

## Supplemental Materials and Methods

### *Populations sampled*

The American populations sampled have been described in Smith *et al.* (2000) except the Aleut, Huichol, Mixtec, and Seri, which have been described in Rubicz *et al.* (2003), Kemp (2006), Hollenbach *et al.* (2001), and Infante *et al.* (1999), respectively.

The sampling locations for the Asian populations are as follows: Chukchi: Anadyr, Chukotka Autonomous Okrug; Koryaks: Ezzo, Kamchatka; Even: Topolinoe, Yakutia; Mongolian: Ulan Bator, Mongolia. The Altaian samples were all collected in the Republic of Altai at the following locations: Northern Altaian: Turochak; Southern Altaian: Mendur-Sokkon; Altai Kazakh: Kosh-Agach. Twenty-five of the Southern Altaian samples in this study have been described in Crawford *et al.* (2002).

### *Ascertainment of the 9RA*

The forward and reverse primers we used, available online from the Marshfield Clinic Mammalian Genotyping Service (MGS), are 5'-TAGGATTTGAGACAAATGAAAGC-3' and 5'-TTAGCTGCTTCTGGGAAAGA-3', respectively. Amplification was performed for 60 cycles with the following parameters: denaturation at 94°C for 30 seconds, annealing at 57 °C for 30 seconds (- 0.1°C each cycle), and elongation at 72 °C for 40 seconds. Genotyping was conducted on an ABI Prism® 310 Genetic Analyzer and fragments were analyzed with GeneScan® Analysis Software. Four of our Native American samples were genotyped for D9S1120 at the MGS to calibrate the size of the amplicons we analyzed with the sizes reported in Zhivotovsky *et al.*(2003).

### *Mean heterozygosity and number of alleles*

To compare  $F_{ST}$  and heterozygosity at D9S1120 with that at other loci, we used a dataset of four American HGDP populations that have been genotyped for 783 microsatellites. For this dataset, mean heterozygosity is significantly different for loci grouped by number of alleles (Welch (1951) ANOVA,  $F=32.2221$ ,  $p<0.0001$ ). There are eight alleles at locus D9S1120 in the four pooled American HGDP populations. The mean heterozygosity is not significantly different for loci with eight alleles compared to nine (ANOVA,  $F=0.2632$ ,  $p=0.6089$ ). Therefore, we reduced the dataset to 116 loci with eight or nine alleles in the four pooled American HGDP populations.

### **References**

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