



Figure S2. Enrichment of genic and non-genic SNPs for values of δ between selected pairs of populations.

Enrichments of genic and nongenic SNPs are calculated within each δ value bin, as in Figure S1 and main text (width 0.1). Bootstrap confidence intervals are indicated by dotted lines (see main text). SNPs where the derived allele is fixed in the first population and absent in the second are depicted on the right side of the plot (near 1); SNPs where the derived allele is fixed in the second population and absent in the first are depicted on the left side of the plot (near -1). The number above the most extreme δ bins indicates the proportion of bootstrap simulations where an enrichment value was defined for the given bin (see Results); if no value is listed, the proportion is 1. Values less than 0.95 can be considered insignificant. (A) Kenyan Bantu and Maasai. (B) \neq Khomani Bushmen and Yoruba. (C) Mbuti and Namibian San. (D) Hadza and Mbuti Pygmies.