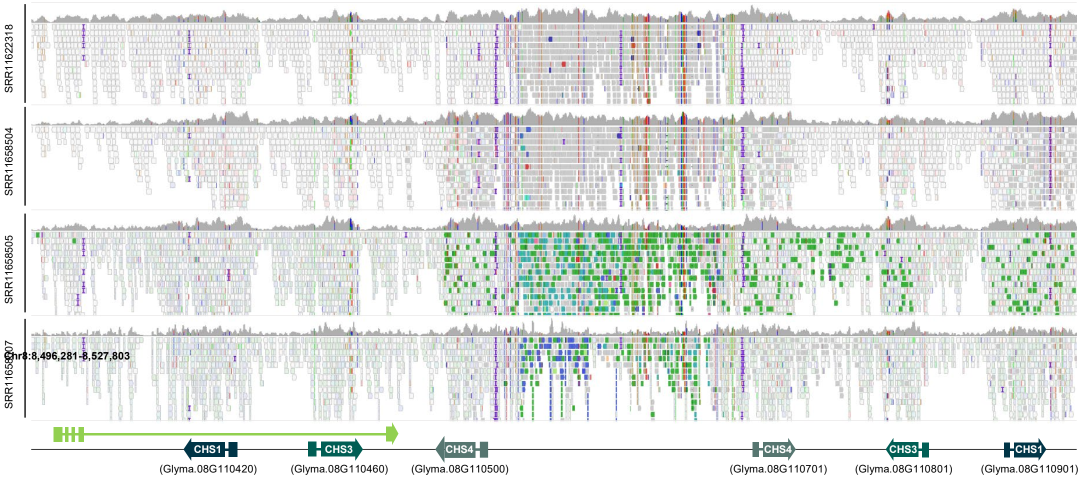

Supplementary Figure 7 | Mapping of Hwangkeum resequencing reads at the *I* locus on the Williams82 reference genome for structural comparison. Four resequencing accessions are shown on the left side of the figure. For each accession, read counts are displayed in the upper lane, and read mapping is shown in the lower lane. The maximum read count is 43. Colors on the mapped resequencing reads indicate sequence mismatches. The features above the lanes represent the structure of the *I* locus, including *CHS* genes and the chimeric transcript.