Figure S1  Mapping of ax2001 and ax2013.

(A-D) Graphs showing the percentage of Hawaiian SNPs (Y axis) along the linkage group indicated (X axis). Each dot represents a unique Hawaiian SNP, only SNPs with frequencies between 20-60% are displayed.

(A) 250 progeny of F1 N2/Hw hybrids (mbk-2(dd5)/mbk-2(dd5)Hw; ax2001/Hw) were grown at 25°C for two generations on one plate and sequenced in one pool. Since ax2001 is dominant, the recombinants are a mixture of ax2001/Hw and ax2001/ax2001 animals. As a result, no distinct region with low Hw SNP frequencies was detected.

(B) Same as in A, except that the recombinants were screened for homozygosity at the suppressor locus before sequencing (Methods). 26 ax2001/ax2001 F2 recombinants were grown for 2 more generations and sequenced in one pool. A 1Mb region with low Hw SNP frequency was detected at the extreme right end of LGII.

(C) Same as in A showing linkage group I for the introgressed mbk-2(dd5)Hw strain. Note the large gap lacking Hw SNPs. This gap is likely due to the N2/Hw incompatibility at the peel-1/zeel-1 locus on LGI and the fact that we used Hw/N2 males to make the introgressed mbk-2(dd5)Hw strain.

(D) Same as in C for a population of F2 recombinants carrying suppressor ax2013. Note the loss of Hw SNPs denoting linkage to the right end of LGI. However because the large gap in the introgressed strain (C), the entire region demarcated by red lines was scanned for novel mutations.