

Population	N <sup>a</sup>	SNPs	Source	Mean relatedness	<i>P</i>
Europeans	28	All <sup>b</sup>	Reported <sup>c</sup>	-0.00016	0.739
			Replication	-0.00016	0.806
		MHC	Reported	-0.043	0.015
			Replication	-0.043	0.014
Yorubans	27	All	Reported	0.00185	<0.001
			Replication	0.00185	<0.001
		MHC	Reported	0.015	0.23 <sup>d</sup>
			Replication	0.015	0.308

**Table S1. Replication of previous findings in Hap2 mate pairs.** Mean relatedness for mate pairs is shown for each population and each set of SNPs under consideration, along with the nominal significance of its deviation from expectation (*P*). Highlights indicate results previously reported to be significant [13], which are the focus of this study. In the interest of completeness, corresponding figures are also shown for results not examined further. <sup>a</sup>Of the 30 couples in each population, the number remaining after exclusions due to the presence of relatives. <sup>b</sup>All autosomal SNPs. <sup>c</sup>Reported by Chaix *et al.* [13]. <sup>d</sup>As reported.