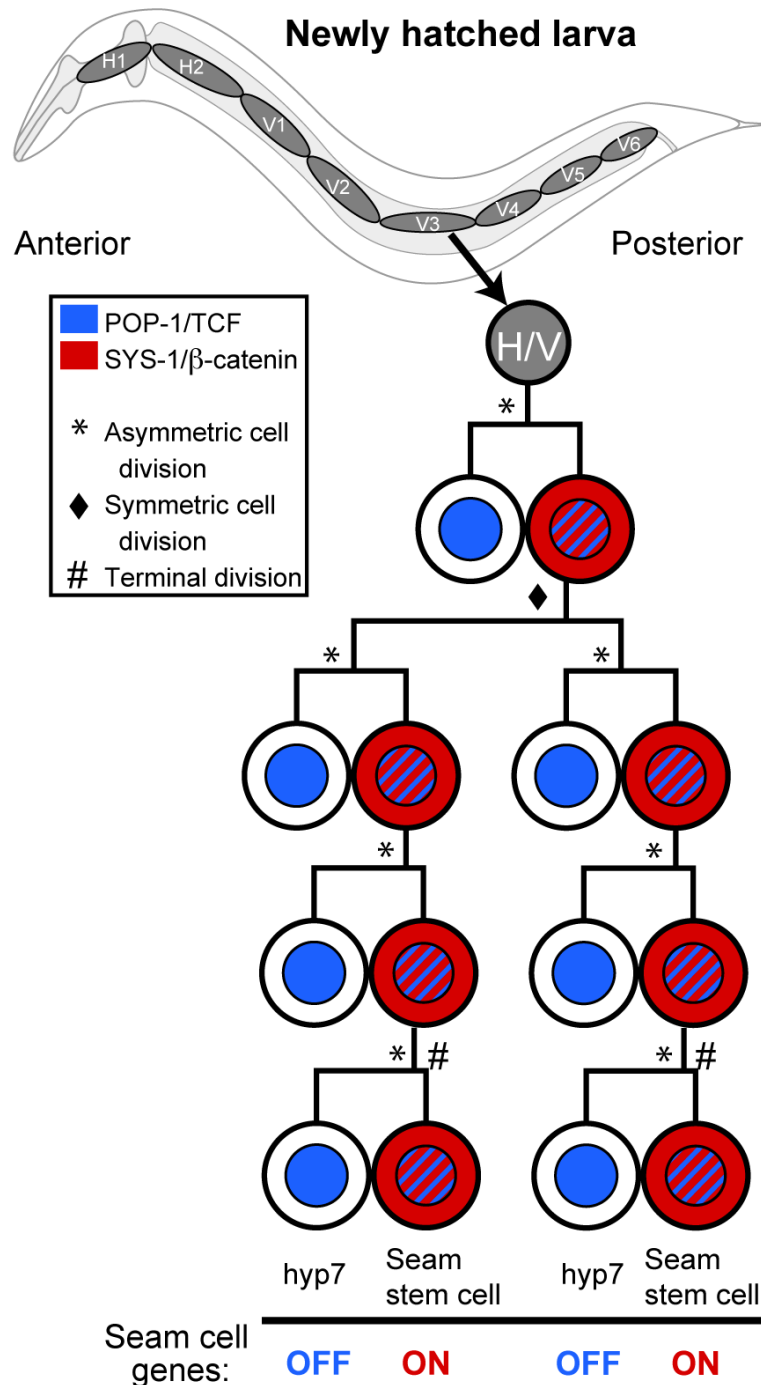
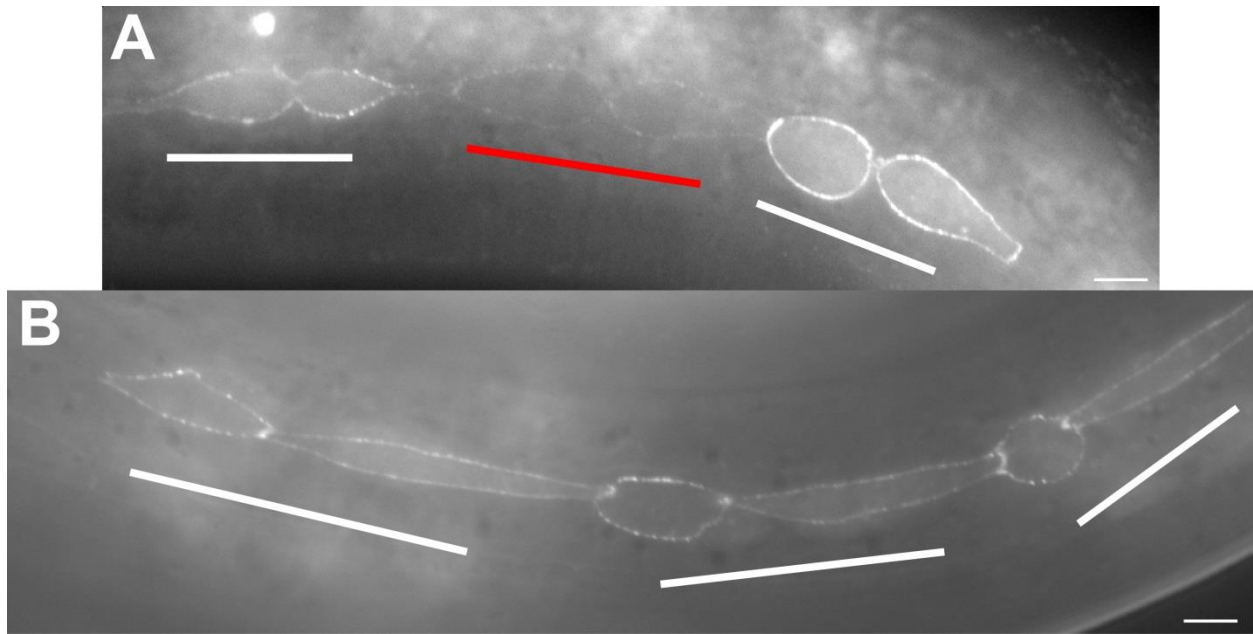


**Figure S1: Model for β-catenin regulation in the seam cells of a wild type worm.**

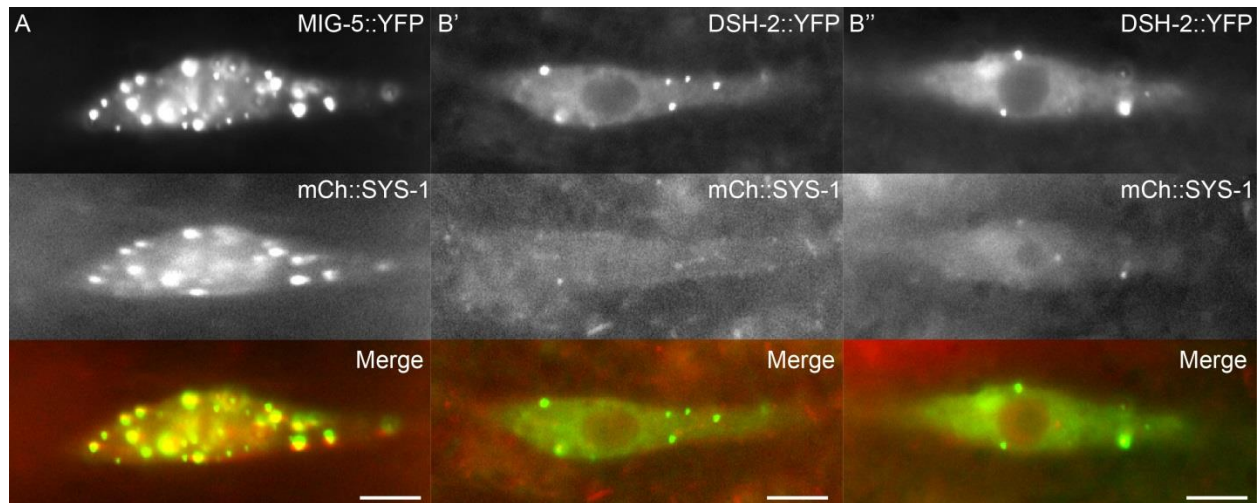
Two pools of APR-1/APC are present in the anterior daughter, a microtubule-associated WRM-1-regulating pool (wrmapr-1, shown in blue) and a KIN-19/CKIα associated SYS-1-regulating pool (sysapr-1, shown in red). Polarized localization of both sysapr-1 and wrmapr-1 is controlled by PRY-1/Axin. Frizzled and Dishevelled presumably localize to the posterior daughter, but how they translate the polarity and activity signal to APR-1 is unknown (denoted by question marks). S, SYS-1/β-catenin (red); W, WRM-1/β-catenin (blue); Ax, SYS-1-regulating PRY-1/Axin (red); Ap, WRM-1-regulating PRY-1/Axin (blue); K, KIN-19/CKIα (red); MT, microtubules; Fz, Frizzled; D, DSH-2, MIG-5/Dishevelled.



**Figure S2: The epidermal seam cells divide in a stem cell-like pattern dependent on the W $\beta$ A signaling pathway.** A cartoon lineage of a representative seam cell. Nuclear POP-1/TCF is high in the anterior nuclei, resulting in target gene repression. Nuclear POP-1 is low in posterior in response to WRM-1/ $\beta$ -catenin-mediated nuclear export, SYS-1/ $\beta$ -catenin levels are high in response to stabilization, and Wnt targets are activated that result in adoption of the seam cell fate. Note that the “#” symbol marks the terminal/final seam cell division, upon which we focus our studies.



**Figure S3: PRY-1::GFP localizes symmetrically to seam cell daughter cortices and does not alter cell fate specification.** A, *osEx229*(*p<sub>pry-1</sub>::PRY-1::GFP*) in wild-type seam cells. Lines indicate daughter pairs. The red line marks a daughter pair with lower *osEx229* expression that still displays symmetric PRY-1::GFP localization. B, *osEx229* expression after division and fate specification. White lines mark daughter pairs. The anterior daughters have correctly adopted the *hyp7* fate and have become smaller and more rounded in anticipation of fusion with *hyp7*, while the posterior daughters have adopted the seam fate and begun elongation. Scale bars = 5  $\mu$ m.



**Figure S4: Dvl puncta are present prior to division.** All images are representative of seam cell mothers in interphase that are expression high/punctate levels of Dvl overexpression. A, top panel: *osEx233*( $p_{SCM}$ ::MIG-5::YFP), middle panel: *uiwls4*( $p_{sys-1}$ ::mCherry::SYS-1), bottom panel: merge. B' & B'', top panels: *osEx225*( $p_{SCM}$ ::DSH-2::YFP), middle panels: *uiwls4*( $p_{sys-1}$ ::mCherry::SYS-1), bottom panels: merge. Scale bars = 5  $\mu$ m.

**Table S1: DSH-1 does not regulate seam cell fate.** Seam cell counts were obtained in early adulthood using the *wls51(scm::GFP)* reporter. EV = empty vector.

Genotype	RNAi treatment	Average seam cell number $\pm$ standard error	N-value
wild-type	EV	15.98 $\pm$ 0.07	62
wild-type	<i>dsh-1 RNAi</i>	15.96 $\pm$ 0.05	62
<i>dsh-1(ok1445)</i>	EV	16 $\pm$ 0.05	61
<i>dsh-2(or302) mig-5(tm2639)</i>	EV	17.66 $\pm$ 0.28	54
	<i>dsh-1 RNAi</i>	17.72 $\pm$ 0.27	59