SUPPLEMENTARY MATERIAL:

Exploring potential germline associated roles of the TRIM-NHL protein NHL-2 through RNAi screening

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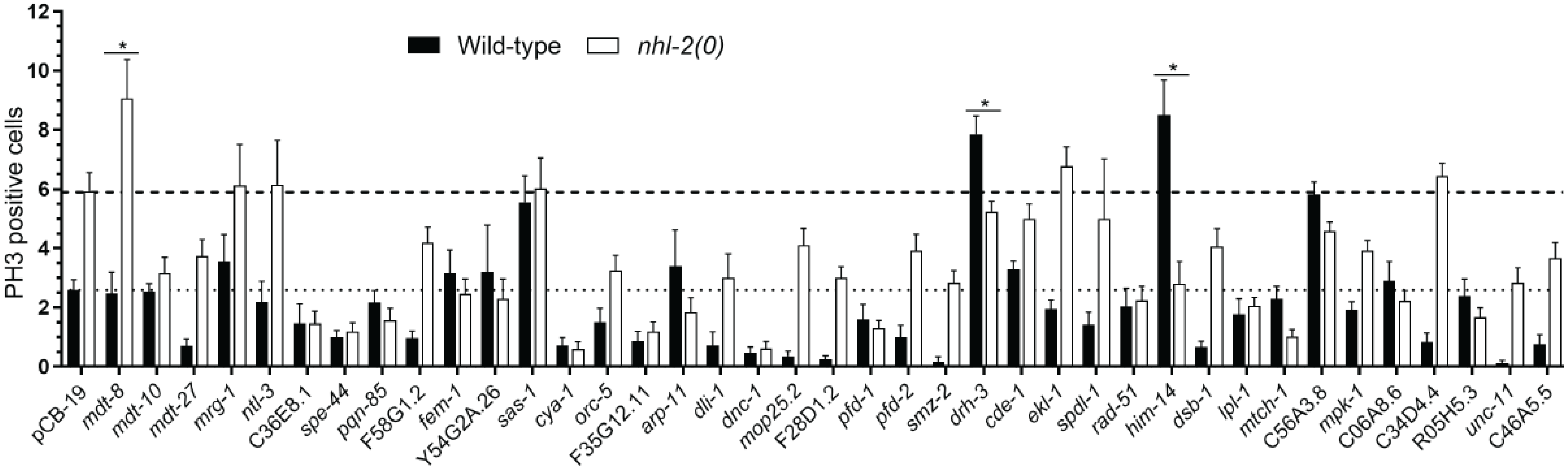

Figure S1: Germ cell proliferation phenotypes of RNAi screen hits in *nhl-2(0)* mutants

Knockdown of high confidence genes as listed in Table 1 immunostained and scored for PH3 positive cells. pCB-19 represents mock-treated RNAi as a positive control. Lower dotted line represents PH3 values in wild-type animals and top dashed line represents PH3 values in mock-treated *nhl-2(0)* mutants. Significance was assigned only when knockdown of a gene was significantly different that observed in *nhl-2(0)* alone. * = P values <0.05, error bars represent standard error of mean.

Table S1: Primary RNAi screen results (Hp = high progeny, S = sterile, El = embryonic lethality, Lp = low progeny, La = larval arrest)

Gene ID	**wild-type/*nhl-2(0)* phenotypes**
K06H7.6	**Hp/S**
ZK287.5	**Hp/S**
B0464.5c	**Mp/S**
C18D4.6a	**Hp/El**
C32E8.10d	**Hp/S**
C32E8.10e	**Hp/S**
D2005.5	**Hp/El**
F32H2.1b	**Mp/S**
F36H1.4c	**Hp/La**
F43C1.2b	**Hp/S**
F44A6.2b	**Hp/El**
F56F3.2	**Hp/El**
F58D5.4b	**Hp/S**
M88.6b	**Mp/La**
R06F6.5b	**Hp/El**
W07B3.2d	**Mp/La**
W09C5.6b	**Mp/S**
Y17G7B.15b	**Hp/S**
Y47D3A.6a	**Mp/La**
ZC410.7a	**Hp/El**
ZK520.4c	**Mp/S**
B0024.9	**Hp/El**
B0205.6	**Hp/S**
B0250.2	**Hp/Lp**
B0280.10	**Hp/Lp**
B0412.1	**Hp/Lp**
B0432.3	**Hp/S**
C01G10.8	**Hp/S**
C01H6.5b	**Hp/El**
C05B5.3	**Hp/S**
C06A8.5	**Hp/Lp**
C06A8.6	**Hp/Lp**
C07H6.8	**Hp/El**
C08F8.1	**Hp/El**
C09G4.3	**Hp/El**
C14B1.7	**Hp/El**
C25G4.4	**Hp/Lp**
C27C12.7	**Hp/S**
C30G12.7	**Hp/S**
C32A3.1	**Hp/S**
C32E8.10	**Hp/Lp**
C33H5.4	**Hp/El**
C34B2.8	**Hp/Lp**

C34C12.8	**Mp/S**
C34D4.4	**Hp/Lp**
C35E7.9	**Hp/Lp**
C36B1.1c	**Hp/S**
C36E8.1	**Hp/La**
C37A5.9	**Hp/Lp**
C39E9.14	**Hp/El**
C46A5.5	**Hp/Lp**
C56A3.8	**Hp/Lp**
D1081.5	**Hp/Lp**
D2013.8	**Hp/El**
E01A2.6	**Hp/Lp**
F08F1.9	**Hp/La**
F08G5.1	**Hp/Lp**
F09G8.2	**Hp/Lp**
F11G11.2	**Hp/El**
F12F6.5	**Hp/S**
F16C3.1	**Hp/Lp**
F18A1.4	**Hp/La**
F20H11.3	**Mp/S**
F21H12.5	**Mp/El**
F22B8.7	**Hp/El**
F22D6.2	**Hp/Lp**
F22D6.6	**Hp/El**
F22F4.2	**Mp/El**
F23H11.4	**Hp/El**
F23H11.7	**Hp/Lp**
F23H12.2	**Hp/S**
F26F4.11	**Mp/S**
F28D1.2	**Hp/La**
F29B9.6	**Mp/S**
F29D10.5	**Hp/Lp**
F31C3.5	**Hp/El**
F32H2.1	**Hp/S**
F33E2.5	**Hp/Lp**
F33H1.3	**Hp/El**
F35D6.1a	**Hp/La**
F35H12.3	**Hp/Lp**
F36A2.7	**Mp/S**
F37C12.1	**Hp/Lp**
F43C1.2	**Hp/Lp**
F43E2.7	**Hp/Lp**
F46A9.4	**Hp/El**
F52F12.4	**Hp/El**
F54C1.9	**Hp/Lp**
F54D7.2	**Hp/Lp**
F57B10.8	**Hp/Lp**

F58A4.9	Mp/S
F58D5.4b	Hp/El
F58G1.2	Hp/Lp
F59A3.3	Hp/S
H20J04.5	Hp/El
H27M09.1	Hp/El
K01A2.5	Hp/S
K08B4.1	Mp/lp
K08E3.5	Hp/Lp
K08E7.3	Hp/El
K10D2.3	Mp/El
K11B4.1	Hp/S
K11H3.3	Hp/Lp
M7.5	Hp/S
R05D7.4	Hp/Lp
R05H5.3	Mp/El
R06C1.3	Hp/El
R09B3.4	Hp/El
R09B5.8	Hp/El
R10H10.2	Hp/S
R11A5.4	Hp/Lp
R12B2.5	Mp/Lp
T01G9.6	Hp/S
T02E1.6	Hp/Lp
T04A8.2	Hp/Lp
T05E11.3	Hp/La
T05F1.4	Hp/Lp
T09A5.5	Hp/S
T09A5.6	Hp/Lp
T09A5.9	Hp/S
T15B12.1	Hp/S
T16H12.3	Hp/S
T17H7.4d	Hp/La
T18H9.6	Hp/Lp
T20B12.2	Hp/S
T20H9.2	Hp/Lp
T21G5.4	Hp/El
T23F11.3	Hp/Lp
T26A5.7	Hp/La
W01G7.3	Mp/S
W02D3.9	Hp/El
W06E11.2	Hp/S
Y111B2A.24	Hp/El
Y37D8A.9	Hp/S
Y39A3A.1	Hp/Lp
Y39E4B.10	Hp/S
Y39E4B.9	Hp/Lp

Y43C5A.6	**Hp/El**
Y43H11AL.3	**Hp/Lp**
Y4C6B.3	**Hp/Lp**
Y53C12A.4	**Hp/Lp**
Y53C12B.3b	**Mp/lp**
Y54G2A.26	**Hp/Lp**
Y56A3A.1	**Hp/S**
Y56A3A.20	**Hp/S**
Y62F5A.1	**Hp/Lp**
Y6B3B.9	**Hp/S**
Y70G10A.2	**Hp/Lp**
Y74C10AR.1	**Mp/La**
Y75B8A.35	**Mp/S**
Y79H2A.6	**Hp/La**
Y95B8A.11	**Hp/Lp**
ZC168.3	**Hp/El**
ZC477.9c	**El/S**
ZK1010.3	**Hp/La**
ZK1058.3	**Hp/Lp**
ZK1098.2a	**Hp/S**
ZK1127.11	**Hp/S**
ZK1127.5	**Hp/La**
ZK1307.5	**Mp/El**
ZK507.6	**Hp/Lp**
ZK512.2	**Mp/S**
ZK512.6	**Hp/El**
ZK525.2	**Hp/Lp**
ZK593.5	**Hp/Lp**
R17.1	**Hp/S**

Table S2: Gene ontology (GO terms) for genes associated with biological processes

GO Terms (biological process)	Genes
anatomical structure development (GO:0048856)	33
embryo development (GO:0009790)	31
reproduction (GO:0000003)	27
cellular nitrogen compound metabolic process (GO:0034641)	11
cell cycle (GO:0007049)	11
locomotion (GO:0040011)	9
biosynthetic process (GO:0009058)	8
cell differentiation (GO:0030154)	8
cell death (GO:0008219)	8
chromosome segregation (GO:0007059)	7
transport (GO:0006810)	6
growth (GO:0040007)	6
cellular component assembly (GO:0022607)	5
response to stress (GO:0006950)	5
vesicle-mediated transport (GO:0016192)	5
mitotic nuclear division (GO:0007067)	4
macromolecular complex assembly (GO:0065003)	4
chromosome organization (GO:0051276)	4
catabolic process (GO:0009056)	4
DNA metabolic process (GO:0006259)	3
signal transduction (GO:0007165)	3
cytoskeleton organization (GO:0007010)	3
protein complex assembly (GO:0006461)	3
aging (GO:0007568)	3
cellular protein modification process (GO:0006464)	3
cytoskeleton-dependent intracellular transport (GO:0030705)	2
protein folding (GO:0006457)	2
cell morphogenesis (GO:0000902)	2
cell division (GO:0051301)	2
developmental maturation (GO:0021700)	1
nucleobase-containing compound catabolic process (GO:0034655)	1
translation (GO:0006412)	1
anatomical structure formation involved in morphogenesis (GO:0048646)	1
small molecule metabolic process (GO:0044281)	1
cell proliferation (GO:0008283)	1
cell motility (GO:0048870)	1
membrane organization (GO:0061024)	1

Table S3: Gene ontology (GO terms) for genes associated with molecular function

GO Terms (molecular function)	Genes
DNA binding (GO:0003677)	3
transcription factor activity, protein binding (GO:0000988)	3
ion binding (GO:0043167)	2
ATPase activity (GO:0016887)	2
kinase activity (GO:0016301)	2
unfolded protein binding (GO:0051082)	2
enzyme binding (GO:0019899)	2
RNA binding (GO:0003723)	1
helicase activity (GO:0004386)	1
ligase activity (GO:0016874)	1
signal transducer activity (GO:0004871)	1
cytoskeletal protein binding (GO:0008092)	1
nucleotidyltransferase activity (GO:0016779)	1
nucleic acid binding transcription factor activity (GO:0001071)	1
nuclease activity (GO:0004518)	1
lipid binding (GO:0008289)	1

Table S4: Gene ontology (GO terms) with genes associated with cellular compartment

GO Terms (cellular compartment)	Genes
cell (GO:0005623)	28
intracellular (GO:0005622)	28
organelle (GO:0043226)	26
nucleus (GO:0005634)	15
cytoplasm (GO:0005737)	14
protein complex (GO:0043234)	13
chromosome (GO:0005694)	12
cytoskeleton (GO:0005856)	6
nuclear chromosome (GO:0000228)	6
nucleoplasm (GO:0005654)	4
microtubule organizing center (GO:0005815)	2
Golgi apparatus (GO:0005794)	2
endoplasmic reticulum (GO:0005783)	1
cytoplasmic vesicle (GO:0031410)	1
cytosol (GO:0005829)	1
mitochondrion (GO:0005739)	1
plasma membrane (GO:0005886)	1