

Figure S1a Diagram of the HA412-HO x RHA415 cross



Figure S1b Diagram of the HA412-HO x RHA415 cross



Figure S1c Diagram of the RHA280 x RHA801 cross

NMS373 x Hopi







Figure S2a



Figure S2b



Figure S2c

Figure S2 On the HA412-HO x RHA415 map, 14 different assays could be used to map two loci each. The resulting data included nine distinct genotypic clusters corresponding to the nine different two-locus genotypes that are expected when two loci are segregating. Because Genome Studio is designed for single locus data, these loci were scored manually. In 8 of 14 cases, both loci could also be mapped to the corresponding chromosomal positions in either the HA412-HO x ANN1238, RHA280 x RHA801, or NMS373 x Hopi populations. In the other six cases, only one of the two loci could be mapped to a corresponding position in one of the other three mapping populations. In Figure S2a, nine distinct clusters of individuals from the mapping population could be identified corresponding to the expected 9 possible genotypes for assay SFW3767. For this example the "a" allele and the "B" allele were effectively "null" alleles and provided no signal. In this example, the two loci mapped to cM 68 of chromosome 12 and cM 6 of chromosome 13. In Figure S2b, 9 distinct clusters of individuals from the mapping population could be identified corresponding to the expected 9 possible genotypes for assay SFW1323. In this case, the "a" allele was effectively a "null" alleles and provided no signal. The two loci mapped to cM 33 of chromosome 14 and cM 48 of chromosome 1. In Figure S2c, 9 distinct clusters of individuals from the mapping population could be identified corresponding to the expected 9 possible genotypes for assay SFW1323. In this case, the "a" allele was effectively a "null" alleles and provided no signal. The two loci mapped to cM 33 of chromosome 14 and cM 48 of chromosome 1. In Figure S2c, 9 distinct clusters of individuals from the mapping population could be identified corresponding to the expected 9 possible genotypes for assay SFW1323. IN this case, the "a" and "B" alleles hybridized more strongly than the second locus with the "a" and "b" alleles, presumably due to a secondary SNP associated with the latter. The two loci



Figure S3a Comparison of map order for RHA280 x RHA801 computed by MSTMap and manually.



Figure S3b Comparison of map order for NMS373 x Hopi computed by MSTMap and manually. MSTMap failed to assemble LG 17 into a single linkage group, and produced two large inversions on LGs 11 and 14, that were not observed on maps from the other three crosses.



Figure S3c Comparison of map order for HA412-HO x RHA415 computed by MapDisto and manually.



Figure S3d Comparison of map order for HA412-HO x ANN1238 computed by MapDisto and manually.



Figure S3e Comparison of map order for RHA280 x RHA801 computed by MapDisto and manually. Mapdisto failed to correctly place a one locus on LG 10, resulting in a much larger chromosome than the one created manually.



Figure S3f Comparison of map order for NMS373 x Hopi computed by MapDisto and manually. Mapdisto failed to correctly place a single loci on LG 17 and made some marker order changes in LG13 and 17, relative to the manual map, these ordering differences we not observed in maps from the other three crosses.



Figure 4a Synteny plot between HA412-HO x RHA415 and HA412-HO x ANN1238.

1,921 SNPs mapped in common between two maps and 1,750 (91.1%) were syntenic.



Figure 4b Synteny plot between HA412-HO x RHA415 and NMS373 x Hopi.

1,404 SNPs mapped in common between two maps and 1,241 (88.4%) were syntenic.



Figure 4c Synteny plot between HA412-HO x RHA415 and RHA280 x RHA801.

1,734 SNPs mapped in common between two maps and 1,569 (90.5%) were syntenic.



Figure 4d Synteny plot between RHA280 x RHA801 and HA412-HO x ANN1238.

1,902 SNPs mapped in common between two maps and 1,685 (88.6%) were syntenic.



Figure 4e Synteny plot between RHA280 x RHA801 and NMS373 x Hopi.

1,447 SNPs mapped in common between two maps and 1,252 (86.5%) were syntenic.



Figure 4f Synteny plot between HA412-HO x ANN1238 and NMS373 x Hopi.

1,537 SNPs mapped in common between two maps and 1,337 (87.0%) were syntenic.



Figure S5a Graphical representation of linkage groups 1-9 of composite map.

	LG10	LG11	LG12	LG13	LG14	LG15	LG16	LG17
0 10 10 15 10 10 10 10 10 10 10 10 10 10								

File S1 Supporting Data

File S1 is available for download as an Excel file at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.112.002659/-/DC1.