

species and can be used to integrate the physical and genetic chromosome maps of wheat with the genome sequence of rice.

As a part of a National Science Foundation-funded

line (two copies of Dt5AS and Dt5AL) was also included in the study. The arm location of the markers involved in a putative pericentromeric inversion were also determined in *Lophophyrum elongatum* Host ditelosomic addition lines Dt5ES and Dt5EL (Dvořák 1980; Tuleen and Hart 1988) and *Hordeum vulgare* L. line Dt5HL (

Sequences showing similarities $\geq 70\%$, over at least 100-bp segments, were considered as significant matches and were used in the analysis of the wheat-rice colinearity. To test the

some having the largest number of significant matches to that particular wheat bin and then used a binominal distribution to calculate the probability of finding the observed number under the null hypothesis $e^{-1} (calp)^{-2663.17} p(r)^{40m-2663.17}$ -ribution

TABLE 1

TABLE 2**Distribution of group 5 wheat EST loci and duplicated loci along the centromere-telomere axis**

Proximal 1/2

centromeric bins on W5L and R12S. These wheat ESTs
particular bin. We have included in the supplemental on-
line materials (<http://>

plain those results: the inversion/deletion hypothesis

wheat chromosome 1B (Sandhu *et al.* 2001; Francki *et al.*

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