

An RNAi-based suppressor screen identifies interactors of the Myt1 ortholog of *C. elegans*

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FIGURE S1

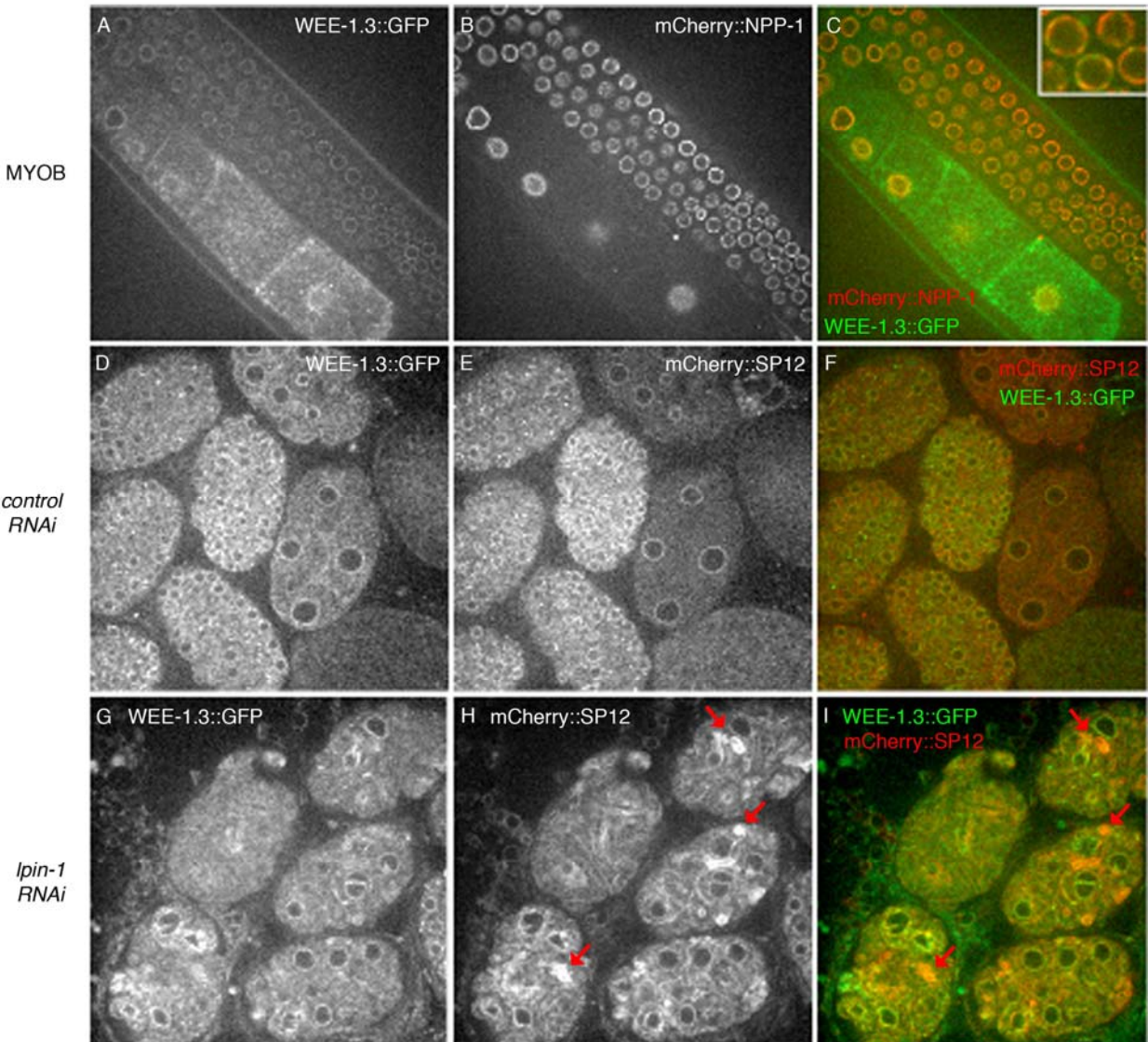


Figure S1 WEE-1.3 is localized to the nuclear envelope and a portion of the endoplasmic reticulum. Single confocal images of live animals expressing WEE-1.3::GFP (green) and mCherry::NPP-1 (red) (A-C) or WEE-1.3::GFP (green) and mCherry::SP12 (red) (D-I). (A-C) Gonad from animal expressing WEE-1.3::GFP and mCherry::NPP-1. Inset in (C) is a blow-up of meiotic nuclei in the more distal germline. (D-I) Embryos from animals expressing WEE-1.3::GFP and mCherry::SP12 subjected to *control* (D-F) or *Ipin-1* (G-I) RNAi. Red arrows in (H) and (I) indicate regions where WEE-1.3::GFP and mCherry::SP12 do not colocalize. Embryos are ~50 μ m in length.

Figure S2

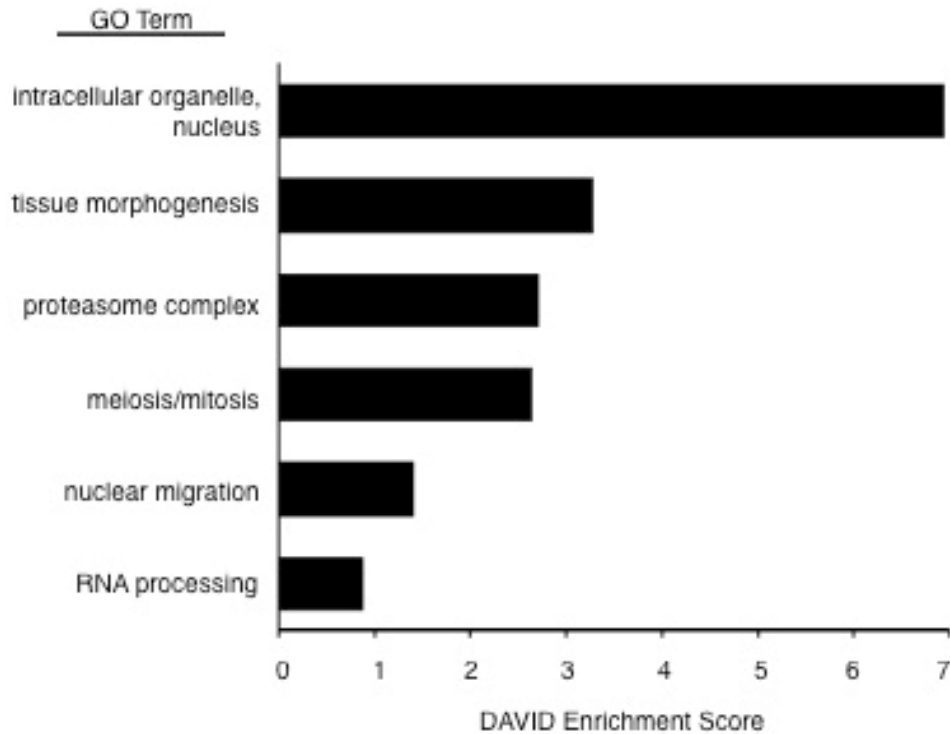


Figure S2 Gene ontology (GO) terms enriched in the set of suppressors identified in the WEE-1.3 RNAi suppressor screen. The top scoring GO: Biological Process and GO: Cellular Component categories with P values of <0.05 are shown. Reported terms are subontologies that belong to either biological process (BP; tissue morphogenesis, meiosis/mitosis, phosphorylation, translation, nuclear migration, RNA processing, and proteolysis) or cellular component (CC; intracellular organelle/nucleus and proteasome complex) categories. Enrichment and P -values are as follows: intracellular organelle/nucleus ($E = 6.92$, P -value = $9.3e-10$), tissue morphogenesis ($E = 3.25$, P -value = $4.4e-4$), proteasome complex ($E = 2.68$, P -value = $1.6e-4$), meiosis/mitosis ($E = 2.62$, P -value = $1.0e-3$), nuclear migration ($E = 1.38$, P -value = $4.3e-2$), and RNA processing ($E = 0.85$, P -value = $1.8e-2$).

FIGURE S3

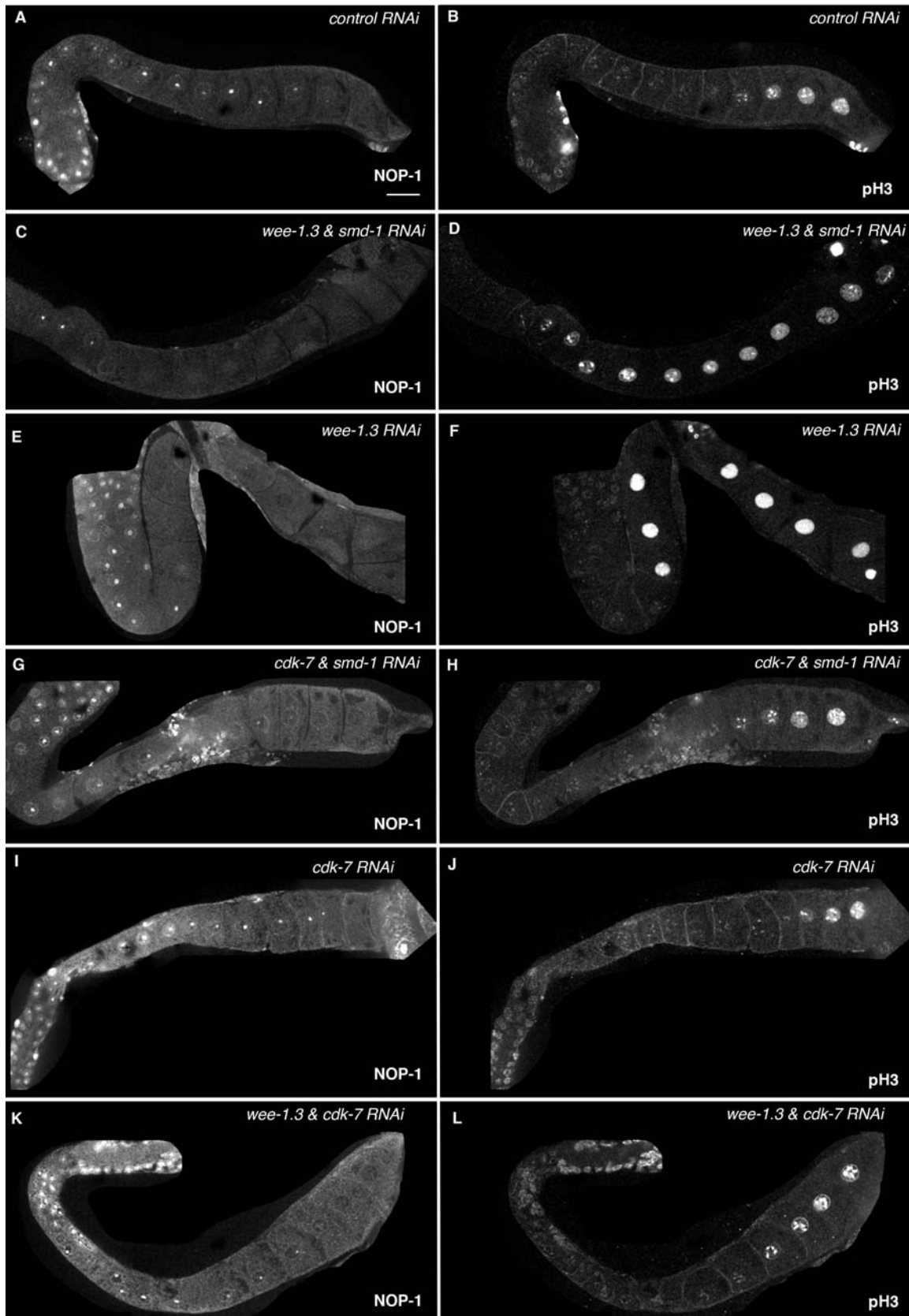


Figure S3 Individual panels of NOP-1 and pH3 staining for images found in Figure 5.

Individual panels for NOP-1 and pH3 antibody images provided in Figure 5. Single-plane confocal images of gonads dissected from mothers treated with the indicated RNAi, fixed, and co-stained with antibodies against the nucleolus (NOP-1; panels A, C, E, G, I, and K) and phosphohistone H3 (Ser10) (pH3; panels B, D, F, H, J, and L). RNAi treatment is as follows: (A-B) control, (C-D) co-depletion of WEE-1.3 and control, (E-F) WEE-1.3-depleted, (G-H) co-depletion of CDK-7 and control, (I-J) CDK-7-depleted, and (K-L) co-depletion of WEE-1.3 and CDK-7. Gonads are oriented with the proximal region to the right in this figure. Scale bar is approximately 20 μ m.

Table S1 Plasmids and Primers Used in This Study

PLASMID	DESCRIPTION OF PLASMID INSERT	PRIMERS USED TO GENERATE PLASMID	DONOR VECTOR USED
pAA11	attL4::wee-1.3 short promoter::attR1	oAKA2 and oAKA3	pDONR(P4-P1r)
pAA13	attR2::wee-1.3 3'UTR::attL3	oAKA6 and oAKA9	pDONR(P2r-P3)
pAA15	attR2::wee-1.3 gene + wee-1.3 3'UTR::attL3	oAKA5 and oAKA9	pDONR(P2r-P3)
pAA32	attL4::wee-1.3 short promoter + wee-1.3 gene::attR1	oAKA51 and oAKA52	pDONR(P4-P1r)
pCR110	attL1-GFP with introns (no stop)-attL2		
pCR347	attL1-mCherry (no stop)-attL2		
pCR319	attR4 - attR3; <i>C.elegans unc-119(+)</i>		
pNU162	<i>fib-1</i> prom::FIB-1::eGFP:: <i>fib-1</i> 3' UTR + <i>unc-119(+)</i>		
pDONR P4 P1R	attP4 – attP1R		
pDONR P2R P3	attP2R – attP3		

PRIMER	PRIMER SEQUENCE (5' → 3')	AMPLIFIES
oAKA2	GGGGACAACCTTTGTATAGAAAAGTTGGCcaacatcagaaattcaag	attB4- <i>wee-1.3</i> promoter (forward)
oAKA3	GGGGACTGCTTTTTGTACAAACTTTGGcatttctactgaaaatg	attB1- <i>wee-1.3</i> promoter (reverse)
oAKA5	ggggacagcttctgtacaaagtggTTATGGACGACACAGAGGGTAACCTC	attB2- <i>wee-1.3</i> gene (forward)
oAKA6	ggggacagcttctgtacaaagtggGTAAtaatgcacaaaaatcagaaa	attB2- <i>wee-1.3</i> 3'UTR (forward)
oAKA9	ggggacaactttgtataataaagtggCgtctactccagactactacaagaacagg	attB3- <i>wee-1.3</i> 3'UTR (reverse)
oAKA51	GGGGACAACCTTTGTATAGAAAAGTTGGCacccaaccattgcaaatatgtg	attB4- <i>wee-1.3</i> promoter (forward)
oAKA52	GGGGACTGCTTTTTGTACAAACTTTGCaacctcgtcgcctgatgatcc	attB1- <i>wee-1.3</i> gene (reverse)
B4F2	ggggacaactttgtatagaaaaagtggcACGTGGATGAATGAGAGCAGC	attB4- <i>cbd-1</i> promoter (forward)
B1R3	ggggactgcttttgtacaaacttggATATCCCGATTATCATCATTGTACG	attB1- <i>cbd-1</i> gene (reverse)
B2rF2	ggggacagcttctgtacaaagtggccTGATAAGTTGTTCTAAACACCCCC	attB2- <i>cbd-1</i> 3'UTR (forward)
B3R1	ggggacaactttgtataataaagtggGCGTCCCTTTACATTTACAG	attB3- <i>cbd-1</i> 3'UTR (reverse)
oAKA70	ggtggttctccgaaagaa	<i>act-1</i> (forward)
oAKA71	gctatgtccagccatccttct	<i>act-1</i> (reverse)
oAKA88	gaataatgtgatcgacgaggctcc	<i>wee-1.3</i> (forward)
oAKA89	tcttctacgtggcgattccgattg	<i>wee-1.3</i> (reverse)
oAKA80	tctcaccatcgttctctcactg	<i>vet-1</i> (forward)
oAKA81	tcggtgggagtgaagaatgg	<i>vet-1</i> (reverse)
oAKA84	gtgctaacttccatccgttg	<i>vet-4</i> (forward)
oAKA85	caaccagtttctctggaagtc	<i>vet-4</i> (reverse)
oAKA76	ggaagaatgtcaagcggcac	<i>vet-6</i> (forward)
oAKA77	tccgtctctgatggcttctctc	<i>vet-6</i> (reverse)

Table S2 is available for download as an Excel file at

<http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013649/-/DC1>