**Supplementary Table 2.** Prediction of the number of meioses separating subjects in a complex

Palauan pedigree.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Pedigree | True M | N | aveRel×100 | maxRel×100 | predM |
| Fig 1 - meiosis 15 | 15 | 8 | 10.1 | 42.2 | 15.4 |
| Fig 1 - meiosis 16 | 16 | 7 | 8.4 | 32.4 | 15.6 |
| Fig 1 - meiosis 21 | 21 | 6 | 2.3 | 5.2 | 21.0 |
| Fig 1 - meiosis 22 | 22 | 9 | 6.5 | 26.7 | 21.8 |
| Fig 1 - meiosis 25 | 25 | 8 | 2.5 | 4.5 | 25.2 |
| Fig 1 - meiosis 32 | 32 | 13 | 4.4 | 23.1 | 32.0 |
| Palau - fam A | 22 | 11 | 11.0 | 34.4 | 22.0 |

 Palau - fam B 25 11 9.2 21.2 25.0

Reassuringly, not only is the fit of the model excellent, the estimated M is highly correlated with the number of affected subjects per haplotype cluster (r = 0.70) in Supplementary Table 1, as expected.