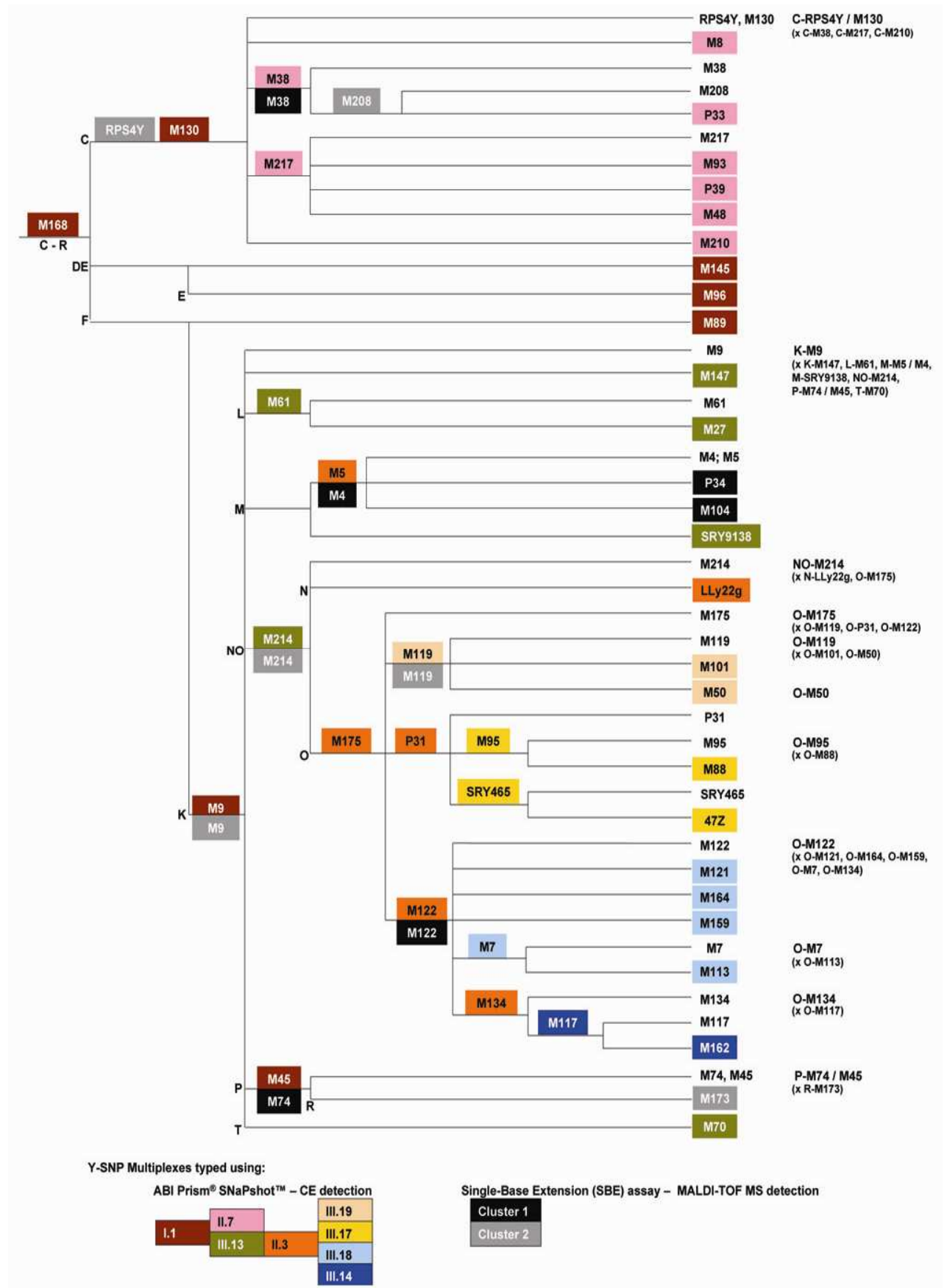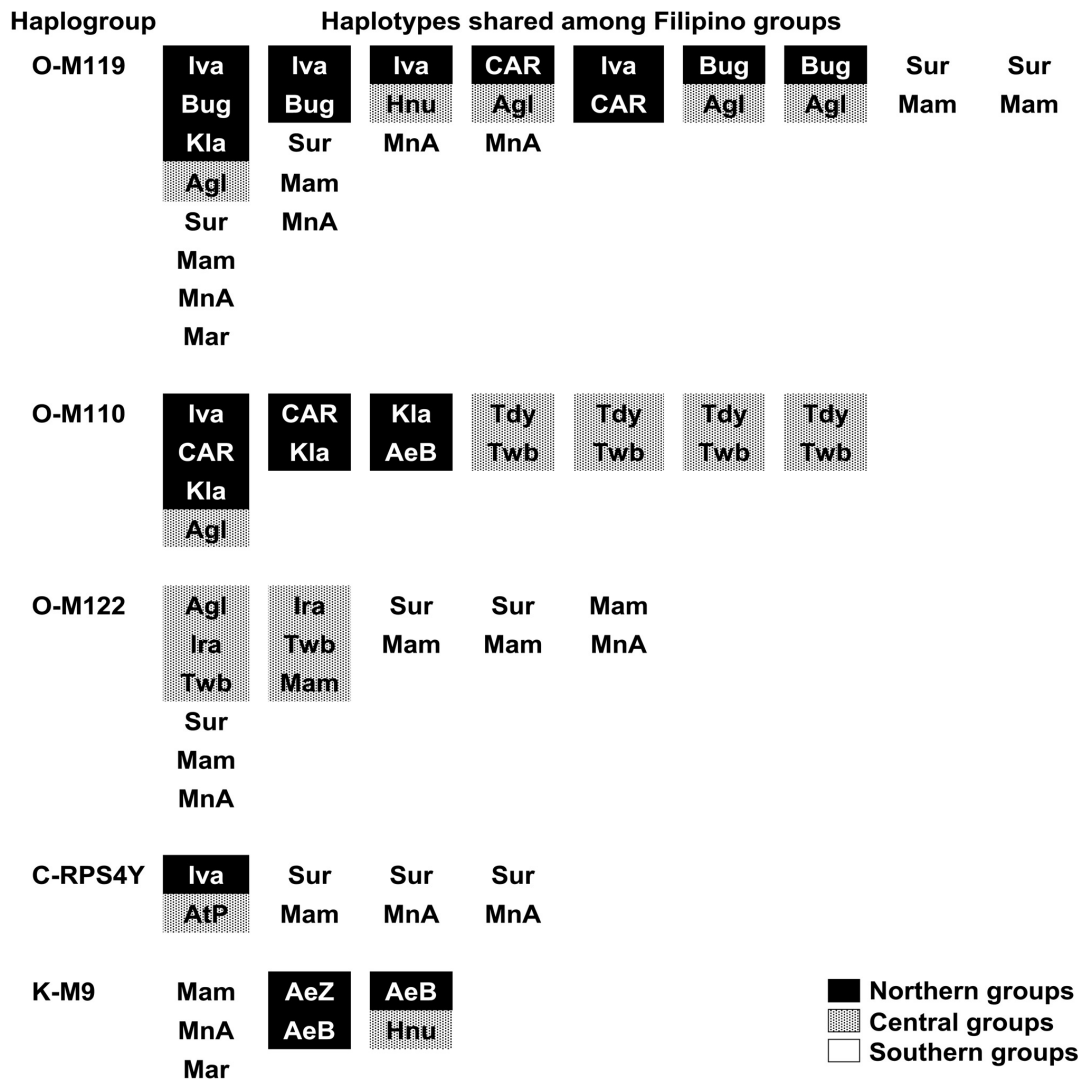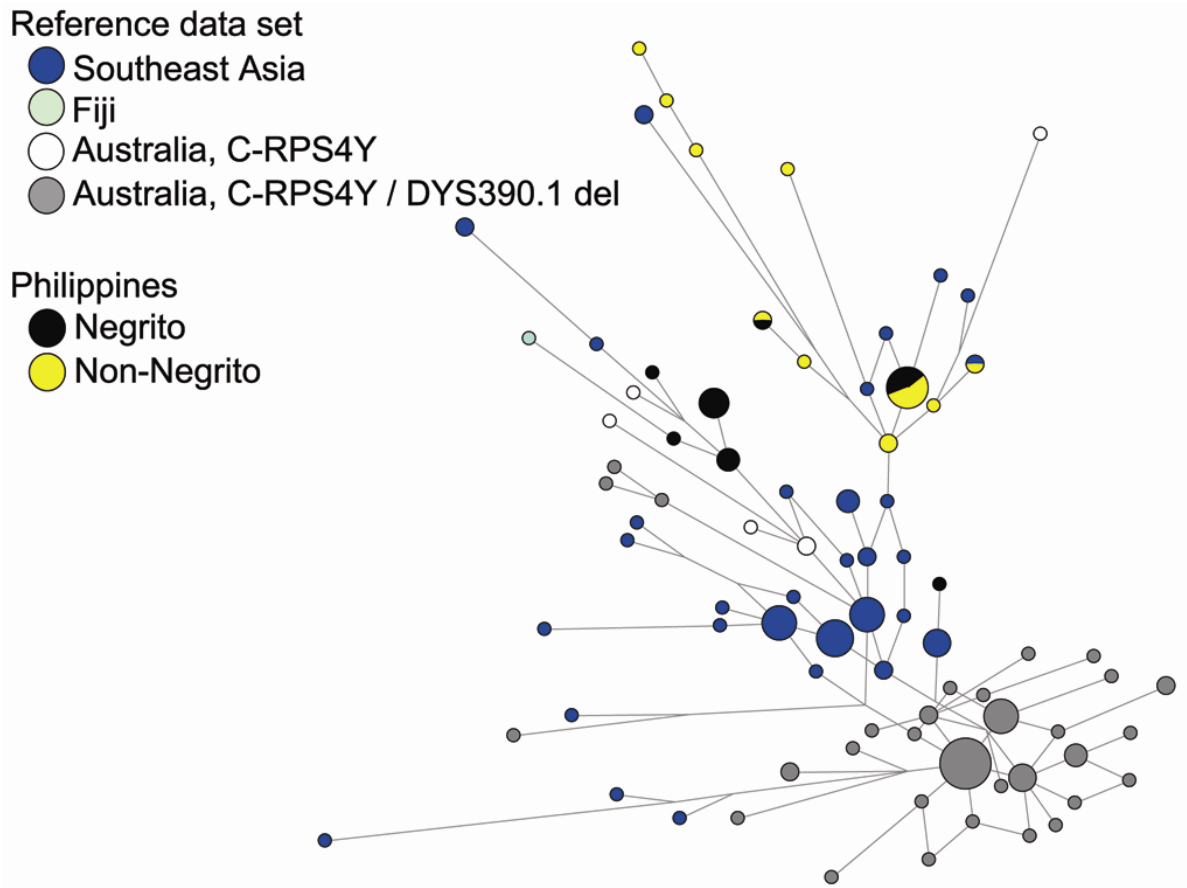# SUPPLEMENTARY FIGURES

Supplementary Figure 1. A schematic representation of the Y-SNP haplogroup tree. The tree shows the phylogenetic relationships of Y-SNPs used in this study. Y-SNPs represented on solid lines were genotyped in this study, while Y-SNPs represented on dashed lines were not typed but were included in the figure for reference purposes. Y-SNP haplogroup labels at particular tips of the tree indicate the Y-SNP haplogroups observed in the Filipino language group data set. Colors distinguish between the different Y-SNP multiplexes. Multiplexes I.1 to III.19 were adopted and modified from previous studies[1,2] and were used in an ABI Prism® SNaPshot™ (Applied Biosystems, Foster, CA, USA) assay. The Cluster 1 and Cluster 2 multiplexes were developed for a SBE assay with detection using MALDI-TOF MS.

Haplogroup   **Haplotypes shared among Filipino groups**

O-M119

Iva	Iva	Iva	CAR	Iva	Bug	Bug	Sur	Sur
Bug	Bug	Hnu	Agl	CAR	Agl	Agl	Mam	Mam
Kla	Sur	MnA	MnA					
Agl	Mam							
Sur	MnA							
Mam								
MnA								
Mar								

O-M110

Iva	CAR	Kla	Tdy	Tdy	Tdy	Tdy
CAR	Kla	AeB	Twb	Twb	Twb	Twb
Kla						
Agl						

O-M122

Agl	Ira	Sur	Sur	Mam
Ira	Twb	Mam	Mam	MnA
Twb	Mam			
Sur				
Mam				
MnA				

C-RPS4Y

Iva	Sur	Sur	Sur
AtP	Mam	MnA	MnA

K-M9

Mam	AeZ	AeB
MnA	AeB	Hnu
Mar		

■ Northern groups
▨ Central groups
□ Southern groups

Supplementary Figure 2. Sharing of Y-STR haplotypes (within Y-SNP haplogroups) among Filipino groups.

Each column refers to a specific haplotype shared by two or more Filipino groups. Codes for Filipino groups are the same as in Figure 1.

Supplemetary Figure 3. Network for Y-SNP haplogroup C-RPS4Y. This network contains all haplotypes shown for C-RPS4Y in Figure 6 including all DYS390.1 del / C-RPS4Y haplotypes from the reference data set.[3] Each network is based on seven haplogroup-associated Y-STR loci. Circles represent Y-STR haplotypes, with the area of the circle proportional to the frequency of the haplotype. Nodes without circles that connect branches are median vectors that represent inferred ancestral haplotypes. Branch lengths are proportional to the number of mutation steps.
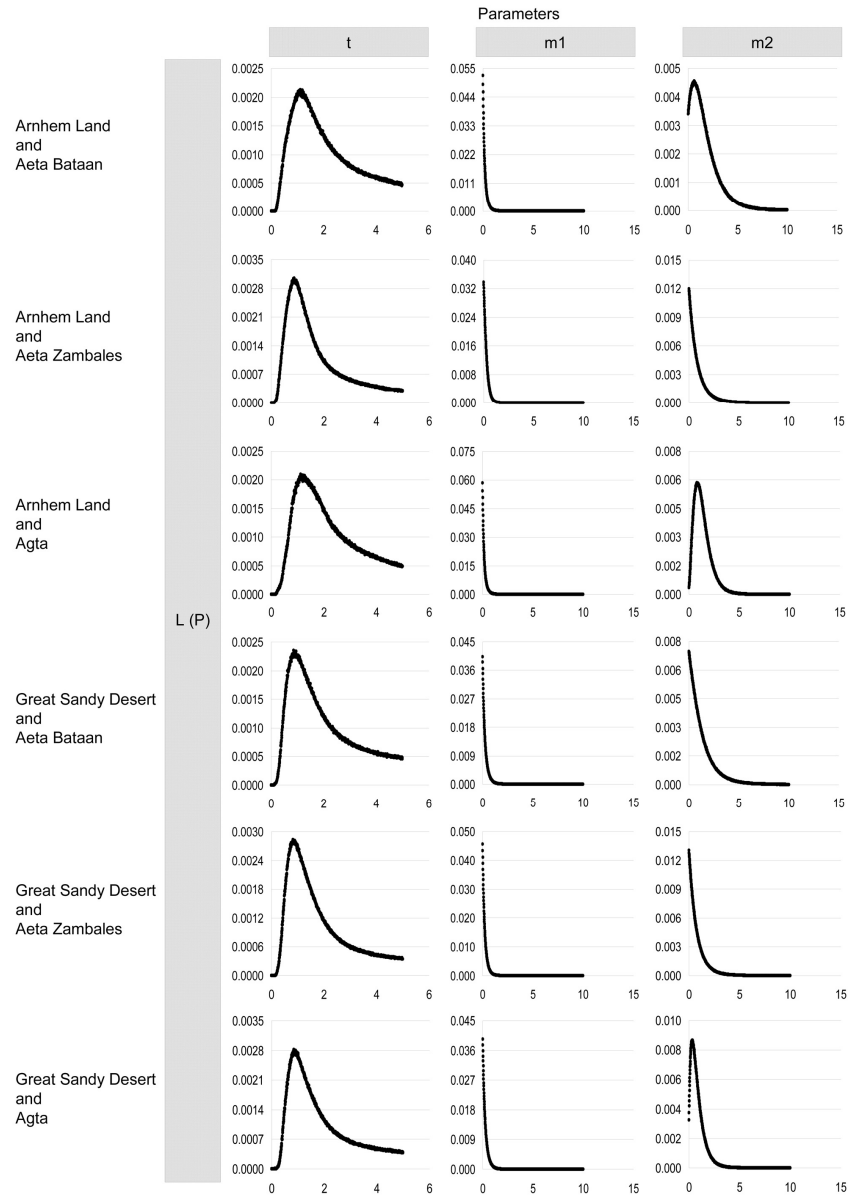
Supplementary Figure 4. Posterior distributions of parameter estimates of divergence times (t) and migration rates (m1 and m2). Parameter estimates are for Negrito groups and indigenous Australians with observed genetic associations, and were obtained for Y-STR haplotype data (7 Y-STRs) using the IM program.[4] The x-axis shows the parameter scales for t, m1 (migration from Negrito groups to Australian groups) and m2 (migration from Australian groups to Negrito groups), respectively; while the y-axis shows the log likelihood values. Scaled values (T, M1 and M2) for the peak (mode) of each distribution are shown in Table 4.

REFERENCES

1. Paracchini S, Arredi B, Chalk R, Tyler-Smith C: Hierarchical high-throughput SNP genotyping of the human Y-chromosome using MALDI-TOF mass spectrometry. Nucleic Acids Res 2002; 30: e27 21-26.

2. Hurles ME, Sykes BC, Jobling MA, Forster P: The dual origin of the Malagasy in island Southeast Asia and East Africa: Evidence from maternal and paternal lineages. Am J Hum Genet 2005; 76: 894-901.

3. Kayser M, Brauer S, Weiss G, Schiefenhövel W, Underhill PA, Stoneking M: Independent Histories of Human Y Chromosomes from Melanesia and Australia. Am J Hum Genet 2001; 68: 173-190.

4. Hey J, Nielsen R: Multilocus methods for estimating population sizes, migration rates and divergence time, with applications to the divergence of *Drosophila pseudoobscura* and *D. perimilis*. Genetics 2004; 167: 747-760.