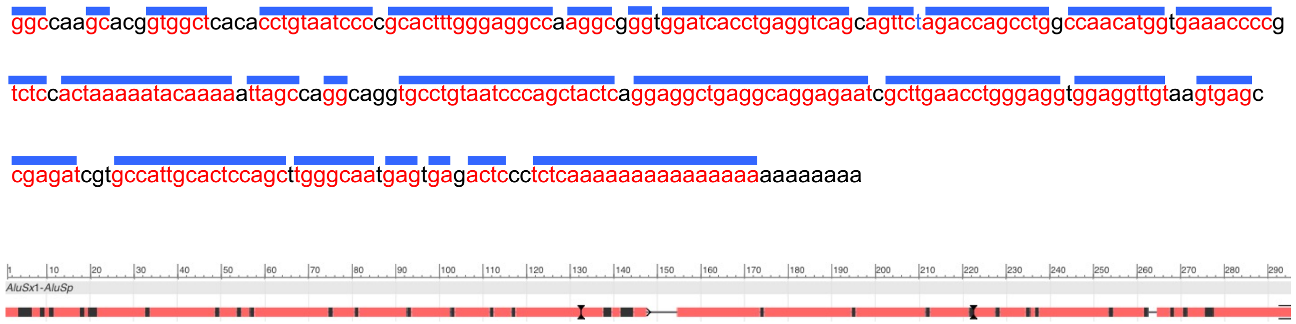
Supplemental Fig S3. The *Alu* pairs utilized in the yeast template switching assay and the position on a consensus *Alu* sequence of the microhomologies at breakpoint junctions. (A-B) The sequence of *Alu*Sx1 (Chr2:32378388-32378684, GRCh37/hg19) is shown, and the microhomologies that align with *Alu*Sp (Chr2:32381110-32381405, GRCh37/hg19, in A) or *Alu*Y (Chr2:32403014-32403315, GRCh37/hg19, in B) are colored in red and marked with a blue line on top. We also represent the *Alu*Sx1 sequence as a rectangle and colored the homologous region in red using NCBI BLAST for easier comparison of the two constructs. (C-E) The relative positions of the microhomologies observed in the *Alu*Sx-*Alu*Sp strain on an *Alu* consensus sequence (lower panel) were presented. Panel C describes the published 74 events (Mayle et al. 2015); D shows the results from the second batch including 250 events (including the published 74 events) and panel E displays the 503 events (including the 250 events in panel C).

A



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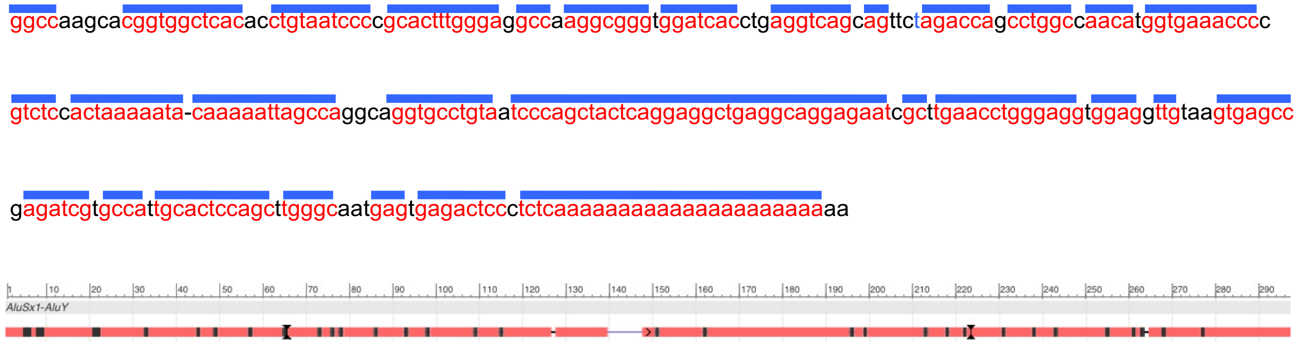

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