

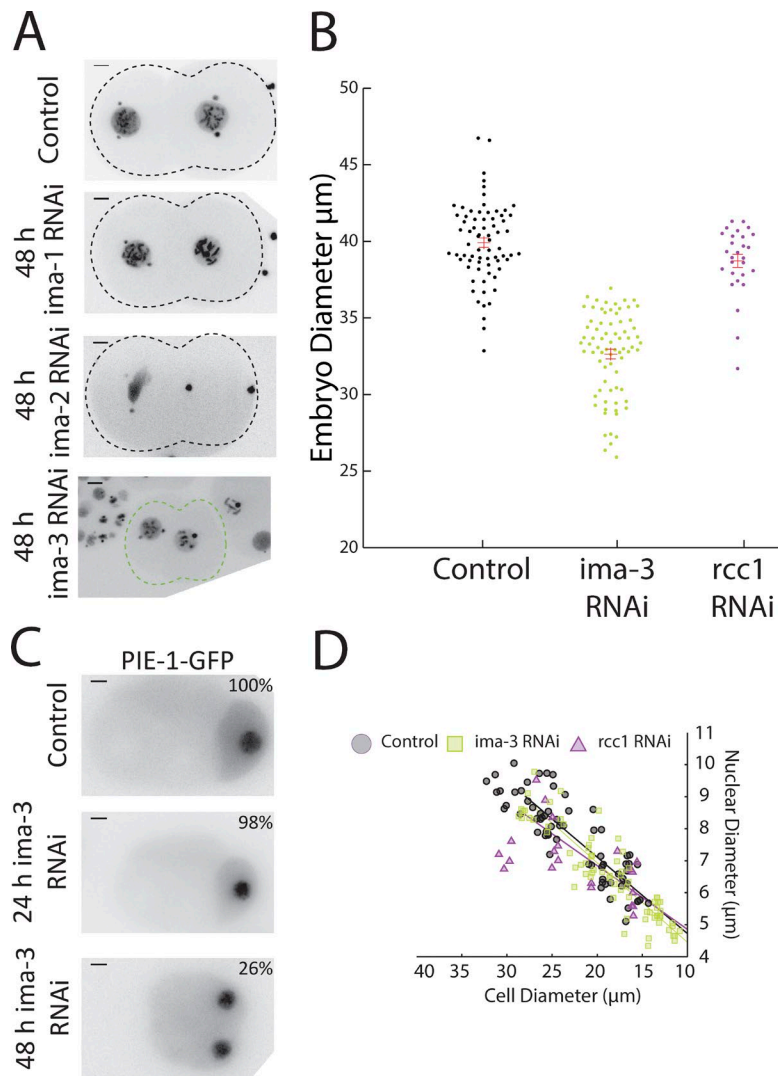
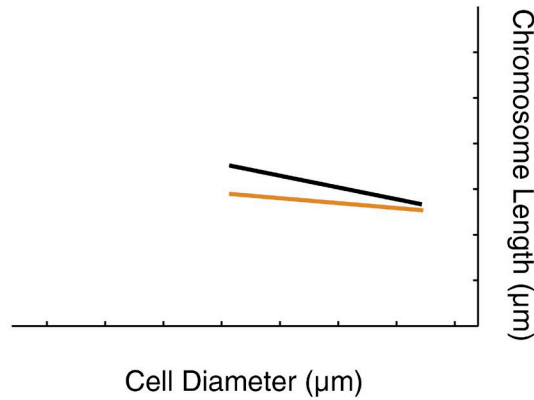
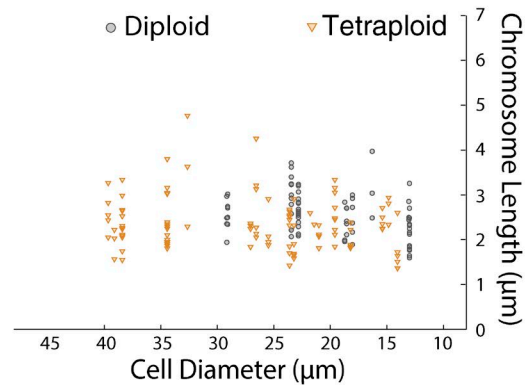
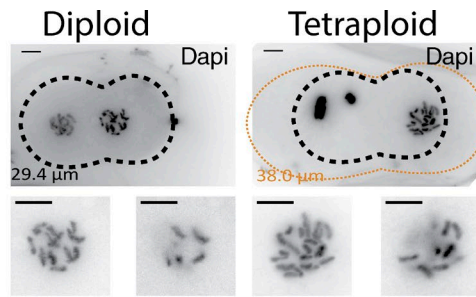
Ladouceur et al., <http://www.jcb.org/cgi/content/full/jcb.201502092/DC1>

Figure S1. **Embryo size differences for IMA-1 to -3 RNAi and RCC1 RNAi, PIE-1::GFP localization at the 4-cell stage, and nuclear to cell diameter relation in control, IMA-3, and RCC1 RNAi embryos.** (A) Embryos depleted of the three importin- α proteins found in *C. elegans*. The outlines of the embryos are depicted with dashed black lines. (B) Embryo diameter in control, ima-3, or rcc1 RNAi. Error bars are standard error of the mean. (C) Percentage of embryos with the indicated localization or mislocalization of Pie-1::GFP in the P2 cell after 48- or 24-h depletion of ima-3. (A and C) Bars, 5 μm . (D) Correlation of cell to nucleus diameter in control or rcc1 RNAi embryos. Linear regression values are presented in Table S3.



	Slope	pValue	Intercept	pValue
Diploid	0.048 +/- 0.014	0.0010702	1.690 +/- 0.275	5.88E-08
Tetraploid	0.020 +/- 0.016	0.2044	1.892 +/- 0.342	6.34E-07

Figure S2. **Chromosome length analysis in diploid versus tetraploid worms.** Representative still images of diploid and tetraploid embryos at the 2-cell stage. Shown is the outline of the embryo and size of the depicted embryo: black, diploid; orange, tetraploid. The diploid outline is overlaid on the tetraploid to illustrate differences in size. Bars, 5 μ m. Chromosome length correlated to cell size in diploid and tetraploid embryos from the 1- to 16-cell stage. Graph and table representing the linear regression of cell size versus chromosome length are shown. Diploid, $n = 97$; tetraploid, $n = 156$.

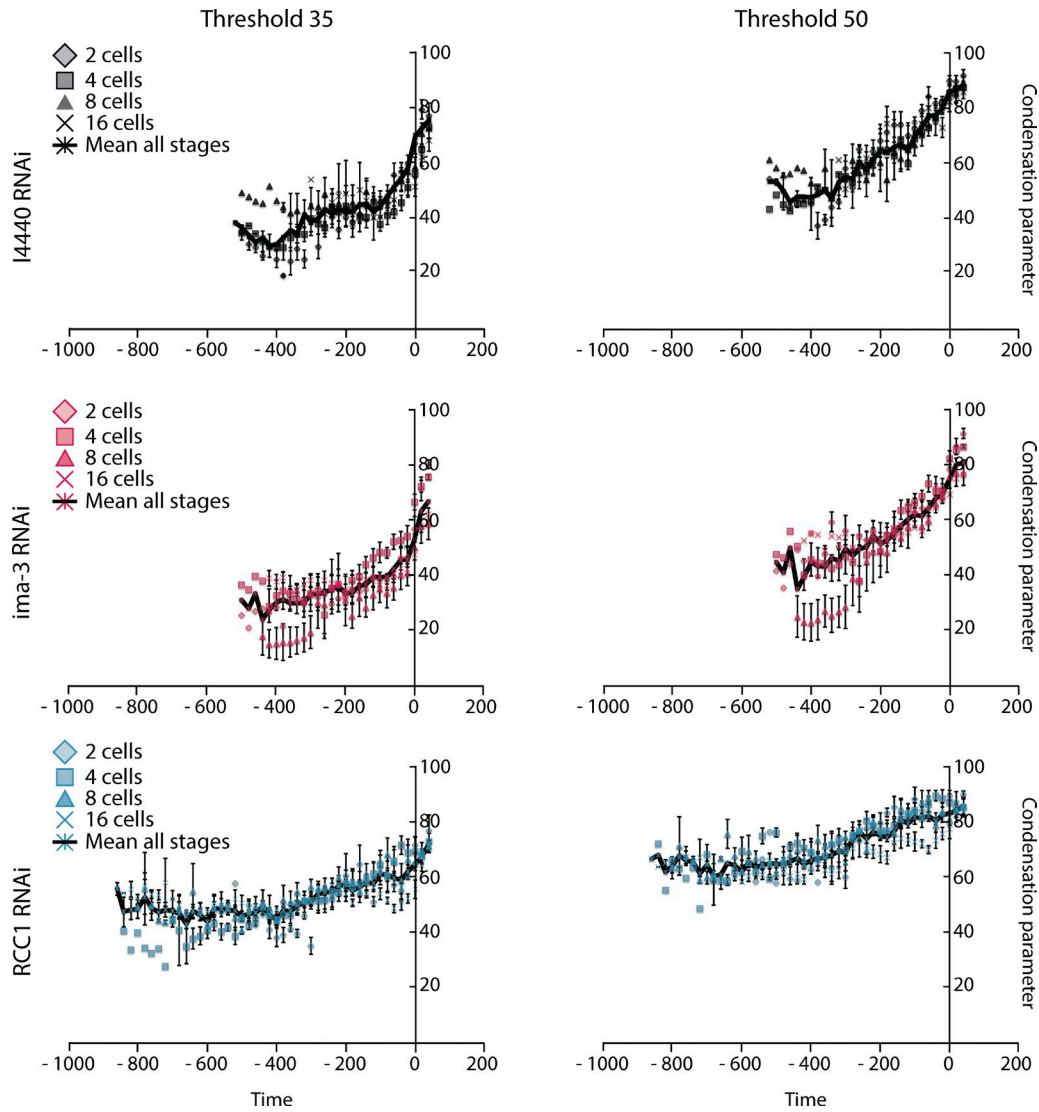


Figure S3. **Plot of condensation dynamics at all developmental stages examined in this study.** The number of pixels with a value below a threshold of either 35 or 50% is shown as indicated. Error bars are standard error of the mean.

Table S1. **One-way ANOVA comparing developmental stage for each RNAi condition or all RNAi conditions at each developmental stage**

Condition/developmental stage	ANOVA significance
Condition	
Control RNAi	P < 0.0001
ima-3 RNAi	P < 0.0001
rcc1 RNAi	P < 0.0001
Developmental stage	
1-cell stage	P < 0.0001
2-cell stage	P < 0.0001
4-cell stage	P < 0.0001
8-cell stage	P < 0.0001
16-cell stage	P < 0.0001

One-way ANOVA comparing chromosome length differences measured in control, ima-3, and rcc1 RNAi at all developmental stages. The top half of the table shows the ANOVA significance for comparisons of chromosome length differences between all developmental stages from 1- to 16-cell stage for each RNAi condition. The bottom half of the table shows the ANOVA significance for comparisons of chromosome length differences between all RNAi conditions for each developmental stage from 1- to 16-cell stage. Using the Bonferroni correction gives a significance threshold of 0.01. Control RNAi, $n = 354$ chromosomes; IMA-3 RNAi, $n = 287$ chromosomes; RCC1 RNAi, $n = 207$ chromosomes.

Table S2. Student's *t* test statistical significance of chromosome length differences comparing all developmental stages for each RNAi condition

Developmental stage	Control RNAi	ima-3 RNAi	rcc1 RNAi
1 cell vs. 2 cell	ns	ns	P ≤ 0.05
1 cell vs. 4 cell	ns	P ≤ 0.05	P ≤ 0.05
1 cell vs. 8 cell	P ≤ 0.05	P ≤ 0.05	P ≤ 0.05
1 cell vs. 16 cell	P ≤ 0.05	P ≤ 0.05	P ≤ 0.05
2 cell vs. 4 cell	ns	ns	ns
2 cell vs. 16 cell	P ≤ 0.05	P ≤ 0.05	P ≤ 0.05
2 cell vs. 16 cell	P ≤ 0.05	P ≤ 0.05	ns
4 cell vs. 8 cell	P ≤ 0.05	ns	ns
4 cell vs. 16 cell	P ≤ 0.05	P ≤ 0.05	ns
8 cell vs. 16 cell	ns	P ≤ 0.05	ns

The multiple comparisons Student's *t* test was corrected using the Bonferroni correction. ns, not significant.

Table S3. Correlation between cell size, nuclei size, and chromosome length in control and IMA-3-, RCC1-, and NTF-2-depleted embryos

Parameter	Slope	P-value	Intercept
Cell diameter vs. chromosome length (μm)			
Control (333)	0.052 ± 0.01	4.11 × 10 ⁻⁷	2.056 ± 0.251
ima-3 RNAi (285)	0.053 ± 0.007	1.38 × 10 ⁻¹¹	1.79 ± 0.144
rcc1 RNAi (185)	0.019 ± 0.012	0.1016	1.857 ± 0.245
Nuclear diameter vs. chromosome length (μm)			
Control (316)	0.130 ± 0.033	0.00011151	2.182 ± 0.252
ima-3 RNAi (272)	0.210 ± 0.026	4.28 × 10 ⁻¹⁴	1.387 ± 0.179
rcc1 RNAi (165)	0.120 ± 0.036	0.0010262	1.436 ± 0.264
Cell diameter vs. nuclear diameter (μm)			
Control (64)	0.239 ± 0.022	2.62 × 10 ⁻¹⁵	2.334 ± 0.477
ima-3 RNAi (70)	0.249 ± 0.016	7.13 × 10 ⁻²⁴	1.965 ± 0.291
rcc1 RNAi (21)	0.199 ± 0.046	0.00056384	2.861 ± 0.954
Cell volume vs. nuclear volume (μm³)			
Control (37)	0.009688 ± 0.0009577	6.25 × 10 ⁻¹²	183.55 ± 13.85
rcc1 RNAi (23)	0.0053036 ± 0.0020787	0.0186	105.63 ± 27.965
nif2 RNAi (27)	0.002163 ± 0.001139	0.0693	120.4 ± 13.22

Bold indicates statistically different from control. P-value is the possibility of the slope being different than 0.

Table S4. Time spent in prophase in control and RCC1-depleted embryos

RNAi	Mean time
l4440	4 min 30 s
Rcc1	4 min 35 s

Time represents time of centrosome growth from duplication to NEBD.

Table S5. Statistical differences of chromosome length variance at all different stages between control and RCC1-depleted embryos

Developmental stage	Variance control	Variance rcc1 RNAi embryos	Statistically different
	<i>μm</i>	<i>μm</i>	
1-cell stage	1.914	1.925	No
2-cell stage	1.751	2.113	No
4-cell stage	1.405	1.966	Yes
8-cell stage	1.858	1.226	No
16-cell stage	1.626	1.245	No