



Figure S1: Probability that the globally minor allele at a locus has a given geographic distribution pattern, considering each of 22 autosomes and the two sex chromosomes. Probabilities are calculated using all non-singleton SNPs on each chromosome and $g = 500$ ($g = 150$ for the Y chromosome). Patterns that are present at greater than 1% frequency on any autosome are indicated, with all other patterns grouped into the “Other” category.