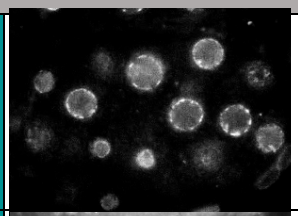
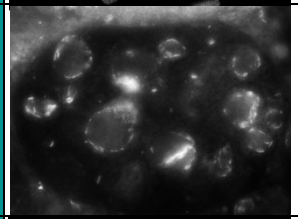
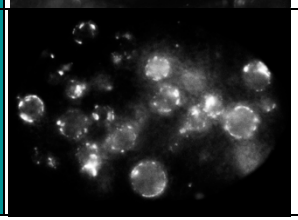
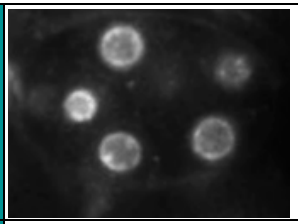
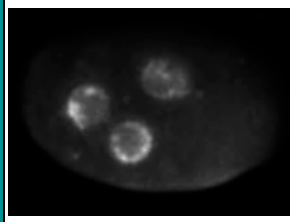
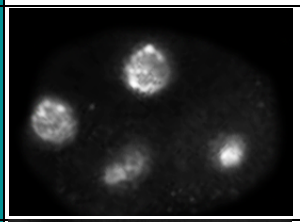
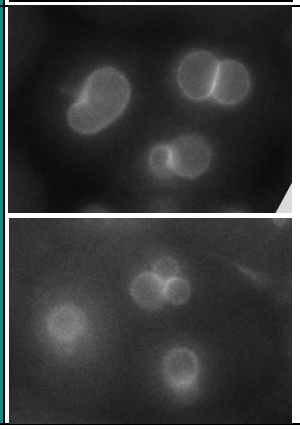
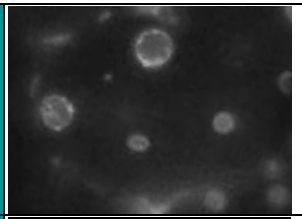
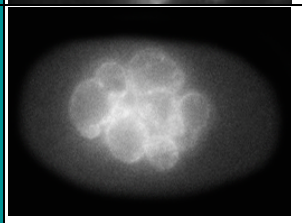
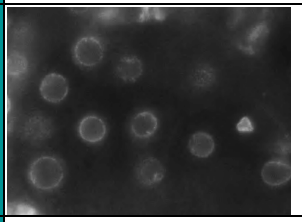
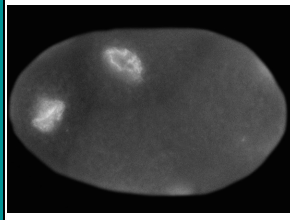
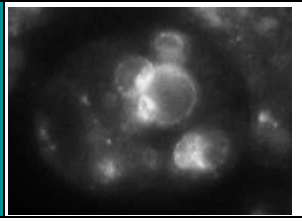
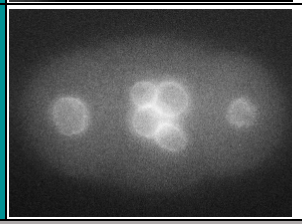
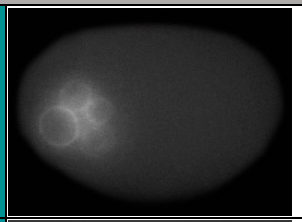
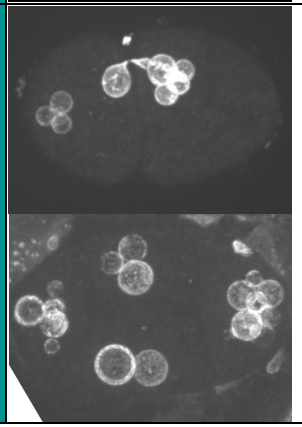
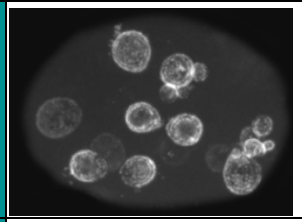
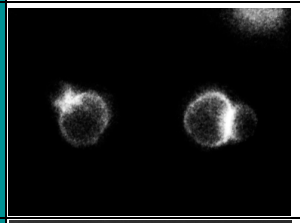
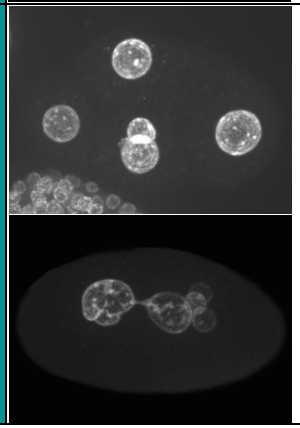
Supplemental Table S1

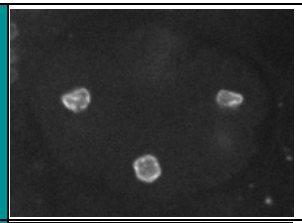
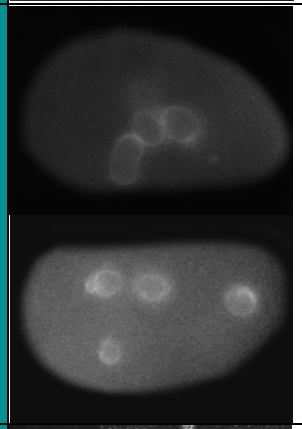
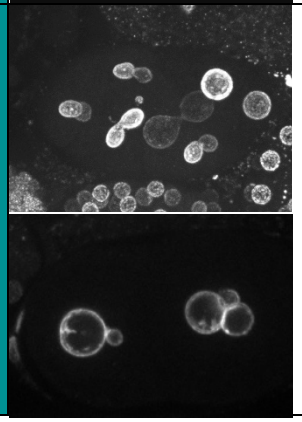
Functional Category	ORF	RNAi location- Chromosome/ Start-Stop[1]	Gene	Protein function[2, 3]	Phenotypes									Representative image(s)	Previously described nuclear phenotypes[4]
					Multi-nucleated				Abnormal shape		NPC distribution defect				
					Paired Nuclei	One-cell stage	2 or more cell stages	Micronuclei	Anaphase bridges	Deformed	Abnormal NE NPC distribution	Cytoplasmic NPCs	Intra-nuclear NPCs		
mRNA processing															
Splicing factors	Y116A8C.42	IV/ 17088015-17088796	*snr-1*	Orthologous to human small nuclear riboprotein Sm D3, involved in pre-mRNA splicing (Barbee *et al.* 2002).							√				NPC distribution defect *(Joseph-Strauss et al. 2012)*; nuclear appearance variant; multi-nucleated oocytes, enlarged nuclei (Green *et al.* 2011).
	W08E3.1	I/ 13347443-13348263	*snr-2*	Orthologous to human small nuclear riboprotein Sm B/B' involved in pre-mRNA splicing (Barbee *et al.* 2002).							√				NPC distribution defect *(Joseph-Strauss et al. 2012)*; nuclear appearance variant, small nuclei (Green *et al.* 2011).
	C52E4.3	V/ 11982323 11981131	*snr-4*	Orthologous to human small nuclear riboprotein Sm D2 involved in pre-mRNA splicing (Barbee *et al.* 2002).							√				NPC distribution defect *(Joseph-Strauss et al. 2012)*; nuclear appearance variant, small nuclei (Green *et al.* 2011); severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).

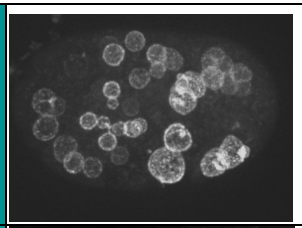
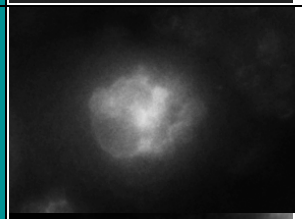
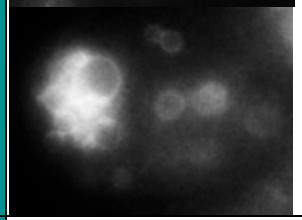
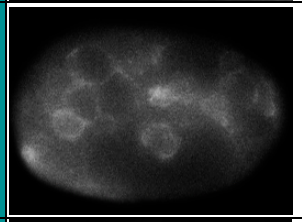
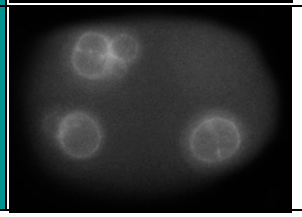
		ZK652.1	III/ 7861988-7862537	*snr-5*	Orthologous to human small nuclear riboprotein Sm F involved in pre-mRNA splicing (Barbee *et al.* 2002).							√				NPC distribution defect *(Joseph-Strauss et al. 2012)*; nuclear appearance variant, small nuclei (Green *et al.* 2011).
		Y49E10.15	III/ 12429440-12429121	*snr-6*	Orthologous to human small nuclear riboprotein Sm E involved in pre-mRNA splicing (Barbee *et al.* 2002).							√				NPC distribution defect *(Joseph-Strauss et al. 2012)*; nuclear appearance variant; small nuclei, nuclear morphology variation in early embryos (Green *et al.* 2011); severe pleiotropic defects including multiple pronuclei (Sonnichsen *et al.* 2005).
		Y71F9B.4	I/ 2727013-2727546	*snr-7*	Orthologous to human small nuclear riboprotein Sm G involved in pre-mRNA splicing (Barbee *et al.* 2002).							√				NPC distribution defect *(Joseph-Strauss et al. 2012);* small nuclei (Green *et al.* 2011).
		B0464.5	III/ 9456536-9462405	*spk-1*	A serine/threonine kinase orthologous to mammalian serine/arginine-rich protein kinases (SRPKs) that phosphorylate SR proteins, required for splicing (Kuroyanagi *et al.* 2000).	√		√								

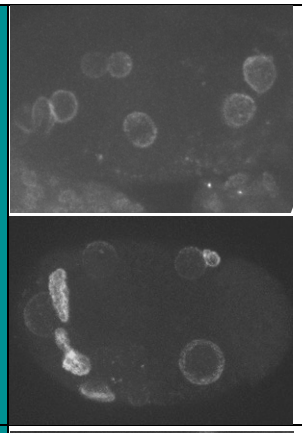
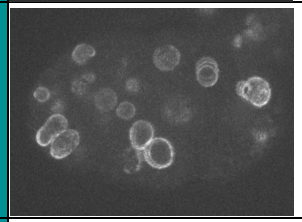
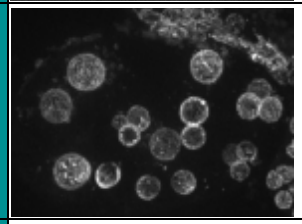
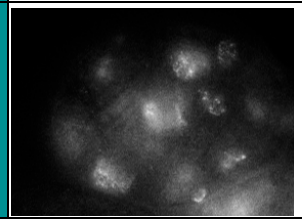
		C41G7.1	I/ 9520156-9519240	*smn-1*	Required for efficient splicing. Orthologous to the human SMN (Gao *et al.* 2014).						√				
		F58D5.1	I/ 12072955-12068329	*hrp-2*	Orthologous to the mammalian heterogeneous nuclear ribonucleoproteins (hnRNP) Q and R, involved in alternative splicing (Kinnaird *et al.* 2004; Kabat *et al.* 2009).		√				√				
		C04H5.6	II/ 14561485-14552390	*mog-4*	A DEAH box protein, orthologous to the budding yeast *PRP16* gene that is required for splicing (Puoti and Kimble 2000).						√				
		Y47G6A.20	I/ 3546908-3543515	*rnp-6*	An RNP (RRM RNA binding domain) containing protein, orthologous to the Drosophila HALF-PINT splicing factor. RNP-6 has a role in alternative splicing (Barberan-Soler and Zahler 2008).						√	√			
	mRNA deadenylation	Y56A3A.20	III/ 11920069-11918698	*ccf-1*	A deadenylase. Orthologous to human CNOT-7 (Nousch *et al.* 2013).			√	√		√				Multi-nucleated cells (Lall *et al.* 2005); nuclear appearance variant, enlarged nuclei (Green *et al.* 2011).

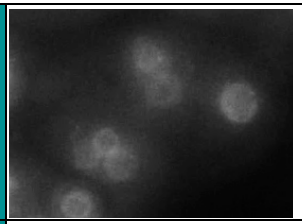
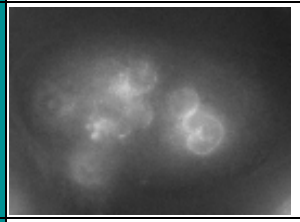
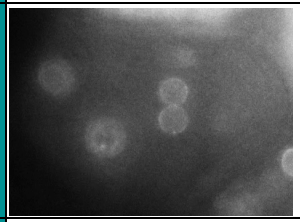
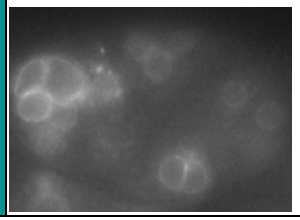
	mRNA binding factors	F53B7.3	V/ 11003278-11002248	*isy-1*	An ortholog of an mRNA binding protein involved in splicing (yeast) or micro-RNA processing (human) (Jiang *et al.* 2018).							√			
		Y18D10A.17	I/ 12912513-12914262	*car-1*	An ortholog of human LSM14A and LSM14B. CAR-1 functions with an RNA helicase CGH-1 and localizes to P bodies, where it likely represses translation (Audhya *et al.* 2005).			√							Anaphase bridges (Audhya *et al.* 2005).
	Translation														
	Ribosome subunits	T22F3.4	V/ 3585891-3585132	*rpl-11.1*	A predicted 60S ribosomal protein L11 (Maciejowski *et al.* 2005).		√								Nuclear appearance variant (Waters *et al.* 2010); enlarged nuclei (Green *et al.* 2011); severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		C14B9.7	III/ 8130493-8129439	*rpl-21*	A predicted 60S ribosomal protein L21.			√	√	√					Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).

		C27A2.2	II/ 5055521-5056203	*rpl-22*	A predicted 60S ribosomal protein L22.			√							Chromosome segregation defects (Sonnichsen *et al.* 2005).
		B0336.10	III/ 5706078-5705475	*rpl-23*	A predicted 60S ribosomal protein L23.			√	√	√					Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); enlarged nuclei (Green *et al.* 2011).
		F52B5.6	I/ 8337704-8337116	*rpl-25.2*	A predicted 60S ribosomal protein L25a.	√					√				Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		F10E7.7	II/ 7105482-7106242	*rpl-33*	A predicted 60S ribosomal protein L35a.	√		√	√	√	√				Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).

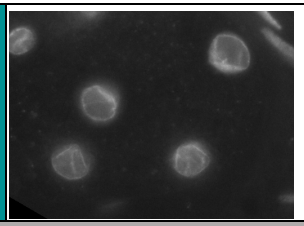
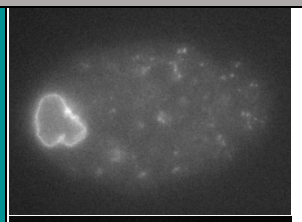
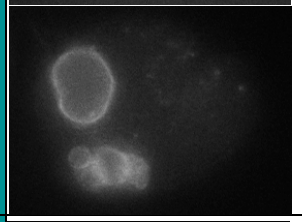
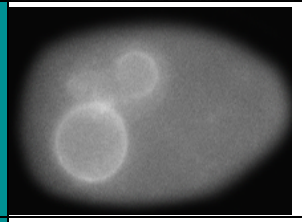
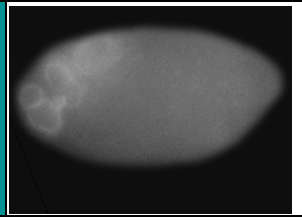
		F40F8.10	II/ 11126275-11125319	*rps-9*	A predicted 40S ribosomal protein S9.					√						Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); small nuclei (Green *et al.* 2011).
		F54E7.2	III/ 5679242-5680134	*rps-12*	A predicted 40S ribosomal protein S12.			√	√		√					Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); small nuclei (Green *et al.* 2011).
		F37C12.11	III/ 7189561-7189070	*rps-21*	A predicted 40S ribosomal protein S21.			√	√	√						Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); small nuclei (Green *et al.* 2011).

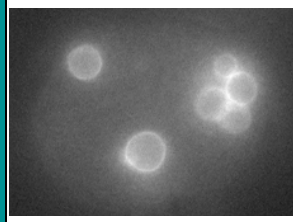
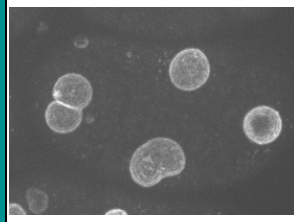
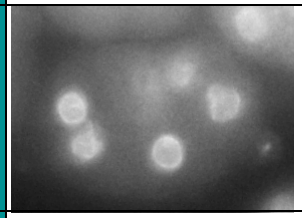
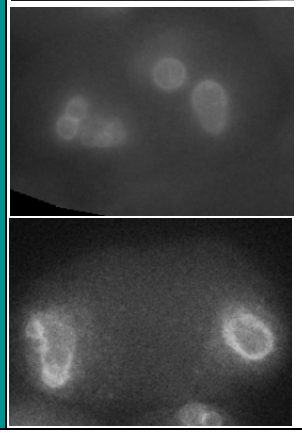
		F53A3.3	III/ 1950524-1951417	*rps-22*	A predicted 40S ribosomal protein S22.	√		√	√		√				Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
	tRNA aminoacylation	B0464.1	III/ 9491130-9489070	*dars-1*	An ortholog of human DARS, an aspartyl(D) tRNA synthetase.			√			√			 	Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); nuclear appearance variant, small nuclei (Green *et al.* 2011).
		C47E12.1	IV/ 9972826-9973962	*sars-2*	An ortholog of human SARS2, a seryl amino-acyl tRNA synthetase.			√							
		F26F4.10	III/ 4917083-4914055	*rars-1*	An ortholog of human RARS, an—arginyl-tRNA synthetase.				√						Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); enlarged nuclei (Green *et al.* 2011).

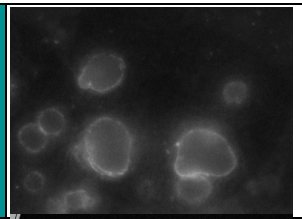
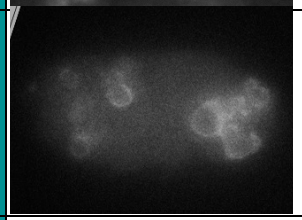
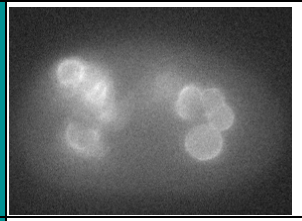
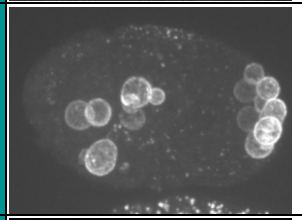
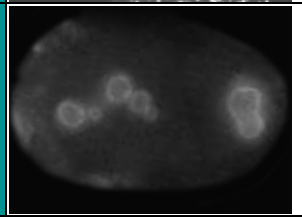
		Y87G2A.5	I/ 13567411-13555717	*glp-4*	An ortholog of human VARS, a valyl-tRNA synthetase (Rastogi *et al.* 2015).	√		√	√		√					Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		T20H4.3	III/ 7238948-7241207	*pars-1*	An ortholog of human EPRS, a glutamyl-prolyl-tRNA synthetase.	√		√			√					Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		T11G6.1	IV/ 10858932-10861264	*hars-1*	An ortholog of human HARS, a histidyl-tRNA synthetase.	√		√								Sister chromatid separation defective causing deformed nuclei (Sonnichsen *et al.* 2005).
		F28H1.3	I/ 3983173-3986917	*aars-2*	An ortholog of human AARS, an alanyl-tRNA synthetase.						√	√				Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).

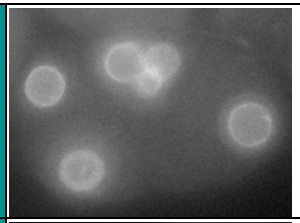
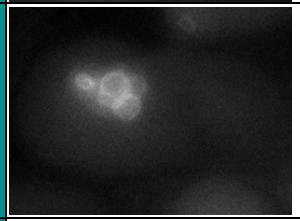
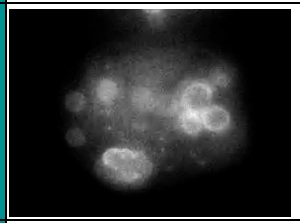
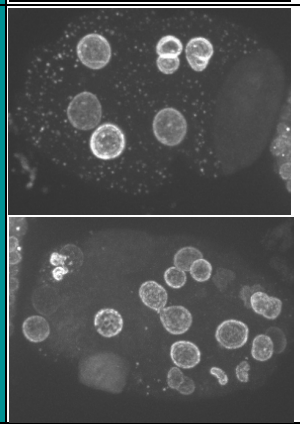
	Translation factors	R08D7.3	III/ 8971486-8969564	*eif-3.D*	An ortholog of human EIF3D, a translation initiation factor (Rhoads *et al.* 2006).			√							Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005); nuclear appearance variant (Green *et al.* 2011).
		C37C3.2	V/ 7857584-7860570	*phi-18*	An ortholog of human EIF5, a eukaryotic translation initiation factor 5 (Rhoads *et al.* 2006).			√			√				Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		Y47H9C.7	I/ 11901771-11899695	*eif-2 β*	An ortholog of human EIF2B2, a translation initiation factor (Rhoads *et al.* 2006).	√									Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		Y39E4B.1	III/ 13092289-13093077	*abce-1*	An ortholog of human ABCE1 which is involved in translation initiation and ribosome recycling (Zhao *et al.* 2004).	√		√			√				

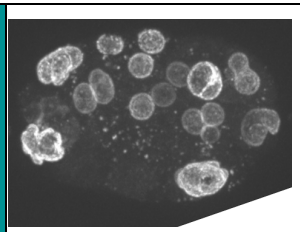
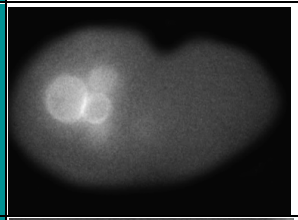
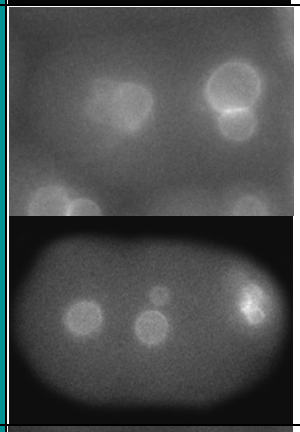
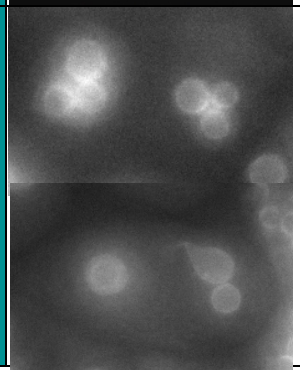
		R03G5.1	X/ 7823586-7825696	*eef-1A.2*	An ortholog of human EEF1A2, a translation elongation factor (Rhoads *et al.* 2006).					√	√				
		F25H5.4	I/ 9171491-9175032	*eef-2*	An ortholog of human EEF2, a translation elongation factor (Ofulue and Candido 1991; Rhoads *et al.* 2006).			√			√				Nuclear appearance variant (Green *et al.* 2011).
	Ribosome biogenesis	T19A6.2	I/ 8402782-8406677	*ngp-1*	A nucleolar GTP-binding protein orthologous to human GNL2. NGP-1 has a role in non-sense mediated decay. Yeast homolog, Nog2, is involved in ribosome biogenesis (Casadio *et al.* 2015).			√							

		Y48G1A.4	I/ 323861-330729	*nol-14*	A nucleolar protein, an ortholog of human NOP14, required for ribosome biogenesis.						√				
	Microtubule function and centrosomes														
	Tubulin	C47B2.3	I/ 12974925-12972741	*tba-2*	α-tubulin, forms microtubules along with β-tubulin (Phillips *et al.* 2004).			√			√		√	 	
		F44F4.11	II/ 10918609-10920067	*tba-4*	α-tubulin, forms microtubules along with β-tubulin.			√			√				
		C36E8.5	III/ 4017607-4015736	*tbb-2*	β-tubulin, dimerizes with α-tubulin to form microtubules (Wright and Hunter 2003; Ellis *et al.* 2004).			√			√				

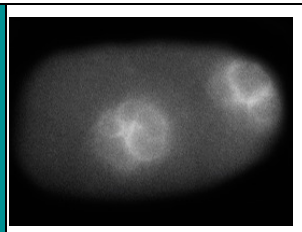
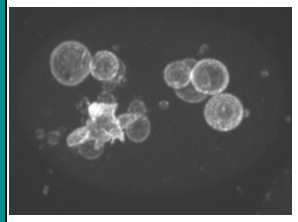
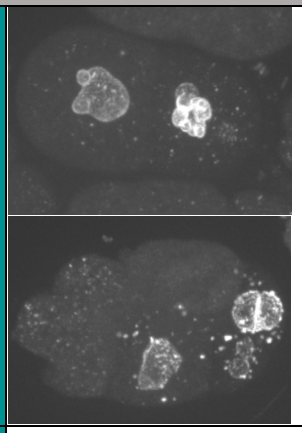
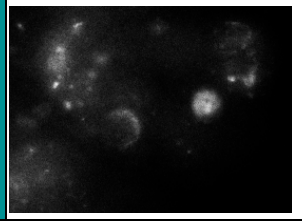
	Motor proteins	M03D4.1	IV/ 6118214-6121751	*zen-4*	A kinesin motor protein belongs to the MKLP/CHO1 subfamily of kinesin. ZEN-4 bundles antiparallel microtubules at the spindle midzone (Raich *et al.* 1998; Mishima *et al.* 2002; Siddiqui 2002).			√							Multi-nucleated cells (Raich *et al.* 1998; Echard *et al.* 2004).
		C06G3.2	IV/ 7040199-7043684	*klp-18*	A kinesin motor protein belongs to the MCAK/KIF2 subfamily of kinesins. Contributes to acentrosomal spindle bipolarity (Siddiqui 2002; Segbert *et al.* 2003; Wolff *et al.* 2016).	√			√		√				Multi-nucleated cells (Piano *et al.* 2002).
		Y43F4B.6	III/ 13306699-13302210	*klp-19*	A kinesin motor protein belongs to the chromokinesin subfamily of kinesins that is associated with chromosomes (Siddiqui 2002; Powers *et al.* 2004).				√	√					Anaphase bridges (Powers *et al.* 2004); chromosome segregation defect (Sonnichsen *et al.* 2005).
		T26A5.9	III/ 6464100-6462844	*dlc-1*	A light chain subunit of dynein, which is a minus-end direct motor. Orthologous to human DYNLL1 and DYNLL2 (O'rourke *et al.* 2007).			√	√		√				Multi-nucleated oocytes (Green *et al.* 2011); nuclear appearance variant, enlarged nuclei (Dorsett and Schedl 2009).

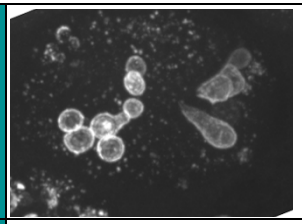
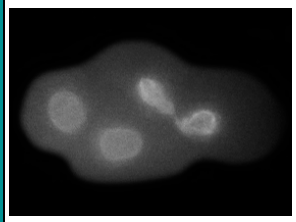
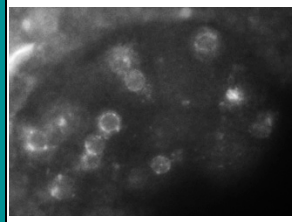
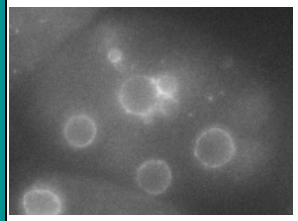
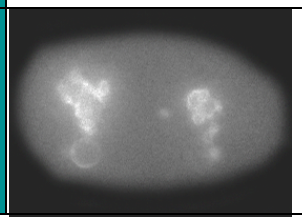
		C17H12.1	IV/ 6778141-6779777	*dyci-1*	A putative intermediate chain subunit of dynein, a minus-end directed motor (O'rourke *et al.* 2007).	√					√				
		C39E9.14	IV/ 13098788-13096975	*dli-1*	A light intermediate chain subunit of dynein, a microtubule minus-directed motor (Yoder and Han 2001).			√			√				Multi-nucleated cells (Yoder and Han 2001).
		F53A2.4	III/ 13340992-13342059	*nud-1*	An ortholog of *Aspergillus* nuclear division protein nudC. NUD-1 associates with dynein (Dawe *et al.* 2001).			√			√				Multi-nucleated cells (Aumais *et al.* 2003); nuclear appearance variant, small nuclei (Green *et al.* 2011).
		ZK593.5	IV/ 10933098-10926708	*dnc-1*	A subunit of dynactin, a dynein associated protein required for cargo binding. *dnc-1* is an ortholog of p150/GLUED/DCTN1 (Skop and White 1998).			√	√		√				Chromosome segregation defect (Skop and White 1998).
		Y53F4B.22	II/ 15120182-15123228	*arp-1*	Actin related protein A, orthologous to human ACTR1. ARP-1 is a component of the dynactin complex (Terasawa *et al.* 2010).			√	√		√				

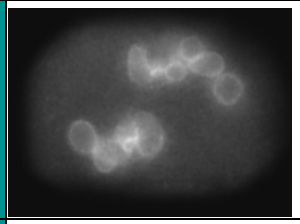
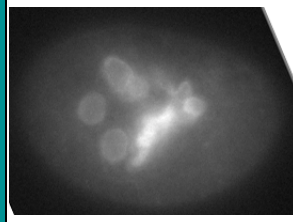
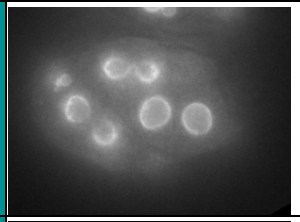
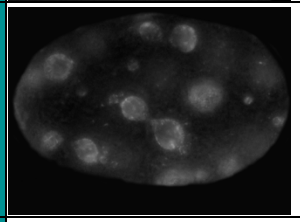
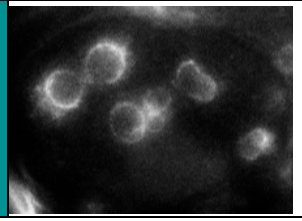
		C49H3.8	IV/ 7901980-7900270	*arp-11*	An actin related protein 10, orthologous to human ACTR10, a component of dynactin complex (Terasawa *et al.* 2010).			√							
	Tubulin/microtubule-interacting proteins	C05D11.3	III/ 6432118-6432915	*txdc-9*	A thioredoxin domain-containing protein, orthologous to human TXNDC9. TXDC-9 is required for tubulin acetylation (Ogawa *et al.* 2004; Chen *et al.* 2015).			√	√		√				
		T06G6.9	I/ 12736231-12737852	*pfd-3*	Predicted to be a subunit of prefoldin. PFD-3 is involved in tubulin folding (Lundin *et al.* 2008).			√			√				
		F22B5.1	II/ 8467088-8467897	*evl-20*	A small GTPase, an ortholog of human ARL2. May regulate microtubule structure (Antoshechkin and Han 2002).	√		√		√	√				

	positioning	C38C10.4	III/ 9393060-9391288	*gpr-2*	A G-protein regulator-regulates the GTPase activity of Gα protein GOA-1. Involved directly in regulating spindle positioning (Gonczy *et al.* 2000; Colombo *et al.* 2003; Srinivasan *et al.* 2003).	√		√			√				Multi-nucleated cells (Piano *et al.* 2002).
	Meiotic spindle	C28C12.2	IV/ 8499307-8500000	*mesp-1*	MESP-1 interacts with KLP-18 for maintaining acentrosomal spindle bipolarity (Wignall and Villeneuve 2009; Wolff *et al.* 2016).			√							Multi-nucleated cells (Piano *et al.* 2002).
		F57B10.12	I/ 6573915-6572812	*mei-2*	A subunit of the katanin complex (along with MEI-1) which has microtubule severing activity. MEI-2 is required for the establishment of the oocyte meiotic spindle (Srayko *et al.* 2000).	√		√	√						
	Centrosome-associated proteins	C45G3.5	I/ 9235046-9240071	*gip-2*	A γ-tubulin interacting protein, a component of the γ-tubulin complex (Hannak *et al.* 2002).			√		√					

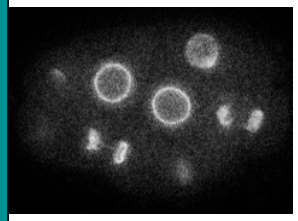
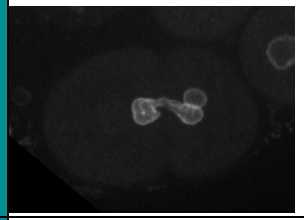
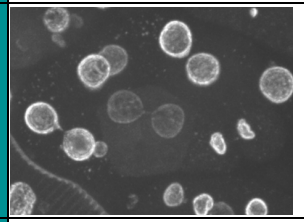
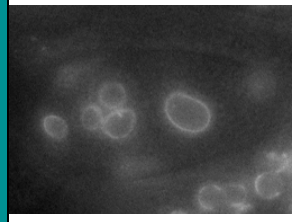
		F58A4.8	III/ 9629050-9626438	*tbg-1*	γ-tubulin, a centrosome component (Bobinnec *et al.* 2000).			√	√		√				Multi-nucleated oocyte, nuclear appearance variant; small nuclei (Green *et al.* 2011); multi-nucleated cells (Piano *et al.* 2002).
		F56A3.4	I/ 5175525-5171286	*spd-5*	A coiled coil, pericentriolar material (PCM) scaffold protein (Hamil *et al.* 2002).			√	√	√	√				Multi-nucleated cells (Piano *et al.* 2002).
		F35B12.5	V/ 11613335-11615644	*sas-5*	A coiled-coil protein that localizes to centrioles and is required for centriole duplication (Delattre *et al.* 2004; Rogala *et al.* 2015).			√			√				Multi-nucleated cells; nuclear morphology variation in early embryos (Schmutz and Spang 2005).

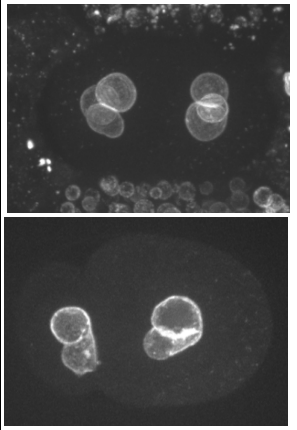
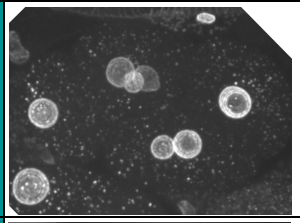
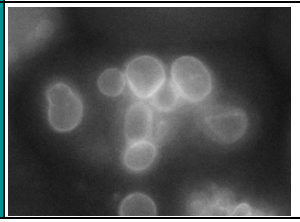
		Y45F10D.9	IV/ 13788695-13786919	*sas-6*	A coiled-coil protein that localizes to centrioles and is required for centriole duplication (Dammermann *et al.* 2004; Leidel *et al.* 2005; Nakazawa *et al.* 2007).			√			√				
		C30B5.1	II/ ‘6198678-6201563	*szy-4*	Protein of unknown function. *szy-4 (loss-of-function)* mutation rescues the centrosome duplication failure caused by *zyg-1(it25)* loss-of-function mutants (Kemp *et al.* 2007).			√	√		√				Multi-nucleated oocytes (Green *et al.* 2011).
	Cell Cycle														
	Cell cycle regulators	T06E6.2	V/ 15398281-15399936	*cyb-3*	A B-type cyclin that activates CDK-1 (Sonneville and Gonczy 2004; Van Der Voet *et al.* 2009).	√		√	√		√	√	√		Multi-nucleated cells, nuclear appearance variant, small nuclei (Green *et al.* 2011).
		Y53C12A.1	II/ 9716375-9713643	*wee-1.3*	Orthologous to the vertebrate Myt1, belongs to the Wee1 family of kinases. WEE-1.3 represses the activity of Cdk-1 (Lamitina and L'hernault 2002; Burrows *et al.* 2006).								√		Multi-nucleated oocytes, nuclear appearance variant, enlarged nuclei (Green *et al.* 2011).

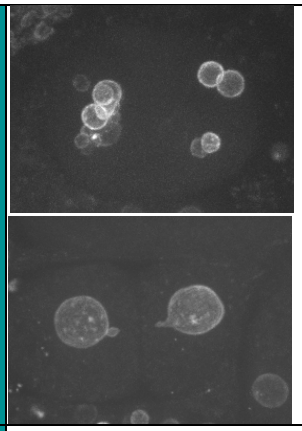
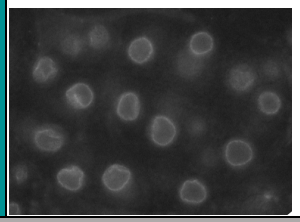
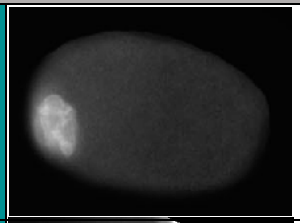
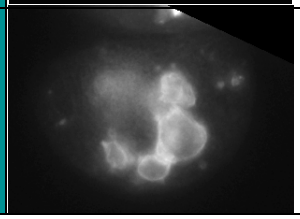
		C09G4.3	IV/ 8513916-8514388	*cks-1*	A cyclin dependent kinase regulatory subunit, an ortholog of human Cks/Suc (Polinko and Strome 2000).	√		√	√	√	√	√	√			Pronuclear morphology defect (Polinko and Strome 2000).
		F26E4.1	I/ 9762170-9765948	*sur-6*	A regulatory subunit of serine/threonine protein phosphatase 2A (PP2A-B). Among the processes regulated by SUR-6 are Ras-mediated signaling, membrane trafficking and centriole duplication (Sieburth *et al.* 1999; Jiu *et al.* 2014).					√						Anaphase bridges (Song *et al.* 2011); multi-nucleated cells (Fraser *et al.* 2000; Zipperlen *et al.* 2001).
		T09A5.9	II/ 7858317-7859638	*sds-22*	Ortholog of human protein phosphatase 1 regulatory subunit. Yeast and human orthologs are involved in processes related to mitosis. SDS-22 is required for centriole duplication (Peel et al. 2017).			√				√				
		K07C11.2	V/ 8224002-8226114	*air-1*	An Aurora A serine/threonine kinase. Regulates chromosome segregation and cell division related processes (Schumacher et al. 1998; Hannak et al. 2001).				√							Nuclear appearance variant, enlarged nuclei (Green *et al.* 2011); multi-nucleated cells (Piano *et al.* 2002; Echard *et al.* 2004); anaphase bridges (Schumacher *et al.* 1998).
		C27A2.3	II/ 5055163-5054128	*ify-1*	A securin like protein, that is degraded at the onset of anaphase following ubiquitination by the anaphase promoting complex-dependent. Inhibits the activity of separase,			√	√		√					Pronuclear size defect (Kitagawa *et al.* 2002).

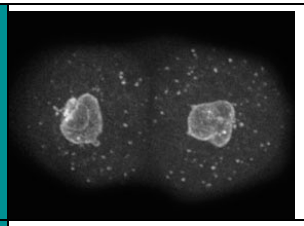
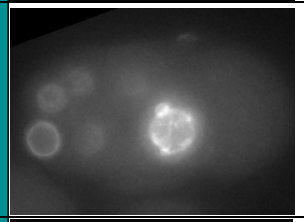
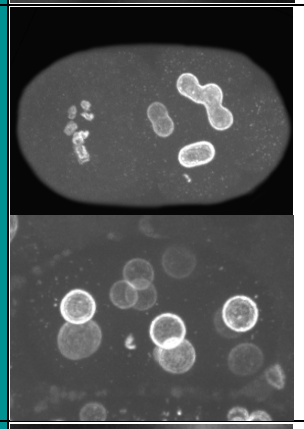
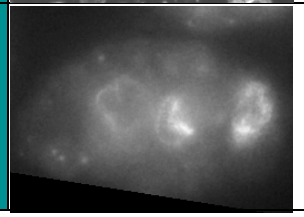
					SEP-1, that is needed for sister chromatid separation (Kitagawa et al. 2002).										
	Anaphase promoting complex	ZK177.6	II/ 5501599-5503874	*fzy-1*	A Cdc20/Fizzy homolog, a substrate recognition subunit of the anaphase promoting complex (Kitagawa et al. 2002).			√			√				
		F35G12.9	III/ 4594387-4593855	*apc-11*	A subunit of anaphase promoting complex, an E3 ubiquitin ligase. Required for anaphase initiation by promoting the ubiquitination of Cyclin B and other proteins (Davis et al. 2002).		√		√		√				
	DNA replication	F58A4.4	III/ 9614173-9612231	*pri-1*	An ortholog of DNA polymerase α-primase subunit D (Encalada et al. 2000).					√					Multi-nucleated cells (Piano *et al.* 2002).
		W02D9.1	I/ 12559588-12560331	*pri-2*	An ortholog of DNA polymerase α-primase subunit C (Encalada et al. 2000).				√	√					Multi-nucleated cells (Piano *et al.* 2002); nuclear morphology variation in early embryos (Fraser *et al.* 2000; Zipperlen *et al.* 2001).
		ZC168.3	IV/ 10734556-10732881	*orc-5*	An ortholog of human Orc5, required for the initiation of DNA replication.			√	√	√	√				

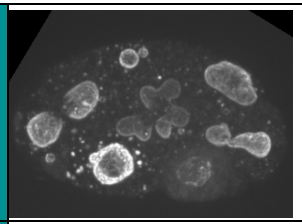
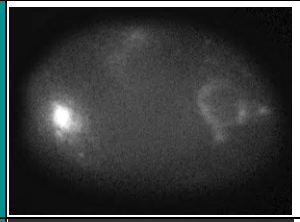
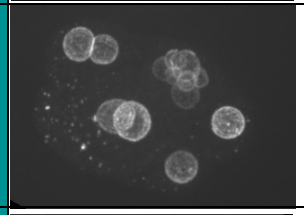
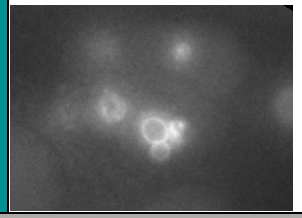
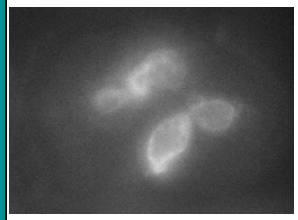
		F32D1.10	V/ 4346978-4349568	*mcm-7*	An ortholog of mammalian MCM7, part of a helicase complex involved in initiation of DNA replication (Woodward et al. 2006; Sonneville et al. 2012).	√		√	√	√	√		√		Multi-nucleated cells (Piano *et al.* 2002).
	Ribonucleotide reductase	T23G5.1	III/ 9228686-9225276	*rnr-1*	A putative large subunit of ribonucleotide reductase involved in deoxyribonucleotide biosynthesis (Hong et al. 1998; Mori et al. 2008).				√		√				
		C03C10.3	III/ 4094896-4093318	*rnr-2*	A putative small subunit of ribonucleotide reductase, involved in deoxyribonucleotide biosynthesis (Mori et al. 2008).	√		√							Enlarged nuclei (Green *et al.* 2011).
	Kinetochore proteins	W01B6.9	IV/ 10086113-10088368	*ndc-80*	An ortholog of the yeast kinetochore protein Ndc80. NDC-80 is required for kinetochore-microtubule interactions (Desai et al. 2003).			√		√	√				Pronuclear size defect; multi-nucleated cells (Piano *et al.* 2002).

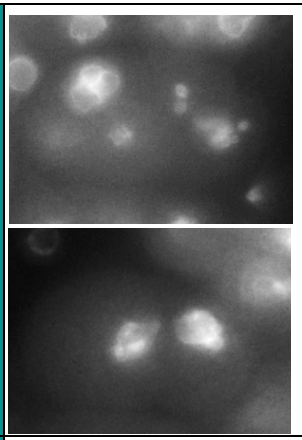
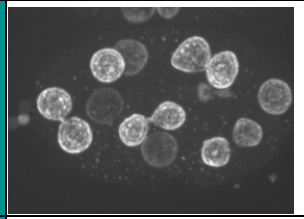
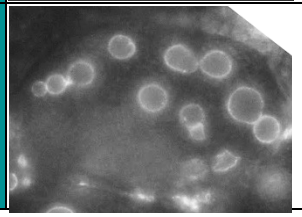
		C06A8.5	II/ 7781497-7783131	*spdl-1*	Homologous to the *Drosophila* coiled coil protein Spindly, which is responsible for recruiting Dynein to kinetochores. SPDL-1 is also required for spindle assembly checkpoint function (Gassmann *et al.* 2008; Yamamoto *et al.* 2008).					√					
		F58A4.3	III/ 9616360-9615218	*hcp-3*	A Histone H3-like centromeric protein, orthologous to human CENP-A (Buchwitz *et al.* 1999; Oegema *et al.* 2001).	√				√	√				Nuclear appearance variant (Green *et al.* 2011).
	Spindle assembly checkpoint	R06C7.8	I/ 7260006-7263287	*bub-1*	A serine/threonine kinase orthologous to the yeast and human BUB1. BUB-1 is required for spindle assembly checkpoint signaling (Oegema *et al.* 2001).	√			√	√					Multi-nucleated cells (Fraser *et al.* 2000; Dawe *et al.* 2001; Zipperlen *et al.* 2001).
	Cytokinesis	K08E3.6	III/ 13770697-13768024	*cyk-4*	A Rho GTPase-activating protein (GAP) protein. CYK-4 is part of the central spindle complex that is required for central spindle formation and cytokinesis (Jantsch-Plunger *et al.* 2000).		√				√				Nuclear appearance variant, small nuclei (Green *et al.* 2011); multi-nucleated cells (Encalada *et al.* 2000; Piano *et al.* 2002; Green *et al.* 2011).
	Signaling															

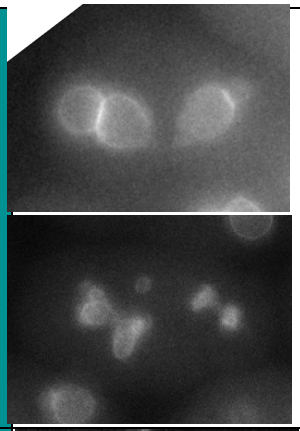
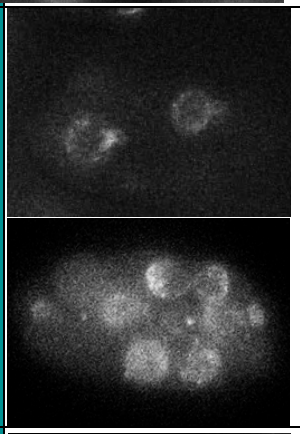
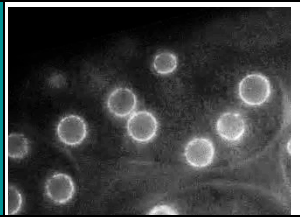
	MAP kinase signaling	F49E11.1	IV/ 13059603-13060644	*mbk-2*	A Serine/threonine kinase, it is a member of the DYRK (dual-specificity Yak1-related kinase) family of proteins (Pellettieri *et al.* 2003; Raich *et al.* 2003).	√		√		√	√				Anaphase bridges (Pellettieri *et al.* 2003).
		ZK792.6	IV/ 11691064-11688203	*let-60*	A GTP-binding RAS protein. LET-60 activity regulates RAS-mediated signaling as part of the part of the MAP kinase cascade (Han and Sternberg 1990).	√		√							Enlarged nuclei (Green *et al.* 2011).
	Rho GTPase	T19E10.1	II/ 10783193-10778791	*ect-2*	A Rho guanine exchange factor (GEF) required for cytokinesis and cell polarity in early embryos (Morita *et al.* 2005; Motegi and Sugimoto 2006).			√			√				Multi-nucleated cells (Echard *et al.* 2004).

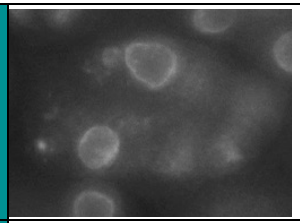
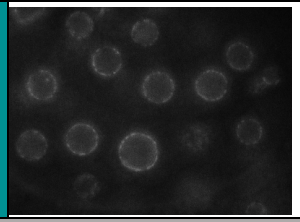
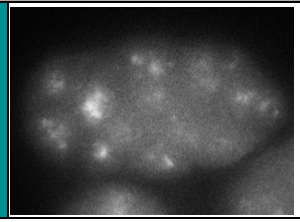
	Wnt pathway related	C03C10.1	III/ 4086610-4084105	*kin-19*	A Casein kinase I homolog. KIN-19 is a serine/threonine kinase In the Wnt signaling pathway (Walston *et al.* 2004; Banerjee *et al.* 2010).	√		√		√					Small nuclei (Green *et al.* 2011).
		Y18D10A.5	I/ 12827264-12832855	*gsk-3*	An ortholog of human GSK3B, a kinase involved in Wnt signaling (Schlesinger *et al.* 1999).						√				
	Protein degradation														
	Proteasome	C30C11.2	III/ 8447260-8449221	*rpn-3*	A putative 19S non-ATPase subunit of the proteasome complex. Orthologous to human PSMD3 (Davy *et al.* 2001).						√				Nuclear appearance variant; enlarged nuclei (Green *et al.* 2011).
		C52E4.4	V/ 11985025-11983065	*rpt-1*	A putative 19S ATPase subunit of proteasome complex. Orthologous to human PSMC2 (Davy *et al.* 2001).		√		√		√				Nuclear appearance variant, enlarged nuclei (Green *et al.* 2011).

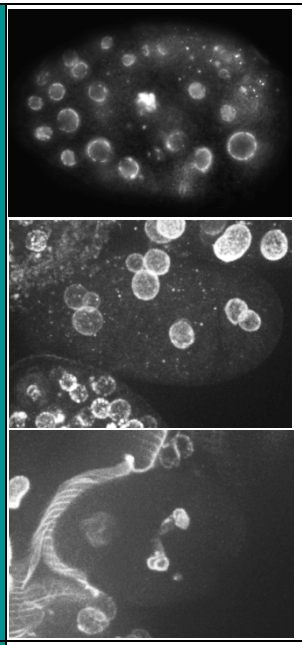
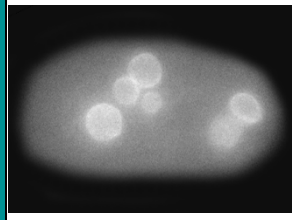
		Y110A7A.14	I/ 5106207-5105113	*pas-3*	A putative 20S α-type proteasome subunit. Orthologous to human PSMA4 (Davy *et al.* 2001).						√		√			Nuclear appearance variant (Green *et al.* 2011).
	Ubiquitylation	M7.1	IV/ 11082233-11081066	*let-70*	A ubiquitin conjugating enzyme, also known as UBC-2. Works with the anaphase promoting complex (Frazier *et al.* 2004).				√		√					Nuclear appearance variant (Green *et al.* 2011).
		ZK858.4	I/ 9140591-9143791	*mel-26*	An ortholog of human SPOP. MEL-26 is the substrate recognition subunit of the CUL-3 ubiquitin ligase. Promotes MEI-1 degradation, thereby facilitating the transition from the meiotic spindle the mitotic one (Dow and Mains 1998; Pintard *et al.* 2003b).	√		√			√					
		ZK520.4	III/ 13686666-13692042	*cul-2*	An E3 ubiquitin ligase, orthologous to human CUL2 (Kipreos *et al.* 1996; Kipreos 2005).			√			√		√			

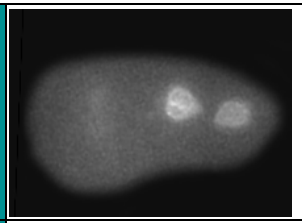
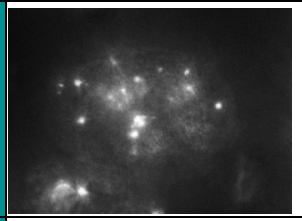
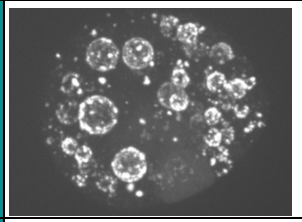
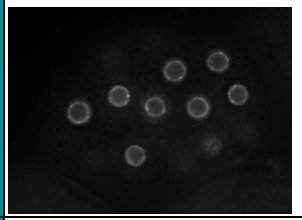
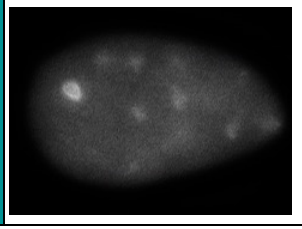
		ZK287.5	V/ 9693198-9692300	*rbx-1*	Part of the CUL-2 ubiquitin ligase complex. Orthologous to human RBX1 (Sasagawa *et al.* 2003; Kipreos 2005).			√	√	√	√					
		F52C6.12	II/ 1929919-1929408		Orthologous to ubiquitin conjugating enzymes (Michelle *et al.* 2009). According to Wormbase it may be a pseudogene.				√		√					
	COP9 signalosome	Y59A8A.1	V/ 17873225-17863962	*csn-1*	A COP9 signalosome complex subunit, regulates E3 ubiquitin ligases. Orthologous to human GPS1 (Pintard *et al.* 2003a).	√		√			√					
		B0547.1	IV/ 5649522-5651047	*csn-5*	A COP9 signalosome complex subunit, which regulates E3 ubiquitin ligases. Orthologous to human COPS5 (Pintard *et al.* 2003a).			√								
	Chromatin and chromosome structure															
	Condensin complex	M106.1	II/ 10824200-10841307	*mix-1*	A component of dosage compensation complex, homologous to SMC2. Required for X chromosome dosage compensation and chromosome condensation (Lieb *et al.* 1996; Hagstrom *et al.* 2002).			√		√	√					Anaphase bridges (Csankovszki *et al.* 2009); Pronuclear size defect (Piano *et al.* 2002).

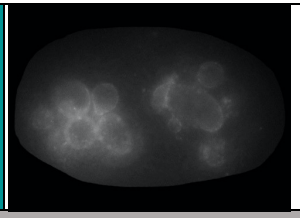
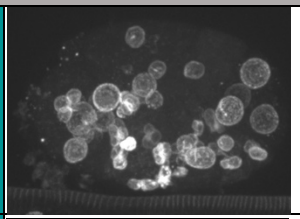
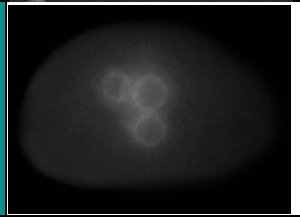
		Y110A7A.1	I/ 5165160-5171301	*hcp-6*	A condensin complex subunit, required for chromosome condensation (Stear and Roth 2002).			√	√	√	√					Anaphase bridges (Csankovszki *et al.* 2009); sister chromatid separation defective causing deformed nuclei (Sonnichsen *et al.* 2005); pronuclear size defect (Piano *et al.* 2002).
		F55C5.4	V/ 12274473-12278252	*capg-2*	A CAP-G condensin subunit, required for chromosome condensation (Ono *et al.* 2003; Csankovszki *et al.* 2009).			√		√	√					Anaphase bridges (Csankovszki *et al.* 2009); multi-nucleated cells (Echard 2004).
	Cohesion complex	F18E2.3	V/ 12766536-12770517	*scc-3*	A cohesin complex subunit. Essential for sister chromatid cohesion (Pasierbek *et al.* 2003; Wang *et al.* 2003).				√	√						Sister chromatid separation defective causing deformed nuclei (Sonnichsen *et al.* 2005).

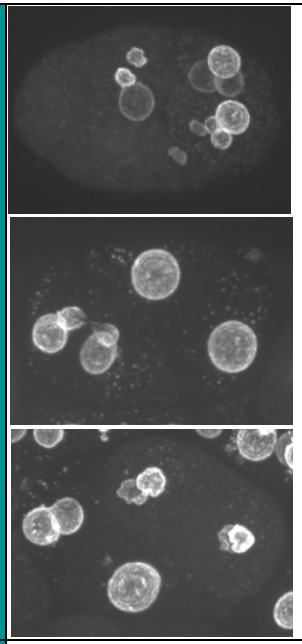
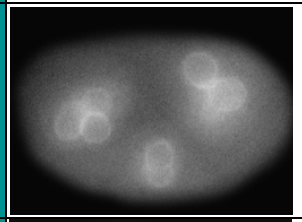
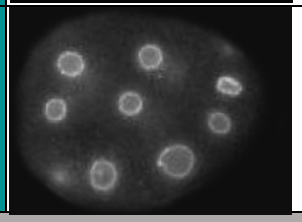
		Y47D3A.26	III/ 11290733-11305795	*smc-3*	A cohesin complex subunit. SMC-3 is required for DNA condensation, cohesion and DNA repair (Chan *et al.* 2003; Baudrimont *et al.* 2011).	√			√	√					
	Histone genes	ZK131.7	II/ 13820101-13820511	*his-13*	Histone H3 (Roberts *et al.* 1989).				√	√	√	√			Anaphase bridges (Kodama *et al.* 2002).
		F45E1.6	X/ 7982016-7981323	*his-71*	A Histone H3.3 variant (Ooi *et al.* 2006).							√			

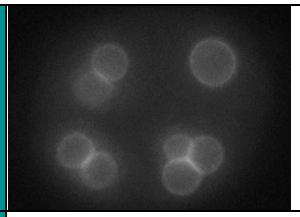
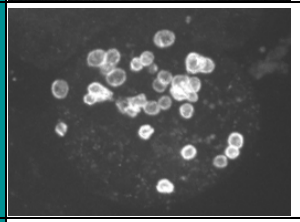
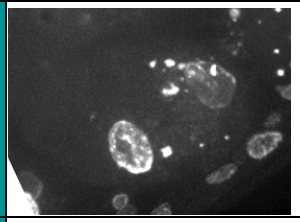
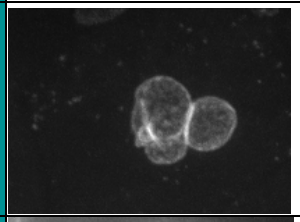
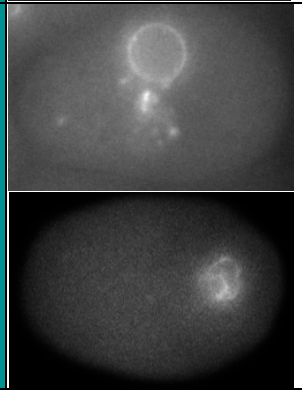
	Other	ZK1127.7	II/ 7038329-7041086	*cin-4*	Orthologous to human topoisomerase II (Stanvitch and Moore 2008).				√		√				Multi-nucleated cells, pronuclear size defect (Piano *et al.* 2002); Sister chromatid separation defective causing deformed nuclei (Sonnichsen *et al.* 2005).
		D1081.8	I/ 8499345-8504358	*phi-7/ cdc-5L*	A putative ortholog of human CDC5L (cell division cycle 5 like). cdc-5L is predicted to have DNA binding activity.							√			Multi-nucleated cells in early embryos (Piano *et al.* 2002).
	Nuclear envelope proteins														
	Nuclear lamina associated proteins	F28B12.3	II/ 5921925-5924791	*vrk-1*	A serine/threonine vaccinia-related protein kinase. VRK-1 is essential for nuclear envelope reassembly at the end of mitosis (Gorjanacz *et al.* 2007).								√		Nuclear appearance variant (Sonnichsen *et al.* 2005).

		DY3.2	I/ 8771044-8773679	*lmn-1*	A nuclear envelope protein required for chromatin organization and structural integrity of the nucleus. It is the only lamin ortholog in *C. elegans* (Riemer *et al.* 1993; Liu *et al.* 2000).	√		√	√	√	√	√			Multi-nucleated oocytes; small nuclei (Green *et al.* 2011); nuclear appearance variant (Liu *et al.* 2000; Green *et al.* 2011) multi-nucleated cells (Gorjanacz and Mattaj 2009); pronuclear size defect (Fraser *et al.* 2000; Zipperlen *et al.* 2001).
		F57B1.2	V/ 13196132-13194062	*sun-1*	A SUN-domain containing inner nuclear envelope protein. Associates with ZYG-12 to form the LINC complex. Required for centrosome attachment to the nuclear envelope, nuclear movement and homologous chromosome pairing in meiosis (Malone *et al.* 1999; Malone *et al.* 2003).			√							

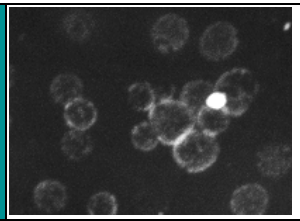
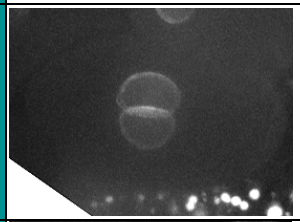
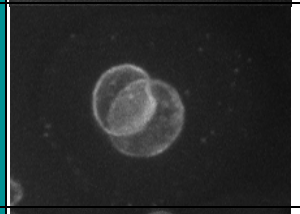
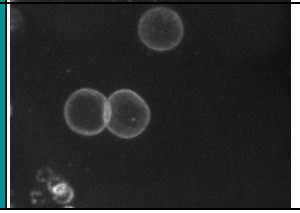
	Nuclear import and export	Y48G1A.5	I/ 323355-318567	*xpo-2*	An ortholog of human CSE1L. A putative importin-β, involved in nuclear export.					√	√					Pronuclear envelope defect in early embryos (Fraser *et al.* 2000; Zipperlen *et al.* 2001; Sonnichsen *et al.* 2005).
		K01G5.4	III/ 10747712-10746411	*ran-1*	A Ran GTPase orthologous to human RAN. Mediates nucleocytoplasmic transport (Askjaer *et al.* 2002; Bamba *et al.* 2002).							√				Multi-nucleated oocytes, enlarged nuclei (Green *et al.* 2011); small nuclei (Askjaer *et al.* 2002; Green *et al.* 2011); pronuclear appearance defect (Sonnichsen *et al.* 2005); pronuclear size defect (Askjaer *et al.* 2002).
		C26D10.1	II/ 8324972-8322555	*ran-3*	A guanine exchange factor (GEF) of RAN-1, orthologous to human RCC1, involved in nucleocytoplasmic transport (Askjaer *et al.* 2002; Bamba *et al.* 2002).			√		√		√	√			Nuclear appearance variant, small nuclei (Green *et al.* 2011); multi-nucleated cells (Piano *et al.* 2002); pronuclear appearance defect (Sonnichsen *et al.* 2005); pronuclear size defect (Askjaer *et al.* 2002).
	Nuclear pore complex subunits	T01G9.4	I/ 8301697-8299361	*npp-2*	A subunit for the nuclear pore complex that mediates nucleocytoplasmic transport. *npp-2* is orthologous to human NUP85 (Galy *et al.* 2003).							√				Pronuclear appearance defect (Sonnichsen *et al.* 2005); nuclear morphology variation in early embryos (Fraser *et al.* 2000; Zipperlen *et al.* 2001; Galy *et al.* 2003).
		F59A2.1	III/ 3404465-3400630	*npp-9*	A subunit for the nuclear pore complex that mediates nucleocytoplasmic transport. npp-9 is orthologous to Nup358/RANBP2 (RAN binding protein 2) (Galy *et al.* 2003).						√		√			Pronuclear appearance defect (Sonnichsen *et al.* 2005); nuclear morphology variation in early embryo (Galy *et al.* 2003).

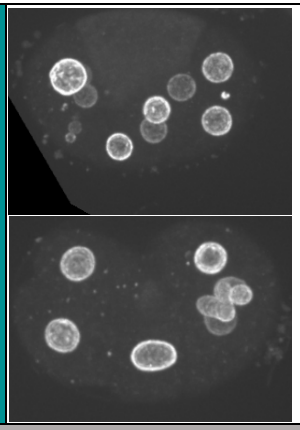
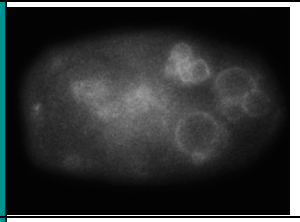
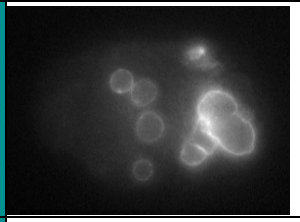
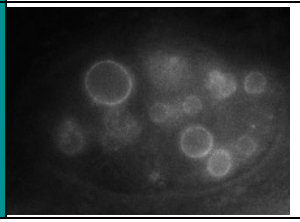
		Y77E11A.13	IV/ 1496025-1490729	*npp-20*	A subunit for the nuclear pore complex that mediates nucleocytoplasmic transport. NPP-20 is orthologous to SEC13 (Casadio *et al.* 2015).			√			√	√				Nuclear morphology variation in early embryo (Galy *et al.* 2003).
	Vesicle trafficking														
		F53G12.1	I/ 110318-108686	*rab-11.1*	A Rab GTPase that functions in endocytosis and regulates endocytic protein sorting (Grant and Hirsh 1999).			√			√					Multi-nucleated cells (Poteryaev *et al.* 2007); nuclear appearance variant (Green *et al.* 2011).
		K02D10.5	III/ 8776160-8777730	*snap-29*	A syntaxin-type SNARE, part of t-SNAREs. Involved in vesicle trafficking (Sato *et al.* 2011).		√									Multi-nucleated oocytes, small nuclei (Green *et al.* 2011).

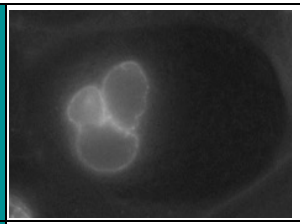
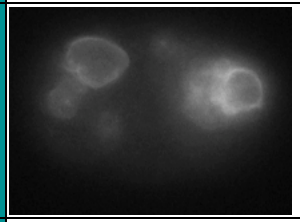
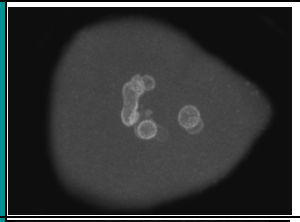
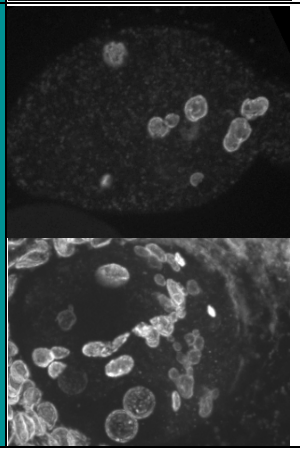
		T01B11.3	IV/ 8457277-8458860	*syx-4*	A syntaxin-type SNARE, part of t-SNAREs. Involved in vesicle trafficking (Jantsch-Plunger and Glotzer 1999).	√		√	√	√	√				Multi-nucleated cells (Jantsch-Plunger and Glotzer 1999); enlarged nuclei (Green *et al.* 2011).
		F55A11.2	V/ 11767492-11769803	*syx-5*	A syntaxin-type SNARE, part of t-SNARE. Involved in vesicle trafficking (Hyenne *et al.* 2015).	√		√			√				Multi-nucleated cells (Echard *et al.* 2004).
		M110.5	II/ 8226029-8228242	*dab-1*	Orthologous to DISABLED, a clathrin binding protein. DAB-1 is required for receptor-mediated endocytosis (Kamikura and Cooper 2003).							√			
Mitochondrial functions															

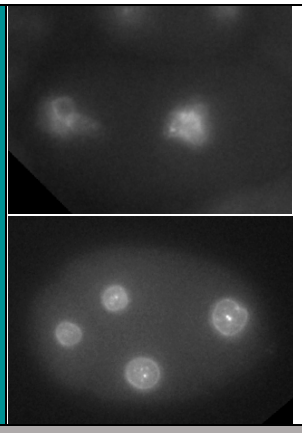
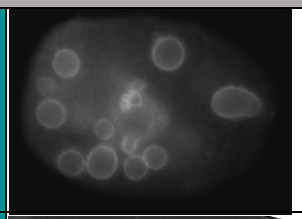
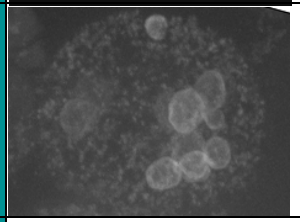
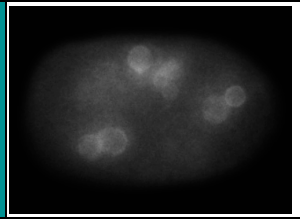
	Mitochondrial fission	C02C6.1	X/ 15568833-15573610	*dyn-1*	A dynamin ortholog, required for various membrane fusion events, including endocytosis, apoptosis and mitochondrial fission (Clark *et al.* 1997).	√		√							Multi-nucleated oocytes (Green *et al.* 2011).
		T12E12.4	IV/ 5538481-5541336	*drp-1*	A dynamin-related protein required for mitochondrial fission (Labrousse *et al.* 1999).	√		√			√				Multi-nucleated cells (Echard *et al.* 2004).
	Electron transport chain	H28O16.1	I/ 12660248-12662673	*atp-1/phi-37*	A putative alpha subunit of mitochondrial ATP synthase, orthologous to human ATP5F1A.						√	√			*(Rahman et al. 2014)*
		C34E10.6	III/ 5228368-5230501	*atp-2*	A putative beta subunit of mitochondrial ATP synthase, orthologous to human ATP5F1B.		√		√		√				*(Rahman et al. 2014)*
		F27C1.7	I/ 5429876-5428542	*atp-3*	A putative OSCP subunit of mitochondrial ATP synthase, orthologous to human ATP5O.						√		√		*(Rahman et al. 2014)*

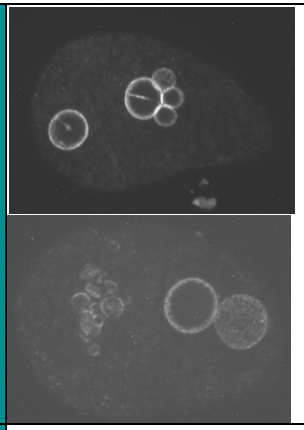
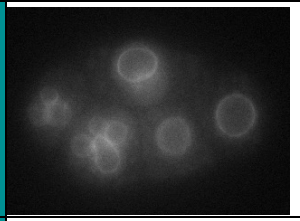
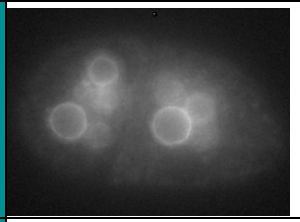
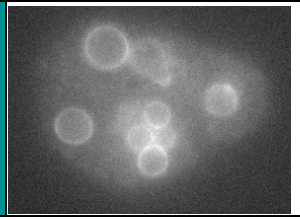
		T05H4.12	V/ 6429792-6428787	*atp-4*	A putative F_6 subunit for mitochondrial ATP synthase, orthologous to human ATP5J.						√		√		*(Rahman et al. 2014)*
		C06H2.1	V/ 11126564-11125409	*atp-5*	A putative D subunit for mitochondrial ATP synthase, orthologous to human ATP5D.		√		√						(Rahman *et al.* 2014)
		C54G4.8	I/ 8032481-8030742	*cyc-1*	Orthologous to human CYC1 (cytochrome c1).			√				√			*(Rahman et al. 2014)*
		F56D2.1	III/ 5592086-5594420	*ucr-1*	Orthologous to human ubiquinol-cytochrome c reductase core protein.	√									*(Rahman et al. 2014)*
		F26E4.9	I/ 9796827-9797972	*cco-1/cox-5b*	Orthologous to human COX5B (cytochrome c oxidase subunit 5B).	√		√							*(Rahman et al. 2014)*

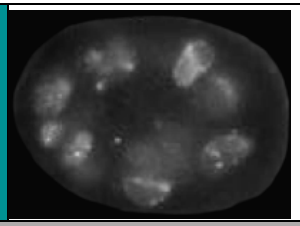
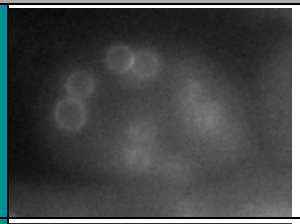
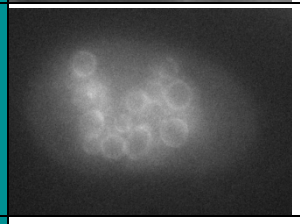
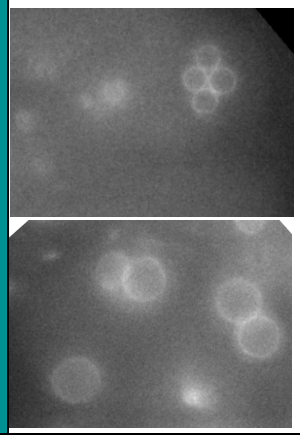
		Y37D8A.14	III/ 12905313-12906435	*cco-2*	Orthologous to human COX5A (cytochrome c oxidase subunit 5A).			√							*(Rahman et al. 2014)*
		F33A8.5	II/ 11049822-11049056	*sdhd-1*	Orthologous to human succinate dehydrogenase complex subunit D.	√									*(Rahman et al. 2014)*
		T07C4.7	III/ 10334107-10334995	*mev-1/sdhc-1*	Orthologous to human succinate dehydrogenase complex subunit C.	√									*(Rahman et al. 2014)*
		K04G7.4	III/ 7158735-7155955	*nuo-4*	Orthologous to human NADH:ubiquinone oxidoreductase subunit A10.	√									*(Rahman et al. 2014)*
		T20H4.5	III/ 7234127-7232849		Orthologous to human NADH:ubiquinone oxidoreductase core subunit S8.	√	√								*(Rahman et al. 2014)*

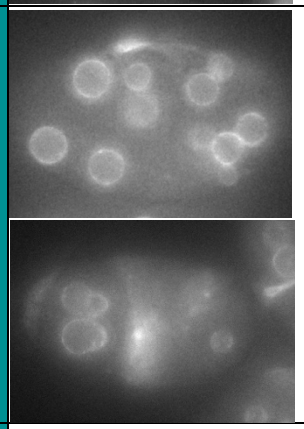
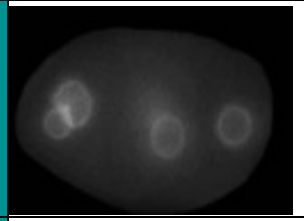
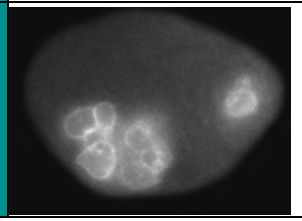
	Mitochondrial protein Degradation	Y47G6A.10	I/ 3467131-3477972	*spg-7*	A putative mitochondrial-AAA metalloprotease that regulates mitochondrial protein degradation (Pena *et al.* 2016).			√	√		√					
	Protein folding														
	Chaperonin	T05C12.7	II/ 8185353-8187520	*cct-1*	A subunit of T complex chaperonin. CCT-1 functions as an ATP-dependent molecular chaperone (Leroux and Candido 1995).			√	√		√					Nuclear appearance variant, small nuclei (Green *et al.* 2011).
		T21B10.7	II/ 8927642-8929643	*cct-2*	A subunit of T complex chaperonin. CCT-2 functions as an ATP-dependent molecular chaperone (Leroux and Candido 1995).			√			√					
		C07G2.3	III/ 4508216-4499167	*cct-5*	A subunit of T complex chaperonin. CCT-5 functions as an ATP-dependent molecular chaperone (Leroux and Candido 1995).			√			√					Multi-nucleated oocytes, nuclear appearance variant (Green *et al.* 2011).

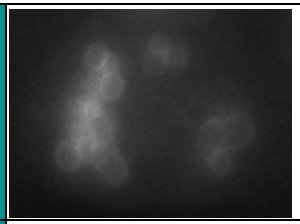
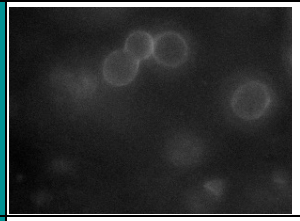
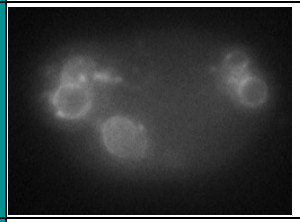
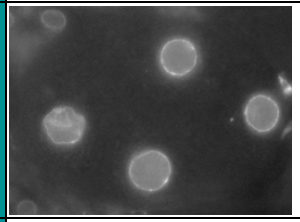
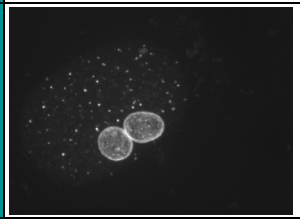
		F01F1.8	III/ 5855643-5853497	*cct-6*	A subunit of T complex chaperonin. CCT-6 functions as an ATP-dependent molecular chaperone (Leroux and Candido 1995).		√				√				Multi-nucleated oocytes, nuclear appearance variant (Green *et al.* 2011).
		T10B5.5	V/ 1872072-1875354	*cct-7*	A putative subunit of T complex chaperonin. CCT-7 functions as an ATP-dependent molecular chaperone (Leroux and Candido 1995).			√	√		√				Severe pleiotropic defects including multiple pronuclei in early embryos (Sonnichsen *et al.* 2005).
		F39B2.10	I/ 14764897-14766826	*dnj-12*	An Hsp40-like J-domain. DNJ-12 has a role in protein folding along with Hsp70 (Nillegoda *et al.* 2015).			√	√		√				
		C30C11.4	III/ 8446824-8443828	*hsp-110*	A member of Hsp70 family of heat shock proteins (Nillegoda *et al.* 2015).			√	√		√				

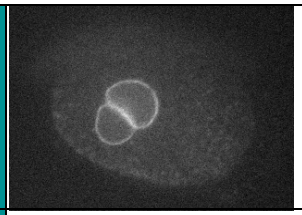
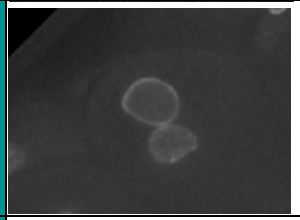
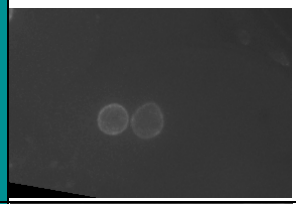
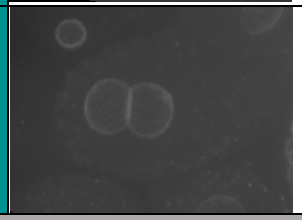
		Y65B4BR.5	I/ 535788-536881	*icd-2*	An ortholog of human NACA (nascent polypeptide-associated complex subunit alpha) (Arsenovic *et al.* 2012).			√			√			√		
	Vacuolar proteins														
	V-ATPase	R10E11.8	III/ 9781134-9781950	*vha-1*	A vacuolar V-ATPase c subunit, an ortholog of human ATP6V0C (Oka *et al.* 1997; Lee *et al.* 2010).			√	√		√					Multi-nucleated in oocytes, nuclear appearance variant, enlarged nuclei (Green *et al.* 2011).
		R10E11.2	III/ 9782050-9783140	*vha-2*	A vacuolar V-ATPase c subunit, an ortholog of human ATP6V0C (Oka *et al.* 1997; Lee *et al.* 2010).		√				√					Nuclear appearance variant, enlarged nuclei (Green *et al.* 2011).
		T01H3.1	II/ 7879254-7877999	*vha-4*	A vacuolar V-ATPase c'' subunit, an ortholog of human ATP6V0B (Oka *et al.* 1997; Lee *et al.* 2010).	√		√								Multi-nucleated oocytes, nuclear appearance variant (Green *et al.* 2011).

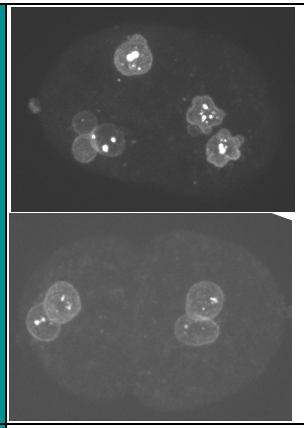
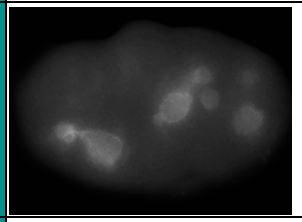
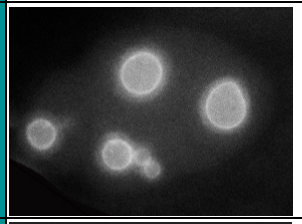
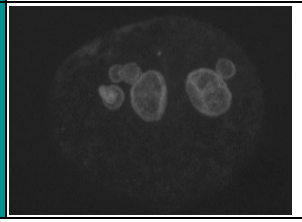
		C17H12.14	IV/ 6791062-6792430	*vha-8*	A vacuolar V-ATPase E subunit (Oka *et al.* 1997; Choi *et al.* 2003; Ji *et al.* 2006; Lee *et al.* 2010).	√		√	√		√					Multi-nucleated early embryos (Choi *et al.* 2003); nuclear appearance variant (Green *et al.* 2011).
		ZK970.4	II/ 10303619-10302449	*vha-9*	A vacuolar V-ATPase F subunit, an ortholog of human ATP6V1F (Lee et al. 2010).			√			√					Nuclear appearance variant, enlarged nuclei (Green *et al.* 2011).
		Y38F2AL.3	IV/ 2314574-2307823	*vha-11*	A vacuolar V-ATPase C subunit, an ortholog of human ATP6V1C1 (Oka and Futai 2000; Lee *et al.* 2010).			√			√					Small nuclei (Green *et al.* 2011).
		F55H2.2	III/ 9507990-9509640	*vha-14*	A vacuolar V-ATPase D subunit, an ortholog of human ATP6V1D (Lee *et al.* 2010).			√								Nuclear appearance variant (Green *et al.* 2011).

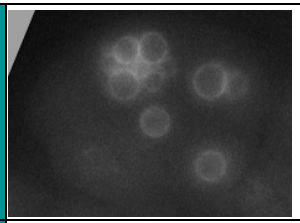
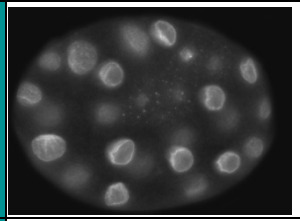
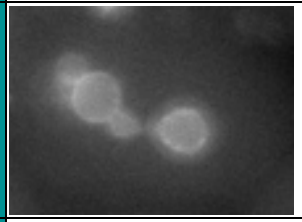
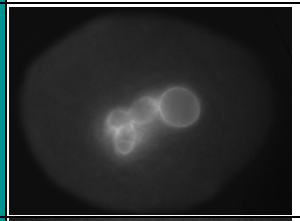
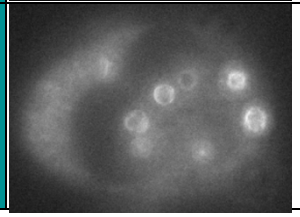
		ZK637.8	III/ 8905517-8911670	*unc-32*	A vacuolar V-ATPase a subunit, an ortholog of human ATP6V0A1 (Pujol *et al.* 2001; Lee *et al.* 2010).						√	√				
	Intermediary metabolism														
	Glycosylation-related processes	T23G11.2	I/ 7707744-7709207	*gna-2*	A Glucosamine phosphate N-acetyl transferase. GNA-2 is required for alpha-GalNAc-modifications of mucin-like proteins, and chitin (Johnston *et al.* 2006).	√		√			√					Multi-nucleated cells (Lee and Schedl 2001).
		F29F11.1	V/ 10664054-10662218	*sqv-4*	A UDP-glucose 6-dehydrogenase. SQV-4 is essential for the biosynthesis of chondroitin and heparan sulfate proteoglycans (Hwang and Horvitz 2002).			√								
		T24D1.1	I/ 9956147-9961020	*sqv-5*	Chondroitin sulphate synthase, which is similar to human chitin synthase. SQV-5 is required for the biosynthesis of chondroitin (Hwang *et al.* 2003).	√		√								Multi-nucleated cells (Mizuguchi *et al.* 2003).

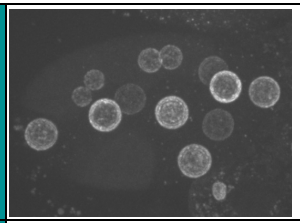
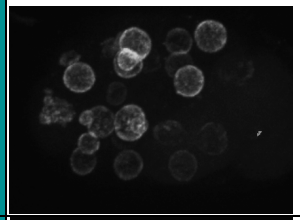
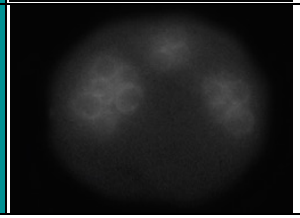
		T01H3.4	II/ 7880729-7882609	*perm-1*	A sugar modifying enzyme, possibly required for the formation of cytidine diphosphate (CDP)-ascarylose in the eggshell (Olson *et al.* 2012).			√	√		√				
		ZK686.3	III/ 7768975-7767493		An ortholog of human MAGT1 and TUSC3. Predicted to be a protein glycosyltransferase subunit.	√		√			√				
	Cytochrome p450	Y17G9B.3	IV/ 4761057-4761057	*cyp-31A3*	Homologous to human CYP7B1, a member of Cytochrome P450 family protein (Benenati et al. 2009).	√					√				
	Phosphate metabolism	C47E12.4	IV/ 9998903-9995447	*pyp-1*	An inorganic pyrophosphatase (Ko et al. 2007).			√			√				

	Nucleoside and nucleotide biosynthesis	R06C7.5	I/ 7256751-7254964	*adsl-1*	An ortholog of human ADSL, an adenylosuccinate lyase. ADSL-1 functions de novo purine biosynthesis (Marsac et al. 2019).			√			√				Nuclear morphology variation (Fraser *et al.* 2000).
		C29E4.8	III/ 7951526-7949916	*let-754*	An ortholog of human AK2, an adenylate kinase.			√			√				Nuclear appearance variant (Green *et al.* 2011).
	Gluconeogenesis and glycolysis	F01F1.12	III/ 5876494-5874189	*aldo-2*	An ortholog of human ALDOA and ALDOC, which have Fructose-bisphosphate aldolase activity. ALDO-2 is involved in glucogenesis and glycolysis.			√			√	√			
		Y46G5A.31	II/ 12877995-12866353	*gsy-1*	A glycogen synthase, orthologous to human GSY1 and GSY2 (Seo et al. 2018).							√			
		T20G5.2	III/ 10216477-10214667	*cts-1*	A citrate synthase ortholog (Hada et al. 2019).	√									(*Rahman et al. 2014*)

		F23B12.5	V/ 14449882-14447926	*dlat-1*	Orthologous to human dihydrolipoyllysine acetyltransferase, a component of the pyruvate dehydrogenase complex.	√									(*Rahman et al. 2014*)
		F42A8.2	II/ 9352704-9350622	*sdhb-1*	Orthologous to human succinate dehydrogenase complex iron sulfur subunit B (Huang and Lemire 2009).	√									(*Rahman et al. 2014*)
		F54H12.1	III/ 4O01 (Ahringer RNAi library)	*aco-2*	Orthologous to human aconitase 2.	√									(*Rahman et al. 2014*)
		F46E10.10	V/ 6519122-6517870	*mdh-2*	Orthologous to human malate dehydrogenase.	√									(*Rahman et al. 2014*)
	Other														

		F22D6.6	I/ 7103551-7106405	*ekl-1*	A putative small RNA regulator. EKL-1 is a tudor domain containing protein (Rocheleau et al. 2008).	√		√			√		√		Anaphase bridges, nuclear appearance variant (Claycomb *et al.* 2009).
		F20D12.1	IV/ 7957569-7961652	*csr-1*	An Argonaute protein. CSR-1 functions by cleaving siRNA-paired mRNA (Yigit et al. 2006; Wedeles et al. 2013).			√	√		√				Anaphase bridges, nuclear appearance variant (Claycomb *et al.* 2009).
		F41E6.4	V/ 8610391-8617668	*smk-1*	An ortholog of human subunits of the PP4 protein phosphatase (Wolff et al. 2006).				√						
		R119.4	I/ 381907-378885	*pqn-59*	Orthologous to human ubiquitin associated proteins UBAP and UBAPL.		√				√				

		B0365.3	V/ 13132588-13128998	*eat-6*	A sodium/potassium ATPase, orthologous to human ATP1A1 and ATP1A3 (Davis et al. 1995).			√							
		K04F10.4	I/ 6350293-6356537	*bli-4*	An endoprotease, belongs to the kex2/subtilisin-like proprotein convertase family that processes proproteins for secretion (Thacker et al. 1995).						√				
		Y37D8A.10	III/ 12874853-12875591	*spcs-2*	An ortholog of human SPCS2, a signal peptidase complex subunit.			√	√						Nuclear appearance variant (Green *et al.* 2011).
		ZC101.2	II/ 14666829-14652045	*unc-52*	Orthologous to the human HSPG2 perlecan, a basement membrane heparan sulfate proteoglycan. Part of the worm extracellular matrix (Rogalski et al. 1995).		√				√				
		C17G10.2	II/ 5594703-5596305	*ttc-4*	An ortholog of human TTC4, a tetratricopeptide repeat domain containing protein of unknown function.			√							

		F37C12.14	III/ 7185524-7184960		Unknown function.	√		√							
		T28D6.6	III/ 11342937-11326482		Orthologous to human DRG1 (developmentally regulated GTP binding protein 1).			√	√		√				
		Y18D10A.20	I/ 12930051-12931584	*pfn-1*	A profilin, an actin associated protein (Severson *et al.* 2002; Velarde *et al.* 2007).			√							

[1] These RNAi clones are in the pL4440-DEST vector.
[2] Protein function is based on WormBase and the indicated references (attached below), if available.
[3] Ortholog designations are based on (Shaye and Greenwald 2011; Kim *et al.* 2018).
[4] References originating from this screen are italicized.

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