Figure S4 INA-1-GFP expression in DTCs. Images were captured by CSU-X1 spinning-disc conforcal system (Yokogawa Electric Corp.) mounted on Axioplan 2 microscope (Zeiss) equipped with a C-apochromat 63X (water immersion; NA 1.2) lens and controlled by MetaMorph software (Molecular Devices Inc.). (A, B, C) *ina-1::GFP* expression. Confocal (upper) and Nomarski (lower) images of L3 hermaphrodites of wild type (A), *fbl-1(tk45)* (B), *emb-9(tk75); fbl-1(tk45)* (C) having *gmIs5* that contain chromosomally integrated *ina-1::GFP* plasmids (Baum & Garriga 1997). The arrowhead indicates the INA-1-GFP expression in DTCs. Scale bar, 20 μm. (D) Fluorescence intensity of INA-1-GFP. The fluorescence intensity for each sample was normalized to that of the wild type. Ten confocal

images of DTCs for each strain were used for quantification. The relative fluorescence intensity was determined as in Figure 5G. Data are shown as the mean ± SD. Results for Student's *t*-test versus wild type are indicated; **, P<0.01; NS, not significant. All images were captured under the same conditions. (E, F) *lag-2p::GFP* expression. As a control, we examined *lag-2p::GFP* expression in DTCs and found that it is not affected by genetic backgrounds used in this work. All strains have *qIs56* that contains chromosomally integrated *lag-2p::GFP* plasmids (Blelloch *et al.* 1999) in their background. The fluorescence intensity for each sample was normalized to that of the wild type. Ten or twelve confocal images of DTCs for each strain were used for quantification. The relative fluorescence intensity was determined as in Figure 5G. Data are shown as the mean ± SD. Results for the Student's *t*-test against the wild-type value are indicated; NS, not significant. All images were captured under the same conditions.