

Fig. S1: Location of populations used in this study. Negrito populations are labeled red and non-Negrito populations are labeled in blue. Map obtained from Google maps.

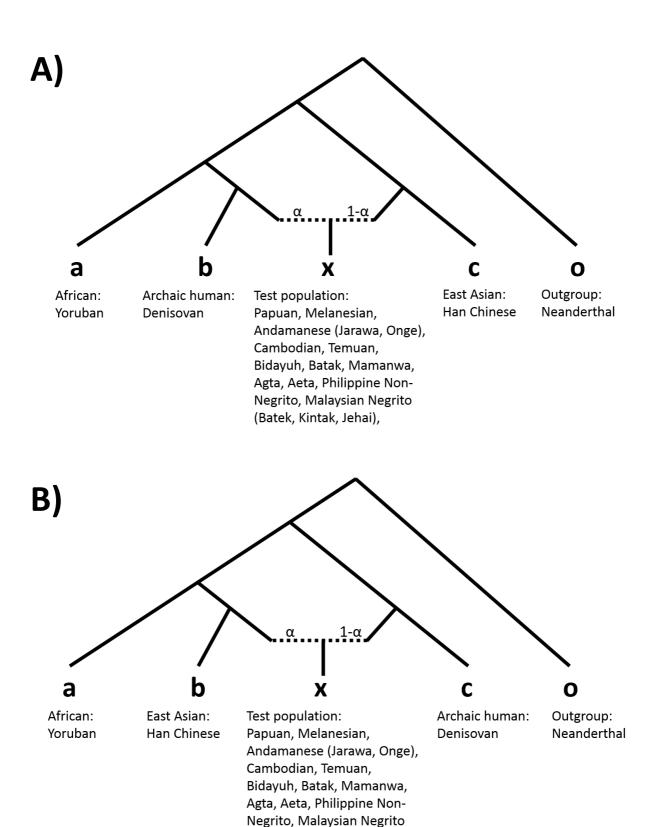


Fig. S2: Assumed topologies for the f_4 ratio test in estimating the proportion of Denisovan genetic component α in tree A) and 1- α in tree B).

(Batek, Kintak, Jehai),

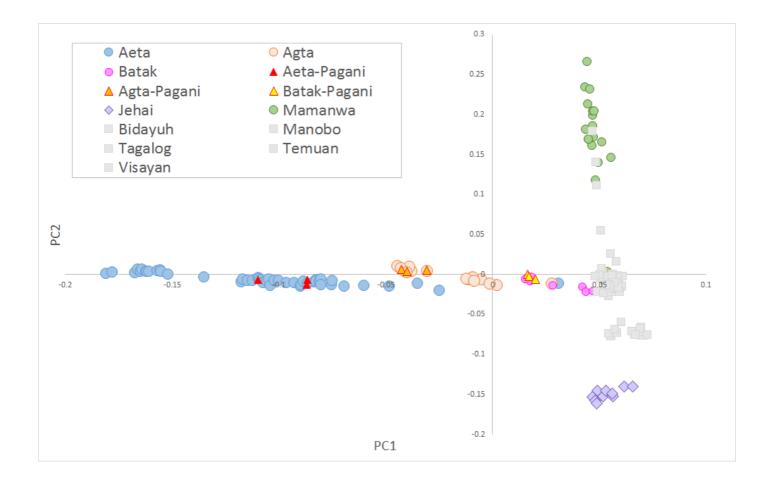


Fig. S3: Principal Component Analysis plot using genome-wide SNP data from this study and variants from whole genome sequencing data of nine Philippine Negrito individuals reported by Pagani et al. 2016.

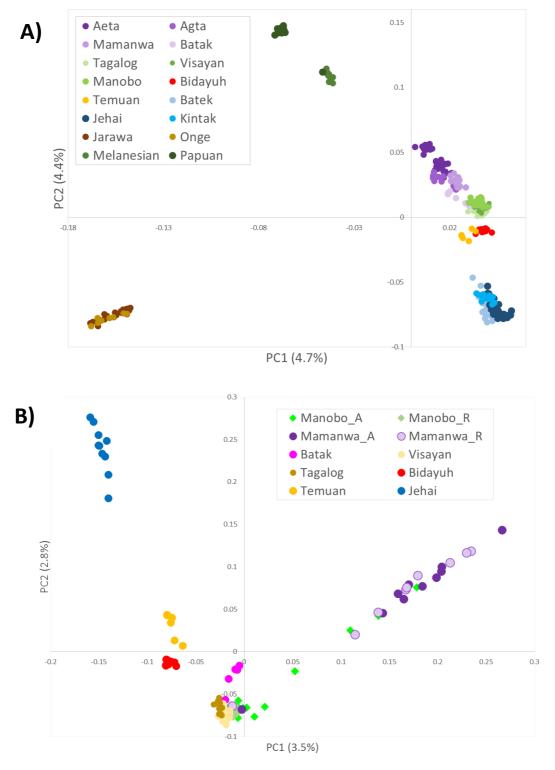


Fig. S4: A) Principal Component Analysis (PCA) plot of the populations in main Figure 1 with the addition of Papuan and Melanesian populations; B) PCA plot of Malaysian and Philippine populations, excluding Agta and Aeta. The A and R suffix for Manobo and Mamanwa individuals represent Archival samples (sampled more than 30 years ago) and Recent samples (sampled less than 10 years ago). These dates use the year 2016 as the reference point.

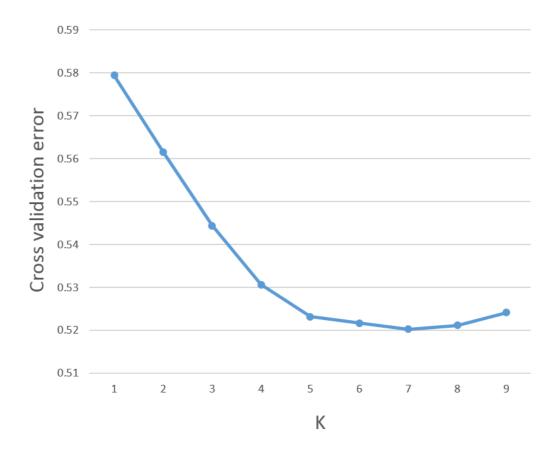


Fig. S5: Cross-validation (CV) error for ADMIXTURE runs assuming k=1 to k=9. Low CV error suggests a more reliable estimate of K.

D (Philippine Negrito, Andamanese; French, x)

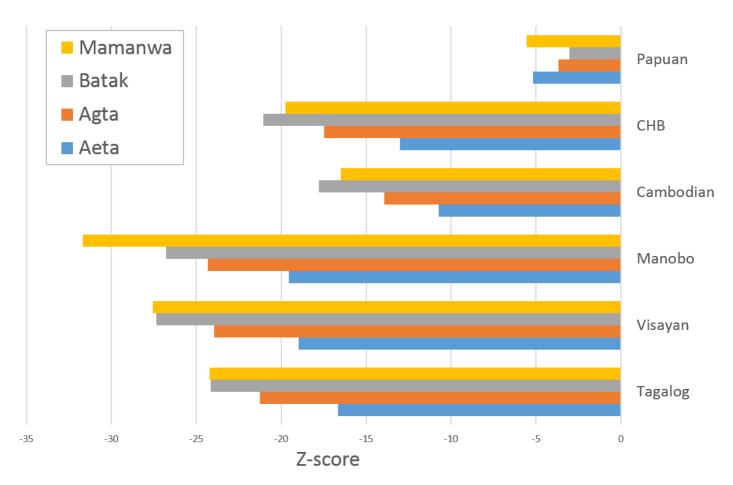


Fig. S6: Formal test for admixture using D statistics. Significantly negative Z-scores suggest admixture between the Philippine Negritos (Mamanwa, Batak, Agta, and Aeta) and Philippine Non-Negritos (Manobo, Tagalog, and Visayan).

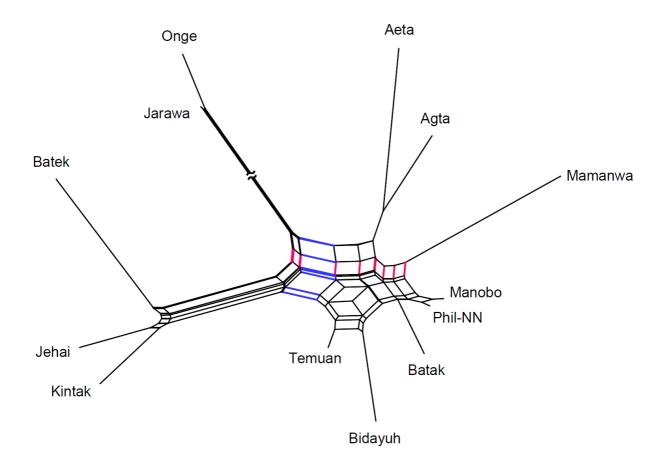


Fig. S7 NeighborNet network based on Fst distances between populations. The long branch length leading to Andamanese (Jarawa and Onge) was truncated for clarity. Splits that group the Andamanese and Malaysian Negritos and those grouping the Andamanese and Philippine Negritos (except for Batak) are shown as blue and red colors, respectively.

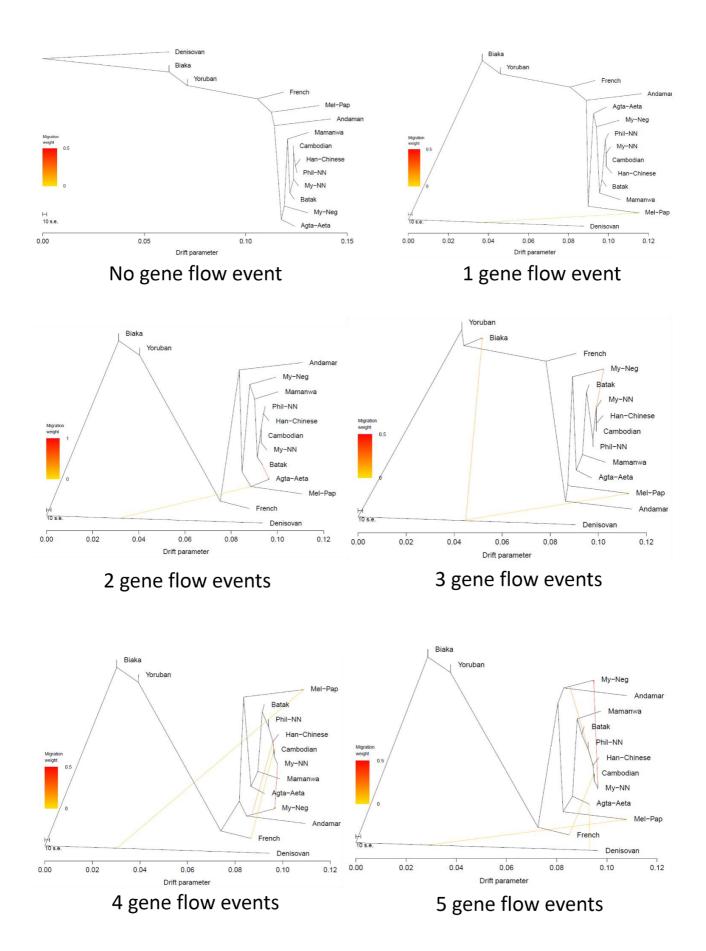


Fig. S8: Treemix results assuming no gene flow events up to 5 events.

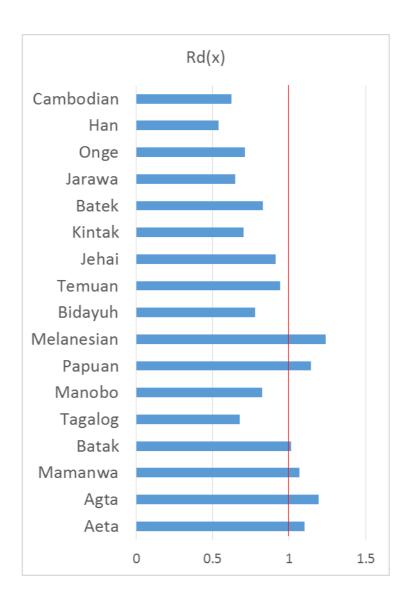


Fig. S9: Detection of Denisovan introgression in various Southeast Asian populations using the $R_D(X)$ statistic (Qin and Stoneking, 2015), which is the ratio of Denisovan and Neanderthal introgression based on the f_4 statistic. Populations with values higher than 1 (red vertical line) suggest to have Denisovan ancestry.

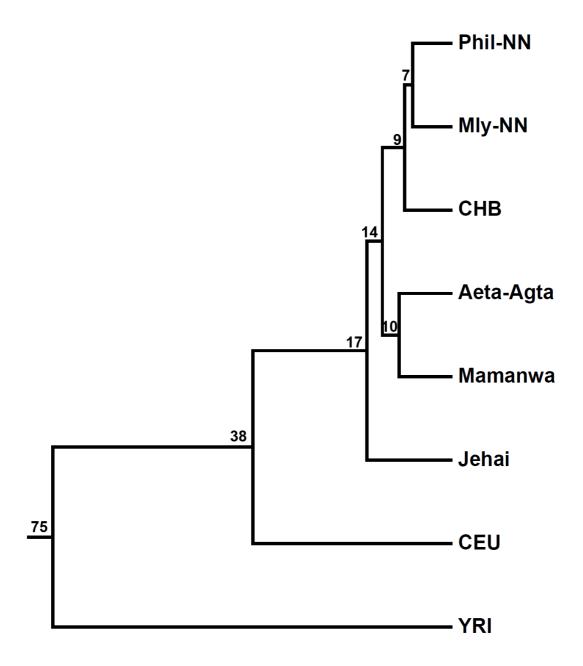


Fig. S10: A UPGMA tree constructed from pairwise divergence times of populations, assuming 30 years generation time. Dataset with Malaysian and Philippine Negritos using 480k SNPs is used. The divergence time estimates are shown as thousand years ago (kya).

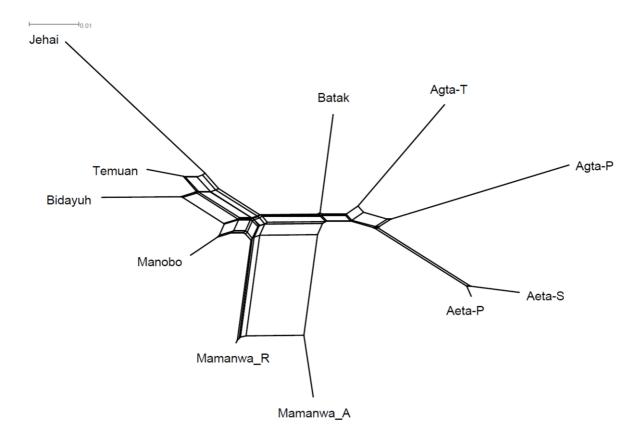


Fig. S11 Neighbor-Net network based on Fst distances between populations. The A and R suffixes for the Mamanwa represent Archival samples sampled more than 30 years ago (at the time of publication) and Recent samples (sampled less than 10 years ago). The T, P, and S suffixes for the Agta and Aeta represent different sampling locations.

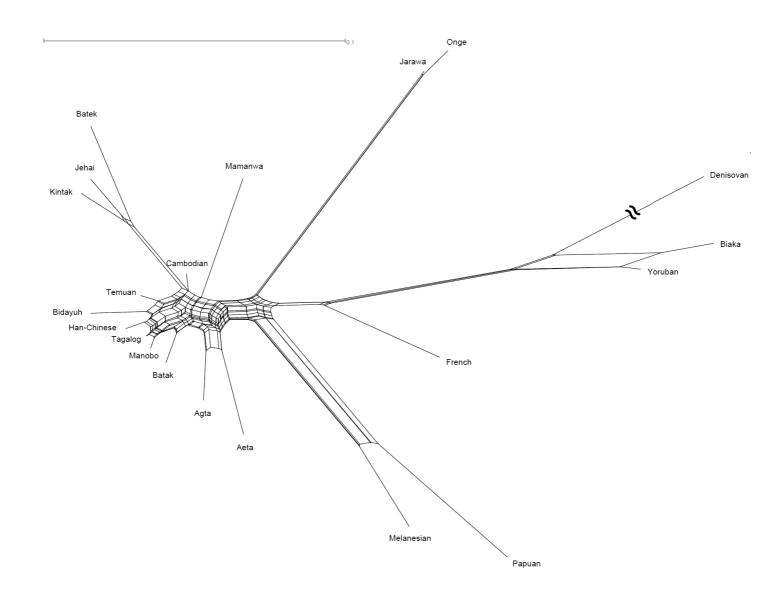


Fig. S12: NeighborNet network based on Fst distances between populations. The long branch length leading to Denisovan was truncated for clarity. Approximately 40k SNPs were used.

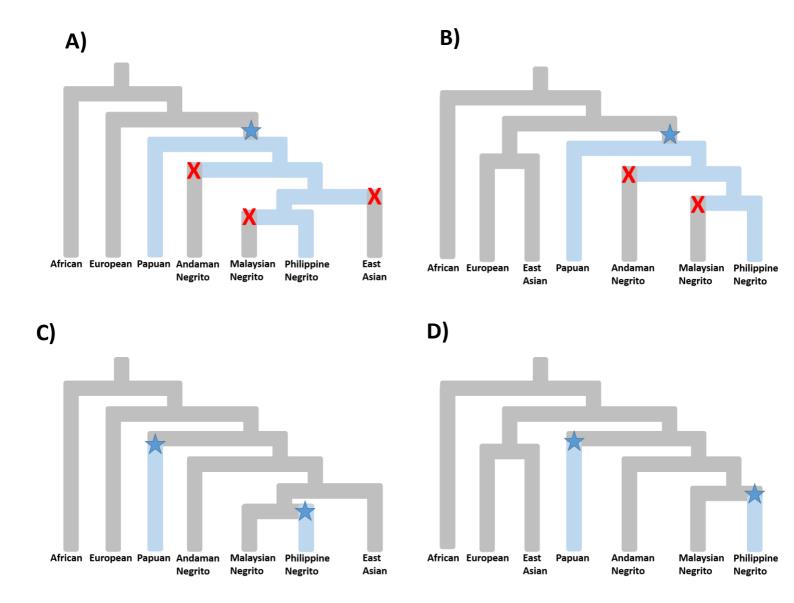


Fig. S13: Possible scenarios of Denisovan introgression in modern humans. A) Single-wave into Asia followed by single Denisovan introgression event in the ancestors of all Asians. Then parallel loss occurred in Andamanese, Malaysian Negritos and East Asians; B) Double-wave into Asia followed by single episode of Denisovan introgression in the common ancestor of Negritos and Papuans. Then parallel loss happened in Andaman and Malaysian Negritos; C) Single-wave into Asia followed by independent introgression in Papuans and Philippine Negritos; D) Double-wave into Asia followed by independent Denisovan introgression in Papuans and Philippine Negritos. Blue stars represent Denisovan admixture events. Red crosses represent loss of Denisovan introgressed regions.