

Genotypes	Couples <sup>a</sup>		SNPs		Het-het <sup>b</sup>	Relatedness				Z	P	Remarks
	Subset	N	Subset	MAF		Mates		Non-mates				
						mean	s.d.	mean	s.d.			
Hap2, Phased	all	28	all	≥5%	.5	-0.043	n/a	n/a	n/a	n/a	0.015	Reported <sup>c</sup>
						-0.043	0.080	-0.0020	0.100	-0.41	0.014	Replication
						-0.020	0.061	-0.0021	0.058	-0.31	0.288	Median <sup>d</sup>
						-0.043	0.080	-0.0020	0.100	-0.41	0.0218	100,000 trials <sup>e</sup>
						-0.043	0.081	-0.0020	0.100	-0.40	0.0217	All in MAF <sup>f</sup>
						-0.043	0.078	-0.0019	0.098	-0.42	0.0190	Permutations of excluded couples <sup>g</sup>
						<b>-0.043</b>	<b>0.081</b>	<b>-0.0020</b>	<b>0.100</b>	<b>-0.40</b>	<b>0.0226</b>	
Hap2, unphased	all	28	all	≥1%	1	-0.040	0.076	-0.0026	0.099	-0.38	0.0304	Permutations of excluded couples <sup>g</sup>
						-0.040	0.080	-0.0027	0.101	-0.37	0.0335	
						<b>-0.068</b>	<b>0.121</b>	<b>-0.0029</b>	<b>0.173</b>	<b>-0.38</b>	<b>0.0348</b>	
						-0.068	0.123	-0.0026	0.174	-0.37	0.0371	
						-0.062	0.120	-0.0037	0.171	-0.34	0.0546	
						-0.061	0.122	-0.0036	0.172	-0.33	0.0592	
						-0.062	0.123	-0.0033	0.172	-0.34	0.0530	
Hap3, unphased	3-only	24	all	≥1%	1	-0.068	0.120	-0.0032	0.174	-0.37	0.0368	Aggregate mean, s.d., P, Z <sup>h</sup>
						-0.063	0.126	-0.0039	0.173	-0.34	0.0727	
						-0.060	0.129	-0.0047	0.170	-0.33	0.0810	
						-0.064	0.124	-0.0052	0.171	-0.34	0.0670	
						-0.063	0.127	-0.0049	0.170	-0.34	0.0670	
-0.014	0.132	-0.0011	0.156	-0.08	0.3512							
-0.020	0.133	-0.0008	0.157	-0.12	0.2792	One-tailed P						

**Table S2. Detailed results for MHC relatedness in European couples.** The mean and standard deviation (s.d.) of relatedness for mate and non-mate pairs are shown, along with the nominal significance (P) and effect size (Z). <sup>a</sup>Subset of couples included for corresponding HapMap Phase, and similarly for SNPs. <sup>b</sup>Identity score assigned to two heterozygous genotypes. <sup>c</sup>Results previously reported by Chaix *et al.* [13]. <sup>d</sup>Median values were used instead of means throughout methods; in this case, values in the mean and s.d. columns are in fact median and median absolute difference, respectively. <sup>e</sup>For these and all subsequent results, 100,000 random trials were conducted. <sup>f</sup>For these and all subsequent results, all samples were included in the calculation of MAF. <sup>g</sup>Results are sorted in decreasing order of significance, and bold type indicates results obtained for the combination used in the previous report [13]. <sup>h</sup>Results are aggregates derived from all permutations of excluded couples.