**FIGURE S3.**—Linkage map of the combined data from the four RIL mapping populations. This map consists of 241 SSR, 1088 SNP, and 10 candidate gene markers. Total map distance is 1961.2 cM. Candidate genes directly mapped are indicated in red. Map intervals containing candidate genes localized by inference indicated as segments with blue diagonal filling, with the candidate gene name in blue positioned at interval midpoint. Map intervals exhibiting significant segregation distortion in the combined analysis indicated as magenta segments on the linkage group. The map interval on chromosome 10 identified as having undergone a selection sweep by Tian *et al.* (2009) is indicated by a pink segment on the linkage group. QTL bars represent the 2-LOD support interval of the QTL position; the middle hash mark of a bar represents the maximum likelihood position of the QTL.