Table S2. Raw genotype and infection data used for logistic regressions and figures.

“B into M” populations, locus *PTC2*

|  |  |  |  |
| --- | --- | --- | --- |
| population | *PTC2* genotype | infected?(1=yes) | number observed |
| M8.2 | BB | 1 | 8 |
|  | BB | 0 | 14 |
|  | BM | 1 | 13 |
|  | BM | 0 | 79 |
|  | MM | 1 | 5 |
|  | MM | 0 | 40 |
| M8-2.2 | BB | 1 | 15 |
|  | BB | 0 | 4 |
|  | BM | 1 | 31 |
|  | BM | 0 | 19 |
|  | MM | 1 | 9 |
|  | MM | 0 | 11 |
| M13.2 | BB | 1 | 10 |
|  | BB | 0 | 11 |
|  | BM | 1 | 17 |
|  | BM | 0 | 28 |
|  | MM | 1 | 6 |
|  | MM | 0 | 13 |
| M17 | BB | 1 | 8 |
|  | BB | 0 | 4 |
|  | BM | 1 | 30 |
|  | BM | 0 | 11 |
|  | MM | 1 | 11 |
|  | MM | 0 | 4 |

“M into B” population, locus *PTC2*

|  |  |  |  |
| --- | --- | --- | --- |
| population | *PTC2* genotype | infected?(1=yes) | number observed |
|  |  |  |  |
| B7.2 | BB | 1 | 3 |
| B7.2 | BB | 0 | 30 |
| B7.2 | BM | 1 | 7 |
| B7.2 | BM | 0 | 57 |
| B7.2 | MM | 1 | 1 |
| B7.2 | MM | 0 | 18 |

F2 entire sample, N = 329, locus *PTC2*

|  |  |  |  |
| --- | --- | --- | --- |
| population | *PTC2* genotype  | infected?(1=yes) | number observed |
| F2(N=329)  | BB | 0 | 69 |
|  | BB | 1 | 24 |
|  | BM | 0 | 140 |
|  | BM | 1 | 29 |
|  | MM | 0 | 58 |
|  | MM | 1 | 9 |

F2 cases & controls, locus *PTC2*

|  |  |  |  |
| --- | --- | --- | --- |
| population | *PTC2* genotype | infected?(1=yes) | number observed |
| F2(case/control) | BB | 0 | 10 |
|  | BB | 1 | 23 |
|  | BM | 0 | 36 |
|  | BM | 1 | 24 |
|  | MM | 0 | 9 |
|  | MM | 1 | 7 |

F2 cases & controls, locus *OPM-04*

|  |  |  |  |
| --- | --- | --- | --- |
| population | *OPM-04* genotype | infected?(1=yes) | number observed |
| F2(case/control) | BB | 0 | 8 |
|  | BB | 1 | 13 |
|  | BM | 0 | 28 |
|  | BM | 1 | 27 |
|  | MM | 0 | 16 |
|  | MM | 1 | 15 |