**Table S1.**

Summary of Illumina GAIIx whole genome sequencing results of Hit9188 and Hit11440 M3 bulks.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Mutant | Sample | Number M3 individuals bulked | Number of Illumina short reads | Total sequence (Gb) | Genome coverage (%)a | Mean depthb |
| Hit9188 | Mutant bulk | 40 | 95,552,424 | 7.17 | 97.4 | 16.5 |
| Wild-type bulk | 40 | 57,925,150 | 4.34 | 95.2 | 9.9 |
| Hit11440 | Mutant bulk | 20 | 67,392,352 | 5.05 | 96.7 | 12 |
| Wild-type bulk | 20 | 62,529,426 | 4.68 | 97.8 | 11.4 |

Illumina short reads were aligned to Hitomebore consensus sequence as described in Material and Methods.

aPercentage of total genomic region of Hitomebore reference sequence aligned by short reads.

bAverage read depth over the whole genome.