SUPPLEMENTARY MATERIAL

Table 1

Primary *dhc-1* phenotypic suppression screen results.

The number of larvae produced in each independent test (1-8 as applicable) of all 238 candidate interacting genes is shown.

Gene name	WormBase ID	Larvae number							
		test 1	test 2	test 3	test 4	test 5	test 6	test 7	test 8
act-1	T04C12.6	0	0	0	0	0			
act-2	T04C12.5	0	0	0	0				
act-3	T04C12.4	0	0	0	0	0			
act-4	M03F4.2	0	0	0	0				
act-5	T25C8.2	0	0	0	0	0			
air-1	K07C11.2	0	0	0					
arf-1.2	B0336.2	0	2	0	0	4			
arf-3	F57H12.1	0	0	0	0	0	0		
arx-2	K07C5.1	0	0	0	0	2			
arx-3	Y79H2A.6	0	0	0	0	0			
arx-5	Y37D8A.1	0	0	0	0	0	2		
arx-7	M01B12.3	0	0	0	0	0	0		
atp-2	C34E10.6	0	0	0					
B0035.4	B0035.4	0	0	0					
B0035.5	B0035.5	0	0	0					
ben-1	C54C6.2	0	0	0					
C01G5.2	C01G5.2	0	0	5					
C05D11.10	C05D11.10	0	1	0					
C07H6.3	C07H6.3	0	0						
C10G6.1	C10G6.1	0	0	1					
C17H12.1	C17H12.1	3	0	0	0	0	2		
C18E3.6	C18E3.6	0	0	1	0	0	0		
C28G1.3	C28G1.3	1	5	0	0				
C30B5.4	C30B5.4	0	0	0					
C31C9.2	C31C9.2	1	1	0	0				
C34B2.7	C34B2.7	0	0	0					
C42C1.10	C42C1.10	0	0	0					
C43G2.1	C43G2.1	0	0	0					

C43G2.2	C43G2.2	0	0	0					
C45G9.5	C45G9.5	0	0	0					
C47B2.2	C47B2.2	0	0	0					
C56C10.10	C56C10.10	0	0						
cap-1	D2024.6	15	16	35	5	5	6	0	
cap-2	M106.5	19	20	15					
cas-1	F41G4.2	0	0	0	0	2			
cdc-42	R07G3.1	0	0	0	0	0	0	0	0
cdh-6	F15B9.7	0	0	0					
cdk-4	F18H3.5	0	0	0					
chs-1	T25G3.2	0	0	0	0	0	0		
cls-2	R107.6	0	0						
cor-1	R01H10.3	1	1	0	0	0			
cpl-1	T03E6.7	2	0	0					
cpn-3	F28H1.2	0	0	0	0	0	0		
csn-5	B0547.1	0	0						
cts-1	T20G5.2	0	0	0	0	0			
cyb-1	ZC168.4	0	0	0					
cyb-2.1	Y43E12A.1	0	0	0					
cye-1	C37A2.4	0	0	0					
cyk-1	F11H8.4	0	0						
D1054.3	D1054.3	0							
daf-4	C05D2.1	0	5	0	0				
dhc-1	T21E12.4	0	0	0					
dlc-1	T26A5.9	0	0	0	0	5	0	0	0
dli-1	C39E9.14	9	11	0					
dnc-1	ZK593.5	0	0	0					
dnj-10	F22B7.5	0	0						
dpl-1	T23G7.1	5	0	0					
drp-1	T12E12.4	0	0						
dsh-2	C27A2.6	0	0	0					
dyn-1	C02C6.1	0	0	0					
eea-1	T10G3.5	0	0	0					
egl-19	C48A7.1	0	1	0	0				
egl-45	C27D11.1	0	0	0					
eif-3.B	Y54E2A.11	0	0	0					
eif-3.H	C41D11.2	0	0	0					
emb-27	F10B5.6	0	0	0					
emb-9	K04H4.1	0	0	0					
epn-1	T04C10.2	0	0	0					

F01G4.6	F01G4.6	0	4				
F09E10.8	F09E10.8	0	0	0			
F10G8.7	F10G8.7	2	0	0			
F21C3.5	F21C3.5	0	0	0	0	0	0
F21D12.3	F21D12.3	0	0	0			
F22B3.4	F22B3.4	0	0	0			
F23B12.5	F23B12.5	0	0	0			
F25B3.6	F25B3.6	0	0	0			
F25H2.5	F25H2.5	1	0	5	5	0	
F26A3.2	F26A3.2	0	0	0			
F27D4.1	F27D4.1	0	0	4			
F37C12.3	F37C12.3	0	0				
F38E9.5	F38E9.5	0	0	2	0	0	0
F43G9.1	F43G9.1	1	0	10			
F52B11.3	F52B11.3	0	0	0	0	0	0
F53B7.3	F53B7.3	0	0	0			
F54D5.12	F54D5.12	0	0	0	0	0	0
F58G6.1	F58G6.1	0	1	0	0	0	
fis-1	F41G3.4	0	0	0			
fkh-10	C25A1.2	1	0	0			
gbh-2	M05D6.7	0	0	0			
gly-2	C55B7.2	0	0	0			
gop-3	C34E10.1	0	0	0			
gpb-1	F13D12.7	0	0				
H37A05.1	H37A05.1	0	0	0			
H43I07.2	H43I07.2	5	0	0			
hda-1	C53A5.3	0	0	0	0	0	
hel-1	C26D10.2	0	0	0			
his-26	ZK131.1	1	0	0			
his-31	F17E9.12	0	0	0			
his-37	C50F4.7	1	0	0			
his-38	K03A1.6	0	0	0			
his-5	F45F2.3	0	0	0			
his-64	F22B3.1	0	0	0			
his-67	T23D8.5	1	0	0			
hmg-1.2	F47D12.4	3	5	0			
hmp-2	K05C4.6	0	0	0			
hsp-4	F43E2.8	0	0				
icd-1	C56C10.8	0	0	0			
itr-1	F33D4.2	0	0	0			

K01H12.2	K01H12.2	0	0					
K07C5.6	K07C5.6	0	0	0				
K08E3.3	K08E3.3	0	1	0				
K08E3.4	K08E3.4	0	0	0	0	0	0	
K08E3.5	K08E3.5	0	0	0	0	0		
kin-10	T01G9.6	0	0	0				
kin-19	C03C10.1	5	0	2				
kin-2	R07E4.6	0	0					
klp-11	F20C5.2	0	0	0				
klp-16	C41G7.2	0	0	0	0	0	0	
krs-1	T02G5.9	0	0					
ldb-1	F58A3.1	0	0	0				
let-23	ZK1067.1	5	5	0	0			
let-70	M7.1	0	5	0	0	0	0	0	0
let-75	R06C7.10	0	4	0	0	0	0	
let-92	F38H4.9	0	0	3	3	0	0	0
lin-11	ZC247.3	0	5	0	0			
lin-26	F18A1.2	0	0	0				
lin-3	F36H1.4	0	0	0				
lin-53	K07A1.12	0	0	0				
lis-1	T03F6.5	22	100	90	20	20	30	
lpd-8	R10H10.1	0	0	0				
M01E5.2	M01E5.2	0	0	0				
M03C11.4	M03C11.4	0	0	0				
M03F8.3	M03F8.3	0	0	0				
mag-1	R09B3.5	0	0	0				
mcm-6	ZK632.1	0	0					
mec-12	C44B11.3	5	0	0				
mek-1	K08A8.1	0	0	0				
mig-10	F10E9.6	5	0	0				
myo-3	K12F2.1	0	0	0	0	0	0	
nhr-69	T23H4.2	0	0	0				
nid-1	F54F3.1	0	0					
nmy-1	F52B10.1	0	0	0	0	5	0	
nmy-2	F20G4.3	0	0	0				
ntl-2	B0286.4	0	0					
nud-1	F53A2.4	0	0	0				
osm-3	M02B7.3	0	0					
paa-1	F48E8.5	0	4	0				
pam-1	F49E8.3	0	0					

Gene	Clone								
pap-1	Y32F6A.3	0	0	0	0	0	0		
par-1	H39E23.1	0	0	0		0	0		
par-3	F54E7.3	5	5	0	0				
par-5	M117.2	0	0						
pbs-2	C47B2.4	0		0					
pbs-4	T20F5.2	0	0						
pbs-5	K05C4.1	0	0						
pbs-7	F39H11.5	0	0						
pes-8	F18G5.2	0	0	0					
pfn-3	K03E6.6	0	0	0	0	0	0		
pha-4	F38A6.1	0	2	0					
pkc-3	F09E5.1	0	0	0					
ppk-3	VF11C1L.1	0	0	0					
ptp-3	C09D8.1	1	5	0	1				
R05G6.7	R05G6.7	0	0						
R09E12.3	R09E12.3	0	5	0	0				
R144.4	R144.4	0	0	0	0	0			
R151.9	R151.9	2	3	10	1	0	0		
R186.1	R186.1	0	0						
rab-1	C39F7.4	0	0	0					
rab-5	F26H9.6	0	0	0					
rab-7	W03C9.3	0	0	0					
rad-51	Y43C5A.6	0	0	0					
ran-1	K01G5.4	0	0	0	0	0	0	0	0
rba-1	K07A1.11	0	0	0					
rbx-1	ZK287.5	0	0	0					
rcq-5	E03A3.2	0	0						
rnp-4	R07E5.14	0	1	0	0				
rnr-1	T23G5.1	0	0	0					
rpl-10	F10B5.1	0	1	0					
rpl-23	B0336.10	0	0						
rpl-7	F53G12.10	0	0	0					
rpn-3	C30C11.2	0	0	0	0	0			
rpn-6	F57B9.10	0	0	0					
rpn-8	R12E2.3	0	0	0					
rpn-9	T06D8.8	0	0	0					
rps-0	B0393.1	0	0	0					
rps-1	F56F3.5	0	0	0					
rps-18	Y57G11C.16	0	0						
rpt-1	C52E4.4	0	0	0					

rpt-3	F23F12.6	0	0	0	0	0	0	0	0
rpt-6	Y49E10.1	0	0	0					
sel-5	F35G12.3	0	0	0	0	1			
sem-5	C14F5.5	0	0	0					
snr-1	Y116A8C.42	0	0	0					
snr-3	T28D9.10	0	0	0					
snt-1	F31E8.2	0	0	0					
sqv-4	F29F11.1	0	0	0					
sur-6	F26E4.1	0	0	0					
T01B11.4	T01B11.4	0	0						
T04C9.1	T04C9.1	0	0	0	0	0			
T09A5.9	T09A5.9	0	0						
T09E8.3	T09E8.3	0	0	0					
T21B10.7	T21B10.7	0	0	0					
T22B11.5	T22B11.5	0	0	0	0	0	0	1	0
T22D1.3	T22D1.3	1	1	0					
T22F3.3	T22F3.3	0	0	1	1	0			
tag-138	F08A8.6	0	0	0	0	0			
tag-216	K08F9.2	0	0	0	0	0			
tba-1	F26E4.8	0	0	0					
tba-2	C47B2.3	0	0	0					
tba-4	F44F4.11	5	5	0	1				
tbb-1	K01G5.7	5	0	0					
tbb-2	C36E8.5	0	0	0					
tbb-4	B0272.1	5	5	0	0				
tbg-1	F58A4.8	0	0	0	0	0	0		
tfg-1	Y63D3A.5	0	0	0					
top-1	M01E5.5	0	0	0					
tre-1	F57B10.7	0	0	1					
ula-1	C26E6.8	0	0	0					
unc-116	R05D3.7	1	0	0					
unc-32	ZK637.8	0	0						
unc-37	W02D3.9	0	0	0	0				
unc-52	ZC101.2	0	0	0					
unc-73	F55C7.7	0	0	0					
unc-78	C04F6.4	0	2	0	0	0			
vab-10	ZK1151.1	0	0	0	0	0	0		
vbp-1	T06G6.9	0	3	5	0	0	0		
vha-1	R10E11.8	0	0						
vha-12	F20B6.2	0	0	0					

vha-2	R10E11.2	0	0					
VW02B12L.3	VW02B12L.3	0	0	0				
W01A11.2	W01A11.2	0		0				
W02D3.6	W02D3.6	0	0	0				
wve-1	R06C1.3	0	0	0				
Y49A3A.1	Y49A3A.1	0	0					
Y49E10.2	Y49E10.2		0	0				
Y66H1B.2	Y66H1B.2	1	0	0				
ZK1128.4	ZK1128.4	0	0	0				
ZK370.3	ZK370.3	0	0	0	0	0	0	

Table 2

Re-screen results for candidate *dhc-1* phenotypic suppressors.

The number of larvae (mean of at least three independent experiments) produced in a first or second 24-hour period of RNAi feeding for all positive candidates from the primary screens (Table 1). Genes are ordered by effectiveness of suppression by RNAi in the first 24-hour period. Gene names (when available) or Wormbase ID are listed (wormbase.org)

Gene name	average number of progeny after 24 hours	average number of progeny after 48 hours
OP50 (neg. ctrl.)	0	0
lis-1	25.5	9.7
cap-2	9.5	5.3
cap-1	6.2	9.4
dli-1	4.2	0.0
vbp-1	1.9	0.2
C08F8.1	0.6	2.5
R151.9	0.5	1.9
C17H12.1	0.4	0.0
F21C3.5	0.3	1.6
B0035.4	0.3	1.3
tba-4	0.3	0.0
dnc-1	0.1	0.0
tba-5	0.1	0.2
H43I07.2	0.0	0.5
cbp-3	0.0	0.7
wsp-1	0.0	0.9
tbb-4	0.0	0.8
mec-12	0.0	0.9
C43G2.2	0.0	0.2
pus-1	0.0	0.2
T22D1.3	0.0	0.0
ptp-3	0.0	0.6
C01G5.2	0.0	0.1
his-26	0.0	0.1
R09E1.2	0.0	0.2
lin-11	0.0	0.1
F25H2.5	0.0	0.1

tbb-6	0.0	0.1
pfn-2	0.0	0.1
pes-8	0.0	0.3
rnp-4	0.0	0.5
K08E3.3	0.0	0.4
F43G9.1	0.0	0.3
F5405.12	0.0	0.1
cct-5	0.3	0.0
F58G6.1	0.0	0.0
cpn-3	0.0	0.0
tba-2	0.0	0.0
him-1	0.0	0.0
unc-116	0.0	0.0
dlc-1	0.0	0.0
nud-1	0.0	0.0
rnh-1.0	0.0	0.0
pfn-3	0.0	0.0
tba-8	0.0	0.0
tba-9	0.0	0.0
klp-11	0.0	0.0
Y66H1B.2	0.0	0.0
cpl-1	0.0	0.0
tbb-1	0.0	0.0
fkh-1.0	0.0	0.0
let-92	0.0	0.0
hmg-1.2	0.0	0.0
his-37	0.0	0.0
C10G6.1	0.0	0.0
C05D11.10	0.0	0.0
rpl-10	0.0	0.0
daf-4	0.0	0.0
mig-10	0.0	0.0
C28G1.3	0.0	0.0
pha-4	0.0	0.0
eea-1	0.0	0.0
his-67	0.0	0.0
1-Apr	0.0	0.0
pfn-1	0.0	0.0
T09E8.3	0.0	0.0
par-3	0.0	0.0

|		
T22B11.3	0.0	0.0
C18E3.6	0.0	0.0
C47B2.2	0.0	0.0
cas-1	0.0	0.0
cor-1	0.0	0.0
arf-1.2	0.0	0.0
arf-3	0.0	0.0
arx-5	0.0	0.0
arx-7	0.0	0.0
F01G4.6	0.0	0.0
F10G8.7	0.0	0.0
F38E9.5	0.0	0.0
wve-1	0.0	0.0
zyg-9	0.0	0.0
osm-3	0.0	0.0
pap-1	0.0	0.0
cct-1	0.0	0.0
cct-4	0.0	0.0
W0D23.6	0.0	0.0
sem-5	0.0	0.0
tac-1	0.0	0.0
let-70	0.0	0.0
let-75	0.0	0.0

Supplementary Figures
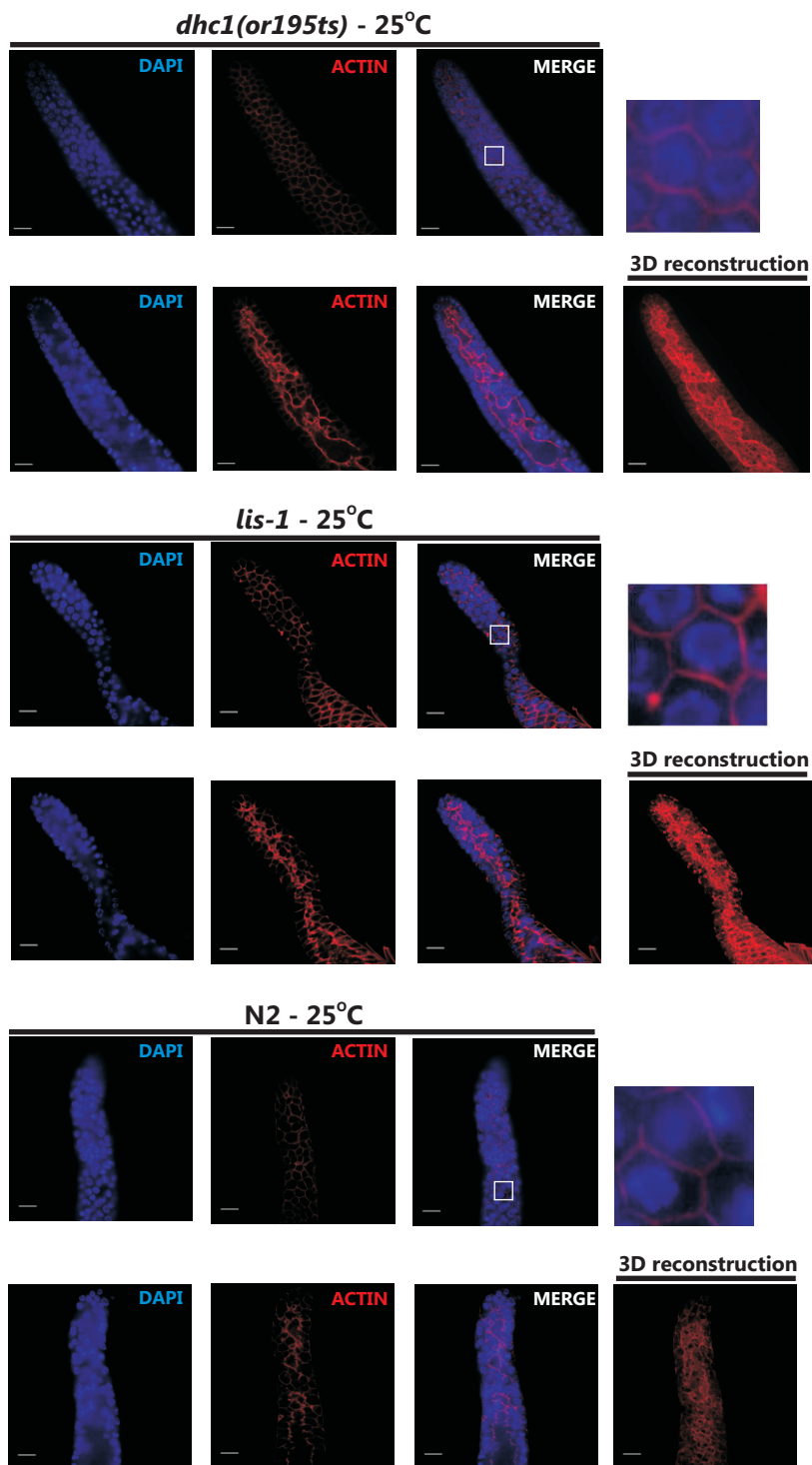
Supplementary Figure 1. Mutations of *dhc-1* and *lis-1* did not show significant changes in F-actin organization in the mitotic and transition regions of the germline.
Phalloidin-rhodamine and Hoechst staining of extruded gonads was used to visualize F-actin (red) and DNA (blue), respectively. A single optical section of the distal part of the gonad and magnification of the single nuclei is showed in the upper row of each panel. Middle section of the gonad and 3D reconstruction of the rachis showed in the lower row of the appropriate panel. Scale bar 10 μM.
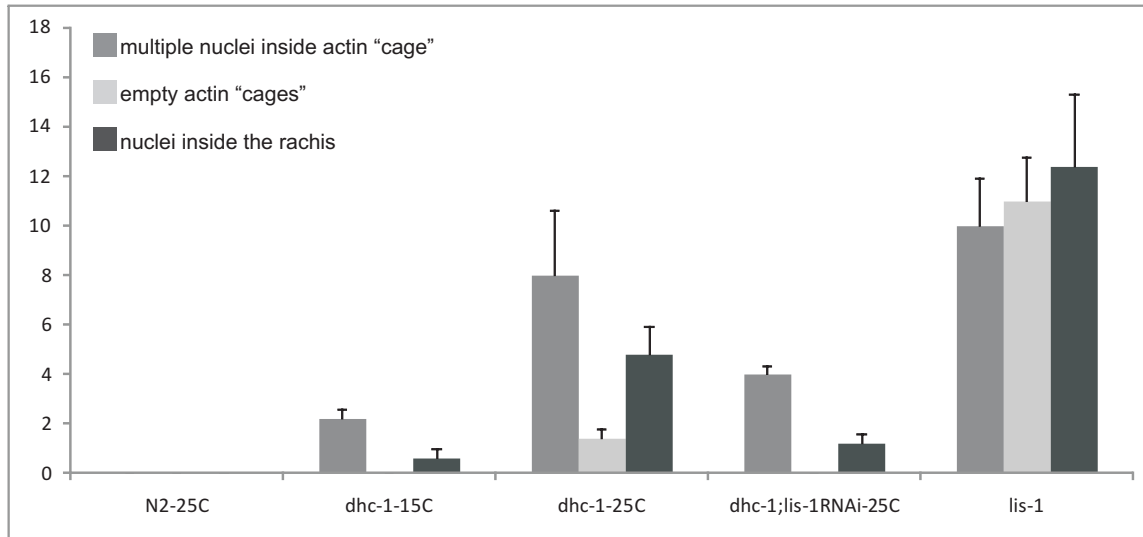
Supplementary Figure 2. Quantification of cytoskeletal nuclear architecture in the pachytene region of the germline.
Quantification of number of nuclei in the rachis of 24 hour adult animals. Average number of multiple-nuclei actin cages (dark gray), empty actin cages (gray) and free nuclei (black) is shown. Error bars represent ±S.E.M.

A

B
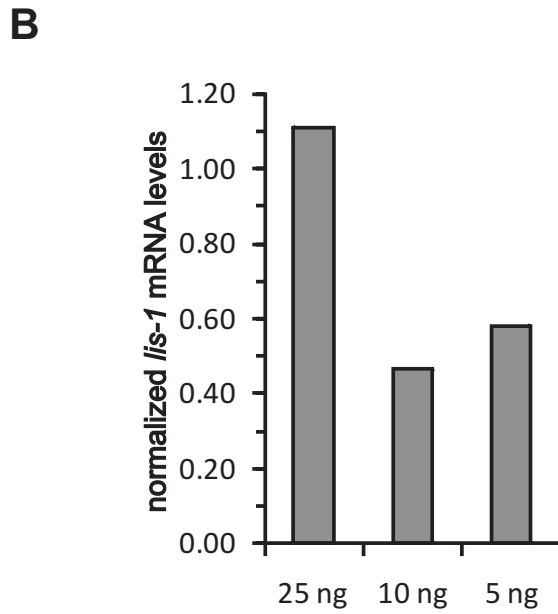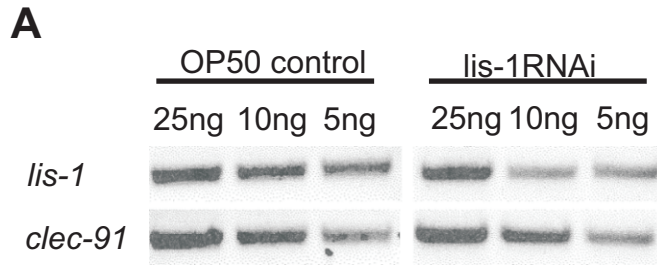
Supplementary Figure 3. Quantification of depletion of *lis-1* mRNA by RNAi.
A) RT-PCR analysis of *lis-1* mRNA levels in total RNA isolated from L4 worms cultured for 24 hours on control (OP50) or *lis-1* (RNAi) bacteria. *clec-91* (ZK858.3) was used as loading control. Various amounts of template RNA (25, 10 and 5 ng) were added to parallel reactions.
B) Quantitation of relative *lis-1* mRNA levels, normalized to control, in each *lis-1*(RNAi) sample.