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Supporting Information

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Using RNA Interference to Identify Specific Modifiers of a Temperature-Sensitive, Embryonic-Lethal Mutation in the *Caenorhabditis elegans* Ubiquitin-Like Nedd8 Protein Modification Pathway E1-Activating Gene *rfl-1*

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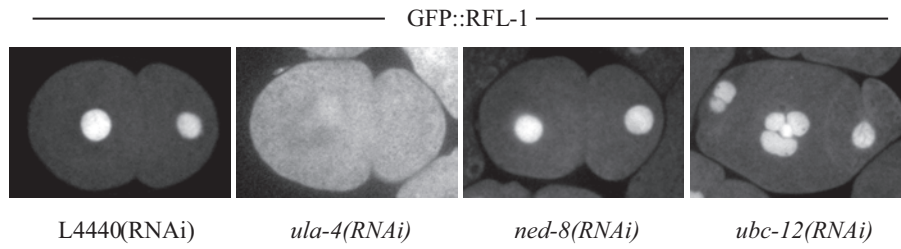


FIGURE S1.—Nuclear localization of GFP::RFL-1 is lost in *ula-1(RNAi)* but not in other neddylation pathway defective backgrounds.

TABLE S1

Summary of modifier effects on embryonic lethality

Table S1 is available for download as an Excel file at <http://www.genetics.org/cgi/content/full/genetics.109.104885/DC1>.

TABLE S2**Summary of *rfl-1(or198ts)* genetic modifiers**

Gene	Encoded Protein	Interaction	Essential	Specific	Human Homolog	Blast P value	% length
<i>csn-5</i>	COP9 Signalosome subunit	suppressor	yes	yes	COPS5	5.2e-100	84.8
<i>csn-2</i>	COP9 Signalosome subunit	suppressor	yes	yes	COPS2	6.81e-151	83.8
<i>mus-101</i>	Nucleotide Excision Repair Factor	suppressor	yes	yes	TOPBP1	3e-50	61.7
R10D12.14	Unknown Function	suppressor	yes	yes	TNRC15	6.4e-06	25.7
<i>mnk-1</i>	Kinase	suppressor	no	yes	Q9BUB5-2	2.1e-31	
F25H5.5	Claspin (kinase)	suppressor	yes	yes	CLSPN	1.4e-25	91.3
F22B8.7	Fe-S Protein	suppressor	no	yes	MOSC1	8.6e-43	85.5
T24C4.3	Novel	suppressor	no	yes	-	-	-
<i>cdr-2</i>	glutathione S-transferase-like	suppressor	no	yes	C6orf168	7.3e-22	82.7
T26E3.6	Fibrillin related protein	suppressor	no	yes	SORL1	0.0001	84.5
<i>elks-1</i>	Rab6 GTPase-interacting protein	suppressor	no	yes	ERC2	6.4e-36	77.3
<i>sri-63</i>	7TM chemoreceptor	suppressor	no	yes	CCR1	0.011	87.7
<i>gcy-20</i>	guanylate cyclase	suppressor	no	yes	NPR1	1.4e-133	89
<i>lgc-20</i>	Acetylcholine receptor	suppressor	no	yes	CHRNB1	1.8e-07	71.6
<i>ugt-16</i>	UDP-glucuronosyl transferase	suppressor	no	yes	UGT2B7	1.6e-43	95.5
<i>col-164</i>	Collagen protein	suppressor	no	yes	Q59HB5	6.4e-43	73
<i>vig-1</i>	RNA Binding Protein	suppressor	yes	no	Q8NC51-4	2.1e-31	97.9
M106.4	GMP Synthase	suppressor	no	no	GMPS	2.7e-151	74.7
<i>aqp-5</i>	Aquaporin	suppressor	no	no	AQP8	6.4e-26	73.8
T05H4.11	Novel	suppressor	no	no	-	-	-
T04C9.1	Rho GTPase-activating protein	suppressor	no	no	ARHGAP10	3.1e-144	79
<i>sel-10</i>	F-Box,WD40 Protein	enhancer	no	yes	FBXW7	1.9e-126	76.7
<i>pha-1</i>	novel	enhancer	yes/no	yes	Q96Q89-3	0.018	71.1
R05A10.8	novel	enhancer	no	yes	-	-	-
<i>srh-292</i>	7TM chemoreceptor	enhancer	no	yes	LMBR1L	.071	75.8
T14E8.1	Protein tyrosine kinase	enhancer	no	yes	MET	1.8e-48	50.8
C24D10.1	Protein tyrosine phosphatase	enhancer	no	yes	Q12923-2	1.2e-06	50.6
<i>abcf-3</i>	ABC transporter	enhancer	no	no	ABCF3	1.3e-183	98
F32B6.9	RNA splicing factor	enhancer	yes/no	no	PRPF18	6e-58	96.6
<i>gpd-4</i>	glyceraldehyde-3-phosphate dehydrogenases	enhancer	yes	no	GAPDH	3.2e-132	99.4
<i>cutl-8</i>	Cuticulin precursor	enhancer	no	no	MAST1	.066	50.9
ZK686.4	Zinc finger protein	enhancer	no	no	ZMAT2	3.4e-50	96.8
<i>mtm-3</i>	Myotubularin-related protein	enhancer	no	no	Q13615-2	1.5e-74	64.1
T01C3.2	Chromatin modifying protein	enhancer	no	no	MIT:ENY2-001	0.0014	92.9

TABLE S3**Statistical analysis of suppressor effects on spindle**

Student T-test		
RNAi	2-tailed p values for spindle angle at NEB compared to <i>rfl-1(or198ts)</i>	significant difference (P=<0.05)
R10D12.14	0.4116	no
<i>mnk-1</i>	0.772	no
<i>mus-101</i>	0.337	no
<i>csn-5</i>	0.038	yes
2-tailed p values for spindle angle at cytokinesis compared to <i>rfl(or198ts)</i>		
R10D12.14	0.0208	yes
<i>mnk-1</i>	0.2752	no
<i>mus-101</i>	0.4244	no
<i>csn-5</i>	0.0174	yes
2-tailed p values for spindle angle at NEB for <i>rfl-1(or198ts)</i> vs wildtype		
empty vector ctrl	0.007	yes
2-tailed p values for spindle angle at cytokinesis for <i>rfl-1(or198ts)</i> vs wildtype		
empty vector ctrl	0.0288	yes