





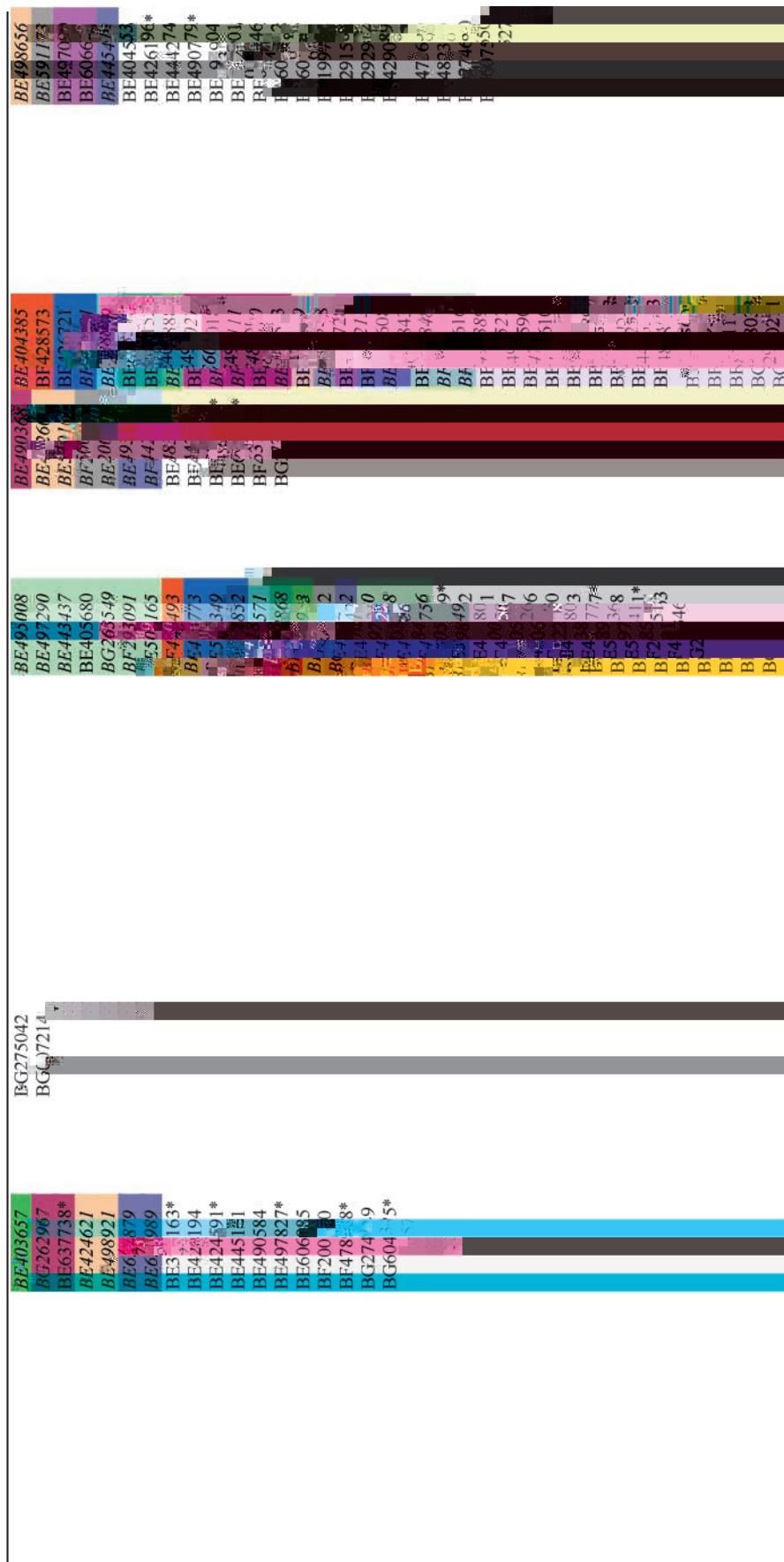
Figure 1.—Deletion maps of wheat chro-



these duplications were observed in the proximal 50% of the red bar chart was drawn to scale using 385 ESTs



TABLE 1  
(Continued)



Colored boxes represent different rice chromosomes, 1–12, with colors as shown in Figure 6. ESTs with discrepant location are marked with an \*. ESTs that are italicized are not mapped on the consensus map. ESTs with regular font but no color are mapped on the consensus map, but have no match with rice sequences. The order of the ESTs within a column from top to bottom corresponds to the order from distal to proximal within bins for the short arm and from proximal to distal on the long arm. The bin desib(otsbin)-333.9 are-333. [ (The)-333flankapping d p proximal tois; (to)-333se(The)-333.8(Figsbin)-3335bin o



slightly different results were observed, depending on methods and criteria. Genetic linkage-map comparisons

the rice and maize genomes. Proc. Natl. Acad. Sci. USA **90**: 7980–7984.

Ahn, S., J. A. Anderson, M. E. Sorrells and S. D. Tanksley, 1993

Homoeologous relationships in 10 T46.911o, T46.9w-333.4(5hods)-1nshin1 5hochr

tion and high-density mapping of gene-rich regions in chromosome group 5 of wheat. *Genetics* **143**: 1001–1012.

Sandhu, D., and K. S. Gill, 2002 Gene-containing regions of wheat and the other grass genomes. *Plant Physiol.* **128**: 803–811.