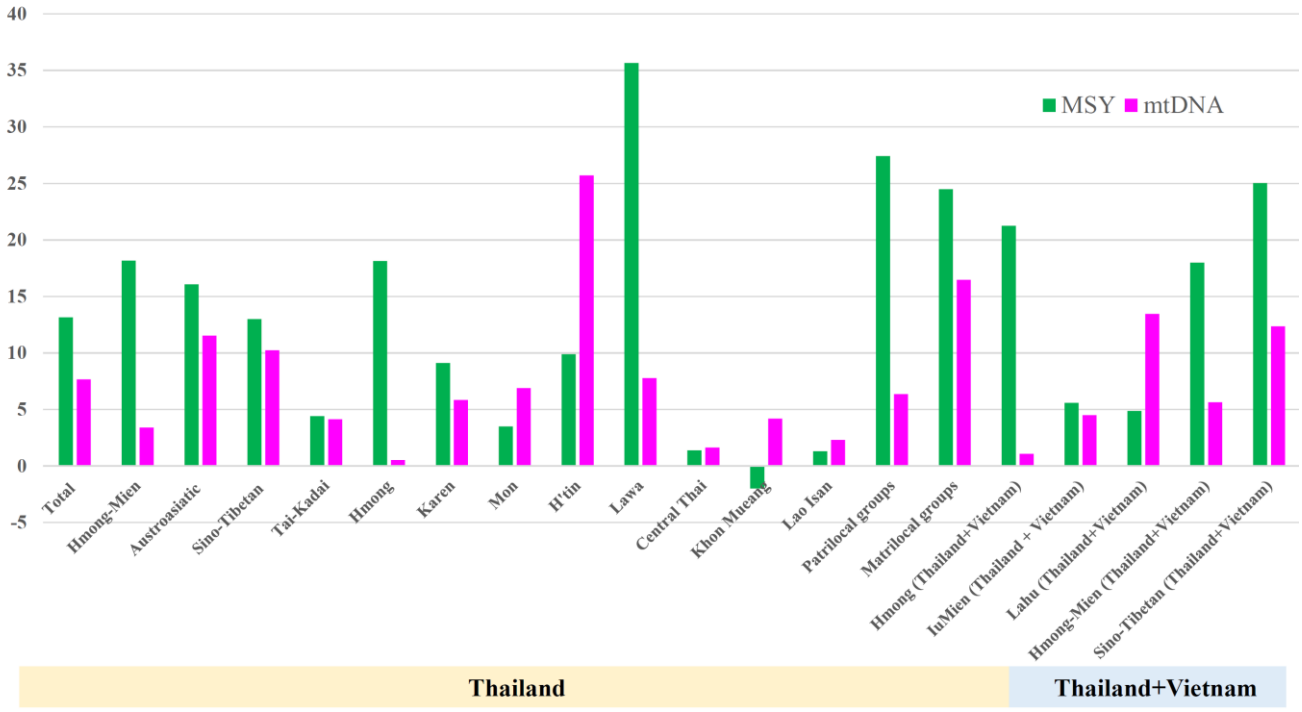

HM4
Ne x generation time (log-scale)
Time
Marker
MSY
mtDNA



Supplementary Fig. S8 The BSPs based on the MSY and mtDNA for 14 populations. Solid lines are the median estimated effective population size (y axis) through time from the present in years (x axis). The 95% highest posterior density limits are indicated by dotted lines.



Supplementary Fig. S9 Bar plots of (A) haplotype diversity and (B) mean number of pairwise differences of patrilocal (blue) and matrilocal (orange). Population abbreviations are in Table S1.



Supplementary Fig. S10. Genetic variation among populations within groups, defined by ethnicity, language and cultural practice.