Supporting Information

Leopold et al. 10.1073/pnas.1501979112

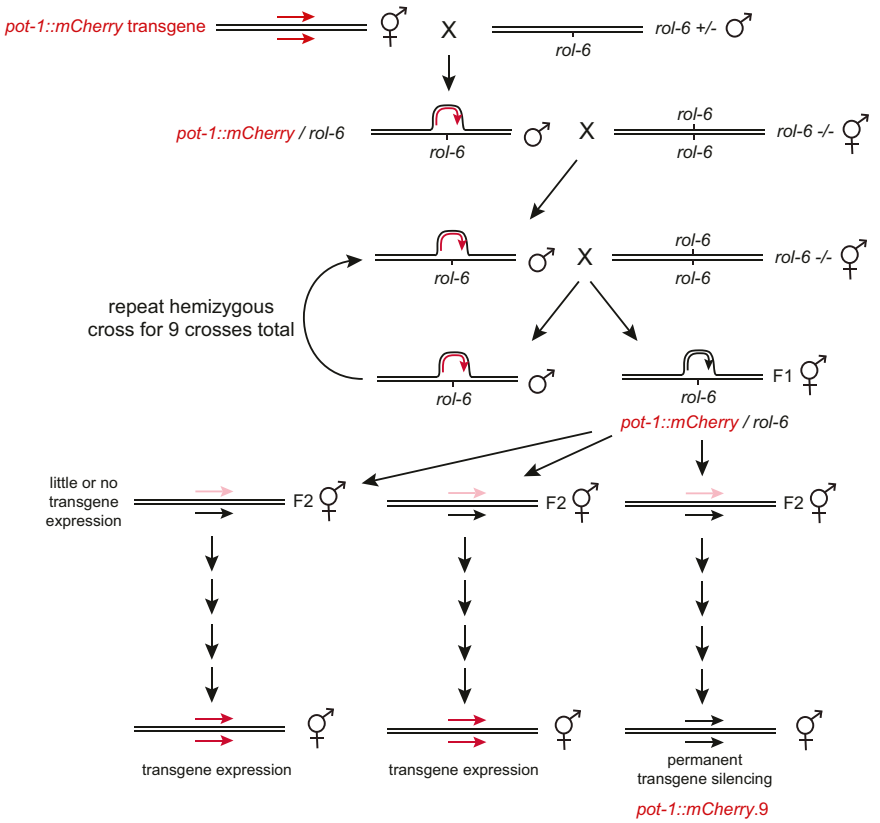

Fig. S1. Crossing scheme that created *pot-1::mCherry.9*.

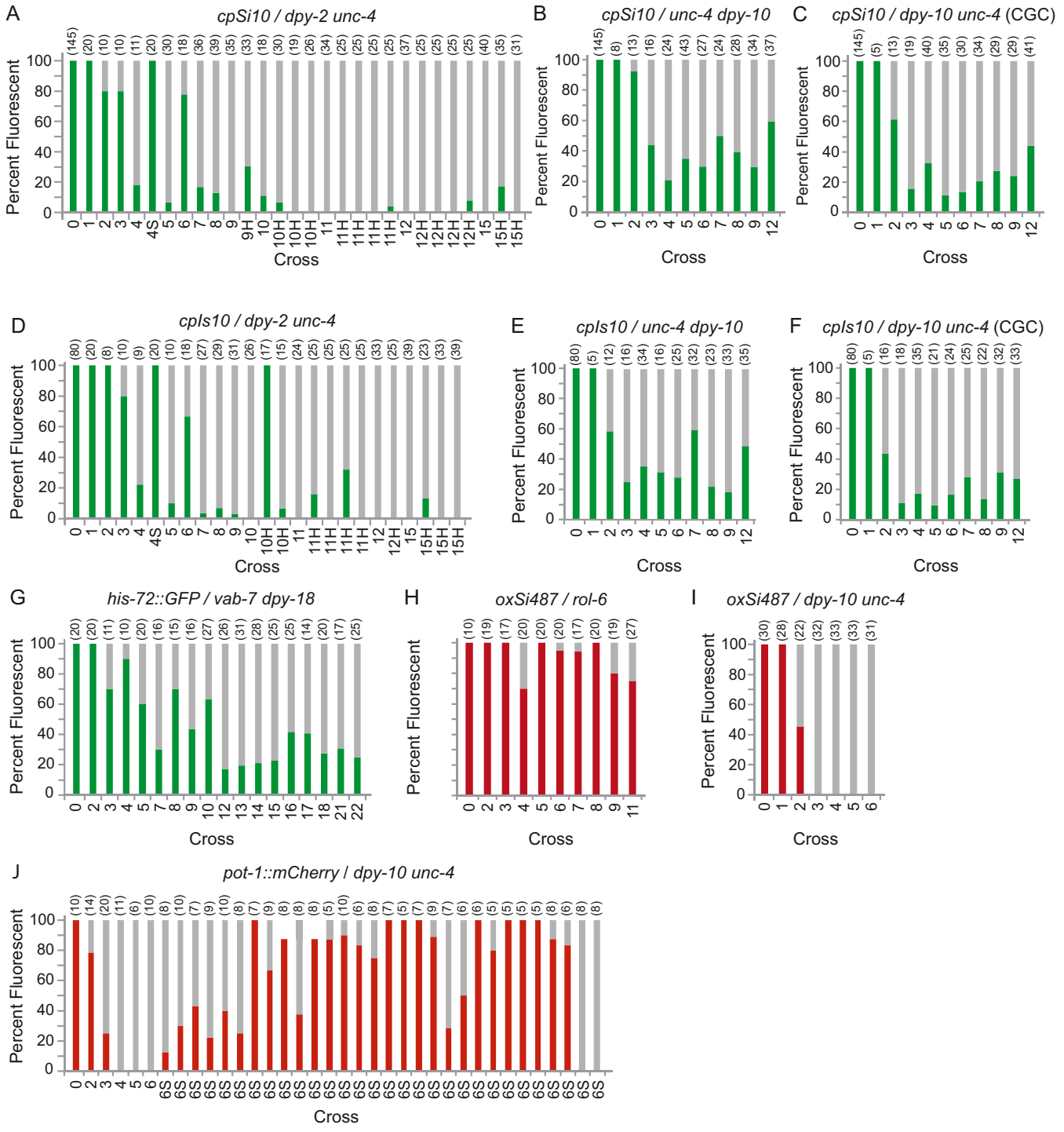

Fig. S2. Crossing various transgenes with various markers induces multigenerational RNAe silencing at variable rates and penetrance levels. Percent of population fluorescent at each round of crossing for (*A–F*) *cpSi10* and *cpIs10* using *dpy-2 unc4*, *unc-4 dpy-10*, or *dpy-10 unc-4* (obtained from *Caenorhabditis* Genetics Center) balancer chromosomes; (*G*) *his-72::GFP* using *vab-7 dpy-18* marker strain; (*H* and *I*) *oxSi487* using either *rol-6* or *dpy-10 unc-4* balancer chromosomes; and (*J*) *pot-1::mCherry* using a *dpy-10 unc-4* balancer chromosome. Numbers at *Top* in parentheses indicate number of worms scored. Bar 0 indicates original transgenic strain before crossing. S denotes homozygous F3 worms derived from starved heterozygous transgene/marker. H denotes homozygous F3 worms derived from heterozygous transgene/marker.

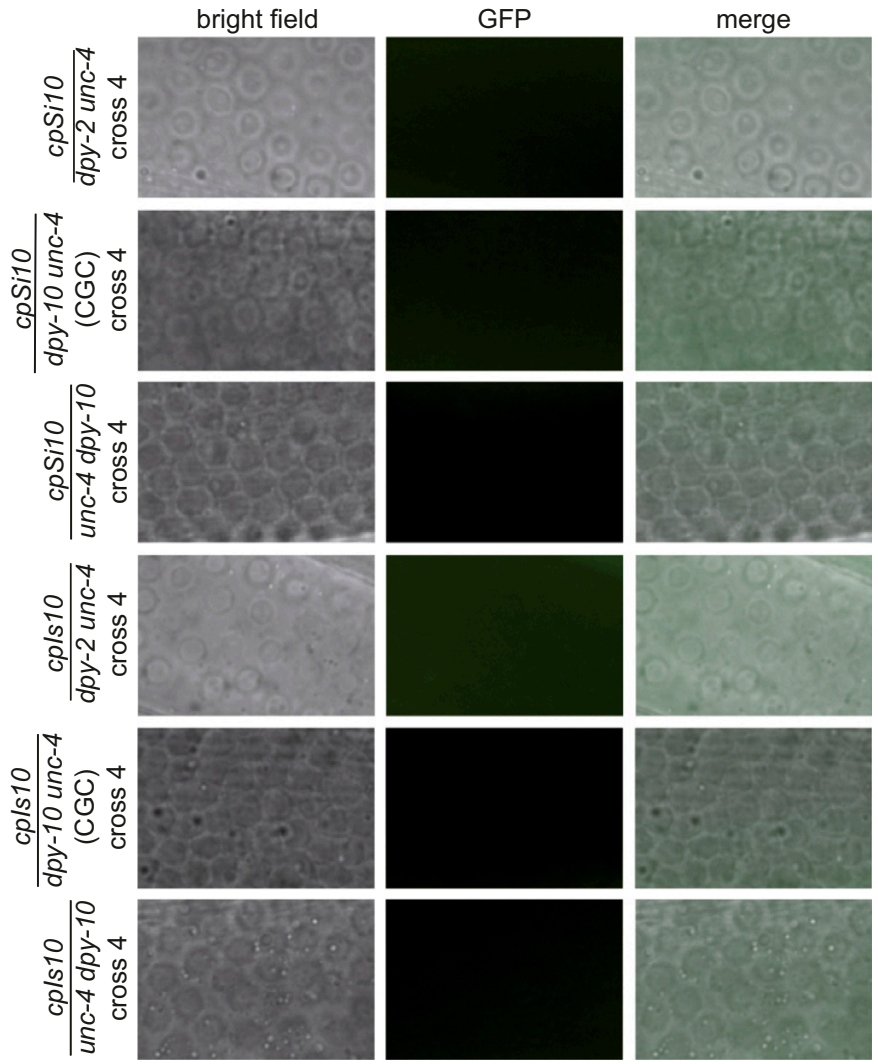

Fig. S3. Widefield microscopy images of brightfield (*Left* column), GFP fluorescence (*Center* column), and a merged image (*Right* column) from silent transgenic strains in Fig. S2 *A–F* (60x).

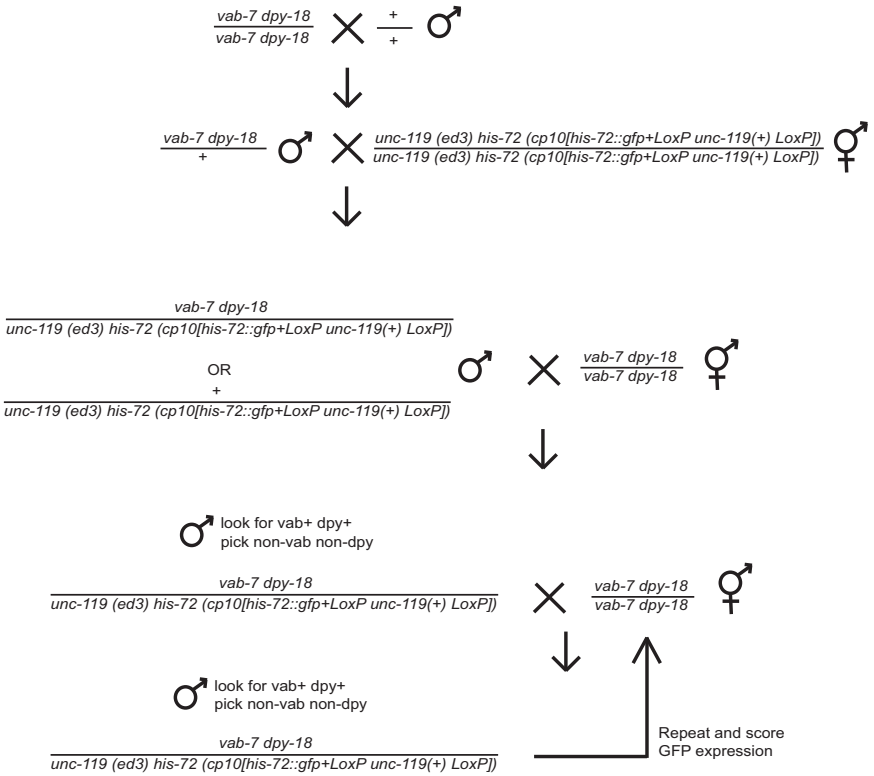

Fig. S4. Schema used to cross the *his-72::GFP* transgene using chromosome *III* marker mutations *vab-7 dpy-18*.