

SUPPLEMENTARY MATERIALS

Malagasy genetic ancestry comes from an historical Malay trading post in Southeast Borneo.

Nicolas Brucato^{1,*}, Pradiptajati Kusuma^{1,2,*}, Murray P. Cox³, Denis Pierron¹, Gludhug A. Purnomo², Alexander Adelaar⁴, Toomas Kivisild^{6,7}, Thierry Letellier¹, Herawati Sudoyo^{2,5} and François-Xavier Ricaut^{1,†}.

¹ Evolutionary Medicine Group, Laboratoire d'Anthropologie Moléculaire et Imagerie de Synthèse UMR 5288 CNRS, Université Toulouse III, Université de Toulouse. France.

² Genome Diversity and Diseases Laboratory, Eijkman Institute for Molecular Biology, Jakarta, Indonesia

³ Statistics and Bioinformatics Group, Institute of Fundamental Sciences, Massey University, Palmerston North, New Zealand

⁴ Asia Institute, University of Melbourne, Melbourne, Australia

⁵ Department of Medical Biology, Faculty of Medicine, University of Indonesia, Jakarta, Indonesia

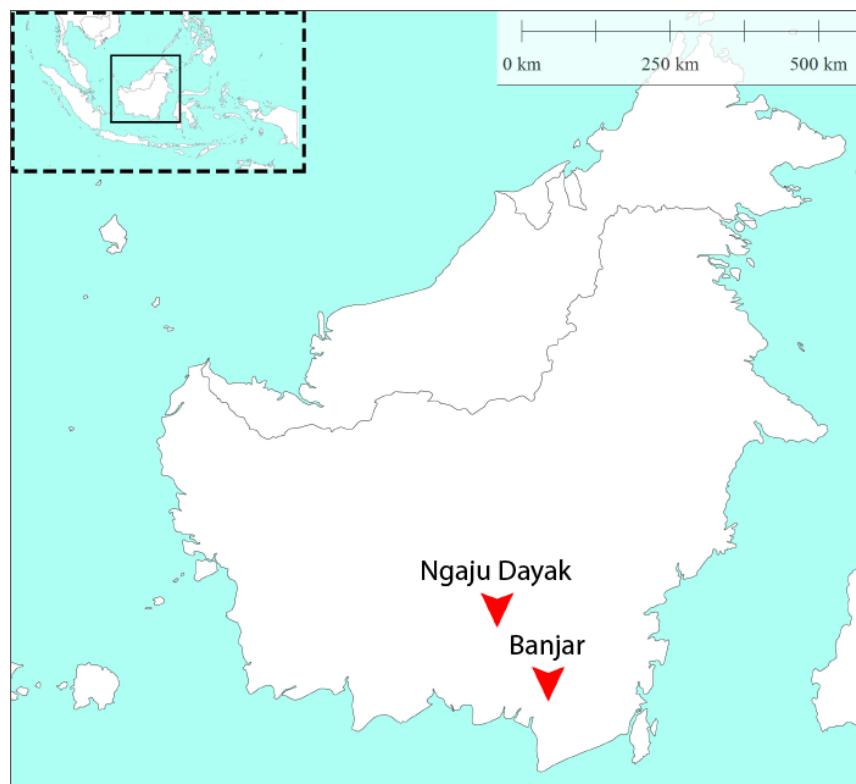
⁶ Department of Biological Anthropology, University of Cambridge, Cambridge, United Kingdom

⁷ Estonian Biocentre, Tartu, Estonia

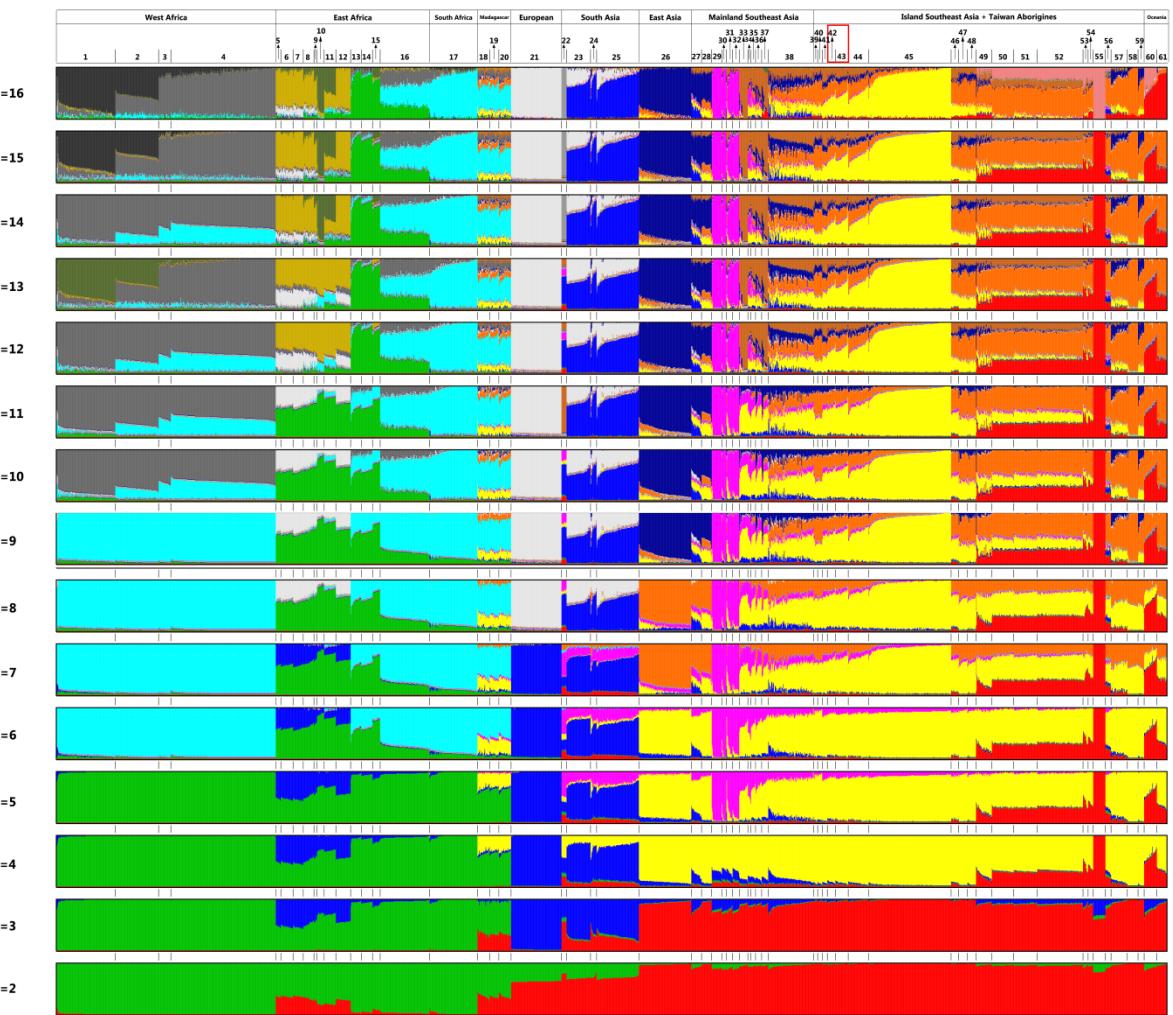
**These authors contributed equally to this work.*

†Corresponding author: F-X.R (francois-xavier.ricaut@univ-tlse3.fr)

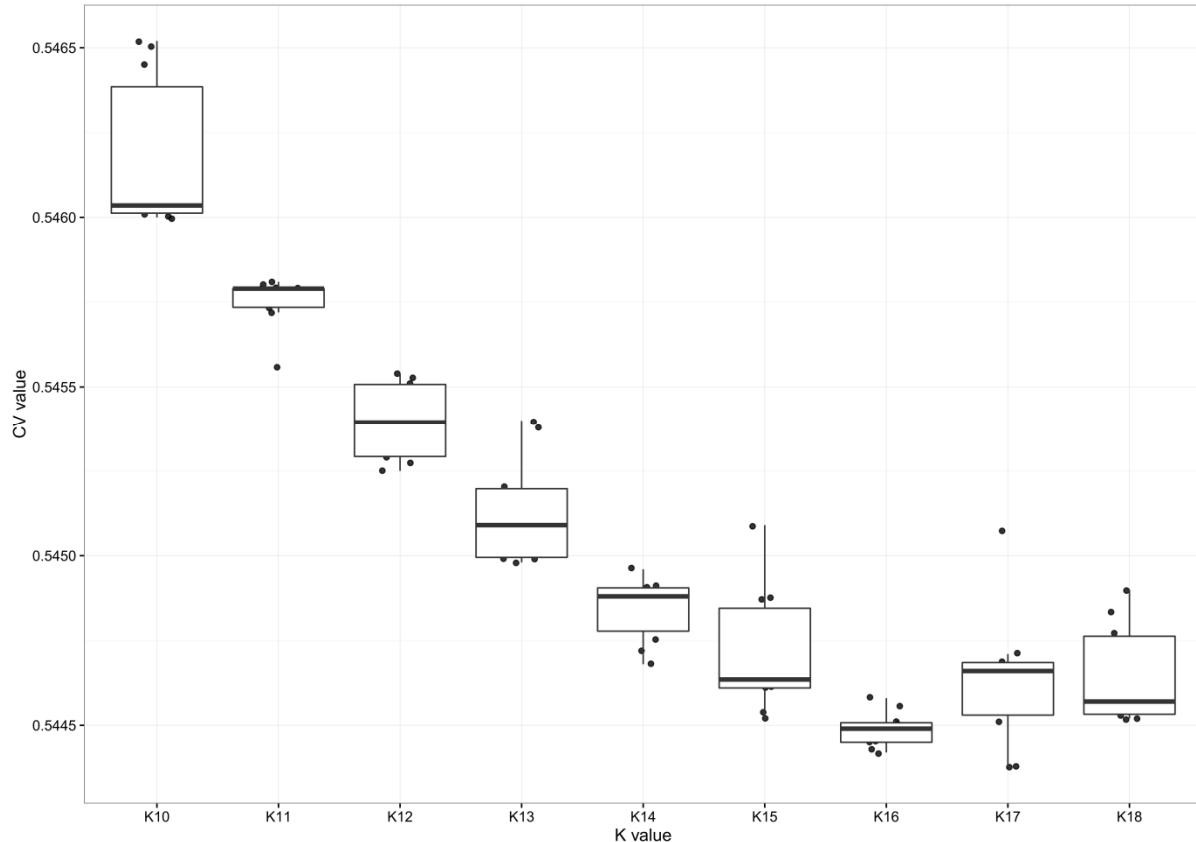
Supplementary Figure S1 - Locations of the sampled groups in Borneo island in Indonesia. The map was generated using Global Mapper v.15 software. (<http://www.bluemarblegeo.com/products/global-mapper.php>)



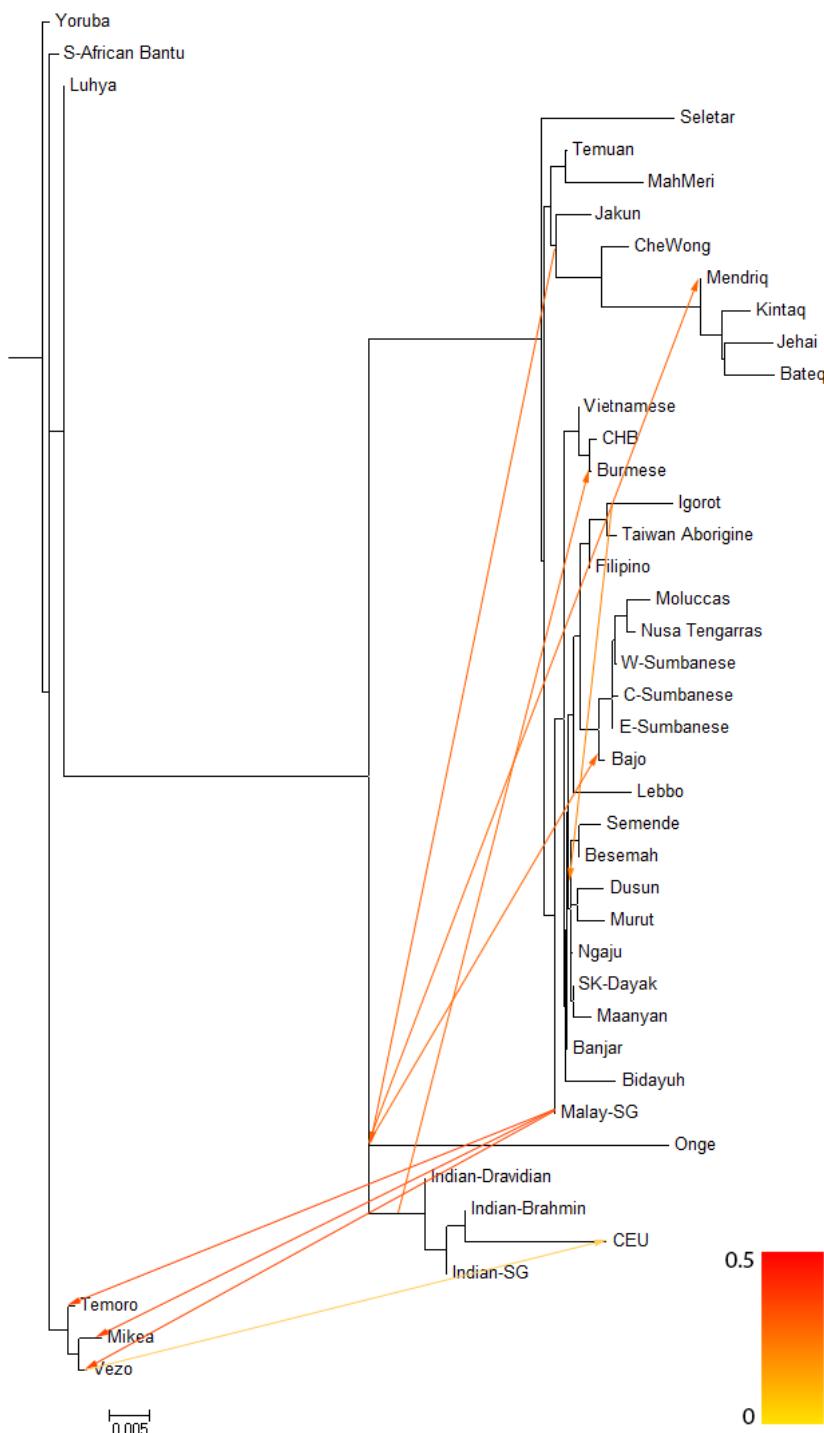
Supplementary Figure S2 - ADMIXTURE plot from K=2 to K=16 of the low SNP density dataset using ADMIXTURE software (Alexander, et al. 2009). The Banjar and Ngaju populations are identified by the red rectangle, respectively labelled 41 and 42. The studied populations are numerically labelled as follows: 1: Gambian; 2: Mende; 3: Beninese; 4: Yoruba; 5: Afar; 6: Amhara; 7: Tygray; 8: Oromo; 9: Wolayta; 10: Ari-Blacksmith; 11: Ari-Cultivator; 12: Somalian; 13: Sudanese; 14: Anuak; 15: Gumuz; 16: Luhya; 17: South African Bantu; 18: Vezo; 19: Mikea; 20: Temoro; 21: US European descendant; 22: Onge; 23: Brahmin; 24: Dravidian; 25: Indian from Singapore; 26: Han; 27: Burmese; 28: Vietnamese; 29: Jehai; 30: Bateq; 31: Mendriq; 32: Kintaq; 33: MahMeri; 34: CheWong; 35: Jakun; 36: Temuan; 37: Seletar; 38: Malay; 39: Besemah; 40: Semende; 41: Bidayuh; 42: Banjar; 43: Ngaju; 44: South Kalimantan Dayak; 45: Ma'anyan; 46: Lebbo; 47: Murut; 48: Dusun; 49: Bajo; 50: Central Sumbanese; 51: East Sumbanese; 52: West Sumbanese; 53: Nusa Tenggara; 54: Moluccas; 55: Papua New Guinea Highlander; 56: Philippines Negrito; 57: Filipino; 58: Igorot; 59: Taiwan Aborigenes; 60: Fiji; 61: Polynesia.



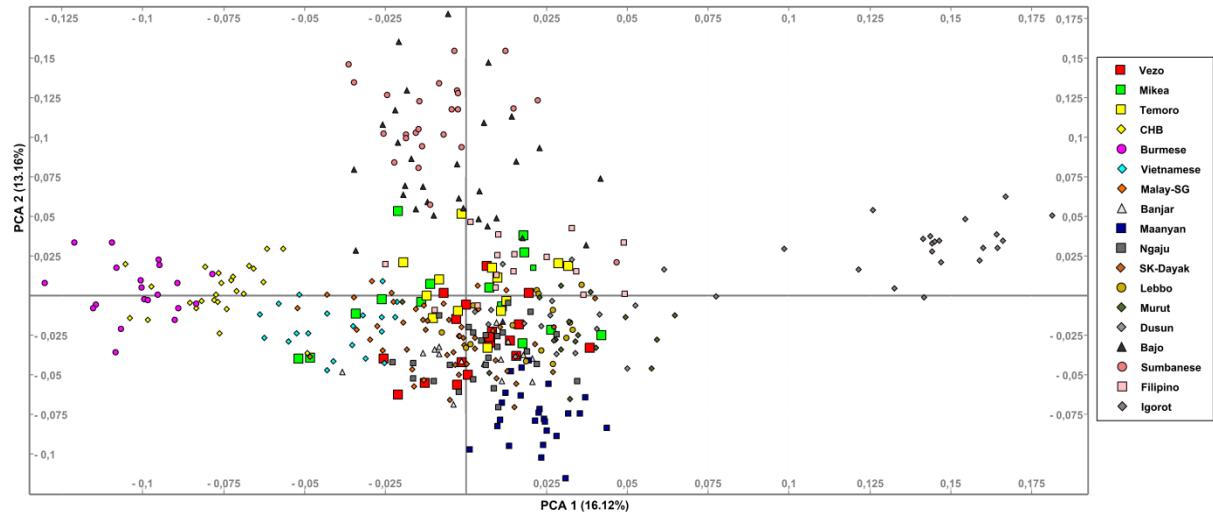
Supplementary File S3 - Cross-validation plot generated from the ADMIXTURE analysis (Alexander et al. 2009) from K=2 to K=18 on the low density SNP dataset from 10 iterations. It shows that K=16 has the lowest median CV value thereby representing the strongly supported ADMIXTURE plot on the analysis.



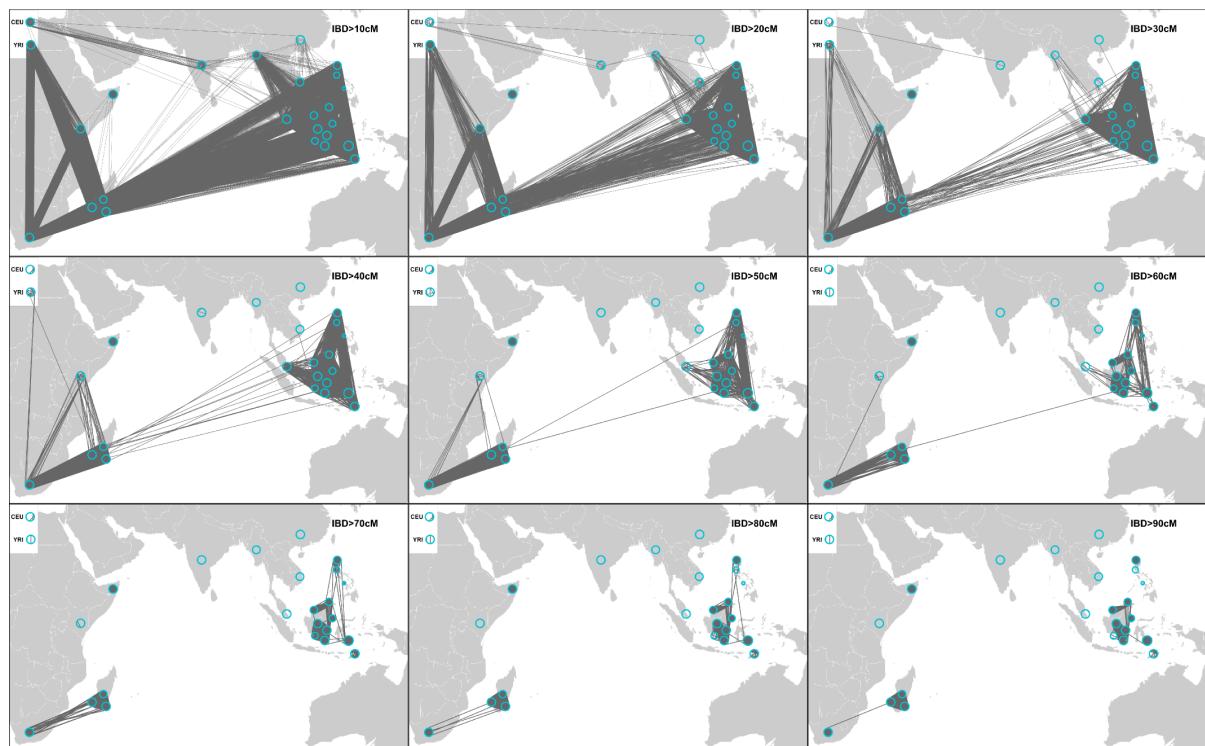
Supplementary Figure S4 -TreeMix analysis on the low density dataset with five migration nodes (99% variability) (Pickrell and Pritchard 2012). The arrows indicate the direction of the gene flow and their colors its intensity. A strong gene flow is identified from a node clustering Southeast Asian populations into the three Malagasy populations.



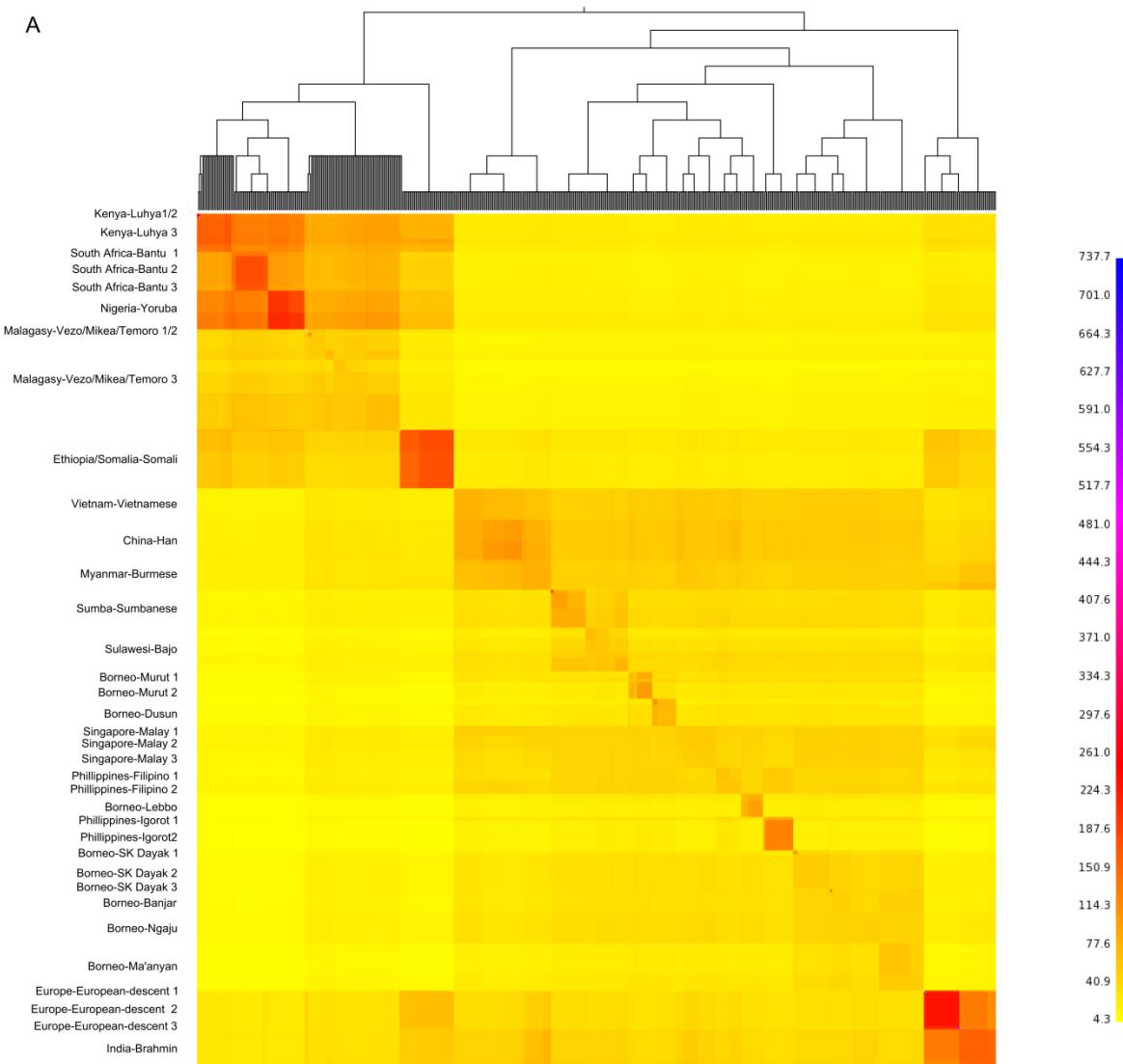
Supplementary figure S5 - Ancestry-specific Principal Component Analysis based on masked SNPs from individuals of the high density dataset obtained after PCAdmix analysis (Brisbin, et al. 2012) and plot with EIGENSOFT v6.0.1 (Patterson, et al. 2006).



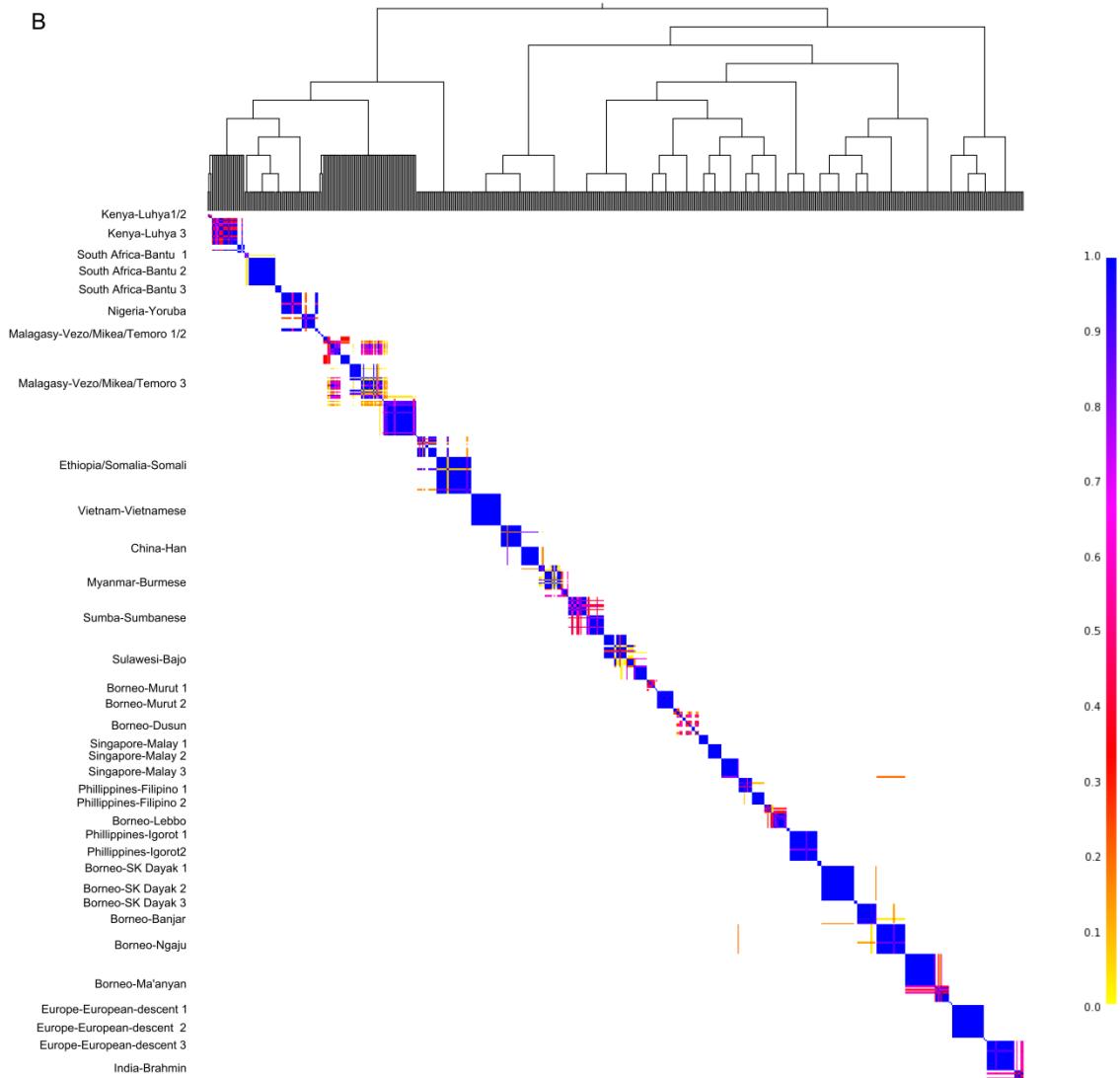
Supplementary Figure S6 - Shared Identity-By-Descent fragments between pairs of individuals in the high density dataset, filtering for different thresholds of shared IBD fragments (from IBD > 10cM to IBD >90cM), calculated with RefinedIBD (Browning and Browning 2007; Browning and Browning 2013). Populations are represented by a blue circle which diameter is proportional to the number of individuals (from n=4 to n=31). Shared IBD fragments between each pair of individuals are represented by a black line with Cytoscape (Shannon, et al. 2003).



Supplementary Figure S7 – Coancestry heat map (A) and pairwise coincidence matrix (B) of the individuals of the high SNP density dataset generated by fineSTRUCTURE (Lawson, et al. 2012). The color scale in (A) indicates the chunk counts between each pair of individuals calculated by Chromopainter. The color scale in (B) indicates the pairwise coincidence between each pair of individuals. Nodes are collapsed below 60% probability. For convenience, close labels are merged (e.g., Kenya-Luhya 1/2 refers to population sub-structure in two groups of the Kenya-Luhya).



B



Supplementary Table S1 - Table of the populations included in both the low and high density SNP datasets used in the study.

Population	Country	N (LDD)	N (HDD)	Reference
Yoruba	Nigeria	206	25	(International HapMap, et al. 2010)
Mende	Senegal	85	-	(International HapMap et al. 2010)
Gambian	Gambia	115	-	(International HapMap et al. 2010)
European	USA	99	25	(International HapMap et al. 2010)
Han	China	103	25	(International HapMap et al. 2010)
Luhya	Kenya	97	25	(International HapMap et al. 2010)
Beninese	Benin	24	-	Fortes-Lima, personal communication
Afar	Ethiopia	10	-	(Pagani, et al. 2012)
Tygray	Ethiopia	20	-	(Pagani et al. 2012)
Amhara	Ethiopia	24	-	(Pagani et al. 2012)
Wolayta	Ethiopia	6	-	(Pagani et al. 2012)
Oromo	Ethiopia	21	-	(Pagani et al. 2012)
Ari-Cutivator	Ethiopia	21	-	(Pagani et al. 2012)
Ari-Blacksmith	Ethiopia	14	-	(Pagani et al. 2012)
Gumuz	Ethiopia	15	-	(Pagani et al. 2012)
Anuak	Ethiopia	22	-	(Pagani et al. 2012)
Sudanese	Sudan	21	-	(Pagani et al. 2012)
Somalian	Somalia	23	23	(Pagani et al. 2012)
Bantu	South Africa	94	25	(May, et al. 2013)
Mikea	Madagascar	18	18	(Pierron, et al. 2014)
Temoro	Madagascar	24	24	(Pierron et al. 2014)
Vezo	Madagascar	24	24	(Pierron et al. 2014)
Lebbo	Indonesia (Borneo)	15	15	(Pierron et al. 2014)
Bajo	Indonesia (Sulawesi)	31	31	(Pierron et al. 2014)
Indian	Singapore	83	-	(Teo, et al. 2009)
Malay	Singapore	89	25	(Teo et al. 2009)
Jehai	Malaysia	20	-	(Aghakhanian, et al. 2015)
Bateq	Malaysia	9	-	(Aghakhanian et al. 2015)
Mendriq	Malaysia	12	-	(Aghakhanian et al. 2015)
Kintaq	Malaysia	13	-	(Aghakhanian et al. 2015)
MahMeri	Malaysia	17	-	(Aghakhanian et al. 2015)
CheWong	Malaysia	6	-	(Aghakhanian et al. 2015)
Jakun	Malaysia	9	-	(Aghakhanian et al. 2015)
Temuan	Malaysia	12	-	(Aghakhanian et al. 2015)
Seletar	Malaysia	13	-	(Aghakhanian et al. 2015)
Onge	Andaman	10	-	(Reich, et al. 2011)

Dravidian	India	12	-	(Reich et al. 2011)
Besemah	Indonesia (Sumatra)	8	-	(Reich et al. 2011)
Semende	Indonesia (Sumatra)	9	-	(Reich et al. 2011)
Bidayuh	Malaysia (Borneo)	10	-	(Reich et al. 2011)
Nusa Tenggara	Indonesia	10	-	(Reich et al. 2011)
Moluccas	Indonesia	10	-	(Reich et al. 2011)
PNG	Papua New Guinea	24	-	(Reich et al. 2011)
Highlander				
Filipino**	Philippines	16	-	(Reich et al. 2011)
Philippines Negrito	Philippines	11	-	(Reich et al. 2011)
Taiwanese Aborigines	Taiwan	12	-	(Reich et al. 2011)
Fiji	Fiji	25	-	(Reich et al. 2011)
Polynesian	Polynesia	19	-	(Reich et al. 2011)
Sumbanese*	Indonesia (Sumba)	180	25	(Cox, et al. forthcoming)
Brahmin	India	47	25	(Mörseburg, et al. forthcoming)
Burmese	Myanmar	20	20	(Mörseburg et al. forthcoming)
Vietnamese	Vietnam	20	20	(Mörseburg et al. forthcoming)
Igorot	Philippines	21	21	(Mörseburg et al. forthcoming)
Filipino**	Philippines	16	16	(Mörseburg et al. forthcoming)
Dusun	Malaysia (Borneo)	17	17	(Mörseburg et al. forthcoming)
Murut	Malaysia (Borneo)	17	17	(Mörseburg et al. forthcoming)
Ma'anyan	Indonesia (Borneo)	162	25	(Kusuma, et al. 2016)
SK.Dayak	Indonesia (Borneo)	40	25	(Kusuma et al. 2016)
Ngaju	Indonesia (Borneo)	25	25	<i>this study</i>
Banjar	Indonesia (Borneo)	16	16	<i>this study</i>

Note: LDD: Low Density of SNP Dataset (40,272 SNPs); HDD: High Density of SNP Dataset (374,189 SNPs). *: Sumbanese of the LDD were sub-grouped in 3 locations of sampling for some analyses: West (W-Sumba), Central (C-Sumba), East (E-Sumba).; **: For some analyses Filipino individuals from (Reich et al. 2011) and (Mörseburg et al. forthcoming) were pooled.

Supplementary Table S2 - Results of *f*3-statistics showing the Z-score <-2 obtained for each combination on populations in the high density dataset to test for admixture.
Only the 15 lowest Z-scores are shown for each tested group.

Tested group	Parental Pop A	Parental Pop B	f3	SD	Z-score	Tested group	Parental Pop A	Parental Pop B	f3	SD	Z-score
Bajo	Luhya	Igorot	-0,00074	0,00015	-4,83578	Mikea	SK-Dayak	Yoruba	-0,00995	0,00010	-100,59000
Bajo	S-African_Bantu	Igorot	-0,00075	0,00016	-4,79533	Mikea	S-African_Bantu	Malay-SG	-0,00946	0,00009	-99,94540
Bajo	Yoruba	Igorot	-0,00073	0,00015	-4,70864	Mikea	Ngaju	Yoruba	-0,00985	0,00010	-99,50600
Bajo	Eth-Somalian	Igorot	-0,00064	0,00015	-4,20585	Mikea	Yoruba	Maanyan	-0,01003	0,00010	-99,44410
Bajo	Somalian	Igorot	-0,00063	0,00015	-4,19374	Mikea	Yoruba	Murut	-0,01017	0,00010	-99,15970
Bajo	Gyan	Igorot	-0,00042	0,00014	-2,91720	Mikea	S-African_Bantu	Dusun	-0,01009	0,00010	-99,13510
Bajo	CEU	Igorot	-0,00038	0,00016	-2,34123	Mikea	Vietnamese	S-African_Bantu	-0,00973	0,00010	-98,79300
Banjar	Gyan	Igorot	-0,00117	0,00009	-12,53420	Mikea	S-African_Bantu	Luzon	-0,00971	0,00010	-98,31260
Banjar	Gyan	Maanyan	-0,00086	0,00007	-11,70650	Mikea	S-African_Bantu	Banjar	-0,00979	0,00010	-98,24890
Banjar	Somalian	Igorot	-0,00112	0,00010	-11,08290	Mikea	Malay-SG	Yoruba	-0,00939	0,00010	-97,83200
Banjar	Eth-Somalian	Igorot	-0,00113	0,00010	-10,98400	Mikea	Dusun	Yoruba	-0,01003	0,00010	-97,10260
Banjar	CEU	Maanyan	-0,00089	0,00008	-10,75080	Ngaju	Gyan	Maanyan	-0,00033	0,00006	-5,42691
Banjar	CEU	Igorot	-0,00113	0,00010	-10,74080	Ngaju	CEU	Maanyan	-0,00030	0,00007	-4,34292
Banjar	Luhya	Igorot	-0,00110	0,00011	-10,40430	Ngaju	Gyan	Igorot	-0,00037	0,00009	-4,23838
Banjar	S-African_Bantu	Igorot	-0,00110	0,00011	-10,30480	Ngaju	Eth-Somalian	Maanyan	-0,00021	0,00006	-3,27339
Banjar	Yoruba	Igorot	-0,00110	0,00011	-10,24280	Ngaju	Eth-Somalian	Igorot	-0,00030	0,00010	-3,01367
Banjar	Eth-Somalian	Maanyan	-0,00077	0,00008	-9,87042	Ngaju	Maanyan	Somalian	-0,00019	0,00006	-2,98514
Banjar	Maanyan	Somalian	-0,00076	0,00008	-9,71601	Ngaju	Luhya	Igorot	-0,00030	0,00010	-2,95500
Banjar	Gyan	Murut	-0,00074	0,00008	-9,13794	Ngaju	Somalian	Igorot	-0,00028	0,00010	-2,92635
Banjar	S-African_Bantu	Maanyan	-0,00073	0,00008	-8,92003	Ngaju	Yoruba	Igorot	-0,00029	0,00010	-2,85123
Banjar	Maanyan	Luhya	-0,00069	0,00008	-8,65876	Ngaju	S-African_Bantu	Igorot	-0,00028	0,00010	-2,68118
Banjar	CEU	Murut	-0,00081	0,00009	-8,63599	Ngaju	CEU	Igorot	-0,00026	0,00010	-2,60884
Burmese	Gyan	CHB	-0,00325	0,00006	-56,17750	Ngaju	S-African_Bantu	Maanyan	-0,00017	0,00007	-2,50506
Burmese	Vietnamese	Gyan	-0,00306	0,00006	-51,65090	Ngaju	Maanyan	Luhya	-0,00017	0,00007	-2,43966
Burmese	CEU	CHB	-0,00316	0,00007	-43,60350	Ngaju	Yoruba	Maanyan	-0,00016	0,00007	-2,32433
Burmese	Vietnamese	CEU	-0,00311	0,00007	-42,84930	Ngaju	Gyan	Murut	-0,00011	0,00007	-1,43415
Burmese	CHB	Somalian	-0,00280	0,00007	-41,56630	SK-Dayak	Maanyan	Burmese	-0,00031	0,00004	-7,90256
Burmese	Eth-Somalian	CHB	-0,00283	0,00007	-40,63090	SK-Dayak	Gyan	Maanyan	-0,00044	0,00006	-7,43457
Burmese	Vietnamese	Somalian	-0,00260	0,00007	-37,29110	SK-Dayak	Maanyan	Sumbanese	-0,00030	0,00004	-7,41106
Burmese	Gyan	Murut	-0,00267	0,00007	-36,73700	SK-Dayak	Vietnamese	Maanyan	-0,00027	0,00004	-7,27878
Burmese	Vietnamese	Eth-Somalian	-0,00260	0,00007	-36,71400	SK-Dayak	Malay-SG	Maanyan	-0,00023	0,00003	-7,08378
Burmese	Gyan	Igorot	-0,00290	0,00008	-36,48650	SK-Dayak	Maanyan	Bajo	-0,00035	0,00005	-7,02357
Burmese	CHB	Luhya	-0,00257	0,00007	-35,51950	SK-Dayak	CEU	Maanyan	-0,00041	0,00007	-6,08851
Burmese	S-African_Bantu	CHB	-0,00261	0,00007	-35,41820	SK-Dayak	Maanyan	CHB	-0,00024	0,00004	-5,80104
Burmese	Yoruba	CHB	-0,00257	0,00007	-34,33380	SK-Dayak	Gyan	Igorot	-0,00049	0,00008	-5,79169
Burmese	SK-Dayak	Gyan	-0,00220	0,00006	-34,22450	SK-Dayak	Temoro	Maanyan	-0,00028	0,00005	-5,32602
Burmese	Gyan	Maanyan	-0,00233	0,00007	-33,86420	SK-Dayak	Vezo	Maanyan	-0,00027	0,00005	-5,20714
Luzon	Gyan	Igorot	-0,00226	0,00008	-26,73450	SK-Dayak	Maanyan	Murut	-0,00021	0,00004	-5,04424
Luzon	Somalian	Igorot	-0,00228	0,00009	-24,00030	SK-Dayak	Maanyan	Luhya	-0,00034	0,00007	-4,91390
Luzon	CEU	Igorot	-0,00233	0,00010	-23,76760	SK-Dayak	Luhya	Igorot	-0,00049	0,00010	-4,90414
Luzon	Eth-Somalian	Igorot	-0,00227	0,00010	-23,51470	SK-Dayak	S-African_Bantu	Maanyan	-0,00034	0,00007	-4,84829
Luzon	Luhya	Igorot	-0,00229	0,00010	-22,86680	Somalian	Yoruba	CEU	-0,00478	0,00010	-47,79240
Luzon	Yoruba	Igorot	-0,00229	0,00010	-22,43360	Somalian	CEU	Luhya	-0,00448	0,00009	-47,43610
Luzon	S-African_Bantu	Igorot	-0,00227	0,00010	-22,24460	Somalian	S-African_Bantu	CEU	-0,00443	0,00010	-44,19020
Luzon	Vezo	Igorot	-0,00161	0,00008	-20,85780	Somalian	Gyan	Luhya	-0,00221	0,00009	-25,10260
Luzon	Mikea	Igorot	-0,00166	0,00008	-20,39340	Somalian	Gyan	Yoruba	-0,00237	0,00009	-24,97390
Luzon	Temoro	Igorot	-0,00160	0,00008	-20,18860	Somalian	S-African_Bantu	Gyan	-0,00205	0,00009	-21,81550
Luzon	Burmese	Igorot	-0,00112	0,00006	-18,23300	Somalian	Burmese	Luhya	-0,00036	0,00010	-3,47382
Luzon	Igorot	Sumbanese	-0,00073	0,00006	-12,37340	Somalian	Yoruba	Burmese	-0,00034	0,00011	-2,98567
Luzon	Malay-SG	Igorot	-0,00069	0,00006	-12,16120	Somalian	CHB	Luhya	-0,00013	0,00011	-1,19885
Luzon	CHB	Igorot	-0,00059	0,00006	-9,63134	Sumbanese	Luhya	Igorot	-0,00065	0,00011	-5,87579
Luzon	Vietnamese	Igorot	-0,00046	0,00006	-7,76522	Sumbanese	S-African_Bantu	Igorot	-0,00065	0,00011	-5,85895
Gyan	CEU	Burmese	-0,00234	0,00008	-30,74300	Sumbanese	Yoruba	Igorot	-0,00065	0,00011	-5,84816
Gyan	Malay-SG	CEU	-0,00235	0,00008	-28,72070	Sumbanese	Eth-Somalian	Igorot	-0,00047	0,00010	-4,53064
Gyan	CEU	Sumbanese	-0,00240	0,00009	-28,18800	Sumbanese	Somalian	Igorot	-0,00045	0,00010	-4,34370
Gyan	Ngaju	CEU	-0,00242	0,00009	-27,79990	Sumbanese	Gyan	Igorot	-0,00021	0,00009	-2,35079
Gyan	SK-Dayak	CEU	-0,00242	0,00009	-27,08320	Sumbanese	CEU	Igorot	-0,00012	0,00011	-1,08230
Gyan	Banjar	CEU	-0,00235	0,00009	-26,65450	Temoro	S-African_Bantu	Ngaju	-0,01130	0,00009	-124,99600
Gyan	Vietnamese	CEU	-0,00238	0,00009	-26,49640	Temoro	S-African_Bantu	SK-Dayak	-0,01141	0,00009	-124,52900

Gyan	Dusun	CEU	-0,00248	0,00009	-26,47620	Temoro	SK-Dayak	Yoruba	-0,01133	0,00009	-123,75300
Gyan	CEU	Maanyan	-0,00238	0,00009	-26,35860	Temoro	Ngaju	Yoruba	-0,01122	0,00009	-123,16300
Gyan	CEU	Murut	-0,00241	0,00009	-25,80560	Temoro	S-African_Bantu	Maanyan	-0,01147	0,00009	-122,94300
Gyan	CEU	Lebbo	-0,00240	0,00009	-25,68800	Temoro	S-African_Bantu	Banjar	-0,01118	0,00009	-122,91200
Gyan	CEU	Luzon	-0,00224	0,00009	-25,41830	Temoro	S-African_Bantu	Malay-SG	-0,01083	0,00009	-122,90400
Gyan	CEU	CHB	-0,00225	0,00009	-24,96840	Temoro	Banjar	Yoruba	-0,01112	0,00009	-121,74100
Gyan	CEU	Bajo	-0,00235	0,00010	-24,66920	Temoro	Yoruba	Maanyan	-0,01137	0,00009	-121,48900
Gyan	CEU	Igorot	-0,00231	0,00010	-23,36910	Temoro	Malay-SG	Yoruba	-0,01073	0,00009	-121,35500
Luhya	Eth-Somalian	Yoruba	-0,00072	0,00005	-15,55730	Temoro	Yoruba	Murut	-0,01149	0,00009	-121,07700
Luhya	Yoruba	Somalian	-0,00071	0,00005	-15,36080	Temoro	S-African_Bantu	Murut	-0,01157	0,00010	-120,65900
Luhya	Yoruba	CEU	-0,00101	0,00007	-14,90660	Temoro	Vietnamese	S-African_Bantu	-0,01114	0,00009	-120,07700
Luhya	S-African_Bantu	Somalian	-0,00062	0,00004	-13,93520	Temoro	S-African_Bantu	Luzon	-0,01108	0,00009	-119,93300
Luhya	Gyan	Yoruba	-0,00087	0,00006	-13,82580	Temoro	Yoruba	Luzon	-0,01099	0,00009	-118,51300
Luhya	S-African_Bantu	Eth-Somalian	-0,00059	0,00005	-12,47290	Vezo	S-African_Bantu	Ngaju	-0,01131	0,00009	-126,64300
Luhya	Yoruba	Burmese	-0,00068	0,00007	-10,42080	Vezo	S-African_Bantu	SK-Dayak	-0,01140	0,00009	-125,42300
Luhya	Malay-SG	Yoruba	-0,00068	0,00007	-10,24830	Vezo	S-African_Bantu	Maanyan	-0,01147	0,00009	-124,43700
Luhya	Yoruba	Sumbanese	-0,00067	0,00007	-10,19040	Vezo	S-African_Bantu	Malay-SG	-0,01079	0,00009	-123,28900
Luhya	Dusun	Yoruba	-0,00070	0,00007	-10,17090	Vezo	S-African_Bantu	Banjar	-0,01118	0,00009	-122,99600
Luhya	SK-Dayak	Yoruba	-0,00068	0,00007	-10,16430	Vezo	SK-Dayak	Yoruba	-0,01132	0,00009	-122,00400
Luhya	Ngaju	Yoruba	-0,00068	0,00007	-10,06140	Vezo	Ngaju	Yoruba	-0,01123	0,00009	-121,63800
Luhya	Yoruba	CHB	-0,00068	0,00007	-10,01850	Vezo	S-African_Bantu	Murut	-0,01161	0,00010	-121,03500
Luhya	Yoruba	Luzon	-0,00067	0,00007	-9,95678	Vezo	S-African_Bantu	Luzon	-0,01109	0,00009	-120,72900
Luhya	Vietnamese	Yoruba	-0,00068	0,00007	-9,92264	Vezo	Yoruba	Maanyan	-0,01138	0,00009	-120,61700
Malay-SG	Gyan	Maanyan	-0,00165	0,00006	-26,43780	Vezo	S-African_Bantu	Dusun	-0,01146	0,00010	-120,42300
Malay-SG	Gyan	Murut	-0,00190	0,00007	-26,38870	Vezo	Vietnamese	S-African_Bantu	-0,01113	0,00009	-120,37100
IMalay-SG	SK-Dayak	Gyan	-0,00144	0,00005	-26,33230	Vezo	Malay-SG	Yoruba	-0,01070	0,00009	-119,67100
Malay-SG	Gyan	Igorot	-0,00202	0,00008	-24,03160	Vezo	Banjar	Yoruba	-0,01112	0,00009	-119,60800
Malay-SG	CEU	Maanyan	-0,00168	0,00007	-23,49810	Vezo	Yoruba	Murut	-0,01153	0,00010	-118,59900
Malay-SG	SK-Dayak	CEU	-0,00151	0,00007	-23,18220	Vietnamese	Ngaju	CHB	-0,00062	0,00004	-16,10290
Malay-SG	CEU	Murut	-0,00196	0,00008	-23,08730	Vietnamese	SK-Dayak	CHB	-0,00054	0,00004	-14,28810
Malay-SG	Dusun	Gyan	-0,00159	0,00007	-22,56590	Vietnamese	Banjar	CHB	-0,00053	0,00004	-12,78690
Malay-SG	Ngaju	Gyan	-0,00121	0,00006	-21,92340	Vietnamese	Maanyan	CHB	-0,00052	0,00004	-12,52290
Malay-SG	SK-Dayak	Somalian	-0,00130	0,00006	-21,53510	Vietnamese	Malay-SG	CHB	-0,00043	0,00004	-11,57120
Malay-SG	Eth-Somalian	Murut	-0,00172	0,00008	-21,37210	Vietnamese	CHB	Murut	-0,00042	0,00005	-9,27405
Malay-SG	SK-Dayak	Eth-Somalian	-0,00129	0,00006	-21,28580	Vietnamese	CHB	Lebbo	-0,00047	0,00005	-9,09139
Malay-SG	Somalian	Murut	-0,00169	0,00008	-21,09710	Vietnamese	Dusun	CHB	-0,00033	0,00005	-7,09284
Malay-SG	Eth-Somalian	Maanyan	-0,00138	0,00007	-20,51370	Vietnamese	Burmese	Igorot	-0,00036	0,00005	-6,54163
Malay-SG	Maanyan	Somalian	-0,00137	0,00007	-20,33400	Vietnamese	CHB	Bajo	-0,00025	0,00005	-4,59526
Mikea	S-African_Bantu	SK-Dayak	-0,01002	0,00010	-103,48400	Vietnamese	CHB	Sumbanese	-0,00013	0,00004	-2,85187
Mikea	S-African_Bantu	Ngaju	-0,00991	0,00010	-102,49300	Vietnamese	Gyan	Igorot	-0,00020	0,00009	-2,18635
Mikea	S-African_Bantu	Maanyan	-0,01012	0,00010	-102,06900	Vietnamese	CEU	Igorot	-0,00012	0,00010	-1,17054
Mikea	S-African_Bantu	Murut	-0,01023	0,00010	-100,83700						

Supplementary Table S3 -*f*3-statistics table obtained for the tree configuration (Malagasy population; Asian population; Yoruba) using the Asian-SNP dataset.

Source 1	Source 2	Target	f3	SE	Z-score	SNPs
Han	Temoro	Yoruba	0.114	0.005	21.092	1595
Burmese	Temoro	Yoruba	0.108	0.005	21.899	1596
Vietnamese	Temoro	Yoruba	0.119	0.006	20.305	1596
Jehai	Temoro	Yoruba	0.109	0.006	18.594	1592
Bateq	Temoro	Yoruba	0.106	0.006	16.485	1590
Mendriq	Temoro	Yoruba	0.11	0.006	17.136	1593
Kintaq	Temoro	Yoruba	0.108	0.006	18.793	1594
Mah-Meri	Temoro	Yoruba	0.111	0.006	19.042	1591
CheWong	Temoro	Yoruba	0.114	0.006	17.852	1585
Jakun	Temoro	Yoruba	0.117	0.006	19.377	1590
Temuan	Temoro	Yoruba	0.115	0.005	21.534	1589
Seletar	Temoro	Yoruba	0.115	0.007	17.066	1593
Malay	Temoro	Yoruba	0.115	0.005	22.628	1597
Besemah	Temoro	Yoruba	0.119	0.006	21.528	1591
Semende	Temoro	Yoruba	0.123	0.006	21.331	1590
Bidayuh	Temoro	Yoruba	0.118	0.006	21.085	1589
Banjar	Temoro	Yoruba	0.121	0.006	21.923	1593
Ngaju	Temoro	Yoruba	0.12	0.005	22.258	1595
SK-Dayak	Temoro	Yoruba	0.121	0.005	23.247	1596
Ma'anyan	Temoro	Yoruba	0.122	0.006	21.937	1597
Lebbo	Temoro	Yoruba	0.117	0.005	21.457	1593
Murut	Temoro	Yoruba	0.119	0.005	22.637	1593
Dusun	Temoro	Yoruba	0.119	0.006	20.81	1594
Bajo	Temoro	Yoruba	0.116	0.005	21.905	1597
C-Sumbanese	Temoro	Yoruba	0.117	0.005	21.529	1597
E-Sumbanese	Temoro	Yoruba	0.113	0.005	20.879	1597
W-Sumbanese	Temoro	Yoruba	0.114	0.005	21.931	1597
Nusa_Tenga	Temoro	Yoruba	0.107	0.006	18.523	1590
Moluccas	Temoro	Yoruba	0.111	0.006	19.981	1587
PNG highlander	Temoro	Yoruba	0.086	0.008	11.34	1578
Philippine Negrito	Temoro	Yoruba	0.109	0.006	19.665	1587
Filipino	Temoro	Yoruba	0.12	0.006	20.97	1596
Igorot	Temoro	Yoruba	0.127	0.006	22.68	1593
Taiwan	Temoro	Yoruba	0.119	0.006	20.335	1594
Aboriginese	Temoro	Yoruba	0.103	0.005	19.196	1594
Fiji	Temoro	Yoruba	0.116	0.006	20.188	1591
Polynesia	Temoro	Yoruba	0.12	0.005	25.6	1620
Han	Vezo	Yoruba	0.112	0.005	24.617	1620
Burmese	Vezo	Yoruba	0.123	0.005	24.012	1621
Vietnamese	Vezo	Yoruba	0.111	0.005	20.357	1616
Jehai	Vezo	Yoruba				

Bateq	Vezo	Yoruba	0.108	0.006	18.361	1614
Mendriq	Vezo	Yoruba	0.113	0.006	20.44	1619
Kintaq	Vezo	Yoruba	0.11	0.006	18.975	1615
Mah-Meri	Vezo	Yoruba	0.118	0.005	21.917	1616
CheWong	Vezo	Yoruba	0.121	0.006	19.101	1605
Jakun	Vezo	Yoruba	0.119	0.006	21.084	1612
Temuan	Vezo	Yoruba	0.119	0.005	23.297	1612
Seletar	Vezo	Yoruba	0.114	0.006	18.853	1615
Malay	Vezo	Yoruba	0.12	0.005	24.098	1622
Besemah	Vezo	Yoruba	0.124	0.005	24.584	1614
Semende	Vezo	Yoruba	0.126	0.005	24.929	1614
Bidayuh	Vezo	Yoruba	0.124	0.006	21.471	1613
Banjar	Vezo	Yoruba	0.127	0.005	25.264	1617
Ngaju	Vezo	Yoruba	0.125	0.005	24.353	1620
SK-Dayak	Vezo	Yoruba	0.126	0.005	26.05	1622
Ma'anyan	Vezo	Yoruba	0.128	0.005	25.407	1622
Lebbo	Vezo	Yoruba	0.122	0.006	21.471	1616
Murut	Vezo	Yoruba	0.124	0.005	22.842	1619
Dusun	Vezo	Yoruba	0.127	0.005	23.517	1619
Bajo	Vezo	Yoruba	0.117	0.005	24.57	1620
C-Sumbanese	Vezo	Yoruba	0.119	0.005	23.606	1621
E-Sumbanese	Vezo	Yoruba	0.116	0.005	23.617	1622
W-Sumbanese	Vezo	Yoruba	0.115	0.005	24.193	1622
Nusa_Tenga	Vezo	Yoruba	0.112	0.006	20.193	1615
Moluccas	Vezo	Yoruba	0.115	0.005	22	1613
PNG highlander	Vezo	Yoruba	0.082	0.008	10.777	1603
Philippine Negrito	Vezo	Yoruba	0.113	0.005	21.12	1609
Filipino	Vezo	Yoruba	0.123	0.005	24.999	1619
Igorot	Vezo	Yoruba	0.13	0.005	23.754	1618
Taiwan						
Aboriginese	Vezo	Yoruba	0.125	0.006	21.543	1618
Fiji	Vezo	Yoruba	0.106	0.005	19.416	1616
Polynesia	Vezo	Yoruba	0.121	0.006	21.102	1614
Han	Mikea	Yoruba	0.116	0.005	22.42	1621
Burmese	Mikea	Yoruba	0.11	0.005	22.506	1622
Vietnamese	Mikea	Yoruba	0.118	0.006	21.511	1621
Jehai	Mikea	Yoruba	0.106	0.005	20.259	1619
Bateq	Mikea	Yoruba	0.103	0.006	16.336	1616
Mendriq	Mikea	Yoruba	0.107	0.006	18.533	1619
Kintaq	Mikea	Yoruba	0.108	0.006	18.301	1616
Mah-Meri	Mikea	Yoruba	0.113	0.005	20.671	1615
CheWong	Mikea	Yoruba	0.115	0.006	19.484	1612
Jakun	Mikea	Yoruba	0.118	0.006	20.018	1616
Temuan	Mikea	Yoruba	0.115	0.005	21.211	1615
Seletar	Mikea	Yoruba	0.109	0.006	19.324	1617
Malay	Mikea	Yoruba	0.115	0.005	22.626	1622
Besemah	Mikea	Yoruba	0.122	0.006	21.96	1615

Semende	Mikea	Yoruba	0.12	0.006	20.337	1616
Bidayuh	Mikea	Yoruba	0.121	0.006	21.17	1616
Banjar	Mikea	Yoruba	0.122	0.005	22.223	1619
Ngaju	Mikea	Yoruba	0.119	0.006	21.055	1622
SK-Dayak	Mikea	Yoruba	0.123	0.005	23.21	1622
Ma'anyan	Mikea	Yoruba	0.123	0.006	21.426	1622
Lebbo	Mikea	Yoruba	0.121	0.006	21.713	1618
Murut	Mikea	Yoruba	0.118	0.005	21.946	1621
Dusun	Mikea	Yoruba	0.124	0.006	20.771	1621
Bajo	Mikea	Yoruba	0.116	0.005	21.556	1622
C-Sumbanese	Mikea	Yoruba	0.116	0.006	19.959	1622
E-Sumbanese	Mikea	Yoruba	0.113	0.006	19.793	1621
W-Sumbanese	Mikea	Yoruba	0.115	0.005	21.267	1621
Nusa_Tenga	Mikea	Yoruba	0.114	0.006	18.352	1618
Moluccas	Mikea	Yoruba	0.116	0.006	17.925	1614
PNG highlander	Mikea	Yoruba	0.089	0.008	10.992	1603
Philippine Negrito	Mikea	Yoruba	0.109	0.006	17.881	1613
Filipino	Mikea	Yoruba	0.121	0.006	21.286	1621
Igorot	Mikea	Yoruba	0.126	0.006	20.052	1618
Taiwan						
Aboriginese	Mikea	Yoruba	0.12	0.006	20.126	1620
Fiji	Mikea	Yoruba	0.107	0.006	18.074	1619
Polynesia	Mikea	Yoruba	0.12	0.006	18.604	1618

Supplementary Table S4 - F_{ST} genetic distances (lower diagonal) between ‘Asian-SNP’ Malagasy and data from the Asian populations of the high density dataset, and the corresponding standard deviation (upper diagonal).

FST \ S.D.	Vezo	Mikea	Temoro	CHB	Burmese	Vietnamese	Malay-SG	Banjar	Ma'anyan	Ngaju	SK-Dayak	Lebbo	Murut	Dusun	Bajo	Sumbanese	Filipino	Igorot
Vezo	0	0.005	0.006	0.004	0.004	0.003	0.004	0.003	0.004	0.003	0.003	0.004	0.004	0.004	0.003	0.003	0.003	0.003
Mikea	0.01	0	0.006	0.005	0.004	0.005	0.004	0.005	0.004	0.004	0.004	0.005	0.005	0.005	0.004	0.004	0.005	0.005
Temoro	0.007	0.016	0	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.005	0.004	0.005	0.004	0.004	0.004	0.005
CHB	0.035	0.041	0.031	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.002
Burmese	0.032	0.034	0.024	0.009	0	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002
Vietnamese	0.026	0.032	0.021	0.007	0.009	0	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002
Malay-SG	0.019	0.028	0.015	0.015	0.009	0.007	0	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.002
Banjar	0.021	0.029	0.016	0.02	0.015	0.009	0.004	0	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.002
Ma'anyan	0.026	0.036	0.021	0.028	0.024	0.017	0.009	0.008	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002
Ngaju	0.021	0.028	0.016	0.021	0.015	0.011	0.003	0.004	0.008	0	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002
SK-Dayak	0.018	0.025	0.015	0.019	0.014	0.01	0.002	0.002	0.005	0.001	0	0.002	0.001	0.001	0.001	0.001	0.001	0.002
Lebbo	0.043	0.046	0.036	0.042	0.036	0.034	0.024	0.027	0.034	0.027	0.025	0	0.002	0.002	0.002	0.002	0.002	0.003
Murut	0.033	0.041	0.027	0.028	0.028	0.021	0.016	0.018	0.024	0.016	0.015	0.035	0	0.002	0.001	0.002	0.001	0.002
Dusun	0.033	0.041	0.026	0.028	0.026	0.02	0.017	0.016	0.022	0.019	0.015	0.036	0.023	0	0.001	0.002	0.001	0.002
Bajo	0.028	0.032	0.018	0.02	0.016	0.014	0.008	0.011	0.019	0.011	0.009	0.028	0.02	0.019	0	0.001	0.001	0.002
Sumbanese	0.031	0.037	0.019	0.025	0.02	0.019	0.011	0.015	0.021	0.014	0.012	0.032	0.025	0.024	0.008	0	0.001	0.002
Filipino	0.023	0.028	0.017	0.013	0.015	0.008	0.006	0.008	0.013	0.009	0.006	0.028	0.013	0.012	0.007	0.012	0	0.002
Igorot	0.051	0.056	0.043	0.047	0.05	0.039	0.037	0.038	0.042	0.038	0.037	0.057	0.04	0.041	0.038	0.044	0.026	0

Supplementary Table S5 – GLOBETROTTER inferred dates (in both generations from present and years, bootstrap 95% CIs given in parenthesis; YBP = years before present), admixing sources, and percentage (%) of admixture for each population of interest (Hellenthal, et al. 2014). We assume a generation time of 25 years. R^2 corresponds to the goodness-of-fit of the tested model. FQ_1 and FQ_2 correspond respectively to the fit of a single admixture event and the fit of the first two principal components capturing the admixture events. M corresponds to the additional R^2 explained by adding a second date versus assuming only a single date of admixture ($M>0.35$ to infer multiple dates event). The admixture models presented in the table correspond to the best fit models considering the ‘best guess’. P: p-value of evidence of any detectable admixture event obtained after 100 bootstrap resamplings of the NULL procedure. Date confidence intervals are based on 100 bootstrap replicates of the date inference.

Target Group	Analysis	P	R^2	FQ_1	FQ_2	M	Best-guess	1-date (gen.)	1-date (YBP)	1-date Best Surrogate 1	1-date Best Surrogate 2	2-date (gen.)	2-date (YBP)	2-date Best Surrogate 1	2-date Best Surrogate 2
Vezo	main	< 0.01	0.996	1	1	0.095	one-date	25	625 (24-27) 25	Banjar (39%)	S.A.Bantu (61%)	-	-	-	-
	main.null	< 0.01	0.996	1	1	0.012	one-date		625 (600-675)	Banjar (38%)	S.A.Bantu (62%)	-	-	-	-
Mikea	main	< 0.01	0.993	1	1	0.142	one-date	27	675 (25-29) 27	Banjar (36%)	S.A.Bantu (64%)	-	-	-	-
	main.null	< 0.01	0.991	1	1	0.255	one-date		675 (625-725)	Banjar (36%)	S.A.Bantu (64%)	-	-	-	-
Temoro	main	< 0.01	0.996	1	1	0.076	one-date	30	750 (29-31) 30	Banjar (37%)	S.A.Bantu (63%)	-	-	-	-
	main.null	< 0.01	0.995	1	1	0.102	one-date		750 (725-775)	Banjar (37%)	S.A.Bantu (63%)	-	-	-	-
Banjar	main	< 0.01	0.621	1	1	0.078	one-date	17	425 (11-20) 23	Ma'anyan (23%)	Malay (77%)	-	-	-	-
	main.null	< 0.01	0.615	1	1	0.042	one-date		575 (350-800)	Ma'anyan (24%)	Malay (76%)	-	-	-	-
Ngaju	main	< 0.01	0.521	1	1	0.082	one-date	16	400 (9-19) 20	Ma'anyan (19%)	Malay (81%)	-	-	-	-
	main.null	< 0.01	0.554	1	1	0.045	one-date		500 (425-575)	Ma'anyan (43%)	Malay (57%)	-	-	-	-

SK Dayak	main	< 0.01 0.463 1 1 0.127	one-date	12 (7-16)	300 (175-400)	Malay (21%)	Ma'anyan (79%)	-	-	-	-
	main.null	< 0.01 0.615 1 1 0.084	one-date	19 (11-35)	475 (275-875)	Malay (27%)	Ma'anyan (73%)	-	-	-	-
Malay	main	< 0.01 0.959 0.972 0.989 0.481	multiple-dates	7 (2-10)	175 (50-250)	Burmese (24%)	Filipino (76%)	42 (29-58)	1050 (725-1450)	Brahmin (14%)	Filipino (86%)
	main.null	< 0.01 0.94 0.979 0.992 0.514	multiple-dates	9 (4-15)	225 (100-375)	Burmese (16%)	Filipino (84%)	66 (43-111)	1650 (1075-2775)	Brahmin (19%)	Filipino (81%)
Bajo	main	< 0.01 0.946 0.882 0.998 0.22	one-date-multiway	35 (32-40)	875 (800-1000)	Sumbanese (23%), Brahmin (12%)	Banjar (25%), Filipino (25%), Malay (11%), Ngaju (6%)	-	-	-	-
	main.null	< 0.01 0.953 0.96 0.999 0.22	one-date-multiway	47 (43-54)	1175 (1075-1350)	Sumbanese (27%), Brahmin (15%)	Banjar (23%), Filipino (27%), Ngaju (8%)	-	-	-	-

Supplementary Table S6 – Estimated dates of admixture in Malagasy ethnic groups using Banjar and South African Bantu data as parental populations with ALDER (Loh, et al. 2013).

Test Pop	Ref A	Ref B	p-value	2-ref z-score	1-ref z-score A	1-ref z-score B	max decay diff (%)	2-ref decay (gen.)	2-ref amp_exp
Temoro	Banjar	South Africa Bantu	5.1e-81	19.34	17.87	22.90	0.03	29.16 +/- 1.08	0.0018 +/- 0.0001
Mikea	Banjar	South Africa Bantu	6.9e-85	19.79	18.70	11.12	0.09	25.21 +/- 1.27	0.0017 +/- 0.0001
Vezo	Banjar	South Africa Bantu	2.6e-69	17.89	18.88	15.81	0.01	22.29 +/- 1.25	0.0017 +/- 0.0001

Supplementary Methods

Sample collection and ethics

A total of 41 DNA samples were analyzed from two groups in Southeast Borneo: the Banjar ($n=16$) and the Ngaju ($n=25$) that were collected in Banjarmasin city (Supplementary Figure S1). Blood samples were collected from healthy adult donors, all of whom provided written informed consent. DNA was extracted using a standard salting-out procedure. All participants were surveyed for language affiliation, current residence, familial birthplaces, and a genealogy of four generations to establish ancestry. This study was approved by the Research Ethics Commission of the Eijkman Institute for Molecular Biology (Jakarta, Indonesia). Genome-wide SNP genotyping for individuals from the two groups were performed using the Illumina Human Omni Express Bead Chip-24 v1.0 (Illumina Inc., San Diego, CA), which characterizes 730,525 single nucleotide markers regularly spaced across the genome. The accession number for the Southeast Borneo samples genotyped for this study is EGA: EGAS00001001841.

Dataset

We gathered data from previously published studies on populations from Madagascar, Southeast Asia, South Asia, East Asia, East Africa, South Africa, and Europe (Supplementary Table S1). Two datasets were compiled respective to their analytical use: a low SNP density dataset of populations covering a large geographical area; and a high SNP density dataset of populations composed by a subset of populations of the latter dataset. To avoid any statistical bias that could be induced by a size effect due to populations over-represented in the high SNP density

dataset, we randomly selected a maximum of 31 individuals in each group, such as each population has a number of individuals between 15 and 31. Quality controls were applied using Plink v1.9 (Chang, et al. 2015) to filter for i) close relatives, using an Identity-by-Descent (IBD) estimation with upper threshold of 0.25 (second degree relatives); ii) SNPs that failed the Hardy-Weinberg exact (HWE) test ($P < 10^{-6}$) were excluded; iii) samples with a call rate <0.99 and displayed missing rates >0.05 across all samples in each population were excluded; and iv) variants in high linkage disequilibrium ($r^2 > 0.5$) were also removed for the low density dataset. After filtering, the low SNP density dataset included 2183 individuals from 61 populations genotyped for 40,272; and the SNPs high SNP density dataset was composed of 551 individuals from 24 populations genotyped for 374,189 SNPs. All genotypes of the high SNP density dataset were then phased together with SHAPEIT v2.r790 (Delaneau, et al. 2012) using the 1000Genomes phased data (Delaneau, et al. 2014) as reference panel and the HapMap phase 2 genetic map (International HapMap 2005).

Statistical Analyses

The low density dataset was described by the following analyses. Principal Components Analysis was computed with EIGENSOFT v6.0.1 (Patterson et al. 2006). ADMIXTURE v1.23 (Alexander et al. 2009) was used to estimate the profile of individual genomic ancestries using maximum likelihood for components $K = 2$ to $K = 18$. Ten replicates were run at each value of K with different random seeds, then merged and assessed for clustering quality using CLUMPP (Jakobsson and Rosenberg 2007), and the cross-validation value was calculated to determine the optimal number of genomic components (here, $K = 16$). ADMIXTURE and PCA plots

were generated with Genesis (Buchmann and Hazelhurst 2014). Three-population (f_3) statistics (Patterson, et al. 2012) were computed for each trios of populations of the low SNP density dataset to identify groups showing potential recent admixture event. TreeMix v1.12 analysis (Pickrell and Pritchard 2012) was performed with all Asian populations and three representative of African groups (Yoruba, Luhya, South African Bantu), to estimate gene flows from Asian groups and their relative intensity, with blocks of 200 SNPs to account for linkage disequilibrium and migration edges added sequentially until the model explained 99% of the variance (the TreeMix outputs in Newick format were visualized with MEGA v7.0.14 (Tamura, et al. 2013)). Population structure of the phased high density dataset was evaluated using the fineSTRUCTURE v2.07 package (Lawson et al. 2012). It uses the detection of shared IBD fragments between each pair of individuals, without self-copying, calculated with Chromopainter v2.0 (Lawson et al. 2012) to perform a model-based Bayesian clustering of genotypes. From the results, a coancestry heat map and a dendrogram were inferred to visualize the number of clusters statistically defined that would describe relevantly the data. FineSTRUCTURE v2 identified 37 groups of individuals that can be statistically defined as natural populations (Lawson et al. 2012), according to their shared Identity-By-Descent (IBD) (bootstrapped nodes>60%; Supplementary figure S7). Most of these correspond to anthropologically defined populations, such as the Banjar or the Ngaju, with few exceptions (e.g., the sub-structuration of the Kenyan Luhya group). Although each Malagasy individual has its closest connections with other Malagasy, regardless of their ethnicity, these ethnic groups were treated separately for anthropological interest. Haplotype sharing between pairs of individuals was estimated from the phased high SNP density dataset by the Refined IBD algorithm of Beagle v4.0

(Browning and Browning 2007; Browning and Browning 2013), filtering for detected fragments with a logarithm of odds ratio (LOD)>3. 10 iterations were realized, randomizing the seed number for each run, and the overlapping shared fragments were merged to favour the detection of long shared IBD. Detected fragments between the same pairs of individuals were summed up and visualized with Cytoscape v3.2.1 (Shannon et al. 2003). IBD sharing data with Malagasy individuals was also averaged per Asian population to geographically plot a gradient map with Surfer v12.0 using the Kriging method (GoldenSoftware 2014). All maps used in the present study were generated using Global Mapper v.15 software. (<http://www.bluemarblegeo.com/products/global-mapper.php>). Local ancestry analysis in Malagasy individuals was performed with PCAdmix v1.0 (Brisbin et al. 2012) using two parental metapopulations of 100 individuals of African ancestry (randomly selected in Yoruba, South African Bantu, Kenyan Luhya and Somali groups), and of Asian ancestry (randomly selected in Han, Igorot, Ma'anyan and Malay groups). The phased Malagasy data were screened using the linkage disequilibrium information to define the probability of common ancestry of each Malagasy haplotype with each 'parental' metapopulation. The Viterbi algorithm was then used to mask all haplotypes according to one or the other ancestry in the Malagasy individuals. Ancestry-specific PCAs and F_{ST} calculations were realized with EIGENSOFT v6.0.1 (Patterson et al. 2006). Three-population (f_3) statistics (Patterson et al. 2012) and TreeMix v1.12 analysis (Pickrell and Pritchard 2012) were also performed on this masked dataset (1,664 SNPs for 18 populations). Haplotype 'painting' with Chromopainter v2 (Lawson et al. 2012) was realized on the high density of SNP dataset, defining each cluster of populations as target or donor/surrogate according to the anthropological question addressed. Mutational

rates and N_e parameters were first estimated with an Estimation-Maximization (EM) algorithm running Chromopainter v2 on all 22 autosomes for the entire dataset with 10 iterations (Lawson et al. 2012). The weighted average of these parameters, according to the SNP coverage of each used chromosomes and the number of individuals, were then used to compute the chromosomal painting. Each cluster of populations has been successively identified as target and the others as surrogates (at the exclusion of the Malagasy cluster which has not been used as surrogate). The obtained painted chromosomes for each cluster were used in GLOBETROTTER v1.0 (Hellenthal et al. 2014) to estimate the ratios and the dates of the potential admixture events characterizing them. Coancestry curves were estimated with and without standardization with a ‘NULL’ individual, and consistency between each estimated parameters was checked. 100 bootstrap resamplings were realized to estimate the p-value of the admixture events (considering the ‘NULL’ individual) and the 95% confidence interval for the obtained dates (without the ‘NULL’ individual). The ‘best-guess’ scenario given by GLOBETROTTER v1.0 (Hellenthal et al. 2014) was considered for each target population. Using the parental populations given by GLOBETROTTER v1.0 (Hellenthal et al. 2014), dates of admixture were also estimated by ALDER v1 (Loh et al. 2013).

REFERENCES

- Aghakhanian F, Yunus Y, Naidu R, Jinam T, Manica A, Hoh BP, Phipps ME 2015. Unravelling the genetic history of Negritos and indigenous populations of Southeast Asia. *Genome Biol Evol* 7: 1206-1215. doi: 10.1093/gbe/evv065
- Alexander DH, Novembre J, Lange K 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* 19: 1655-1664. doi: 10.1101/gr.094052.109
- Brisbin A, Bryc K, Byrnes J, Zakharia F, Omberg L, Degenhardt J, Reynolds A, Ostrer H, Mezey JG, Bustamante CD 2012. PCAdmix: Principal components-based assignment of ancestry along each chromosome in individuals with admixed ancestry from two or more populations. *Human Biology* 84: 343-364. doi: 10.3378/027.084.0401
- Browning BL, Browning SR 2013. Improving the accuracy and efficiency of identity-by-descent detection in population data. *Genetics* 194: 459-471. doi: 10.1534/genetics.113.150029
- Browning SR, Browning BL 2007. Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *The American Journal of Human Genetics* 81: 1084-1097. doi: 10.1086/521987
- Buchmann R, Hazelhurst S. 2014. Genesis Manual. University of the Witwatersrand, Johannesburg.
- Chang CC, Chow CC, Tellier LCAM, Vattikuti S, Purcell SM, Lee JJ 2015. Second-generation PLINK: rising to the challenge of larger and richer datasets. *GigaScience* 4: 7. doi: 10.1186/s13742-015-0047-8

Cox MP, Hudjashov G, Sim A, Savina O, Karafet TM, Sudoyo H, Lansing JS forthcoming. Small traditional human communities sustain genomic diversity over microgeographic scales despite linguistic isolation. *Molecular Biology and Evolution*.

Delaneau O, Marchini J, Genomes Project C, Genomes Project C 2014. Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature Communications* 5: 3934. doi: 10.1038/ncomms4934

Delaneau O, Marchini J, Zagury JF 2012. A linear complexity phasing method for thousands of genomes. *Nat Methods* 9: 179-181. doi: 10.1038/nmeth.1785

GoldenSoftware. 2014. Surfer v.12.01.

Hellenthal G, Busby GB, Band G, Wilson JF, Capelli C, Falush D, Myers S 2014. A genetic atlas of human admixture history. *Science* 343: 747-751. doi: 10.1126/science.1243518

International HapMap C 2005. A haplotype map of the human genome. *Nature* 437: 1299-1320. doi: 10.1038/nature04226

International HapMap C, Altshuler DM, Gibbs RA, Peltonen L, Altshuler DM, Gibbs RA, Peltonen L, Dermitzakis E, Schaffner SF, Yu F, Peltonen L, Dermitzakis E, Bonnen PE, Altshuler DM, Gibbs RA, de Bakker PI, Deloukas P, Gabriel SB, Gwilliam R, Hunt S, Inouye M, Jia X, Palotie A, Parkin M, Whittaker P, Yu F, Chang K, Hawes A, Lewis LR, Ren Y, Wheeler D, Gibbs RA, Muzny DM, Barnes C, Darvishi K, Hurles M, Korn JM, Kristiansson K, Lee C, McCarrol SA, Nemesh J, Dermitzakis E, Keinan A, Montgomery SB, Pollack S, Price AL, Soranzo N, Bonnen PE, Gibbs RA, Gonzaga-Jauregui C, Keinan A, Price AL, Yu F, Anttila V, Brodeur W, Daly MJ, Leslie S, McVean G, Moutsianas L, Nguyen H, Schaffner SF, Zhang Q, Ghori MJ, McGinnis R, McLaren W, Pollack S, Price AL, Schaffner SF,

- Takeuchi F, Grossman SR, Shlyakhter I, Hostetter EB, Sabeti PC, Adebamowo CA, Foster MW, Gordon DR, Licinio J, Manca MC, Marshall PA, Matsuda I, Ngare D, Wang VO, Reddy D, Rotimi CN, Royal CD, Sharp RR, Zeng C, Brooks LD, McEwen JE 2010. Integrating common and rare genetic variation in diverse human populations. *Nature* 467: 52-58. doi: 10.1038/nature09298
- Jakobsson M, Rosenberg NA 2007. CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics* 23: 1801-1806. doi: 10.1093/bioinformatics/btm233
- Kusuma P, Brucato N, Cox MP, Pierron D, Razafindrazaka H, Adelaar A, Sudoyo H, Letellier T, Ricaut F-X 2016. Contrasting Linguistic and Genetic Influences during the Austronesian Settlement of Madagascar. *Scientific Reports* 6:26066. doi: doi: 10.1038/srep26066
- Lawson DJ, Hellenthal G, Myers S, Falush D 2012. Inference of population structure using dense haplotype data. *PLoS Genet* 8: e1002453. doi: 10.1371/journal.pgen.1002453
- Loh PR, Lipson M, Patterson N, Moorjani P, Pickrell JK, Reich D, Berger B 2013. Inferring admixture histories of human populations using linkage disequilibrium. *Genetics* 193: 1233-1254. doi: 10.1534/genetics.112.147330
- May A, Hazelhurst S, Li Y, Norris SA, Govind N, Tikly M, Hon C, Johnson KJ, Hartmann N, Staedtler F, Ramsay M 2013. Genetic diversity in black South Africans from Soweto. *BMC Genomics* 14: 644. doi: 10.1186/1471-2164-14-644
- Mörseburg A, Pagani L, Ricaut F-X, Yngvadottir B, Harney E, Castillo C, Antao T, Hoogervorst T, Kusuma P, Razafindrazaka H, Cardona A, Pierron D, Letellier T, Wee J, Abdullah M, Metspalu M, Kivisild T forthcoming. Multi-layered population

structure and local adaptations in Island Southeast Asians. European Journal of Human Genetics.

Pagani L, Kivisild T, Tarekegn A, Ekong R, Plaster C, Gallego Romero I, Ayub Q, Mehdi SQ, Thomas MG, Luiselli D, Bekele E, Bradman N, Balding DJ, Tyler-Smith C 2012. Ethiopian genetic diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool. Am J Hum Genet 91: 83-96. doi: 10.1016/j.ajhg.2012.05.015

Patterson N, Price AL, Reich D 2006. Population structure and eigenanalysis. PLoS Genet 2: e190. doi: 10.1371/journal.pgen.0020190

Patterson NJ, Moorjani P, Luo Y, Mallick S, Rohland N, Zhan Y, Genschoreck T, Webster T, Reich D 2012. Ancient admixture in human history. Genetics 192: 1065-1093. doi: 10.1534/genetics.112.145037

Pickrell JK, Pritchard JK 2012. Inference of population splits and mixtures from genome-wide allele frequency data. PLoS Genet 8: e1002967. doi: 10.1371/journal.pgen.1002967

Pierron D, Razafindrazaka H, Pagani L, Ricaut F-X, Antao T, Capredon M, Sambo C, Radimilahy C, Rakotoarisoa J-A, Blench RM, Letellier T, Kivisild T 2014. Genome-wide evidence of Austronesian–Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. Proceedings of the National Academy of Sciences 111: 936-941. doi: 10.1073/pnas.1321860111

Reich D, Patterson N, Kircher M, Delfin F, Nandineni MR, Pugach I, Ko AM, Ko YC, Jinam TA, Phipps ME, Saitou N, Wollstein A, Kayser M, Paabo S, Stoneking M 2011. Denisova admixture and the first modern human dispersals into Southeast Asia and Oceania. Am J Hum Genet 89: 516-528. doi: 10.1016/j.ajhg.2011.09.005

- Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T 2003. Cytoscape: A software environment for integrated models of biomolecular interaction networks. *Genome Research* 13: 2498-2504. doi: 10.1101/gr.1239303
- Tamura K, Stecher G, Peterson D, Filipski A, Kumar S 2013. MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. *Molecular Biology and Evolution* 30: 2725-2729. doi: 10.1093/molbev/mst197
- Teo YY, Sim X, Ong RT, Tan AK, Chen J, Tantoso E, Small KS, Ku CS, Lee EJ, Seielstad M, Chia KS 2009. Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. *Genome Res* 19: 2154-2162. doi: 10.1101/gr.095000.109