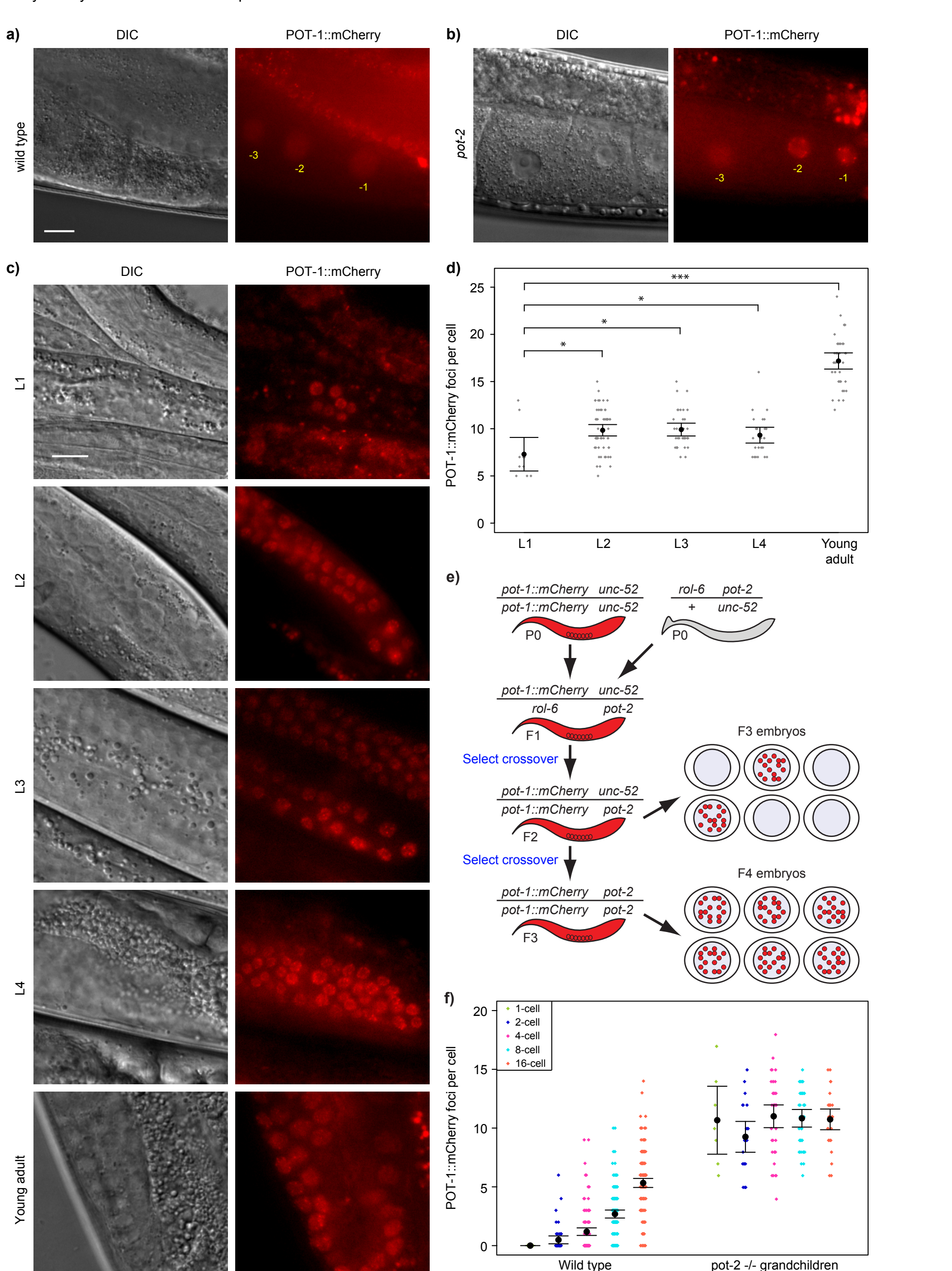


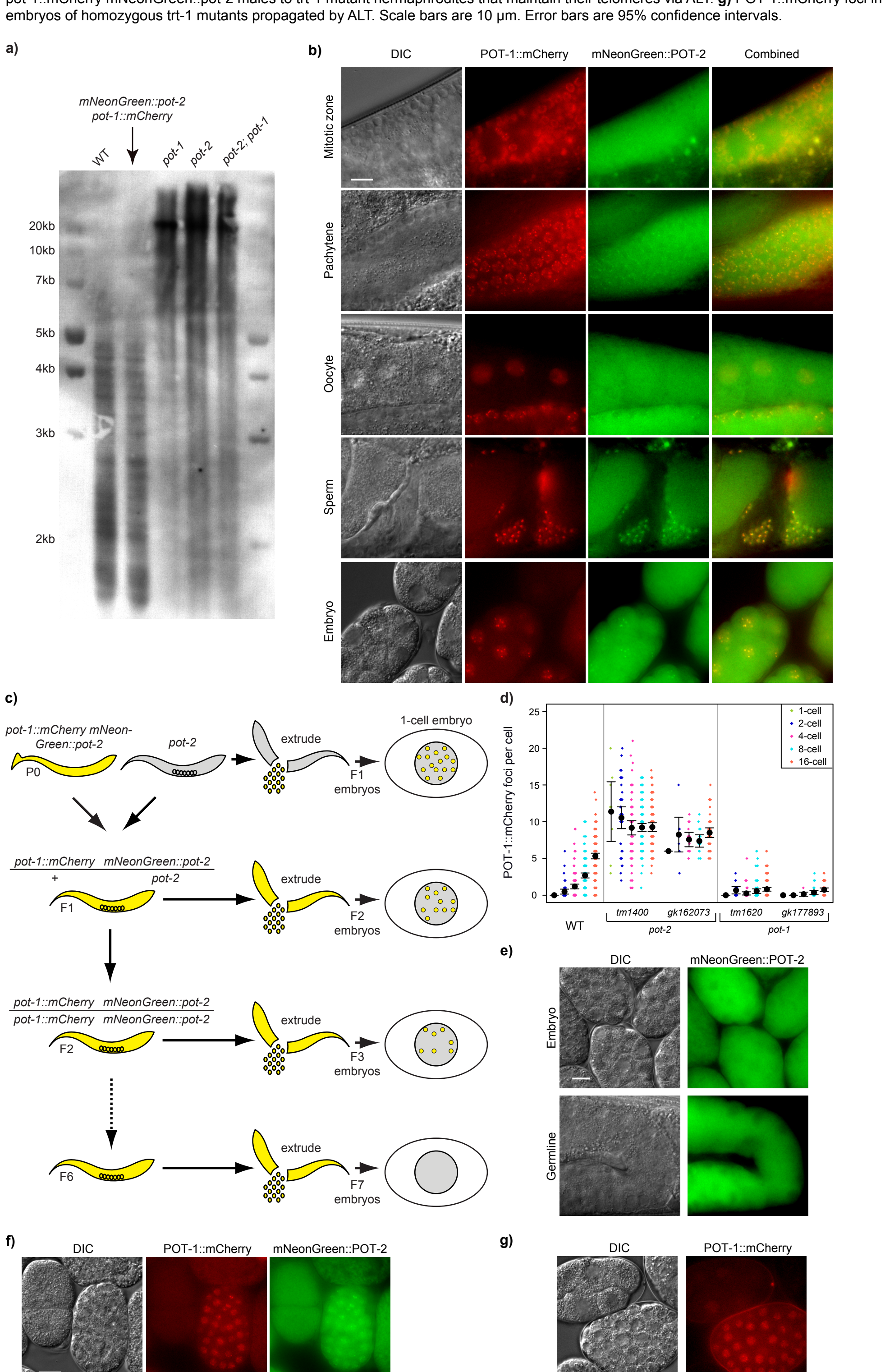
Supplementary Figure 1

a-b) POT-1::mCherry foci in wild type (a) and *pot-2* mutant (b) backgrounds. Oocyte position is indicated with yellow text. **c)** POT-1::mCherry in the distal germline of L1-L4 larvae and young adult worms. **d)** Quantification of POT-1::mCherry in distal germ cells of L1-L4 larvae and young adults. * $p < 0.05$, *** $p < 10^{-5}$. **e)** Diagram of crosses using outcrossed *pot-2* mutants with wild-type telomere lengths. **f)** *pot-2* mutants possessing normal telomere lengths, corresponding to F4 embryos shown in panel e, have elevated levels of Pot1 foci in early embryos. Scale bars are 10 μm . Error bars are 95% confidence intervals.



Supplementary Figure 2

a) A Southern blot of genomic DNA prepared from the indicated genotypes. **b)** DIC and fluorescent images of *pot-1::mCherry* mNeonGreen::*pot-2* worms. Representative images from the germline mitotic zone, pachytene zone, oocytes, sperm, and embryos of early and late stages. **c)** Diagram of the experimental setup used to quantify Pot1 foci in the wild-type descendants of *pot-2* mutants. **d)** Pot1 foci counts in the F2 descendants different *pot-1* and *pot-2* mutants. These independent mutations correspond to results shown in panels 2a and 2c. **e)** mNeonGreen::POT-2 localization in the embryos and germline of *pot-1* mutant homozygotes. **f)** F2 embryos obtained by crossing *pot-1::mCherry* mNeonGreen::*pot-2* males to *trt-1* mutant hermaphrodites that maintain their telomeres via ALT. **g)** POT-1::mCherry foci in embryos of homozygous *trt-1* mutants propagated by ALT. Scale bars are 10 μm . Error bars are 95% confidence intervals.



Supplementary Figure 3

a) Quantification of POT-1::mCherry foci in F2 embryos derived from crosses of *pot-1::mCherry* males with hermaphrodites mutant for the indicated alleles. These are independent alleles of mutations shown in Fig. 3b. **b)** Quantification of POT-1::mCherry foci in homozygous mutant backgrounds for the indicated genes. **c)** Southern blot using genomic DNA from *met-2*, *set-25*, and *set-32* mutants. Error bars are 95% confidence intervals.

