Table 3. Haseman-Elston linkage analyses

Chromosome	**Location, cM**	**Marker allele frequencies**	**Beta**	**Beta SE**	***P* value**
9	95	Maximum likelihood	0.1813	0.0547	0.0006
9	95	Equal	0.1933	0.0554	0.0003
9	95	Complement	0.1943	0.0552	0.0003

Here we demonstrate calculations of the *P* value for linkage on chromosome 9 at 95 cM by using the Haseman-Elston method and employing the maximum likelihood estimate of marker allele frequencies (row 1), compared to setting all marker allele frequencies equal (row 2), and compared to setting all marker allele frequencies proportional to [1–(maximum likelihood estimate)] (row 3). Beta is the coefficient of regression on the allele sharing estimate.