

Supporting Information

Pugach et al. 10.1073/pnas.1211927110

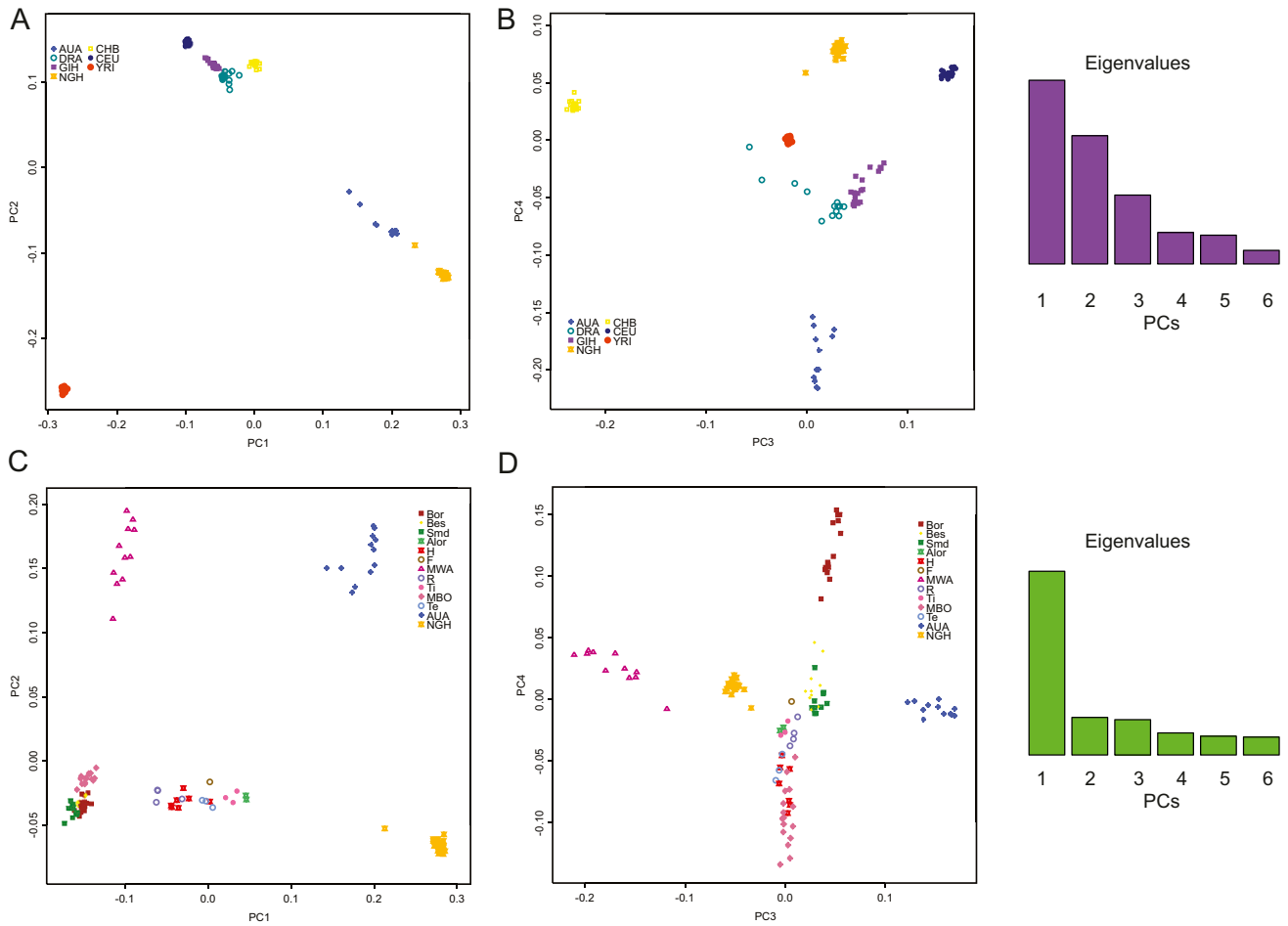


Fig. S1. Results of the PCA. (A) The first two PCs for the AUA, NGH, DRA, and the HapMap populations. (B) PC3 vs. PC4 for the AUA, NGH, DRA, and the HapMap populations. (C) PC1 vs. PC2 for the AUA, NGH, and populations of SE Asia, including the MWA, a Negrito group from the Philippines. (D) PC3 vs. PC4 for the AUA, NGH, and populations of SE Asia. All abbreviations are described in Table S1.

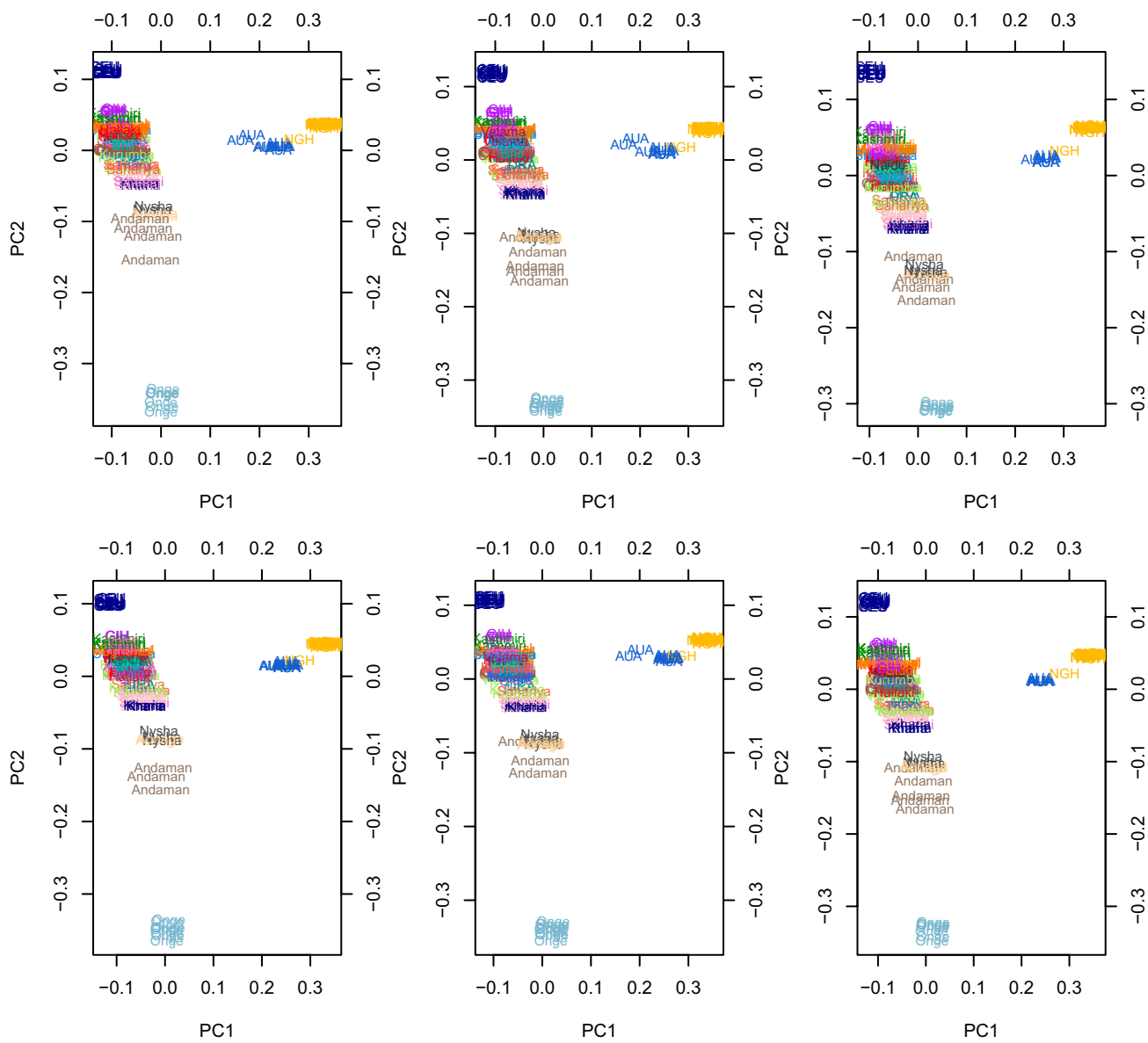


Fig. S2. Results of six runs of PCA, each performed on randomly sampled 70% of the samples.

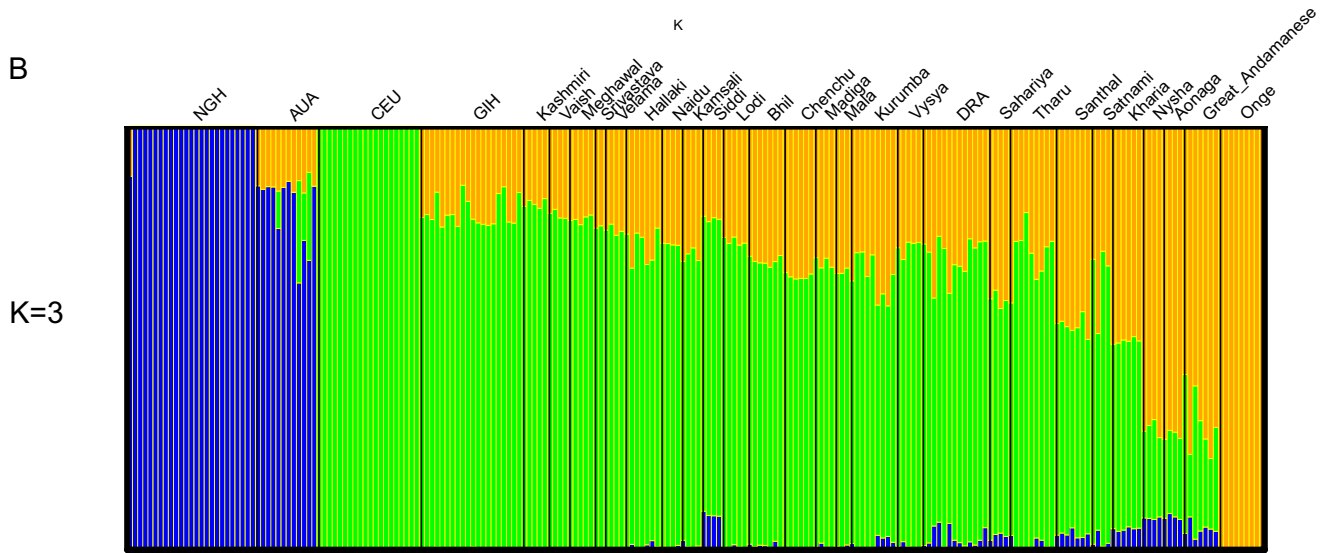
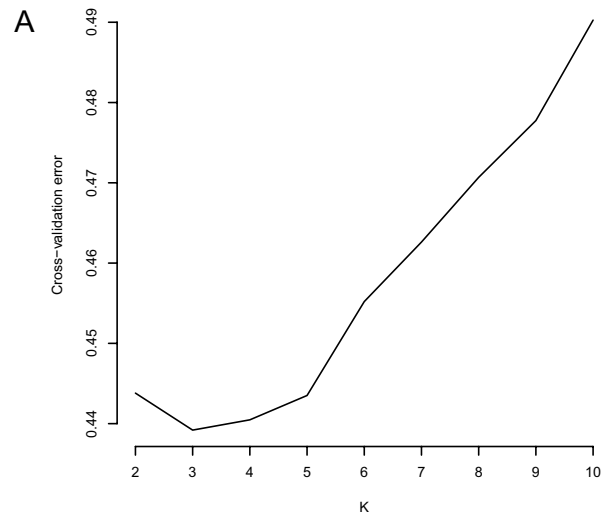


Fig. S3. (A) Estimated cross-validation error for the ADMIXTURE runs involving NGH, AUA, CEU, and Indian populations for K = 2 through K = 10. (B) Results of the ADMIXTURE analysis for K = 3.

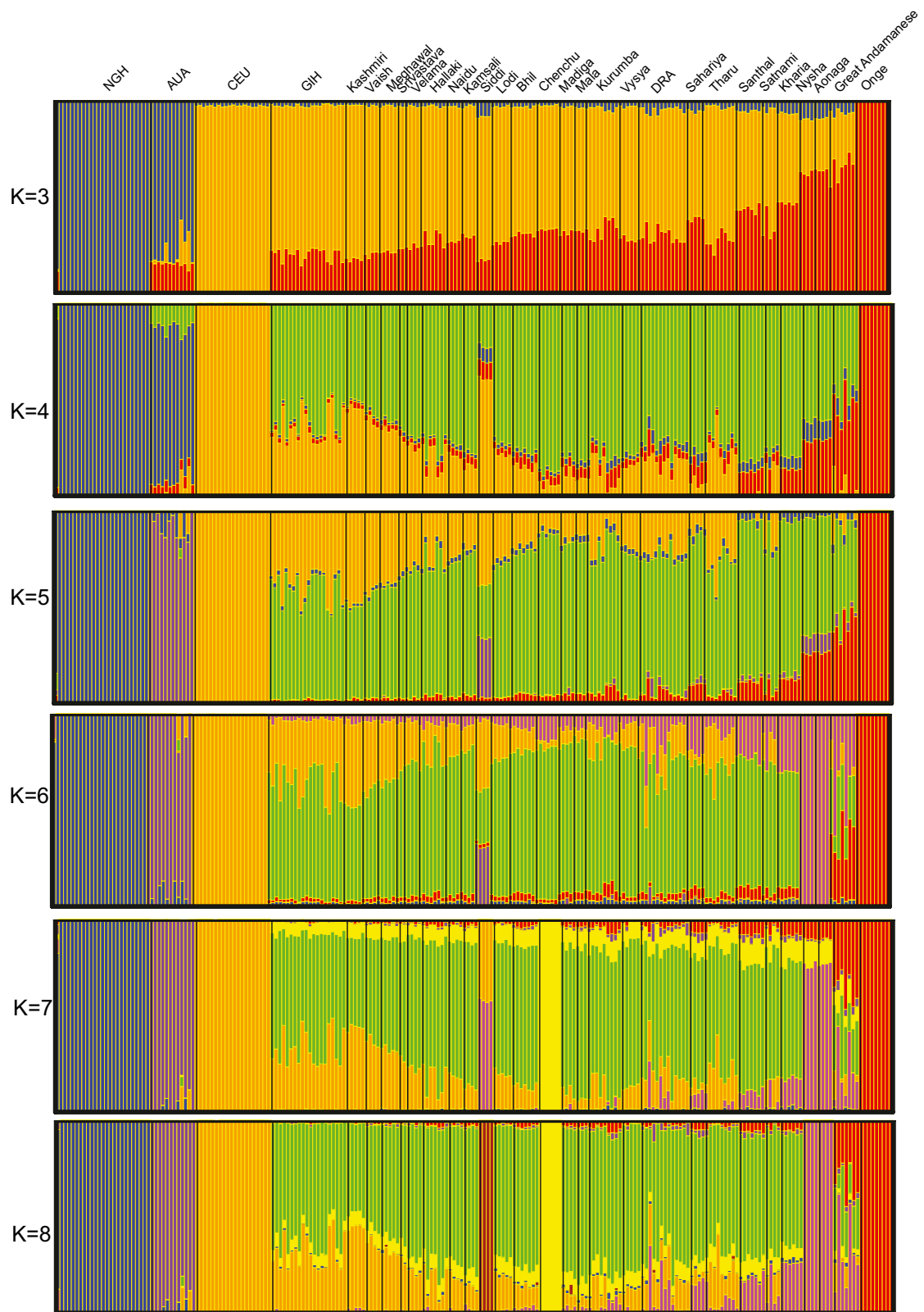


Fig. S4. Results of the *frappe* analysis based on ~450,000 markers, not thinned for SNPs in LD. We tested $K = 3$ through $K = 8$ and performed three independent runs for each value of K . The highest K value that gave the same results across all three runs was $K = 4$, for which Australians are assigned a component that is present at high frequency in mainland India and shared exclusively between Australia and India.

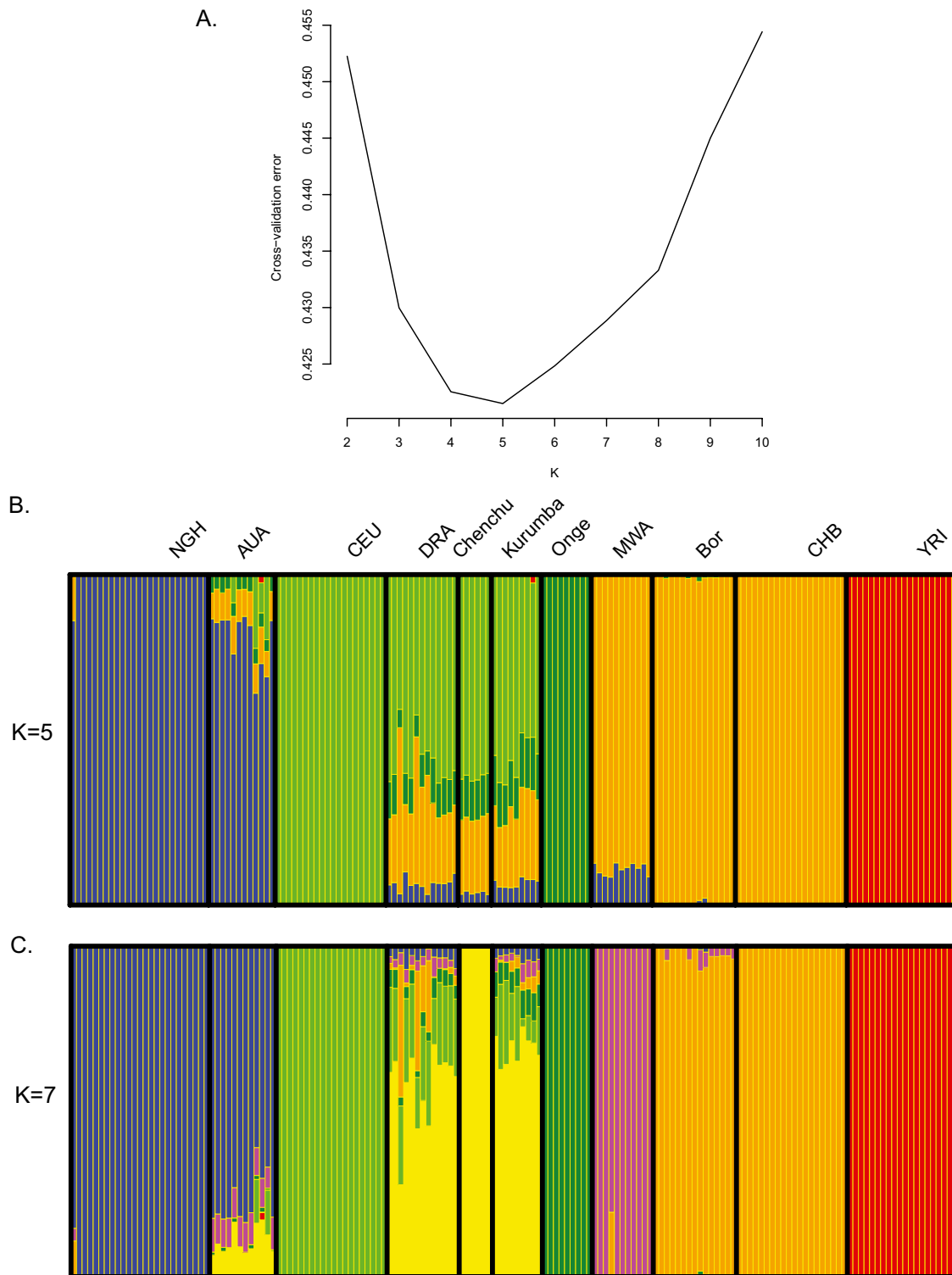


Fig. S5. Results of the ADMIXTURE analysis with individuals of African, European, Asian, and SE Asian ancestry, including the Mamanwa, a Negrito population from the Philippines. (A) Estimated cross-validation error. (B) Results for $K = 5$. The proportion of Australian ancestry not shared with the New Guineans most closely resembles ancestry profile of the three Indian populations (light green, dark green, and orange). (C) Results for $K = 7$. Eleven percent of the Australian ancestry is attributed to India (yellow), and an additional 9% is attributed to the Mamanwa (purple).

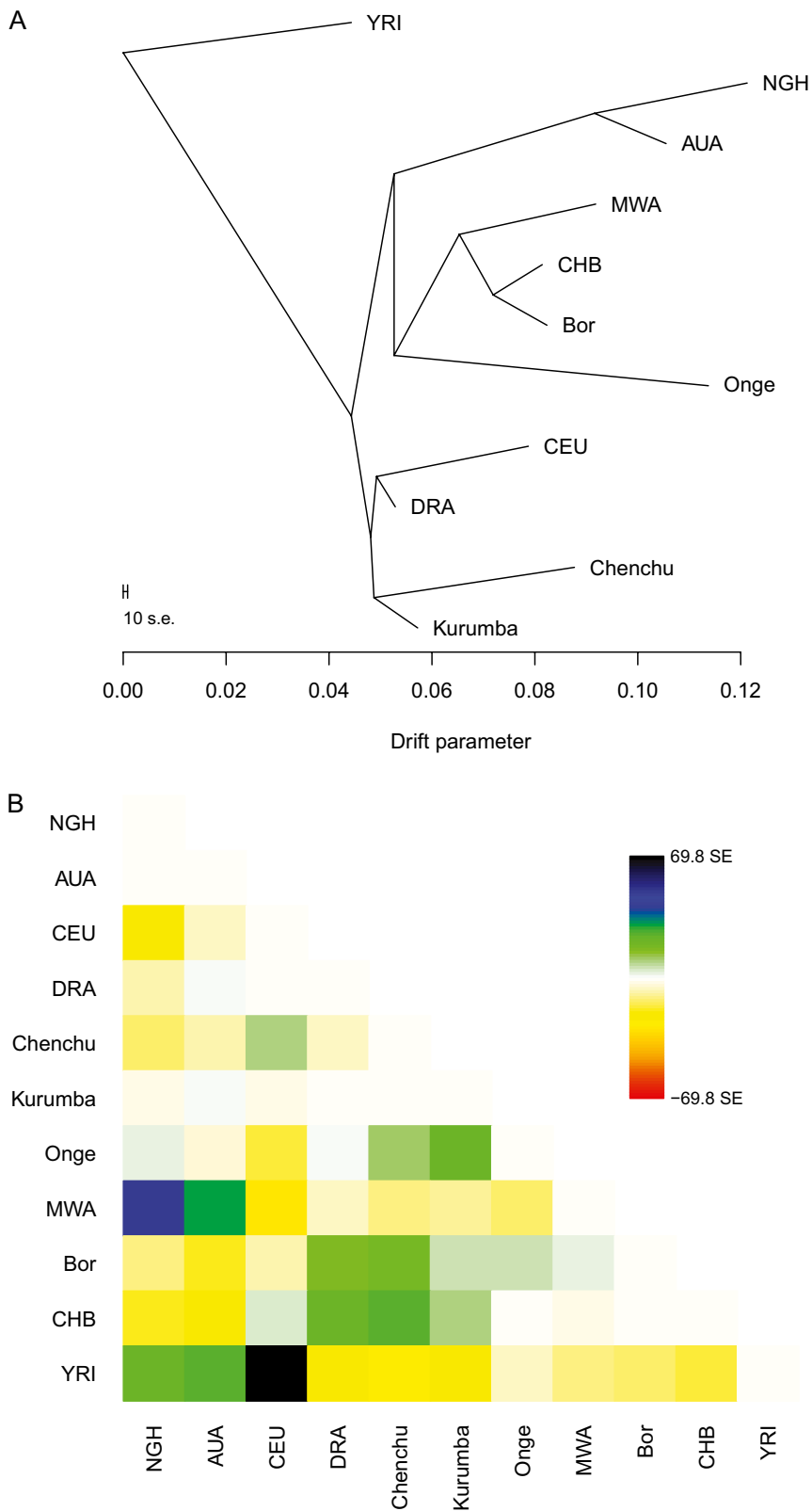


Fig. S6. (A) Maximum-likelihood tree of 11 populations, including YRI and CEU. (B) Residual fit from this tree.

Parental populations: Papua New Guinea (NGH) and India
Admixed: Aboriginal Australian (AUA)

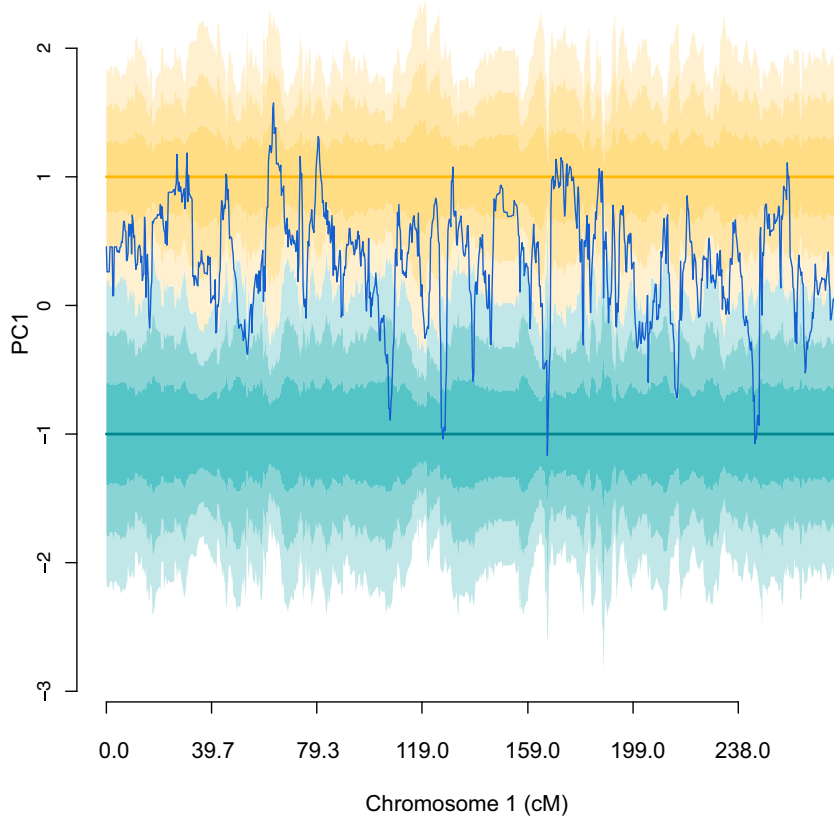


Fig. S7. StepPCO results for an unphased chromosome 1 of an aboriginal Australian individual. Indian (blue) and NGH (orange) populations are used as parental groups. Chromosomal regions of the admixed genome are assigned to either “blue” or “orange” ancestry, with heterozygous regions falling in the middle. The mean PC1 coordinates for each parental population are centered at 1 and -1; progressively lighter shading surrounding the mean of each parental group indicate ± 1 , ± 2 , or ± 3 SDs from the mean.

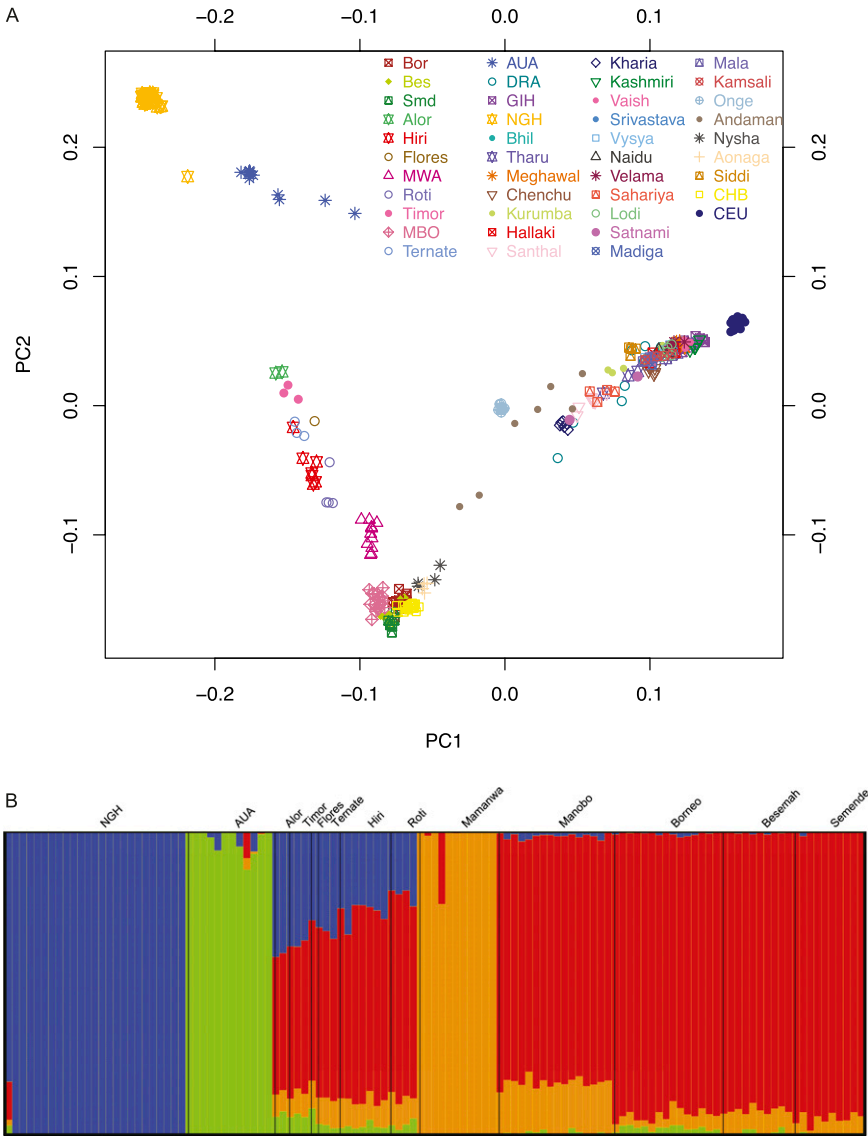


Fig. 58. (A) Results of the PC analysis, carried out on populations of Greater Australia, SE Asia, and India. Two Indian populations Ao Naga and Nyshi belong to the Asian grouping; these two groups come from the northeastern part of India and speak Tibeto-Burman languages, and their east Asian ancestry has been shown previously (1). East Indonesian populations form a cline between Borneo and New Guinea, reflecting the Papuan and Asian (associated with the Austronesian expansion) genetic ancestry of these populations (2). (B) Results of the *frappe* analysis on populations of Greater Australia and SE Asia. Neither the PCA nor *frappe* results show any signal of gene flow between SE Asia and Australia.

1. Chaubey G, et al. (2011) Population genetic structure in Indian Austroasiatic speakers: The role of landscape barriers and sex-specific admixture. *Mol Biol Evol* 28(2):1013–1024.
 2. Xu S, Pugach I, Stoneking M, Kayser M, Jin L; HUGO Pan-Asian SNP Consortium (2012) Genetic dating indicates that the Asian-Papuan admixture through Eastern Indonesia corresponds to the Austronesian expansion. *Proc Natl Acad Sci USA* 109(12):4574–4579.

Table S1. Information on samples used in this study

Sampling location	Population	Abbreviation	Sample size	Ref(s).
Australia Northern Territories	Australians	AUA	12	Redd and Stoneking (1); Reich et al. (2)
Papua New Guinea	Highlanders	NGH	25	Wollstein et al. (3)
Borneo	Land Dayak	Bor	15	
Sumatra	Besemah	Bes	10	
	Semende	Smd	10	
Philippines	Manobo	MBO	16	
	Mamanwa (Negrito)	MWA	11	
Indonesia: Nusa Tenggara	Alor	Alor	2	
	Flores	Flor	1	
	Roti	Roti	4	
	Timor	Tim	3	
Moluccas	Hiri	Hiri	7	
	Ternate	Ter	3	
South India	Dravidian	DRA	13	Reich et al. (2)
India	Bhil		7	
	Meghwal		5	
	Chenchu		6	
	Kurumba		9	
	Hallaki		7	
	Santhal		7	
	Kharia		6	
	Kashmiri		5	
	Vaish		4	
	Srivastava		2	
	Vysya		5	
	Naidu		4	
	Velama		4	
	Sahariya		4	
	Lodi		5	
	Satnami		4	
	Madiga		4	
	Mala		3	
	Kamsali		4	
	Onge		9	
	Andaman		7	
	Nysha		4	
	Ao Naga		4	
	Siddi		4	Reich et al. (4)
Houston, TX	Gujarati Indians	GIH	20	
Utah	European ancestry	CEU	20	
Ibadan, Nigeria	Yorubans	YRI	20	
Beijing, China	Han Chinese	CHB	20	Altshuler et al. (5)

1. Redd AJ, Stoneking M (1999) Peopling of Sahul: mtDNA variation in aboriginal Australian and Papua New Guinean populations. *Am J Hum Genet* 65(3):808–828.
2. Reich D, et al. (2011) Denisova admixture and the first modern human dispersals into Southeast Asia and Oceania. *Am J Hum Genet* 89(4):516–528.
3. Wollstein A, et al. (2010) Demographic history of Oceania inferred from genome-wide data. *Curr Biol* 20(22):1983–1992.
4. Reich D, Thangaraj K, Patterson N, Price AL, Singh L (2009) Reconstructing Indian population history. *Nature* 461(7263):489–494.
5. Altshuler, DM, et al. (2010) Integrating common and rare genetic variation in diverse human populations. *Nature* 467(7311):52–58.