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February 11–16, 2001. The detailed protocols are available on line at http://wheat.pw.usda.gov/NSF/project/mapping\_data. html and were as described in Qi *et al.* (2003). Five Southern blots (each we270(localioso2an70(se8.32(fe)-caliosoa-caliosototal-calioson)-28lioso130)-28lioso-211...9(al.P)TJ/Ft) ]43472.237(Eco Tc(Q1)Tj/F3)

Figure 1.—An example of local-

## TABLE 1

Selected chromosome- and genome-specific ESTs of wheat

gene density among A-, B-, and D-genome chromosomes. The gene density was less than one for A-genome chromosomes (except 4A and 6A) and more than one

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## TABLE 2

## Selected patterns of intra- and interchromosome duplications and the lack of homeology displayed by multicopy ESTs of wheat



Figure 2.—Number of observed and expected EST loci for the A, B, and D genomes of wheat.

Mickel son-Young *et al.* 1995). With large-scale EST mapping, we have uncovered further structural changes in 4A and confirmed the 4B inversion and additional chromosomal structural changes in most of the B-genome



Figure 3.—Gene density in the 42 chromosome arms of wheat. Gene density was calculated by the ratio of observed to expected loci (on the basis of chromosome length).

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Gale, 1992 Homoeologous translocations between group 4, 5 and 7 chromosomes in wheat and rye. Theor. Appl. Genet. 83: 305–312.

throughput sequencing facilitates genome characterization and gene discovery. Genome Res. 12: 795–807. Qi, L. L., and B. S. Gill