**Supplemental figure legends**

**Figure S1.** Schematic of the genomic regions uncovered by existing balancer systems in *C. elegans* (Edgley *et al.* 2006; Dejima *et al.* 2018). The red boxes represent uncovered regions. The orange lines denote pairing centers (Rog and Dernburg 2013).

**Figure S2.** Traditional multiple sgRNAs strategy failed to induce chromosomal inversions covering pairing centers. (A) Schematic of the strategy to generate chromosomal inversions covering pairing centers of LG II. The red arrows indicate the sgRNA targets, and the white arrows show the orientation of the chromosome. The yellow bars represent pairing centers. The positions of PCR primers for genotyping are indicated. (B) Summary of the microinjection experiments using sgRNAs targeting *dpy-9* and *rde-8* simultaneously. (C) Schematic of the strategy to generate chromosomal inversions covering pairing centers of LG X. The positions of sgRNA-guided cleavage sites and PCR primers for genotyping are indicated. (D) Summary of the microinjection experiments using sgRNAs targeting *nrde-3* and *dpy-3* simultaneously.

**Figure S3.** Insertion of *gfp* and *mCherry* cassettes into designed chromosomal loci using CRISPR/Cas9 technology. (A, C and E) Schematic of the genomic loci selected for the insertion of *gfp* or *mCherry* cassettes. The positions of sgRNA-guided cleavage sites and PCR primers for genotyping are indicated. (B, D and F) PCR detection of the mutants carrying integrated cassettes.

**Figure S4.** Summary of the genome editing experiments in this study.

**Figure S5.** The position of selected SNPs used to map the suppressed recombination regions. The blue bars represent the inverted chromosomal regions. The vertical orange lines indicate the pairing centers (Rog and Dernburg 2013).

**Figure S6.** An extrachromosomal (Ex) array of *dpy-8(+)* can rescue the *dpy-8(-)* phenotype in *ustIn3*.

**Table S1.** Strains generated in this study.

**Table S2.** Summary of sgRNA sequences.

**Table S3.** Primer sequences used for the construction of sgRNA-expressing plasmids.

**Table S4.** PCR primers used to construct non-sgRNA plasmids used in this study. TheDNA fragments were amplified and recombined with each other to generate final plasmids via the Gibson assembly method.

**Table S5.** The injection mixes of the CRISPR/Cas9 system.

**Table S6.** PCR primers used to screen for mutants generated by the CRISPR/Cas9 technology and the Mos1 system-mediated Cre insertion.

**Table S7.** PCR primers used to genotype SNPs.

**REFERENCE**

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