**Table S1**. Probability of each case-parents triad genotype in a population with random mating, Mendelian inheritance and Hardy-Weinberg equilibrium at the locus under study.

|  |  |  |  |
| --- | --- | --- | --- |
| Genotypes (number of variant alleles) | | | Cell probabilities: |
| Mother (*M*) | Father (*F*) | Child (C) |  |
|  |  |  |  |
| 2 | 2 | 2 |  |
|  |  |  |  |
| 2 | 1 | 2 |  |
| 2 | 1 | 1 |  |
| 1 | 2 | 2 |  |
| 1 | 2 | 1 |  |
|  |  |  |  |
| 2 | 0 | 1 |  |
| 0 | 2 | 1 |  |
|  |  |  |  |
| 1 | 1 | 2 |  |
| 1 | 1 | 1 |  |
| 1 | 1 | 0 |  |
|  |  |  |  |
| 1 | 0 | 1 |  |
| 1 | 0 | 0 |  |
| 0 | 1 | 1 |  |
| 0 | 1 | 0 |  |
|  |  |  |  |
| 0 | 0 | 0 |  |
|  |  |  |  |

Notes:

1. is the frequency of the variant allele; .

. The sum of the cell probabilities is one since

3. is calculated by summing all cell probabilities where for . The resulting row vector giving the genotype distribution among children is . Analogous calculations give and and show that the genotype distribution among mothers and that among fathers are the same as the genotype distribution among children; in other words, , the Hardy-Weinberg equilibrium distribution.

4. The 3×3 matrix containing as the entry in row *c* and column *m*, as given in the main text, is calculated by first calculating by summing all cell probabilities where and and then dividing those probabilities by . For example,