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Supplemental Data

Population Genetic Structure of the People of Qatar

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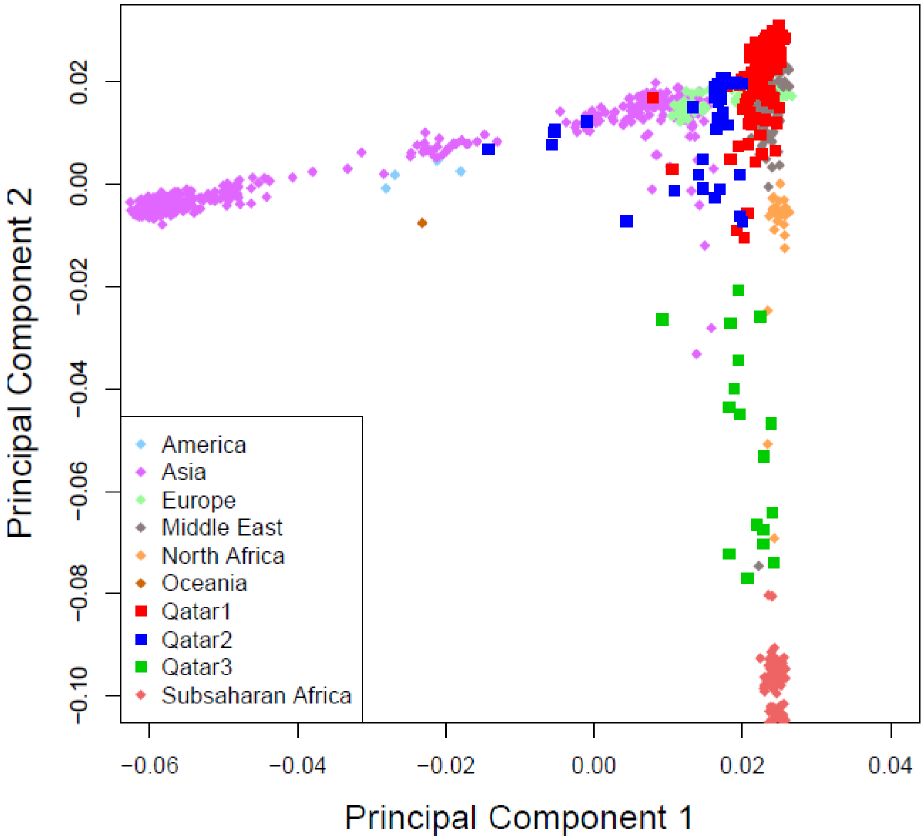

Figure S1. PCA of HGDP and Qatari Samples on Low-F_{ST} SNPs

We calculated F_{ST} for all SNPs between the Qatari samples and the HGDP European populations and selected a subset of SNPs that had F_{ST} below the mean. We repeated the PCA analysis on these SNPs and plotted the results. The resulting figure differs little from the original Figure 2 and, most importantly, the three clusters of the Qatari subgroups are still clearly visible as in the original figure. Therefore, although ascertainment bias may have more subtle effects on the analysis of the Qatari population sample, the discovery of the three Qatari subpopulations, as well as subsequent analysis on these three subgroups, seems robust to the choice of genotyped SNPs.

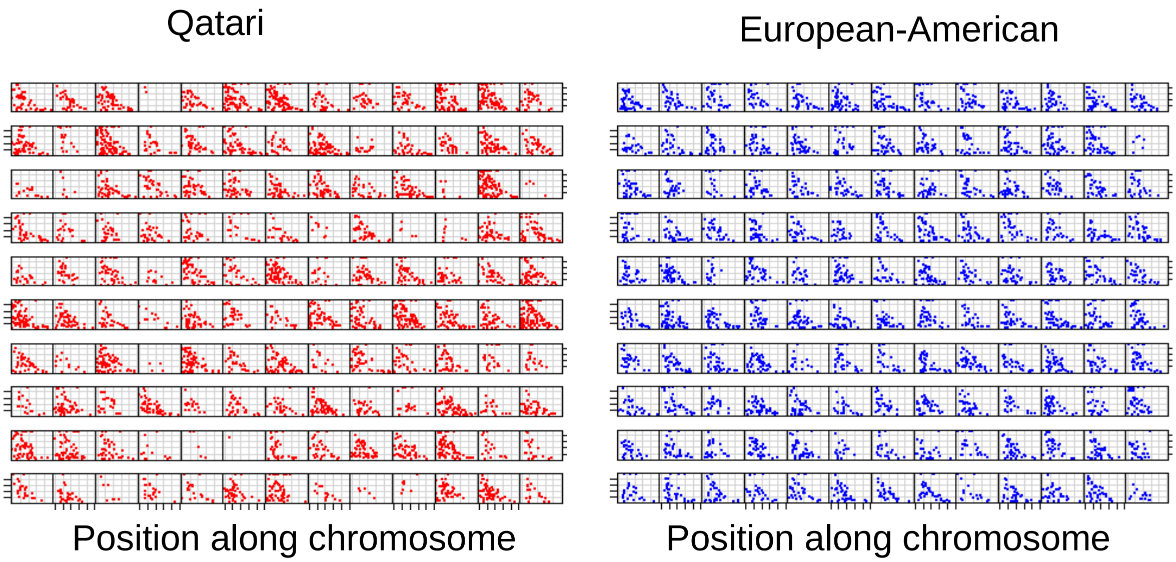

Figure S2.

On the left are plotted results from 130 individuals from the Qatari sample, and on the right are results from 130 individuals from the European-American population sample. Each cell of the figure is a different individual, and within each cell, the x axis is the position along a chromosome (0 -250 Mbp) and the y axis is the chromosome number. Each colored segment represents a block of sequence in which SNP marker genotypes are homozygous. Note the great range in homozygosity among the Qatari compared to the European-Americans.