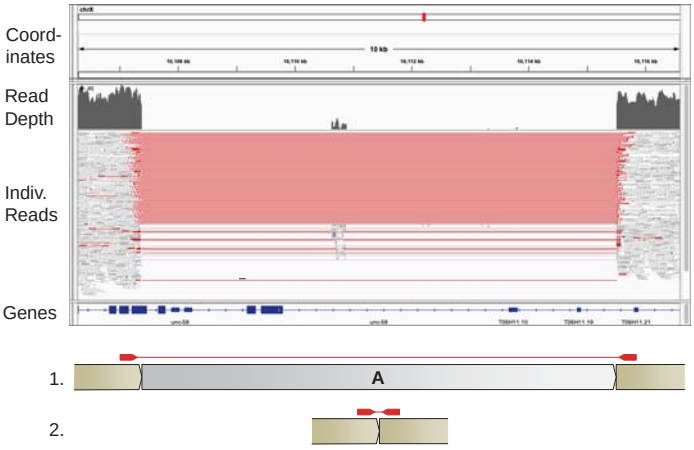
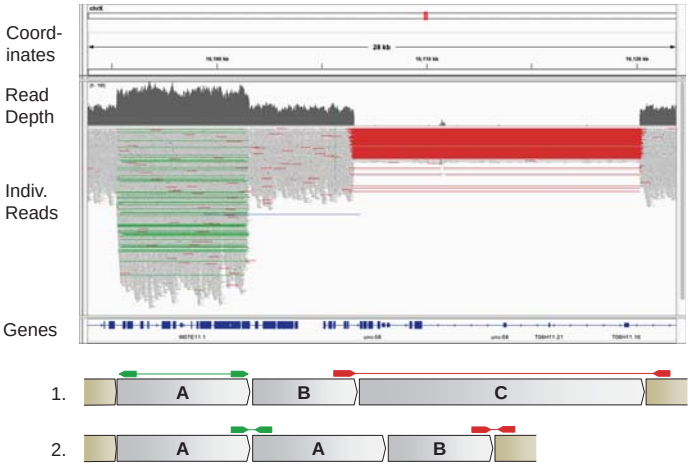
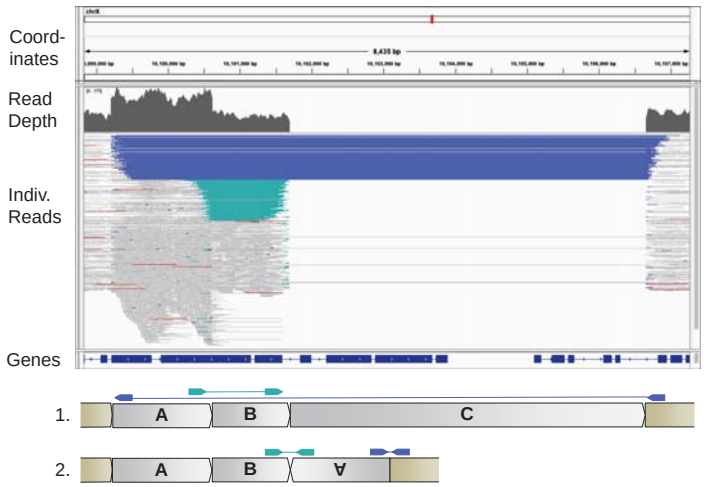
A. *gcna-1(ne4356)*_5 rearrangement



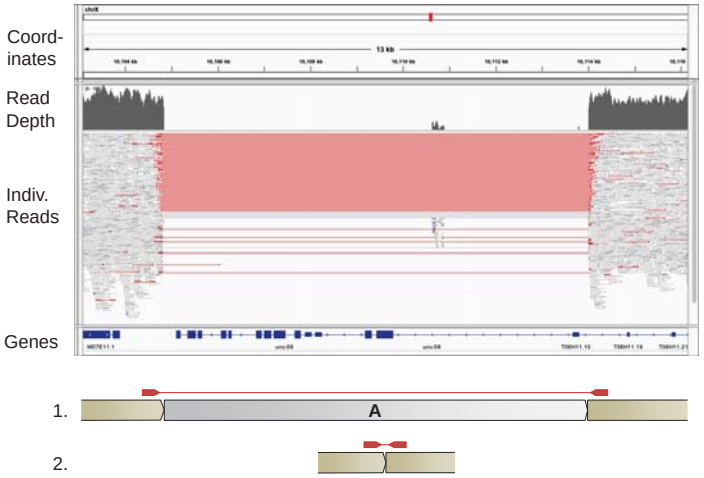

B. *gcna-1(ne4356)*_4 rearrangement



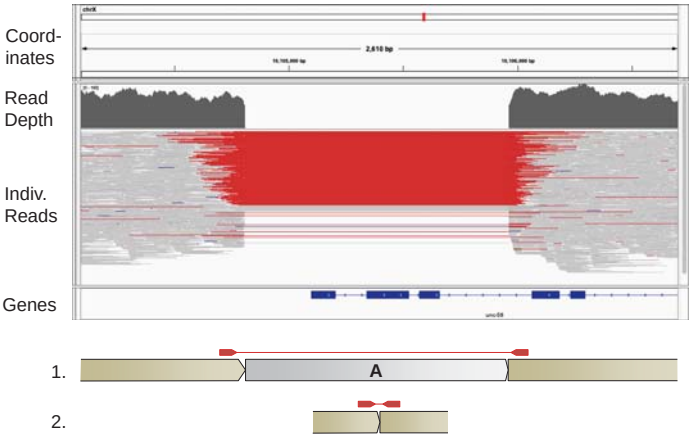

C. *gcna-1(ne4356)*_10 rearrangement




D. *dvc-1(ok260)*_6 rearrangement




E. *dvc-1(ok260)*_7 rearrangement




F. *dvc-1(ok260)*_22 rearrangement

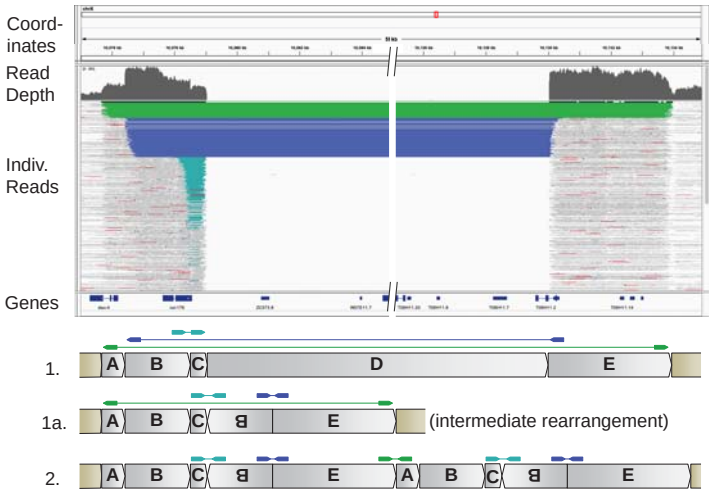


**Figure S3: Related to Figure 3. Integrative Genomics Viewer (IGV) visualization of alignments of paired-end Illumina reads to the reference genome sequence at the *C. elegans unc-58* locus.** Panels A-C represent rearrangements in gcna-1*(ne4356);unc-58(e665)* revertants and panels D-F represent those in *dvc-1(ok260);unc-58(e665)* revertants from the mutator assay in Figure 3. Reads are color coded according to IGV convention: Black, normal paired reads that map with the expected distance and orientation relative to the reference sequence; Red, reads that align with the expected orientation but whose ends are further apart in the genome than expected based on the insert size of the library (implies deletion); Cyan and Blue, reads from both ends of a pair map to the same strand (Cyan, +/+, Blue, -/-, both imply inversion); Green, outward facing reads (implies duplication or translocation). In each panel, Line 1 shows how discordant reads map to the reference sequence. Line 2 shows the rearrangement that can resolve the discordantly mapping reads and account for the copy number variations inferred from the read depth. Segments, defined by inferred rearrangement borders, are labeled alphabetically according to their order in the reference sequence. Inverted letters indicate that an inversion of a segment has taken place.