



Figure S6. Estimated copy number of TE (estimated via dividing the average coverage of the TE in a sample by the average coverage of chromosome 2R) vs. the fraction of dysgenic offspring observed in a cross (12 lines from Florida population [described in Figure S5] crossed to M26 [in red] and M252 [in black]), with lines showing the fit of a binomial generalised linear model. **A.** The correlation between the copy number of P-element and the proportion of dysgenic offspring from the paternal Florida crosses (Supplementary Table 2; z value = 6.49, $p = 8.49e-11$). The equivalent association between dysgenesis and P-element copy number for *D. melanogaster* is shown with clear points (Bingham *et al*, 1982). **B.** The correlation between the copy number of P-element and the proportion of dysgenic offspring from the maternal Florida crosses (Supplementary Table 2; z value = -1.128, $p = 0.259$). **C.** The correlation between the copy number of Tom1 and the proportion of dysgenic offspring from the paternal Florida crosses (Supplementary Table 2; z value = -0.551, $p = 0.581$). **D.** The correlation between the copy number of Tom1 and the proportion of dysgenic offspring from the maternal Florida crosses (Supplementary Table 2; z value = 0.135, $p = 0.893$).