Figure S3  Combined linkage maps for A) the S-G cross and B) the B-G cross estimated using a multipoint maximum likelihood algorithm in JoinMap v. 4.0 on genotypes of the male progeny from each set of backcrosses. Genetic markers were selected to span each chromosome and be informative in both sets of crosses whenever possible. Note that the marker order between linkage maps estimated for the two sets of crosses was highly congruent with two exceptions. First, three markers were typed on the proximal end of chromosome 2 in the B-G cross, but not in the S-G cross, which extended the mappable region on that chromosome in the B-G cross. Second, several X-linked markers in the S-G cross appear to segregate together, indicating the presence of a small inversion that reduces recombination between the S and G X chromosomes.