Dissecting the genetic structure and admixture of four geographical Malay populations

Running title: **Genetic Diversity of Malay**

Keywords: Malay; Single nucleotide polymorphism; Population structure; Genetic admixture.

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Supplementary Information

Figure and Table Legends

Figure S1. Neighbor-joining tree of 27 populations.

YRI is the outgroup. The pair-wise population distance was measured by global F_{ST} with 1,000 bootstrapping repeats. Bootstrap values are noted on the branches. Population IDs are shown in Supplementary Table S4. Geographical groups are indicated with colors as shown in the legend. The four Malay populations are highlighted in bold font with red asterisks.

Figure S2. Principal component analysis.

(A) 2,546 individuals representing 81 populations from South Asia, Southeast Asia and East Asia. (B) 1,469 individuals representing 59 populations from Southeast Asia and East Asia, excluding South Asian and Southeast Asian aborigines (Malaysian Negrito and Senoi) from (A). (C) 1,451 individuals representing 58 populations from Southeast Asia and East Asia, excluding Thai Mlabri from (B). (D) 1,275 individuals representing 47 populations from Southeast Asia, excluding East Asian, Filipino Negritos, East Indonesian and Oceanian (Melanesian).

Figure S3. Correlation between geographical coordinates and population differentiation in the Malays.

(A) and (B) present the correlation between geographical coordinates and Malay differentiation with the vertical axis showing the value of PC1 for each individual in the Figures above, and the horizontal axis showing the populations IDs. PCA results in (A) shows 199 individuals representing 7 Malay populations, among which MY-KN and MY-MLY are combined as PMM from Kelantan, and SG-MAS and SG-MY are combined as SGM; (B) shows 156 individuals representing 5 Malay populations (excluding SLM and Minangkabau). The PC1 values are summarized in the box plot for each population. Latitudes and longitudes of the populations, as well as the Pearson’s correlation coefficient (PCC) and statistical significance (p-value) are summarized in the tables below. PMM^{K} and PMM^{M} denote Kelantan Malay and Minangkabau, respectively. Other population IDs are shown in Supplementary Table S4.

Figure S4. Cross-validation error and population clusters of ADMIXTURE analysis.

(A) The vertical axis represents the five-fold cross validation error of the ADMIXTURE analysis, from K = 2 to K = 12. The cross validation error is nearly stable after K > 6. In (B), each color represents an independent cluster. On all levels of K, the components of East Asian, South Asian and Southeast Asian consistently appear in the Malays. Compared to K < 9, Oceanian, Central Asian and Southeast Asian 2 decomposed from Southeast Asian 1 as the newly appeared components in K = 9, among which only Southeast Asian 2 has non-trivial contributions to the Malay populations. Southeast Asian 1 and Southeast Asian 2 are represented by aborigines from Taiwan and Malaysia, respectively, and better reflect the population genetic diversity in Southeast Asia than taking the various Southeast Asian components as a whole. On the other hand, at K > 9, the Negrito component and Southeast Asian 2 component were further decomposed, which did not provide additional insight to our understanding of the Malay populations. Therefore, we chose K = 9 as optimal for the interpretation of the admixture pattern in the Malays. Population IDs are shown in Supplementary Table S4.

Table S1. Dating the gene flow to the Malays.
Populations in the second column are gene flow donors, and those in the first row are gene flow receptors. The date (mean ± sd) is estimated for each donor-receptor pair and is measured by generations. NA: No available data.

Table S2. Correlation between ancestral components and PC1 in the Malays.
PCC (Pearson product-moment correlation coefficient) measures the correlation between the proportion of each ancestral component in the 5 Malay populations (SLM, Kelantan Malay, Minangkabau, SGM and IDM) and the values along PC1 in the PCA analysis (Supplementary Figure S2A).

Table S3. Sri Lankan ancestral contributions (%) to the Sri Lankan Malays.
Populations in the first column and the first row are ancestral populations, which are combined into different pairs of ancestries of the Sri Lankan Malays. In each population, we randomly sampled 10 individuals to minimize the bias caused by the inconsistent sample size.

Table S4. Details of the populations included in the present study
Individual QC (quality control) was conducted for each population independently. Samples with missing rate of >5% were excluded from subsequent analyses. The sample size of each population before and after QC are summarized in the third and forth columns. More detailed data information can be found in the references indicated in the fifth column.

Table S5. Summary of datasets used in various analyses.
[1] Population with sample size of <10 were excluded from the analysis.
[2] SNPs shared within each donor-acceptor pair were used.
[3] Ten samples were randomly selected from each population.
[4] SNPs shared within each ancestry pair were used.

Figure S1. Neighbor-joining tree of 27 populations.

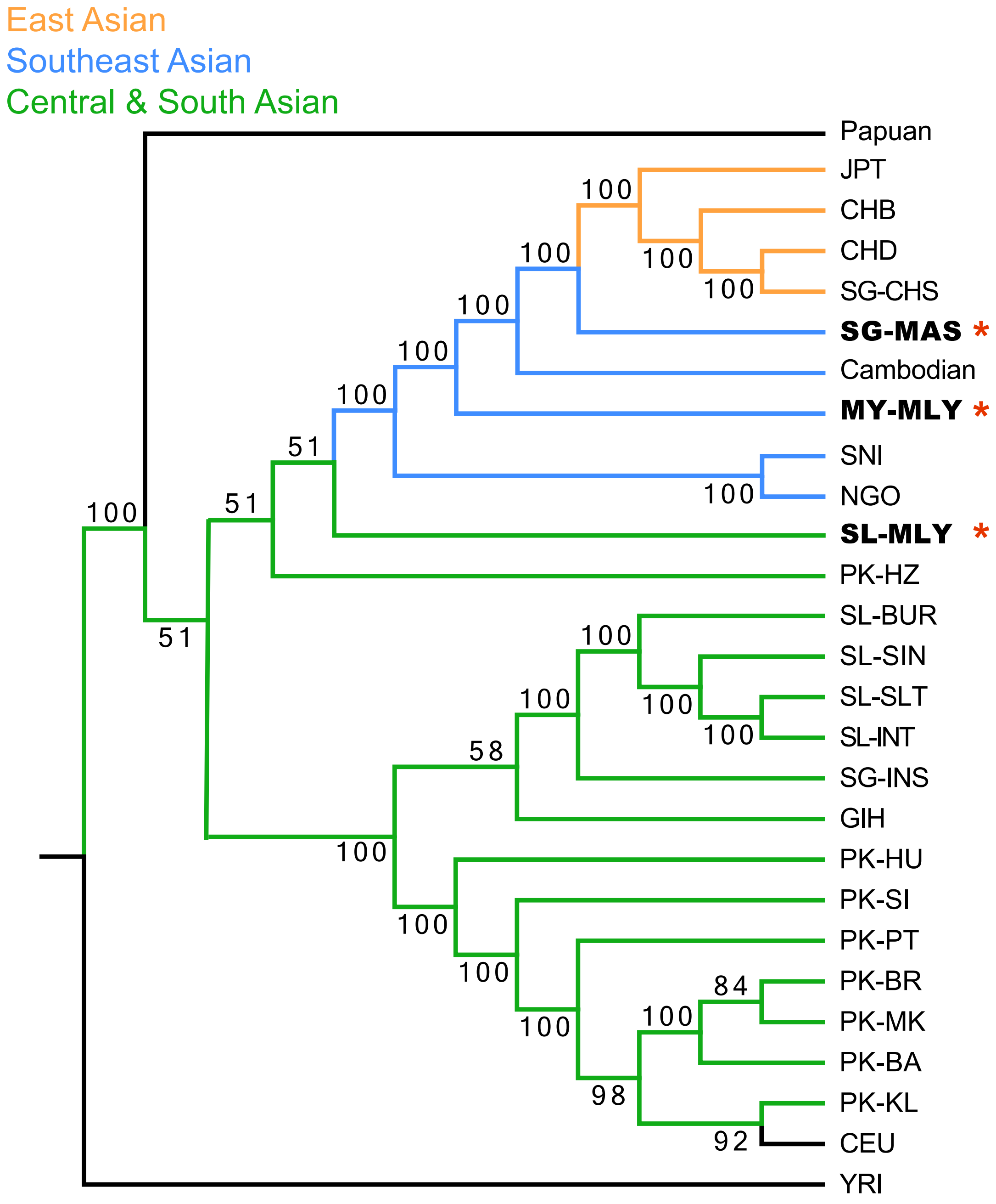


Figure S2. Principal component analysis.

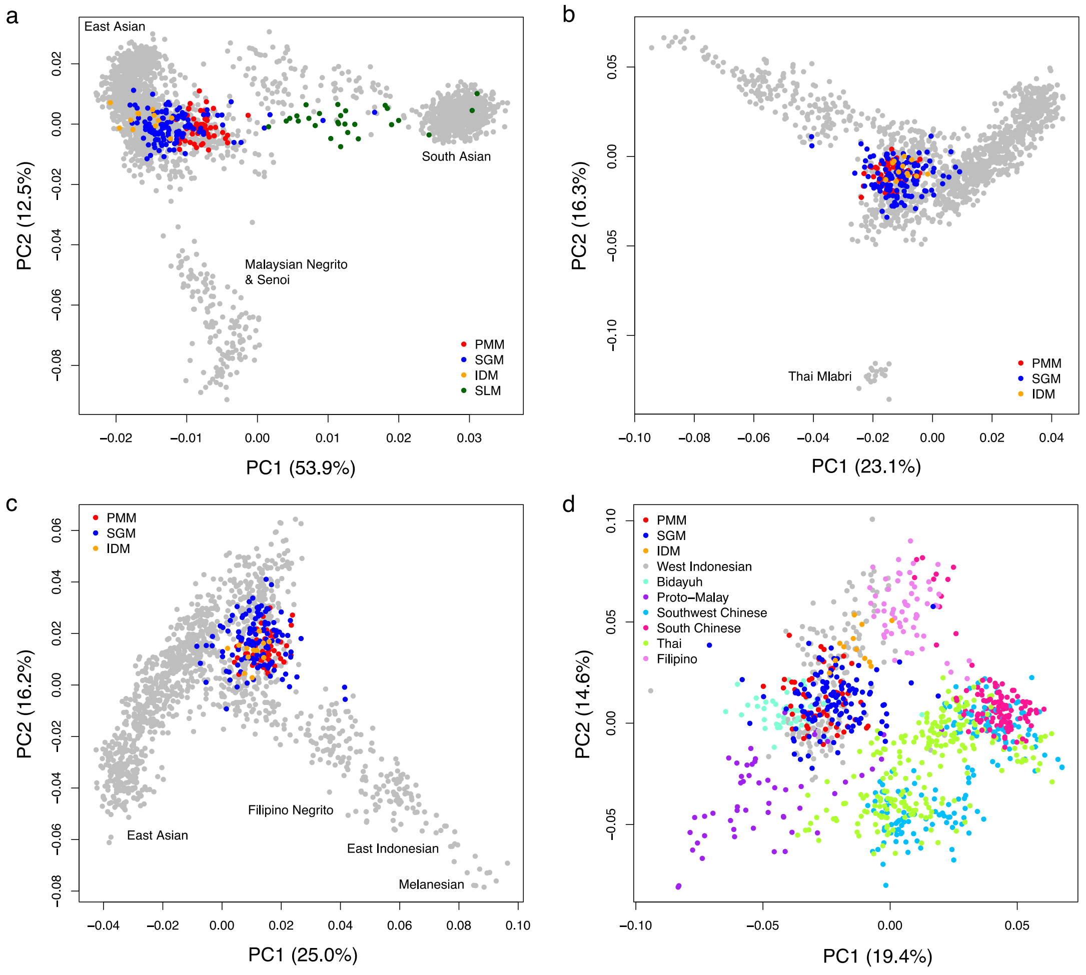
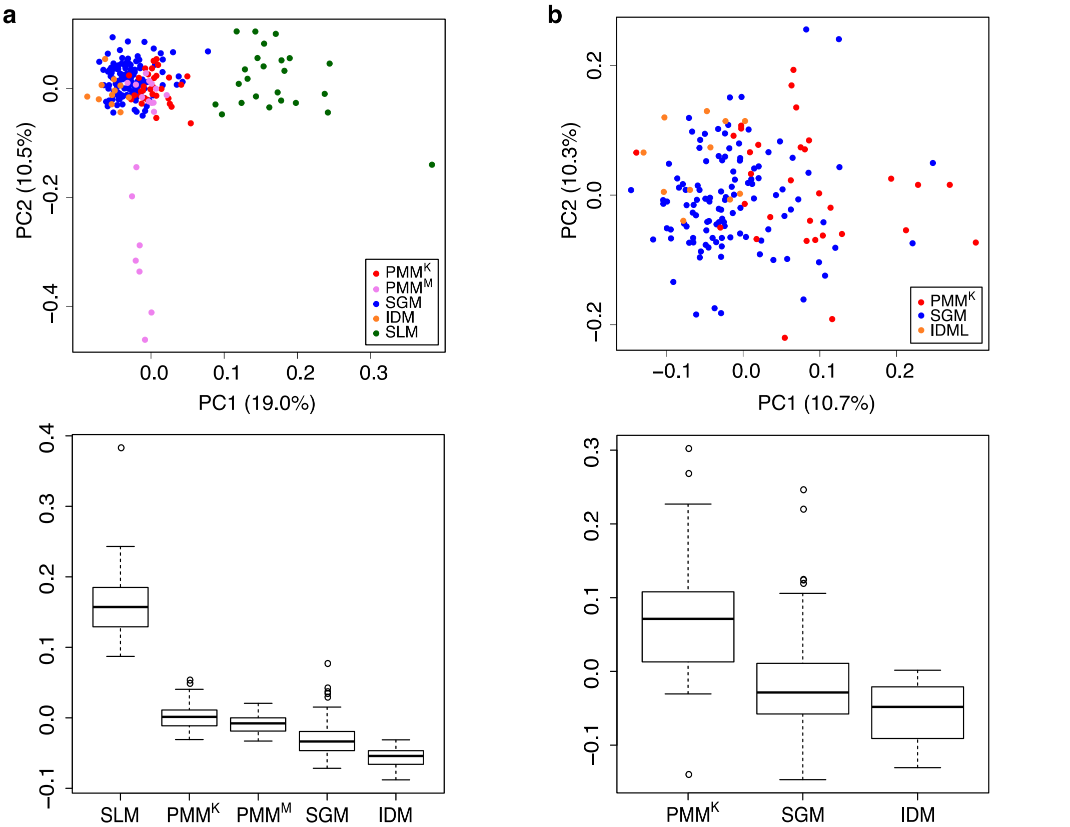


Figure S3. Correlation between geographical location and population differentiation in the Malays.



Latitude	8	5.3	2.8	1.4	-3	PCC = 0.9 p < 2.2e-16
Longitude	80	102	102.2	103.8	104.7	PCC = -0.781 p < 2.2e-16

Latitude	5.3	1.4	-3	PCC = 0.5
				p = 1.819e-11

Longitude	102	103.8	104.7	PCC = -0.475
				p = 2.262e-10

Figure S4. Cross-validation error and population clusters of ADMIXTURE analysis.

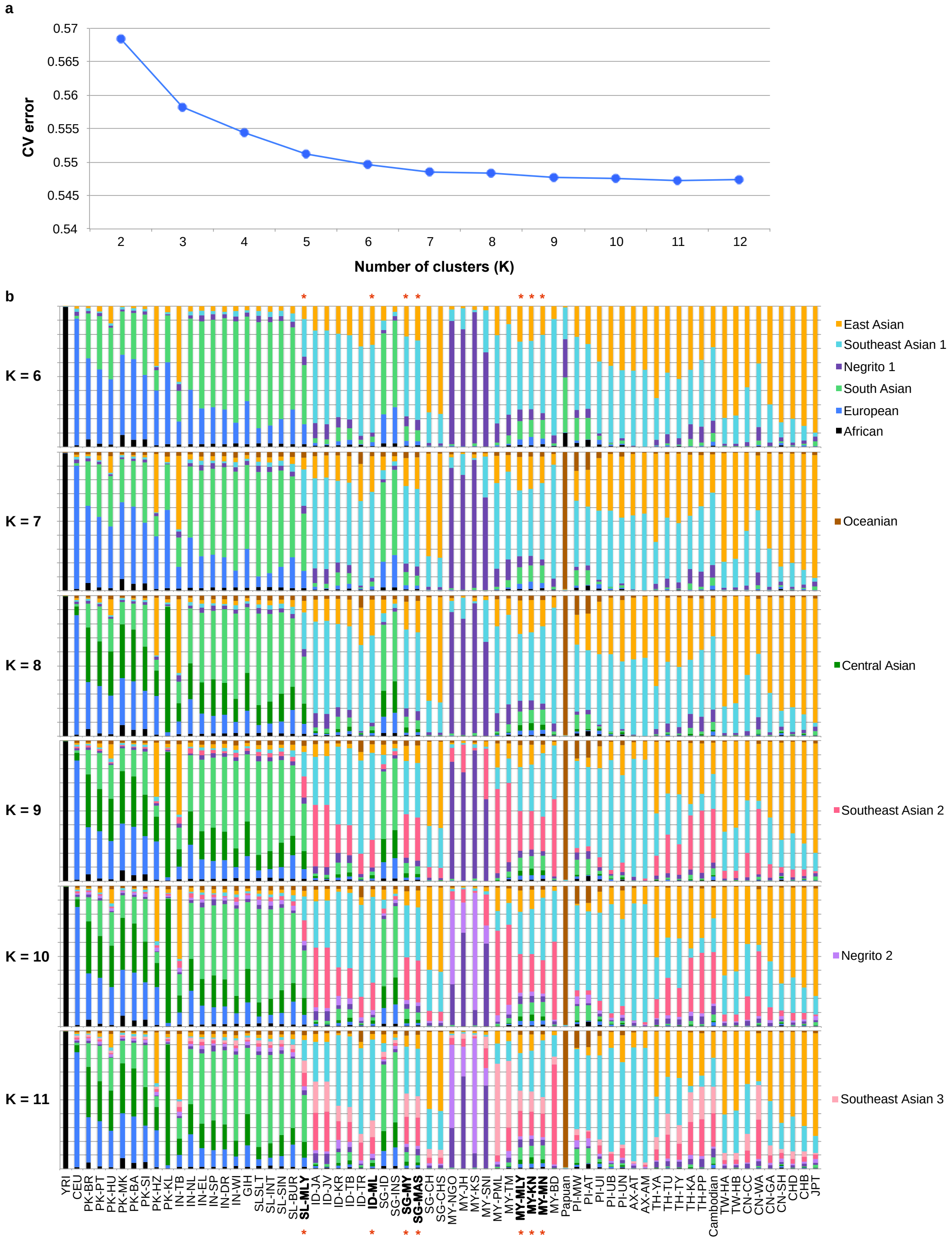


Table S1. Dating the gene flow to the Malays.

Group	Pop	PMM			SGM		IDM	SLM
		MY-MLY	MY-KN	MY-MN	SG-MAS	SG-MY		
European	CEU	35.93 ± 5.79	30.88 ± 6.34	31.21 ± 7.38	9.12 ± 0.68	17.96 ± 4.24	NA	7.92 ± 0.82
Southeast Asian 1	AX-AM	NA	261.46 ± 113.84	NA	30.30 ± 11.55	NA	NA	6.91 ± 1.14
	AX-AT	NA	NA	NA	28.75 ± 4.52	NA	NA	7.75 ± 0.90
Southeast Asian2	MY-TM	NA	NA	NA	NA	NA	NA	6.41 ± 1.04
South Asian	GIH	28.19 ± 6.23	35.77 ± 10.70	29.94 ± 5.01	8.41 ± 0.74	18.94 ± 3.87	NA	6.84 ± 0.52
	IN-DR	37.24 ± 9.61	30.85 ± 6.43	36.38 ± 7.14	8.73 ± 1.36	16.49 ± 3.18	62.30 ± 23.13	6.62 ± 1.66
	IN-EL	36.33 ± 15.52	34.83 ± 8.78	34.96 ± 6.60	9.60 ± 1.80	16.74 ± 6.13	71.15 ± 33.25	10.25 ± 2.70
	IN-IL	39.81 ± 13.16	33.95 ± 5.46	35.21 ± 9.77	10.16 ± 2.05	20.50 ± 4.87	103.33 ± 21.71	7.82 ± 1.40
	IN-NI	88.43 ± 37.57	NA	54.88 ± 13.18	8.99 ± 4.08	27.88 ± 8.53	NA	NA
	IN-NL	37.23 ± 12.84	34.97 ± 5.25	34.44 ± 8.96	9.38 ± 1.87	20.81 ± 6.18	NA	6.95 ± 0.84
	IN-SP	36.26 ± 9.86	37.54 ± 5.18	36.60 ± 8.25	10.57 ± 1.62	14.75 ± 4.36	NA	9.32 ± 2.03
	IN-WI	41.76 ± 14.73	42.08 ± 6.99	32.50 ± 7.47	10.11 ± 2.19	17.98 ± 4.79	67.22 ± 24.71	8.83 ± 1.58
	IN-WL	51.66 ± 12.12	31.04 ± 6.98	33.83 ± 6.57	9.45 ± 1.93	14.48 ± 3.09	NA	10.79 ± 1.65
	SL-BUR	32.16 ± 4.93	27.06 ± 9.61	32.89 ± 5.43	7.81 ± 0.68	12.07 ± 4.79	57.93 ± 14.32	NA
	SL-SIN	31.44 ± 5.05	33.63 ± 10.34	33.22 ± 6.84	10.75 ± 1.19	15.36 ± 3.95	NA	NA
	SL-INT	30.99 ± 4.61	33.94 ± 10.03	33.37 ± 5.46	10.02 ± 0.84	15.76 ± 5.32	NA	6.89 ± 0.61
	SL-SLT	31.17 ± 4.65	32.97 ± 9.51	33.03 ± 6.10	10.43 ± 0.94	15.42 ± 5.16	NA	NA
East Asian	CHB	6.83 ± 2.55	NA	NA	4.28 ± 0.65	NA	NA	6.94 ± 0.37
	JPT	NA	NA	NA	5.94 ± 1.78	NA	NA	7.03 ± 0.83
	JP-ML	NA	NA	NA	NA	NA	NA	7.34 ± 0.91
	KR-KR	NA	NA	NA	4.59 ± 1.50	NA	NA	7.83 ± 0.84
	CN-SH	NA	NA	NA	NA	NA	NA	8.03 ± 0.86
	SG-CH	NA	NA	NA	NA	NA	NA	7.63 ± 0.90

Table S2. Correlation between ancestral components and PC1 in the Malays.

Ancestral Population	South Asian	Central Asian	Southeast Asian 1	European	Southeast Asian 2	East Asian	African	Oceanian	Negrito
PCC	0.927	0.807	0.697	0.579	0.517	0.268	0.152	0	0
p-value	<2.2E-16	<2.2E-16	<2.2E-16	<2.2E-16	1.09E-14	1.03E-4	0.020	0.769	0.803

Table S3. Sri Lankan ancestral contributions (%) to the Sri Lankan Malays.

Ancestral Population	PMM			SGM		IDM
	MY-MLY	MY-KN	MY-MN	SG-MAS	SG-MY	
SL-BUR	60.6	56.9	58.5	57.7	57.9	60.9
SL-SIN	58.1	55.7	57.6	56.9	55.1	59.7
SL-SLT	57.6	55.4	57.2	55.4	55.7	59.3
SL-INT	57.9	55.5	57.4	54.9	55.9	60.3

Table S4. Details of the populations included in the present study.

Population ID	Details	No. Samples before QC	No. Samples after QC	Reference
YRI	Yoruba in Ibadan, Nigeria	116	116	[11]
CEU	Utah residents with Northern and Western European ancestry from the CEPH collection	112	112	[11]
GIH	Gujarati Indians in Houston, Texas	88	88	[11]
CHD	Chinese in Metropolitan Denver, Colorado	85	85	[11]
CHB	Han Chinese in Beijing, China	84	84	[11]
JPT	Japanese in Tokyo, Japan	86	86	[11]
PK-HZ	Hazara in Pakistan	22	22	[12]
PK-BR	Brahui in Pakistan	25	25	[12]
PK-BA	Balochi in Pakistan	24	24	[12]
PK-SI	Sindhi in Pakistan	24	24	[12]
PK-HU	Hunza Burusho in Pakistan	25	25	[12]
PK-KL	Kalash in Pakistan	23	23	[12]
PK-MK	Makrani in Pakistan	25	25	[12]
PK-PT	Pathan in Pakistan	22	22	[12]
Cambodian	Cambodian in Cambodia	10	10	[12]
Papuan	Papuan in New Guinea	17	17	[12]
SG-CHS	Chinese in Singapore	96	96	[14]
SG-MAS	Malay in Singapore	89	89	[14]
SG-INS	Indian in Singapore	83	83	[14]
MY-MLY	Malay in Kelantan, Malaysia	17	17	[5]
MY-PML	Proto-Malay in Malaysia	4	4	[5]
MY-SNI	Senoi in Malaysia	17	17	[5]
MY-NGO	Negrito in Malaysia	46	22	[5]
SL-MLY	Malay in Sri Lanka	27	27	-
SL-BUR	Burger in Sri Lanka	35	35	-
SL-SIN	Sinhalese in Sri Lanka	200	200	-
SL-INT	Tamil in Sri Lanka with Indian ancestry	200	200	-
SL-SLT	Tamil in Sri Lanka	103	103	-
AX-AM	Ami in Taiwan, China	10	10	[8]
AX-AT	Atayal in Taiwan, China	10	10	[8]
AX-ME	Melanesian in Pacific	5	5	[8]
CN-CC	Zhuang in China	26	26	[8]
CN-GA	Han Chinese in Guangdong, China	30	30	[8]
CN-HM	Hmong in China	26	26	[8]

(Continued)

Population ID	Details	No. Samples before QC	No. Samples after QC	Reference
CN-JN	Jinuo in China	29	29	[8]
CN-SH	Han Chinese in Shanghai, China	21	19	[8]
CN-UG	Uyghur in China	26	26	[8]
CN-WA	Wa in China	55	55	[8]
ID-AL	Alorese in Indonesia	19	19	[8]
ID-DY	Dayak in Indinesia	12	12	[8]
ID-JA	Javanese in Indonesia	34	34	[8]
ID-JV	Javanese in Indonesia	18	18	[8]
ID-KR	Batak Karo in Indonesia	17	17	[8]
ID-LA	Lamaholot in Indonesia	20	20	[8]
ID-LE	Lembata in Indonesia	19	19	[8]
ID-ML	Malay in Indonesia	12	11	[8]
ID-MT	Mentawai in Indonesia	15	15	[8]
ID-RA	Manggarai in Indonesia	17	17	[8]
ID-SB	Kambera in Indonesia	20	20	[8]
ID-SO	Manggarai in Indonesia	19	19	[8]
ID-SU	Sundanese in Indonesia	25	25	[8]
ID-TB	Batak in Indonesia	20	20	[8]
ID-TR	Toraja in Indonesia	19	19	[8]
IN-DR	Upper-caste in India	24	24	[8]
IN-EL	Upper-caste in India	16	15	[8]
IN-IL	Upper-caste in India	15	14	[8]
IN-NI	Tharu in India	20	20	[8]
IN-NL	Upper-caste in India	15	11	[8]
IN-SP	Upper-caste in India	22	22	[8]
IN-TB	Ladakhi in India	23	23	[8]
IN-WI	Bhil in India	24	24	[8]
IN-WL	Upper-caste in India	14	14	[8]
JP-ML	Japanese in Japan	71	71	[8]
JP-RK	Ryukyuan in Japan	49	49	[8]
KR-KR	Korean in Korea	90	83	[8]
MY-BD	Bidayuh in Malaysia	49	47	[8]
MY-JH	Negrito (Jehai) in Malaysia	50	50	[8]
MY-KN	Malay in Kelantan, Malaysia	18	13	[8]
MY-KS	Negrito (Kensiu) in Malaysia	30	30	[8]
MY-MN	Malay (Minangkabau) in Malaysia	20	19	[8]
MY-TM	Proto-Malay (Temuan) in Malaysia	49	44	[8]

(Continued)

Population ID	Details	No. Samples before QC	No. Samples after QC	Reference
PI-AE	Negrito in the Philippines	8	2	[8]
PI-AG	Negrito in the Philippines	8	3	[8]
PI-AT	Negrito in the Philippines	23	9	[8]
PI-IR	Negrito in the Philippines	9	2	[8]
PI-MA	Manobo in the Philippines	18	11	[8]
PI-MW	Negrito in the Philippines	19	3	[8]
PI-UB	Urban in the Philippines	20	20	[8]
PI-UI	Urban in the Philippines	20	20	[8]
PI-UN	Urban in the Philippines	18	18	[8]
SG-CH	Han Chinese in Singapore	29	29	[8]
SG-ID	Tamil in Singapore with Indian ancestry	30	30	[8]
SG-MY	Malay in Singapore	30	30	[8]
TH-HM	Hmong in Thailand	19	19	[8]
TH-KA	Karen in Thailand	20	19	[8]
TH-LW	Lawa in Thailand	19	19	[8]
TH-MA	Mlabri in Thailand	18	18	[8]
TH-MO	Mon in Thailand	19	18	[8]
TH-PL	Palong in Thailand	18	18	[8]
TH-PP	Plang in Thailand	18	18	[8]
TH-TK	Tai Kern in Thailand	18	18	[8]
TH-TL	Tai Lue in Thailand	20	19	[8]
TH-TN	H'Tin in Thailand	17	16	[8]
TH-TU	Tai Yuan in Tailand	20	20	[8]
TH-TY	Tai Yong in Tailand	18	18	[8]
TH-YA	Yao in Thailand	19	18	[8]
TW-HA	Han Chinese in Taiwan, China	48	48	[8]
TW-HB	Han Chinese in Taiwan, China	32	32	[8]

Table S5. Summary of datasets used in various analyses.

Dataset	No. Samples	No. SNPs	Analysis
HapMap + SGVP + PASNP + Sri Lankan dataset + Malaysian ethnicities dataset	3025[1]	7012	Population phylogeny (Figure 1)
HapMap + SGVP + HGDP + Sri Lankan dataset + Malaysian ethnicities dataset	1677[1]	90634	Population phylogeny (Supplementary Figure S1)
HapMap + SGVP + PASNP + Sri Lankan dataset + Malaysian ethnicities dataset	3053	3240	PCA (Figure 2, Supplementary Figure S2, Supplementary Figure S3)
HapMap + SGVP + HGDP + PASNP + Sri Lankan dataset + Malaysian ethnicities dataset	2604	4894	ADMIXTURE clustering analysis (Figure 3, Supplementary Figure S4)
HapMap + SGVP + PASNP + Sri Lankan dataset + Malaysian ethnicities dataset	1414	14720-1159620[2]	Gene flow estimation (Table 1, Supplementary Table S1)
SGVP + PASNP + Sri Lankan dataset + Malaysian ethnicities dataset	100[3]	5209-8299[4]	Supervised STRUCTURE analysis (Supplementary Table S3)