Supplementary Information for:

Ancestry, admixture and selection in Colombian genomes

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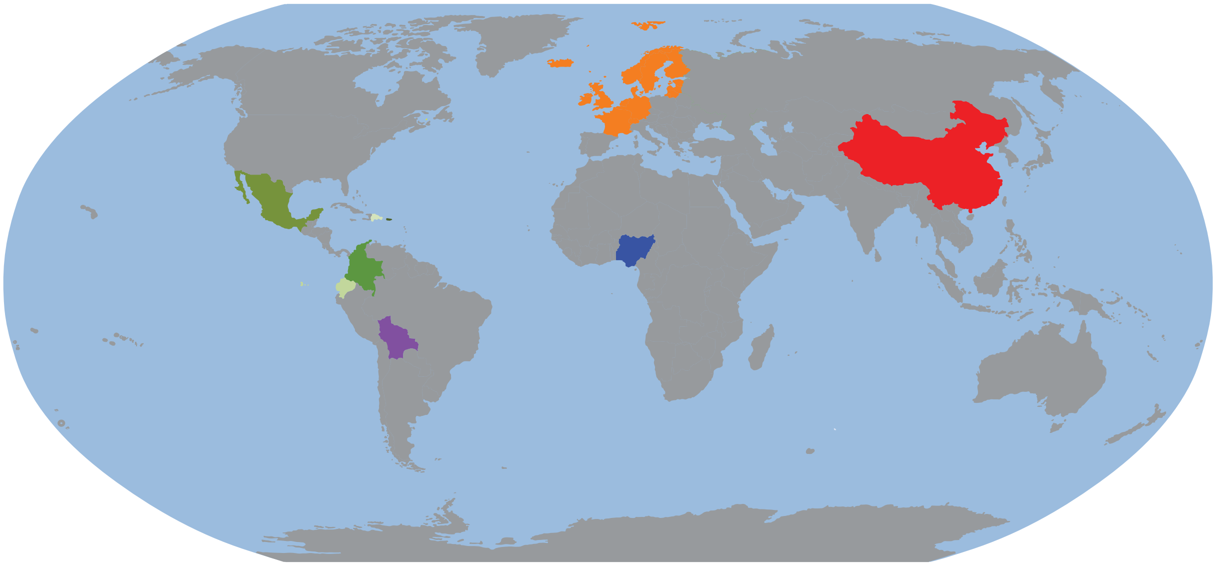


Ancestral Populations from Around the World

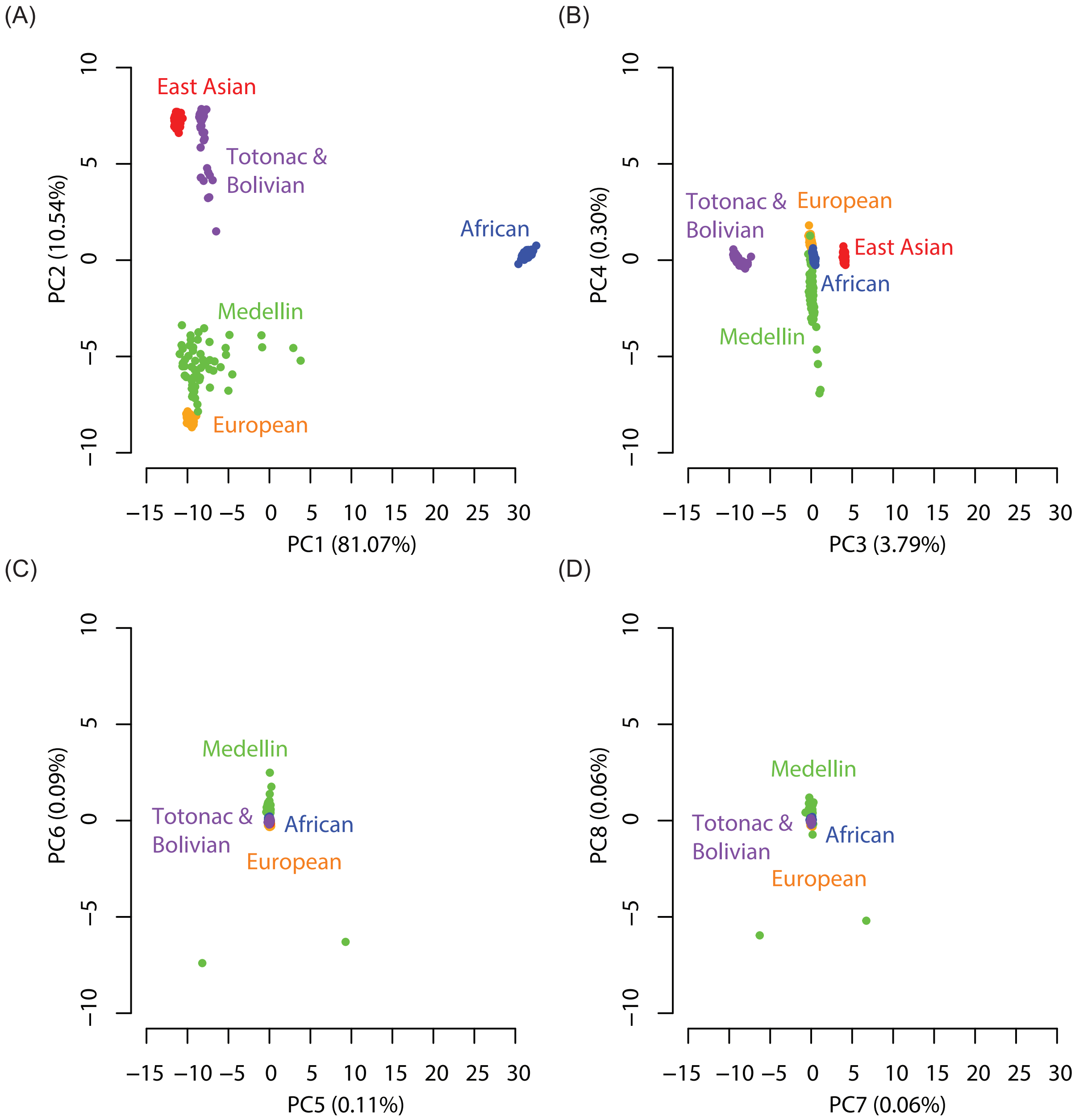
Name	Color	Ancestral Origin	n	Source (PMID)	Platform
CEU	🟧	Northern & Western Europe	85	23128226	Whole genome sequencing
CHB	🟥	Beijing, China	92	23128226	Whole genome sequencing
Totonac & Bolivian	🟪	Mexico & Bolivia	45	22606979	SNP microarray
YRI	🟦	Nigeria	87	23128226	Whole genome sequencing

Admixed Populations from the Americas

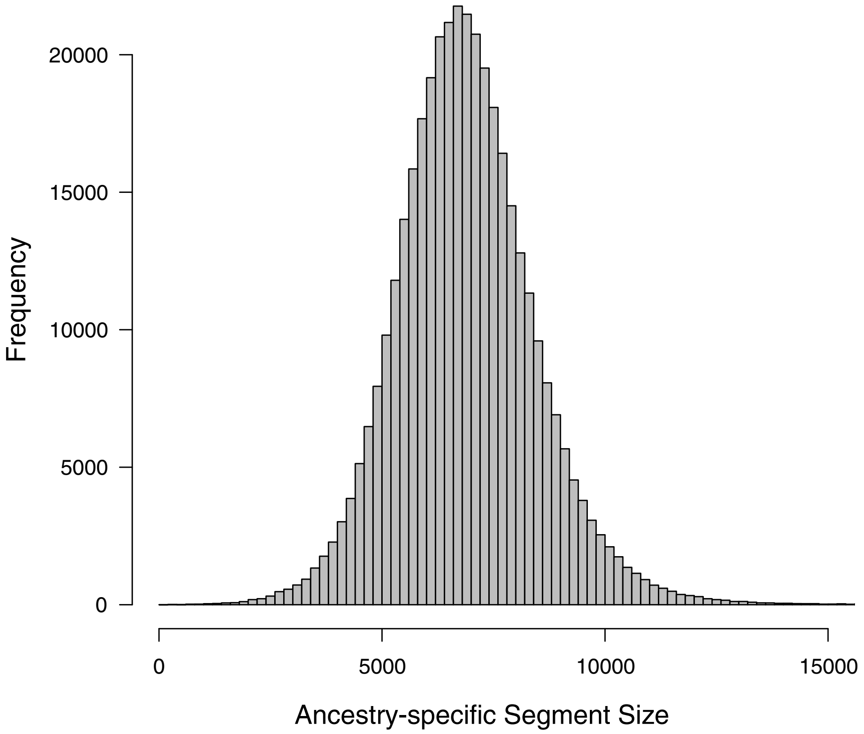
Name	Color	Country	n	Source (PMID)	Platform
CLM	🟩	Medellin, Colombia	60	23128226	Whole genome sequencing
Colombian	🟩	Colombia	26	20445096	Illumina 610K array
Dominican Republican	🟩	Dominican Republic	27	20445096	Illumina 610K array
Ecuador	🟩	Ecuador	20	20445096	Illumina 610K array
Mexican	🟩	Mexico	112	20445096	Affymetrix GeneChip 500K Array Set
Puerto Rican	🟩	Puerto Rico	27	20445096	Illumina 610K array

S1 Figure. World-wide source of genome sequence and genotype data analyzed in this study. The global locations of putative ancestral populations are shown – African (blue), Asian (red), European (orange) and Native American (purple) – along with the locations of admixed American populations (green). Information on the source populations, number of samples, supporting publication and genome characterization platform is provided.

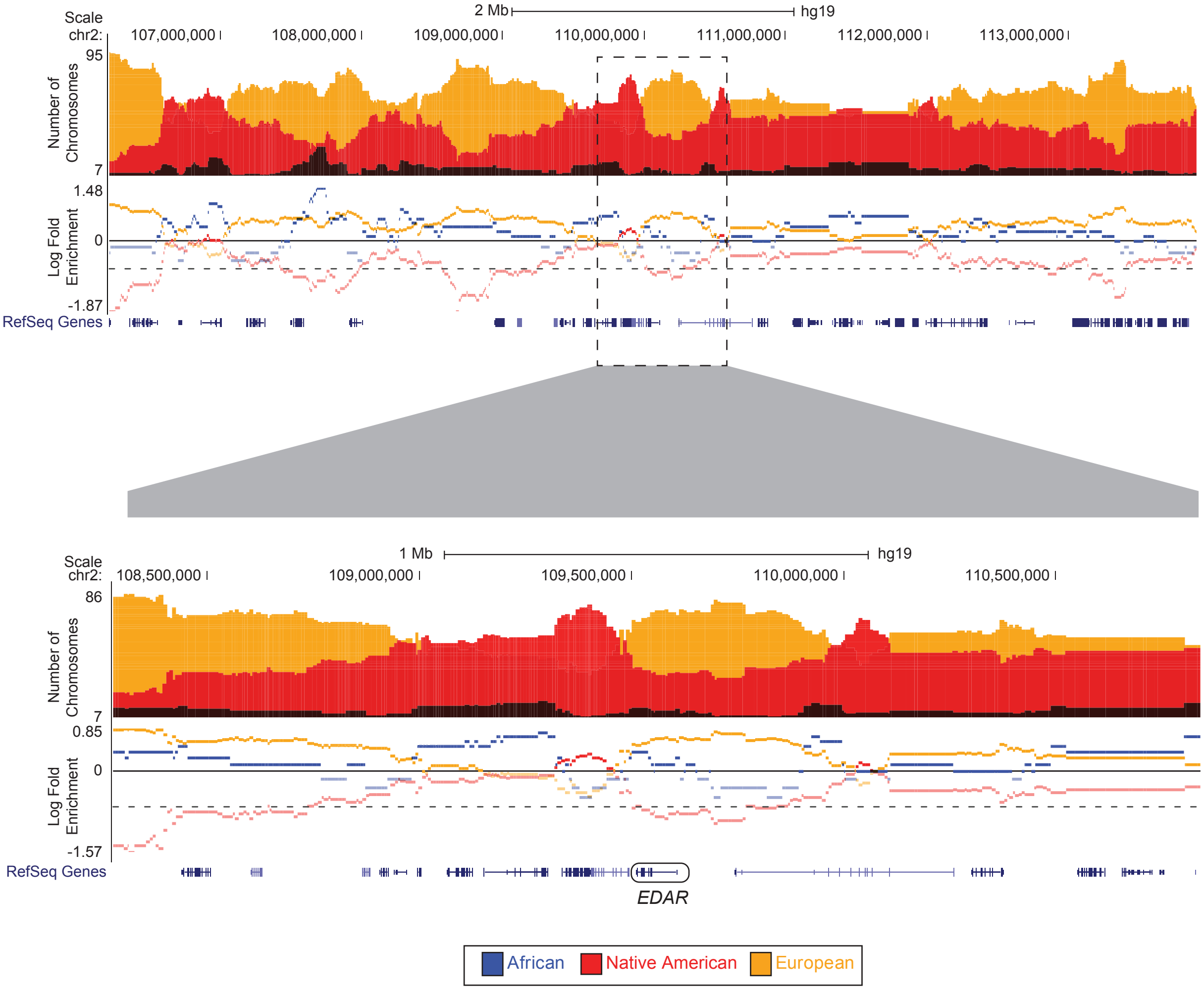
Note: The global map shown here was modified from http://commons.wikimedia.org/wiki/File:World_Map_Blank_-_with_blue_sea.svg, which has been released into the public domain and thus free to be used by anyone for any purpose.



S2 Figure. PCA of pairwise allele sharing distances among admixed Colombian genomes from Medellin compared to putative ancestral populations from Africa, the Americas, Asia and Europe. The panels have comparisons of the successive principal components (PCs): (A) PC1-PC2, (B) PC3-PC4, (C) PC5-PC6 and (D) PC7-PC8.



S3 Figure. Size distribution of the ancestry-specific chromosomal segments used for the ancestry enrichment analysis.



S4 Figure. Example of an Asian (American)-depleted region found at the EDAR locus. Population-wide chromosome counts from the three ancestry-components are shown above the genomic axis and log-fold enrichment values (observed counts/genomic average counts) for the ancestry components are shown below the axis. The upper panel shows a ~7Mb region surrounding the locus on chromosome 2, and the lower panel shows a zoomed in view centered on the Asian (American) ancestry-depleted gene EDAR.