In the published research [1], we have defined significant inter-chromosomal interactions (see methods) and found the sequence similarities were significantly higher for the anchored region pairs of inter-chromosomal interactions than for the intra-chromosomal interacting pairs or random pairs (Fig2c, d). Meanwhile, the within-subgenome interactions were much more significant when the multi-mapped read pairs were included (Fig1), indicating that the sequence with high similarity may greatly affected the within-subgenome interactions. Then we have found the anchored pairs were significantly enriched with subgenome-dominant TEs as compared to randomly sampled read pairs (Fig 2h).

Here, as a supplement, we continued to analyze the lengths of different types of biased TEs in these high similarity anchor pairs and calculated their foldchanges relative to balanced TEs. From the results with and without multi-mapped reads of AK58 and Chinese Spring, we found the specific types of subgenome-biased TE's contribution to interactions within or between the subgenomes.



1. Jia JZ, Xie YL, Cheng JF, Kong CZ, Wang MY, Gao LF, Zhao F, Guo JY, Wang K, Li GW, et al: **Homology-mediated inter-chromosomal interactions in hexaploid wheat lead to specific subgenome territories following polyploidization and introgression.** *Genome Biology* 2021, **22**.