

Table S1. Linkage of CHR markers in the FOM-infected *r*-T BC₁ population

| Chromosome 1 | | | Chromosome 2 | | | Chromosome 3 | | | Chromosome 4 | | | Chromosome 5 | | |
|---------------------|-----------------|-----------------|--------------|-------|------|---------------------|-------|------|--------------|-------|------|--------------|-------|-------|
| Marker ^a | Rf ^b | cM ^c | Marker | Rf | cM | Marker ^c | Rf | cM | Marker | Rf | cM | Marker | Rf | cM |
| CHR1.1 | — | 0.0 | CHR2.1 | — | 0.0 | CHR3.1 | — | 0.0 | CHR4.1 | — | 0.0 | CHR5.1 | — | 0.0 |
| CHR1.2 | 0.193 | 19.3 | CHR2.2r | 0.107 | 10.7 | CHR3.2 | 0.206 | 20.6 | CHR4.2 | 0.107 | 10.7 | CHR5.2m | 0.264 | 26.4 |
| CHR1.3 | 0.237 | 43.1 | CHR2.3o | 0.271 | 37.8 | CHR3.3 | 0.118 | 32.4 | CHR4.3 | 0.124 | 23.0 | CHR5.3 | 0.074 | 33.8 |
| CHR1.4 | 0.169 | 60.0 | CHR2.4s | 0.212 | 59.0 | CHR3.4 | 0.257 | 58.1 | CHR4.4 | 0.124 | 35.4 | CHR5.4 | 0.199 | 53.8 |
| CHR1.5 | 0.112 | 71.2 | CHR2.5 | 0.096 | 68.6 | CHR3.5 | 0.107 | 68.8 | CHR4.5 | 0.140 | 49.4 | CHR5.5 | 0.101 | 63.9 |
| CHR1.6 | 0.146 | 85.9 | CHR2.6 | 0.251 | 93.6 | CHR3.6 | 0.058 | 74.6 | CHR4.6 | 0.048 | 54.2 | CHR5.6 | 0.096 | 73.5 |
| CHR1.7n | 0.112 | 97.1 | | | | CHR3.7 | 0.129 | 87.5 | CHR4.7 | 0.278 | 82.0 | CHR5.7 | 0.129 | 86.4 |
| CHR1.8 | 0.224 | 119.5 | | | | CHR3.8 | 0.112 | 98.7 | | | | CHR5.8 | 0.129 | 99.3 |
| CHR1.10 | 0.112 | 130.8 | | | | | | | | | | CHR5.9m | 0.237 | 123.1 |
| CHR1.9 | 0.231 | 153.9 | | | | | | | | | | | | |

^a DNA markers are described in Methods.

^b Recombination frequency is between marker and above marker.

^c Map position is in centiMorgans.