Table S2. Identification of genes required for DTC plexus formation in an L1 RNAi experiment.

Sequence Name	Gene ID	Total Scored	DTC Plexus Defect	Other Phenotypes Observed
Y77E11A.7	*Y77E11A.7*	6	+++	
Y48G1C.7	*Y48G1C.7*	8	+++	**fgcs, large nuclei**
C15F1.4	*ppp-1*	6	+++	**fgcs**
B0491.5	*B0491.5*	7	+++	
Y48G1A.4	*Y48G1A.4*	11	+++	**fgcs,** Rbs
F10C2.6	*dars-2*	13	+++	**fgcs**
C33H5.9	*sec-10*	8	+++	**large nuclei**
W02B12.9	*W02B12.9*	9	+++	Rbs
Y66H1A.4	*Y66H1A.4*	7	+++	Sick
W07E6.2	*W07E6.2*	12	+++	**fgcs**
F26F4.11	*rpb-8*	10	+++	**fgcs**
C39E9.14	*dli-1*	5	+++	Egl
M18.5	*ddb-1*	13	+++	
F20H11.3	*mdh-2*	21	+++	
F22D6.5	*prpf-4*	17	+++	**fgcs**
ZC64.3	*ceh-18*	12	+++	**large nuclei**
W01G7.3	*rpb-11*	22	+++	**fgcs**
Y38E10A.24	*Y38E10A.24*	16	+++	
F23B12.7	*F23B12.7*	13	+++	
K04A8.6	*dre-1*	20	+++	**fgcs**
C16A3.5	*C16A3.5*	21	++	
H35B03.2	*H35B03.2*	14	++	
F52D10.3	*ftt-2*	11	++	Rup, Egl
R02D3.5	*fnta-1*	20	++	
F43G6.9	*patr-1*	21	++	
R06C1.2	*fdps-1*	17	++	**no oocytes**
Y41E3.11	*Y41E3.11*	13	++	
F42G8.10	*F42G8.10*	13	++	
C17H12.14	*vha-8*	22	++	
F10G8.3	*npp-17*	19	++	**fgcs, increased sperm**
M106.1	*mix-1*	20	++	**differentiating gcs, fgcs,** Mig
C37C3.6	*mig-6*	5	++	Mig
T27C4.4	*lin-40*	21	++	
T22H9.1	*T22H9.1*	16	++	Rup
Y55F3AM.15	*csn-4*	17	++	Sick
C09F9.2	*C09F9.2*	17	++	
T05H10.6	*T05H10.6*	23	++	
F21H12.5	*fbf-2*	18	++	
F10E9.4	*F10E9.4*	18	++	**fgcs**
F29B9.10	*F29B9.10*	18	++	
Y48E1B.5	*Y48E1B.5*	19	++	

C09H10.3	*nuo-1*	26	++	**fgcs**
Y49E10.6	*his-72*	20	++	
C04C3.3	*C04C3.3*	20	++	
T04A8.11	*T04A8.11*	20	++	**fgcs,** Muv, Mig
Y73C8B.4	*lag-2*	133	+	**fgcs**

Penetrance of DTC defect observed was scored as follows: +++, ≥ 30% penetrance defect; ++, ≥ 15% defect; +, ≥ 5% defect. As a positive control, *lag-2* RNAi was examined and showed a low penetrance defect (10/133 animals). Phenotypes reported were observed in ≥ 3 animals. Animals were scored as 1-1.5-day-adults following exposure to RNAi from the L1 larval stage. fgcs (fewer germ cells), Rbs (Reduced brood size), Ste (Sterile), Egl (Egg-laying defective), Rup (ruptured through the vulva), Mig (DTC migration defective), Muv (Multivulva). Germ cell phenotypes are bolded. Sick animals were small and sluggish.