

Web Note D. We made 86 modifications to the sequence assembly of the August 2001 freeze supported by our genetics data. In a large fraction of these 86 cases, our preferred ordering is supported by data from one or more alternative sources such as the BAC clone fingerprint contig (FPC) data from Washington University and Sanger Center, marker to BAC hybridization data (generated by our laboratory or in the public domain), the Marshfield map, and previous sequence assemblies. Modifications to the assembly were made in a conservative manner. In addition to the 86 cases, there are 20 cases where the preferred order of the genetic data reduced the number of obligate recombinations by two or more and there are 10 cases which reduced the number of obligate recombinations by 1, but we decided not to modify the sequence assembly at this juncture because of the lack of support from other sources of data and that there did not exist any easy way to modify the sequence assembly. For each of these 30 cases, our support for an alternative order cases can be narrowed to one or two genotypes, and these genotypes are a subset of the 2123 genotypes removed when the data were used to estimate genetic distances based on the current marker order. Since an alternative order supported by some of these genotypes may yet prove to be the correct one, for anyone utilizing the data to order the markers, we recommend the use of the full data set including the 2123 flagged genotypes.

Another 18 modifications to the August 2001 sequence freeze were made where our genetic data lack resolution, but the changes had strong support from the alternative sources. In many of these 18 cases, our modifications agreed with one or more assemblies released previously.