1.2, and 1.3 for 2A, 2B, and 2D, respectively) from physical measurement of C-banded mitotic chromosomes (Gill *et al.* 1991). Analysis of the distribution of EST loci between the long and short arms was performed on the subset of 965 loci mapped to chromosome arms or bins (excluding loci mapped fragments, (ii) structural rearrangement, or (iii) technical error. In the first case, the unmapped restriction fragments may have been located in syntenous bins, while the nonsyntenous mapped fragments may have been interbin duplication events.

Duplications: ESTs with mapped loci in two different bins

TABLE 1

Number and distribution of EST loci among group 2 chromosomes in wheat

TABLE 2

Distribution of EST loci between the group 2 chromosome arms and among the chromosome bins

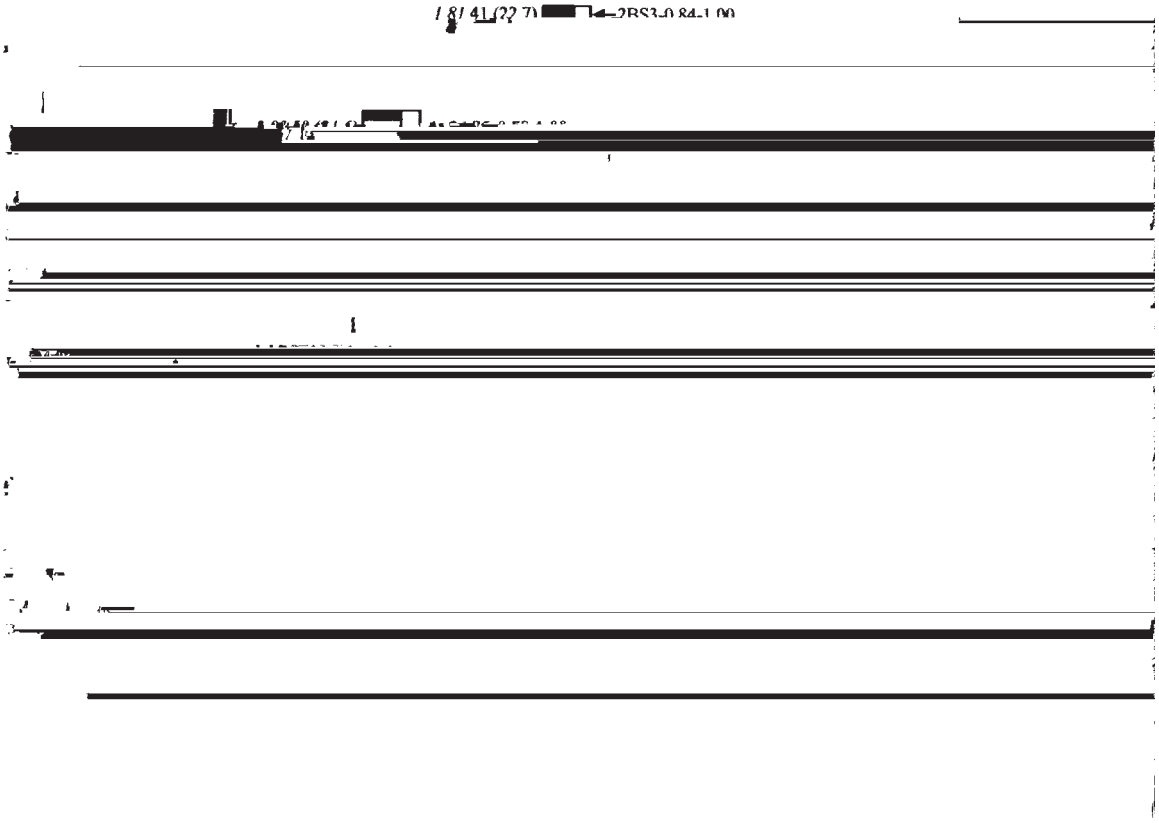

Figure 1.—Distribution of EST loci among group 2 chromosome bins. Italicized numbers indicate the gene density ratios (mean over all bins is 1.0); numbers outside parentheses are the observed number of loci; within parentheses are the expected number based on the physical size of the bin. The bin fraction is indicated to the right of each chromosome. The solid horizontal bands on each chromosome depict heterochromatic regions. Hatched horizontal bands are heterochromatic regions not consistently observed (Gill *et al.* 1991). The figure is based on 854 loci generated from only those ESTs having all restriction fragments mapped and assigned to chromosome bins.

0.76), which contained significantly fewer than expected EST loci ($P < 0.001$). Bin 4S contained 28.3% of the EST loci mapping to short-arm consensus bins, yet accounted of of.on.58J-11221 -1.111ge5rouFLge54300.53.1375)ge5rou the ge5rou expressed

ments mapped to other homoeologous groups. Therefore, many of these anomalies occurred in higher-copy ESTs with complex patterns of duplication. One-half of (anomalies were detected by only

plication analysis was restricted to duplication to other group 2 bins and to other homoeologous groups. Only 25 ESTs (2.3%, based on the confirmed set of ESTs with loci mapping to homoeologous group 2 chromosomes) detected loci in two or more bins within a homoeologous group 2 chromosome, 15 of which involved duplication to bins on opposite arms. The 25 ESTs generated eight duplicate loci on 2A, 14 on 2B, and 6 on 2D.

Three hundred sixty ESTs (32.4%) had at least one locus mapped to a homoeologous group 2 chromosome and at least one locus mapped to a different homoeologous group chromosome. On a whole-chromosome ba-

TABLE 3

TABLE 4

Colinearity between the wheat group 2 consensus map and the rice genome

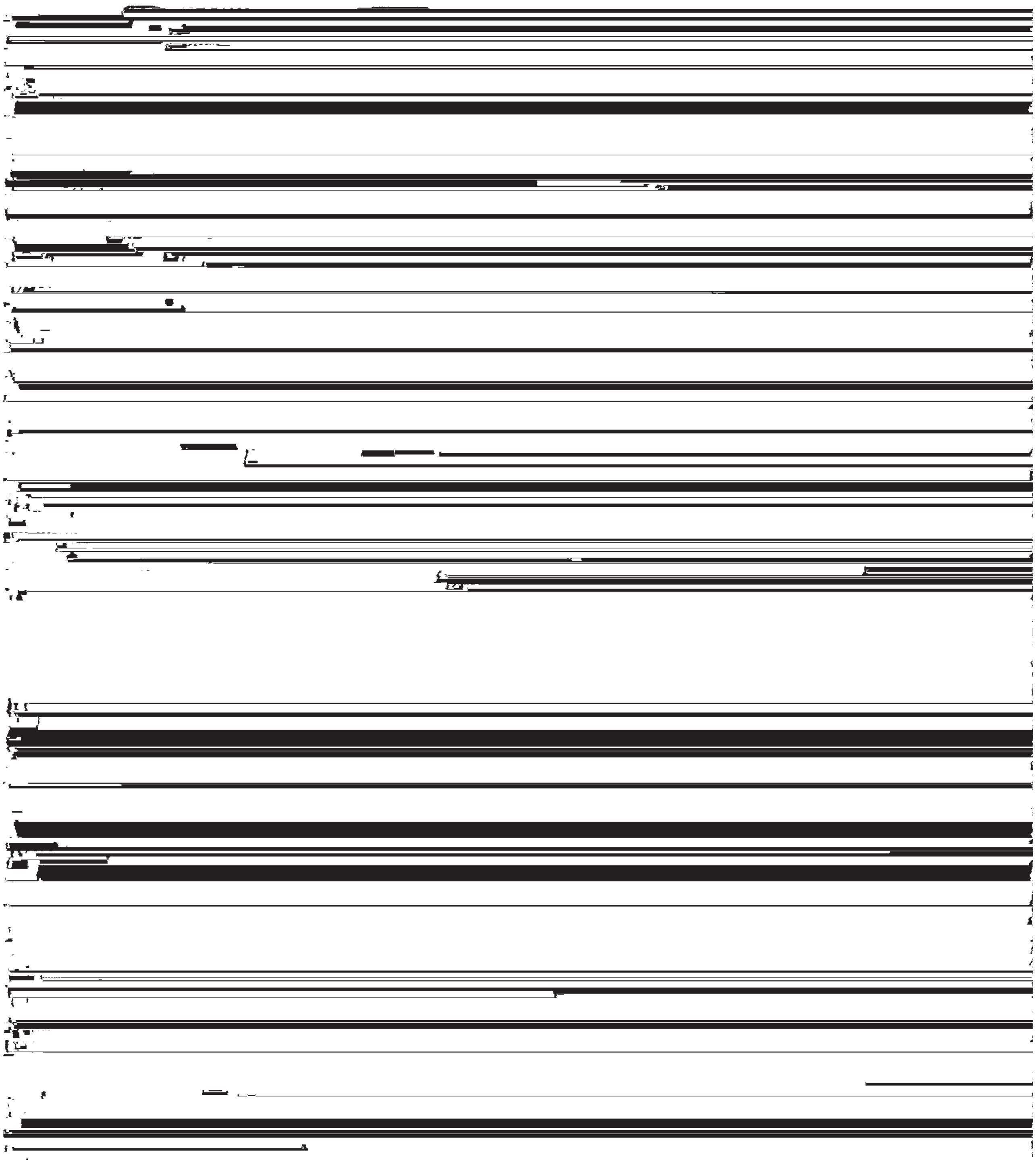

Figure 3.—Depiction of wheat consensus group 2 and rice syntenous blocks. Wheat group 2 ESTs are listed in their putative order within consensus bins on the basis of comparison with ordered rice BAC/PAC clones. The wheat EST consensus map showing loci with matches to the rice colinear chromosomes is flanked by the genetic maps of rice BAC/PAC clones for rice chromosomes 4 (left) and 7 (right). Solid lines connect syntenous blocks between wheat ESTs and rice BAC/PAC clones. Dotted lines indicate significant blast matches between a wheat EST and rice BAC/PAC showing synteny disruptions at the consensus bin level. ESTs involved in synteny disruptions are shown in boldface, underlined type. Thin solid lines connect EST-rice BAC/PAC matches that are syntenous at the bin level, but havthe matcC to the syntenouson rce
indicatd, yth4311.1(hick,)-400(solid)4311.2horizontal, line.th4311.1Cumultative entitongafdicalehomosom.e

Consensus bins provided a higher resolution frame-

sensus bins, 6S and 6L. These results were consistent with previous findings that synteny levels tend to de-