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Figure S2: Determination of the hT2 breakpoint using Integrative Genomics Viewer. The hT2 breakpoint was determined by arranging segments of chromosome I and III into 10 Kb and 5 Kb bins, followed by a script that identified major drops in average coverage at the target region. (A) The state of the genome observed from the sequence. Breakpoints were identified on IGV. A, B, C, D represents chromosomal segments of DNA flanked by the breakpoints. (B) The order of chromosomal segments rearranged to fit the sequence. (C) Proposed structure of the original chromosome segments prior to gamma-irradiation, identified by lining up breakpoints. (D) The hT2 breakpoint on chromosome III visualized using IGV. Multicolored alignments indicate mismatched reads.