The map position of the hT2 breakpoint was determined by McKim et al., 1993, which was used to identify the hT2 physical breakpoint at 11 Mbp. The physical location was inferred from the position of pes-2.2, the gene closest to the hT2 physical breakpoint.

**Figure S1:** Genetic map of mitomycin C-induced lethal mutations in the hT2-balanced region of chromosome I. The h alleles depicted were mapped to chromosome I using three-factor mapping. The numbers displayed beside each h allele represent the mapped genetic location, and the dotted lines represent 95% confidence intervals of three-factor mapping. The genes bli-3, dpy-5, unc-13, and unc-101 are shown as references. Map positions of lethal mutations are displayed as map units.