TABLE 3: 133 genes on chromosome III associated with DIC phenotyp

A. Meiotic divisions and early post-fertilization events

A1. Progress through meiotic divisions (11 genes)			
Male and female pronuclei do not become visible; embryos seem arrested during meiotic divisions.			
Gene	**Brief identification**	**P.**	**Main comments**
C02F5.9	proteasome component C5	EL	
C23G10.4	19S proteasome regulatory particle subunit	EL	rare embryos do not arrest
C30C11.2	26S proteasome regulatory subunit S3	EL	some embryos progress to one cell stage, where there is a block during
F23F12.6	26S proteasome regulatory complex subunit p48A	EL	
F25B5.4	polyubiquitin (*ubq-1*)	EL	
F35G12.9	RING-finger containing protein (APC11-like)	EL	some embryos progress to one cell stage, where there is a block during
F54C8.3	APC4 homologue (*emb-30*) *	EL	
F57B9.10	26S proteasome regulatory complex subunit p42B	EL	
K06H7.5	APC subunit 2	EL	K06H7.5 and K06H7.6 probably constitute a single open reading frame.
T05G5.3	Cdk1/Cdc2 kinase (*ncc-1*) *	EL	
ZK1010.1	ubiquitin (*ubq*-2)	EL	

A2. Fidelity of meiotic divisions (27 genes)			
Multiple female pronuclei; irregular cytoplasm; aberrant pseudoclevage stage; spindle unstable during anaphase; karyomeres in AB/ P1; AB/P1 nuclei off-center; often semi-sterile.			
B0336.10	60S ribosomal protein L17A	EL	semi-sterile
B0393.1	40S ribosomal protein SA	EL	semi-sterile; partial eos; somewhat slow
B0412.4	40S ribosomal protein S29	EL	semi-sterile; partial eos; only partial EL
B0464.1	aspartyl-tRNA synthetase	EL	semi-sterile; muliple pronuclei were not observed; somewhat slow
C14B9.7	ribosomal protein L21	EL	
C16A3.9	40S ribosomal protein S13	EL	
C23G10.3	ribosomal protein S3	EL	low penetrance multiple pronuclei
C27D11.1	translation initiation factor 3 subunit 10 (*egl-45*)	EL	semi-sterile; partial eos
C54C6.1	60S ribosomal protein L37	EL	
F13B10.2	60S ribosomal protein L3	EL	semi-sterile
F26F4.10	arginyl tRNA synthetase	EL	semi-sterile
F37C12.4	ribosomal protein YL39	EL	
F37C12.9	ribosomal protein S14	EL	semi-sterile
F37C12.11	ribosomal protein S21	EL	
F53A3.3	40S ribosomal protein	EL	semi-sterile; somewhat slow
F54E7.2	ribosomal protein S12	EL	semi-sterile; partial eos
F56F3.5	ribosomal protein S3a	EL	semi-sterile; partial eos; somewhat slow
F57B9.3	eukaryotic initiation factor 4A	EL	semi-sterile; somewhat slow
H06I04.4	ubiquitin-like ribosomal protein S27A fusion	EL	semi-sterile
R08D7.3	translation initiation factor eIF3 p66 subunit	EL	somewhat slow
R13A5.8	ribosomal protein L9	EL	semi-sterile
R74.1	leucyl-tRNA synthetase	EL	lack of P1 rotation
R151.3	ribosomal protein ML16	EL	
T05G5.10	translation initiation factor eIF5A	EL	muliple pronuclei or karyomeres were not observed
T10F2.1	glycyl-tRNA synthetase	EL	muliple pronuclei were not observed
T20H4.3	prolyl-tRNA synthetase region	EL	semi-sterile; partial eos
ZK652.4	60S ribosomal protein L35	EL	semi-sterile

A3. Entry into interphase (2 genes)			
Delay before entering interphase; vigorous cytoplasmic and cortical movements; aberrant number and/or position of pronuclei; aberrant spindle position.			
F48E8.5	protein phosphatase 2A regulatory subunit	EL	pronuclei not visible
ZK520.4	cullin (*cul-2*) *	EL	

A4. Pseudocleavage stage (2 genes)			
Little/no cortical ruffing or pseudocleavage furrow.			
C34C12.3	serine/threonine protein phosphatase	WT	no/little transverse spindle oscillations during anaphase
Y49E10.19	homologies to anilin (actin-binding protein)	EL	aberrant polar body; multiple female pronuclei

B. Nuclear appearance

B1. Pronuclear/nuclear appearance (5 genes)			
Pronuclei and nuclei in daughter blastomeres are not/poorly visible; spindle is not/poorly visible; often failure in cytokinesis			
C29E4.3	Ran-GAP1	EL	
C38D4.3	weak homologies to calpastatin	EL	
F59A2.1	Ran-binding protein 2 (NUP 358)	EL	
K01G5.4	Ran	EL	embryos often small
ZK328.5	NUP 98 (nucleoporin)	EL	

B2. Nuclear appearance (5 genes)			
Nuclei in daughter blastomeres are not/poorly visible (but pronuclei appear normal).			
C29E4.2	no clear homologies	EL	P1 division late
F34D10.2	strong homologies to CDC45	EL	P1 division late
R10E4.4	DNA replication licensing factor MCM5	EL	
Y55B1BR.3	contains chromo domain	EL	
ZK632.1	DNA replication licensing factor MCM6	EL	

C. Cell division processes in the early embryo

C1. Pronuclear migration (6 genes)			
Lack of male pronuclear migration; female pronuclear migration variable; sometimes multiple female pronuclei; no/small spindle (see comments).			
C05D11.3	putative ATP binding protein	EL	no spindle in most embryos
C28H8.12	dynamitin (p50) (*dnc-2*) *	EL	small spindle
C36E8.5	β-tubulin	EL	female pronucleus close to male pronucleus; no spindle
K01G5.7	β-tubulin	EL	female pronucleus close to male pronucleus; no spindle
T03F6.5	LIS-1 homologue	EL	no spindle
T26A5.9	dynein 8kd light chain	EL	small spindle

C2. Spindle assembly (2 genes)			
Spindle is either very small or no bipolar spindle is observed; karyomeres are generated			
F58A4.8	γ-tubulin	EL	
H04J21.3	no clear homologies	EL	most embryos not affected in one cell stage, but spindle assembly fails in AB or P1

C3. Fidelity of mitotic divisions (cross-eye phenotype) (3 genes)			
Daughter nuclei stay close to the central cortex; usually karyomeres in daughter blastomeres.			
C02F5.1	homologies to coiled coil containing proteins	EL	
F35G12.8	SMC-1 condensin	EL	
F58A4.3	histone H3-like protein (homology to CENP-A)	EL	

C4. Fidelity of mitotic divisions (karyomeres only) (3 genes)			
More than one nucleus (karyomeres) in daughter blastomeres AB and/or P1.			
F54C8.2	histone H3-like protein (homology to CENP-A)	EL	
R107.6	homologous to *Drosophila orbit*	EL	spindle is attenuated and bends during anaphase
Y43F4B.6	kinesin (KIF4-like)	EL	

C5. Anaphase spindle positioning (symmetric division) (4 genes)			
No posterior spindle displacement during anaphase; symmetric first division.			
C38C10.4	no clear homologies outside *C. elegans*	EL	fairly synchronous AB and P1 divisions; no P1 rotation; paralog of F22B7.13 (cross-RNAi?)
F22B7.13	no clear homologies outside *C. elegans*	EL	fairly synchronous AB and P1 divisions; no P1 rotation; paralog of C38C10.4 (cross-RNAi?)
F54E7.3	PDZ containing protein PAR-3 (*par-3*) *	EL	AB and P1 divide synchronously; rotation in AB as well
F58B6.3	RING-finger containing protein PAR-2 (*par-2*) *	ND	AB and P1 divide synchronously; no P1 rotation

C6. Cytokinesis (5 genes)			
Cleavage furrow not visible or regresses (see comments)			
B0464.5	serine/threonine kinase; similar to *S. pombe* DSK-	EL	sometimes no visible cleavage furrow
C56G7.1	nonmuscle myosin regulatory light chain (*mlc-4*)	EL	aberrant pseudocleavage stage; no cytokinesis
F11H8.4	formin homology protein (*cyk-1*) *	EL	cleavage furrow regresses
K08E3.6	Rho family GTPase activating protein (*cyk-4*) *	EL	cleavage furrow regresses
T25C8.2	actin (*act-5*)	EL	semi-sterile; aberrant pseudocleavage stage; no cytokinesis

C7. P1 rotation (2 genes)			
No rotation of centrosome/nuclear complex in P1.			
F55H2.3	*let-99* homologue	EL	jerky centration/rotation; paralog of *let-99* (K08E7.3) (cross-RNAi?)
Y39E4B.1	RNAse L inhibitor	EL	some embryos small

D. Pace of development

D1. General pace of development (overall slow) (12 genes)			
Slow overall pace of development (over 30 min between pronuclear migration and AB division -compared to 18-22 min in wt).			
C29E4.8	adenylate kinase	EL	irregular cytoplasmic appearance; incomplete centration
C34E10.6	ATP synthase β chain	EL	
F23H11.5	no clear homologies	LA	
F35G12.2	isocitrate dehydrogenase	AD	partially penetrant DIC phenotype; F1 sterile
F35G12.10	ATP synthase B chain	EL	occasional multiple female pronuclei
F54H12.1	aconitate hydratase	EL	
F56D2.1	mitochondrial processing protease enhancing	EL	
K04G7.4	NADH dehydrogenase	LA	
T07C4.7	succinate dehydrogenase cytochrome b chain	EL	
T20G5.2	citrate synthase	EL	
T27E9.1	ADP/ATP mitochondrial carrier protein	EL	
ZK637.8	vacuolar H+-ATPase (TJ6/proton pump) (*unc-32*)	EL	

D2. Pace of development (8 genes)			
Slow between pseudocleavage stage and pronuclear envelope breakdown; P1 division delayed with respect to that of AB.			
C03C10.3	ribonucleotide reductase small subunit	EL	nuclei in daughter blastomeres not/poorly visible
F31E3.3	replication factor C complex protein	EL	no P1 rotation
F44B9.7	replication factor C subunit 3	EL	no P1 rotation
F58A4.4	DNA primase 49Kd subunit	EL	no P1 rotation
R01H10.1	DNA polymerase alpha/primase complex chain B	EL	
T23G5.1	ribonucleotide-disphosphate reductase large chain	EL	nuclei in daughter blastomeres not/poorly visible
T24C4.5	DNA primase subunit	EL	possibly no P1 rotation
Y47D3A.29	DNA polymerase alpha-subunit	EL	possibly no P1 rotation; this gene is no longer present in ACeDB

E. Embryo appearance and morphology

E1. Osmotic integrity and other processes (16 genes)			
Embyros loose structural integrity upon dissection ; limited phenotypic analysis done in utero.			
B0336.2	ADP ribosylation factor 1 (*arf-1*)	EL	slow
B0361.10	glycosyl transferase group 1 protein	EL	mixture of eos and wt-looking embryos
C07H6.5	RNA helicase (DEAD-box protein family)	EL	
C36A4.4	UDP-N-acetylglucosamin	EL	slow; multinucleate cells
D2045.1	no clear homologies	EL	possible cytokinesis defects
F08F8.2	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	EL	
F55H2.2	probable vacuolar ATP synthase subunit D	EL	extremely slow
K10D2.6	NADPH-cytochrome P450	EL	extremely slow
K12H4.4	signal peptidase subunit	EL	
PAR2.4	has regions of homologies to uncharacterized proteins in other metazoans	EL	slow; possible cytokinesis defects; partial EL
T05G5.7	no clear homologies outside *C. elegans*	EL	slow; possible cytokinesis defects
T12A2.2	oligosaccharyl transferase STT3 subunit	EL	slow; karyomeres
ZK328.1	ubiquitin carboxyl-terminal hydrolase	EL	slow; possible cytokinesis defects

ZK512.5	homologies to uncharacterized Drosophila and human predicted proteins	EL	
ZK686.3	homologies to oligosaccharyl transferase 34 kd	EL	possible cytokinesis defects
Y76A2B.1	coronin-like protein (*pod-1*) *	EL	

E2. Cytoplasmic appearance (sparse yolk granules) (4 genes)			
Density of yolk granules throughout embryo is markedly reduced.			
C45G9.5	no clear homologies	LA	
T20G5.1	clathrin heavy chain	EL	jerky centration/rotation
ZK1098.5	putative secretory protein (Bet3p-like)	AD	partial eos; Dumpy adults
Y37D8A.10	homologies to signal peptidase complex 25 kDa	EL	partial eos; pronucleai/nuclei slightly small

E3. Cytoplasmic appearance (irregular) (3 genes)			
Uneven or irregular distribution of yolk granules.			
C03C10.1	casein kinase I	EL	cytoplasm is irregular and seems to contain vacuole-like structures
T20B12.1	homologies to O-linked GlcNAc transferase	EL	uneven distribution
Y49E10.15	small nuclear ribonucleoprotein E (snRNP E)	EL	areas lacking yolk granules; centration/rotation sometimes incomplete; blastomeres poorly separated

F. Unique phenotypes (13 genes)

Phenotypes associated with single genes: see specifics for each gene		
C07G2.3	T-complex protein 1, epsilon subunit (*cct-5*) *semi-sterile; complex phenotype; partial eos; areas lacking yolk granules; failure in microtubule-based processes*	EL
C14B9.4	polo-like kinase (*plk-1*) * *in most embryos: partial eos, no progress to two cell stage; in other embryos: spindle assembly and cytokinesis defects; contains exons from C14B9.4 and neighbouring K06H7.1*	EL
C18D11.5	homologies with transcription factors *additional anterior furrow during pseudocleavage; spindle drifts in some*	EL
F01F1.8	T-complex protein 1, zeta subunit (*cct-6*) *semi-sterile; complex phenotype; partial eos; areas lacking yolk granules; failure in microtubule-based processes*	EL
F10E9.8	no clear homologies *failure of spindle assembly at 2 cell stage, often in only one daughter blastomere*	EL
H38K22.2	regions of homologies to uncharacterized proteins in other eukaryotes *complex phenotype; multiple pronuclei, centration/rotation and spindle positioning*	EL
K11D9.1	kinesin CeMCAK (KIF2/XKCM1-like) *spindle snaps in two during anaphase; abnormally large polar body*	EL
R151.9	homologies to c-myc binding protein MM-1 *no centration/rotation; spindle sets up vertically in posterior of embryo*	EL
T04A8.7	1,4-alpha-glucan branching enzyme *very mobile cortical area and unusual cell shape in Aba*	WT
Y79H2A.11	doublecortin-related kinase *anaphase spindle moves too much to posterior; Y79H2A.11 and Y75B8A.36 probably constitute the same open reading frame*	WT
Y41C4A.10	Elongin B (regulator of RNA polymerase II) *P1 division late (but not slow in first cell stage)*	EL
Y49E10.1	26S proteasome regulatory subunit 8 *delay between breakdown of pronuclei and end of anaphase; excess cortical movements following cell division*	EL
Y56A3A.20	CCR4-associated factor 1 *complex phenotype; small embryos; irregular ctyoplasm; slow; centration/rotation and cytokinesis defects*	EL