Biology Open

Supplementary Material

Takeshi Yamaguchi et al. doi: 10.1242/bio.20123111

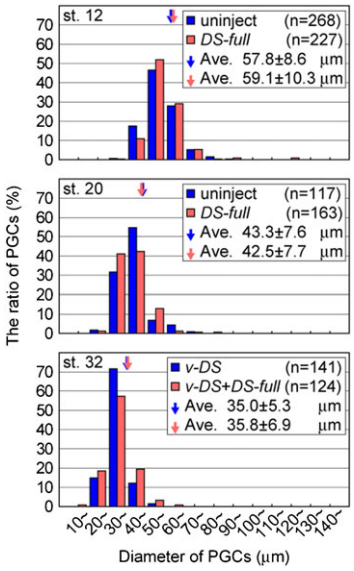

Fig. S1. Overexpression of the *DEADSouth* gene does not affect PGC size. The size distribution of PGCs at stages 12, 20 and 32 from embryos injected with *DS-full*. All mito-EGFP- (at stages 12 and 20) and *v-DS*-labeled PGCs (at stage 32) from injected or uninjected (control) embryos were isolated to measure their diameter. Total numbers of PGCs after each injection are shown as 100%. 'n' indicates total numbers of PGCs. Arrows indicate average diameters from the indicated experiments (*DS-full*/control; 59.1±10.3/57.8±8.6 at stage 12, 42.5±7.7/43.3±7.6 at stage 20, 35.8±6.9/35.0±5.3 at stage 32).

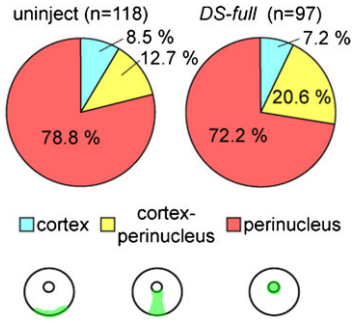

Fig. S2. Overexpression of the *DEADSouth* gene does not affect translocation of germ plasm. Ratio of PGCs with three localization patterns of germ plasm from stage 12 embryos uninjected and injected with *DS-full*. According to the localization patterns, 118 (uninjected) and 97 (*DS-full*) PGCs were classified into three groups; cortex, perinucleus and intermediate (cortex–perinucleus) shown at the bottom of the figure.

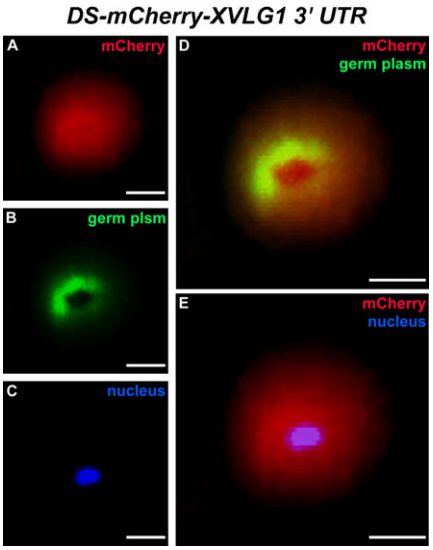

Fig. S3. The 3′UTR of *XVLG1* mRNA does not localize the protein to the germ plasm. Subcellular localization of DEADSouth-mCherry fusion protein in the PGCs of stage 12 embryos injected with *DEADSouth-mCherry-XVLG1 3′UTR* (**A–E**). PGCs were isolated from mito-EGFP embryos injected with the mRNA, fixed, stained with Hoechst 33342 and examined for the location of the mCherry signal (in red), germ plasm (mitochondria, in green) and nucleus (in blue). Note that the mCherry signal is distributed throughout PGCs. Scale bars: 10 μm.