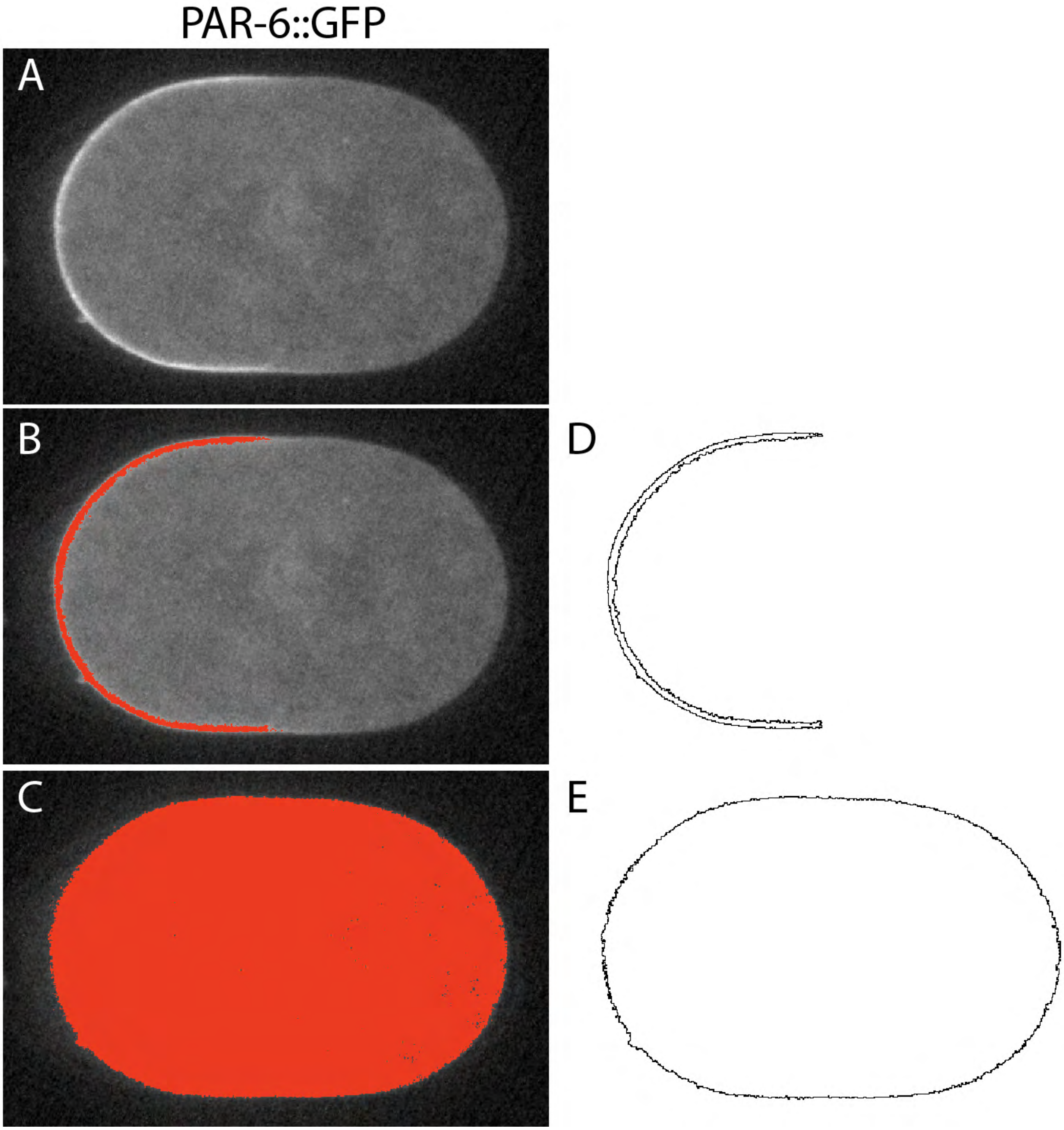

Fig. S1. Procedure to determine the domain size of PAR-6::GFP. (**A-C**) Confocal midsection of a representative PAR-6::GFP embryo at nuclear envelope breakdown. The red overlay on the embryo in B represents the threshold mask applied in order to measure the area of the PAR-6::GFP cortical domain. The red overlay in C shows the threshold mask used to measure the area of the embryo cross-section. (**D**,**E**) The area within the outline in D was designated as area of the cortical PAR-6::GFP domain and the area defined by the outline in E was designated as the area of the embryo.

Movie 1. Control showing distribution of LGL-1::GFP in *lgl-1::gfp; par-2(lw32)*. Time-lapse florescence micrographs of *lgl-1::gfp; par-2(lw32)* embryos.

Movie 2. CHIN-1 is required for the cortical maintenance of LGL-1::GFP in *lgl-1::gfp; par-2(lw32)*. Time-lapse florescence micrographs of *lgl-1::gfp; par-2(lw32); chin-1(RNAi)* embryos.

Table S1. Comparison of measured changes in cortical PAR-6::GFP levels using alternative methods for quantifying cortical PAR-6::GFP. Two alternative methods for calculating the cortical PAR-6::GFP signal were applied to the *cgef-1(RNAi)* and the *par-2(RNAi)* data sets. The column on the left shows the percentage change in cortical PAR-6::GFP and the associated s.e.m. obtained using the method of averaging a set of lines drawn on the cortex that is described in the Materials and methods. The column on the right shows the results obtained by using the average signal associated with the full area of the cortical signal. Both methods led to the same conclusions; the measured changes in PAR-6::GFP relative to the negative control were not significant using either method. The *P* value associated with each comparison is shown in parentheses next to the measured change.

	Change in cortical signal (%)	
cgef-1(RNAi)	7.3±7.8% (0.35)	-1.2±10.0% (0.18)
par-2(RNAi)	4.3±4.2% (0.21)	3.5±2.2% (0.35)

Table S2. Embryonic lethality in *par-2; lgl-1* after depleting CGEF-1.

Genotype		**Embryonic lethality**		
***par-2* allele**	***lgl-1* allele**	**Empty vector**	***cgef-1(RNAi)***	***P* value**
lw32	*tm2616*	100% (n=563)	99.9±0.4% (n=765)	0.17
lw32	*it31*	100% (n=788)	68.3±8.3% (n=687)	$7.4\text{x}10^{-6}$
it5	*tm2616*	100% (n=628)	100% (n=556)	1
it5	*it31*	97.2±3.4% (n=714)	83.0±15.3% (n=1731)	0.001