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Supplementary Materials for

In Vivo Identification of Regulators of Cell Invasion Across Basement Membranes

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This PDF file includes:

Table S3. RNAi depletion of 99 genes results in an AC invasion defect.
Table S4. Timing and degree of AC invasion into the vulval epithelium: mutant analysis and off-target RNAi controls.
Table S5. Timing and degree of AC invasion into the vulval epithelium: uterine-specific RNAi.
Table S6. Extrachromosomal array and integrated strain generation.
Table S7. Primer sequences and templates used for PCR fusions and restriction enzyme cloning.

Other Supplementary Material for this manuscript includes the following:
(available at www.sciencesignaling.org/cgi/content/full/3/120/ra35/DC1)

Table S1. 539 Pvl and Egl genes targeted by RNAi for AC invasion defects (Excel file).

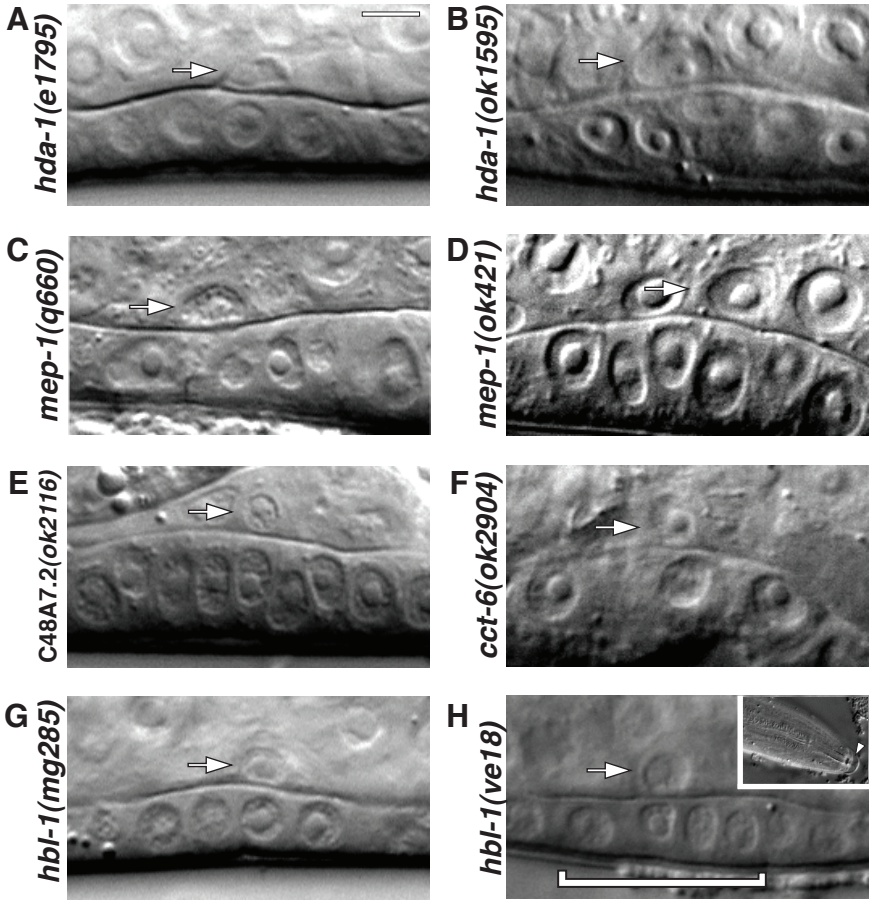

Figure S1. Putative null alleles of *mep-1, hda-1, cct-6,* C48A7.2, and *hbl-1* show AC invasion defects. Anterior is left, ventral is down; white arrows point to the AC, and scale bar represents 5µm in this and all other supplementary figures. (**A** to **H**) With the exception of *cct-6(ok2904)* (F), at the P6.p 4-cell stage of 1˚ VPC division in putative null alleles, ACs failed to breach the BM as evidenced by an unbroken phase-dense line underneath the AC. (**F**) In *cct-6(ok2904)* animals, most homozygous worms (n=32) die before reaching the time of AC invasion (table S4), although one animal survived, and showed an AC invasion defect at the P6.p 8-cell stage of 1° VPC division. (**G** and **H**) *hbl-1* alleles show precocious VPC division and AC invasion defects. (**H**) At the time of the L2/L3 molt, as evidenced by the loosening of pharyngeal cuticle at the anterior (white arrowhead; inset) the P6.p VPC (white bar) has undergone two precocious rounds of division, but the AC has not invaded. This phenocopies *hbl-1* RNAi depletion (fig. S5B). See Table S4 for scoring data for these and other mutant alleles.

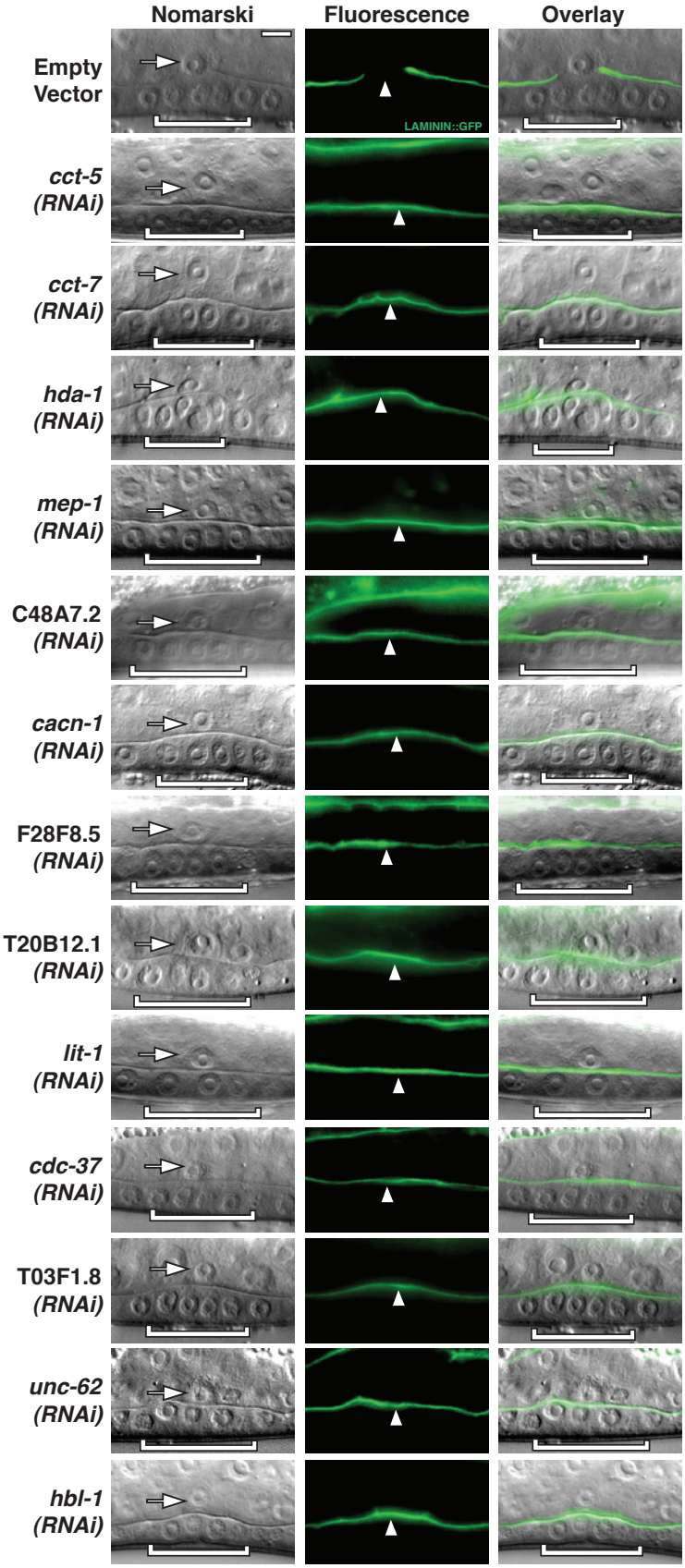

Figure S2. LAM-1::GFP (laminin) is intact following RNAi targeting the *cct* complex and 11 other pro-invasive genes at the P6.p 4-cell stage of VPC division. Anterior is left, ventral is down; brackets denote 1° VPCs, and white arrows point to the AC (Nomarski image, left; corresponding wide-field fluorescence, middle; overlay, right). In animals fed L4440 empty vector control RNAi, the BM is removed underneath the AC, as visualized by the absence of the phase-dense line in the Nomarski micrograph and the absence of LAM-1::GFP in the fluorescence micrograph (white arrowhead) underneath the AC. Following RNAi depletion of the *cct* complex and the remaining 11 genes identified here, whenever an AC invasion defect was observed, the BM underneath the AC was intact, as visualized by the presence of the phase-dense line underneath the AC and uninterrupted LAM-1::GFP expression (n > 10 animals scored for each RNAi target).

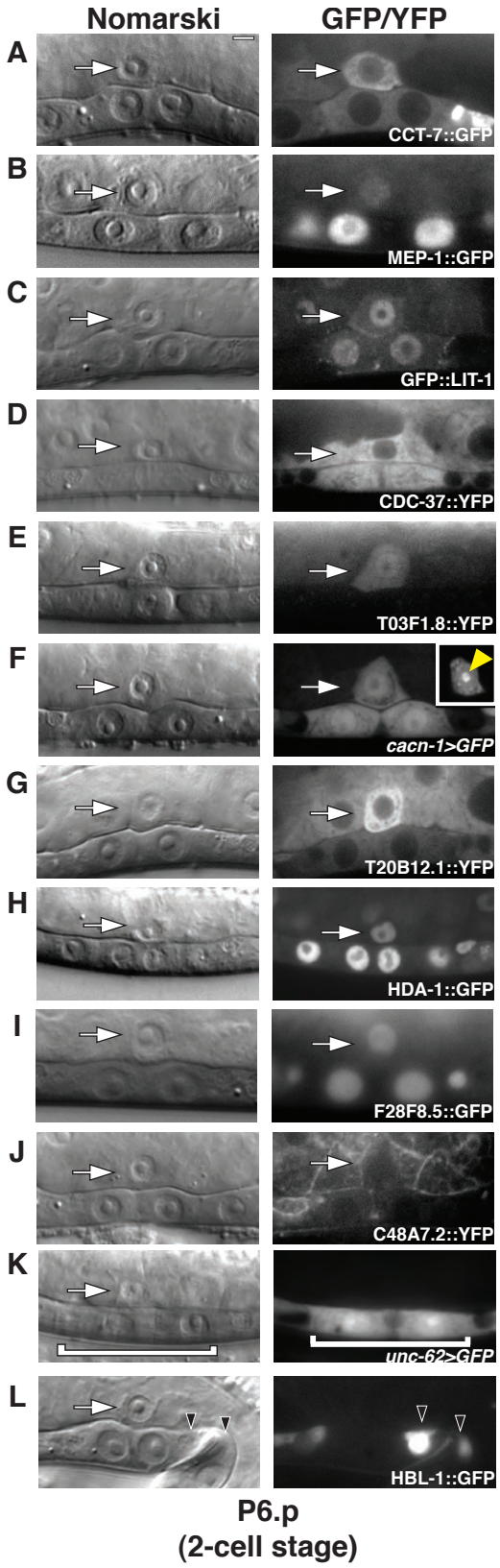

Figure S3. Transgene reporter localization of newly identified pro-invasive genes at the P6.p 2-cell stage of VPC division. Nomarksi, left; corresponding fluorescence, right. All images are confocal z-slices except (C) and (D), which are wide-field fluorescence images. (**A** to **J**) Translational (::) and transcriptional (>) reporter constructs for the *cct* complex [as shown by *cct-7::GFP* in (J)] and nine of the remaining 11 newly identified pro-invasive genes showed AC-enriched (arrow) GFP localization in a variety of subcellular compartments before and during AC invasion. (**I**) A transcriptional reporter for *cacn-1* (*cacn-1>GFP*) is up-regulated in the AC. A translational CACN-1::GFP fusion (*cdh-3>cacn-1::GFP*) is localized throughout the AC, and is enriched in the nucleolus (inset; yellow arrowhead). (**K**) A transcriptional reporter for *unc-62* (*unc-62>GFP*) shows expression in VPCs (white brackets). (**L**) A translational reporter for HBL-1 (*hbl-1::GFP*) is localized to the cell bodies of the ventral nerve cord (VNC) (black arrowheads). Although HBL-1::GFP is not found in the VPCs at the P6.p 2-cell stage of VPC division, it does show VPC localization hours earlier (fig. S5).

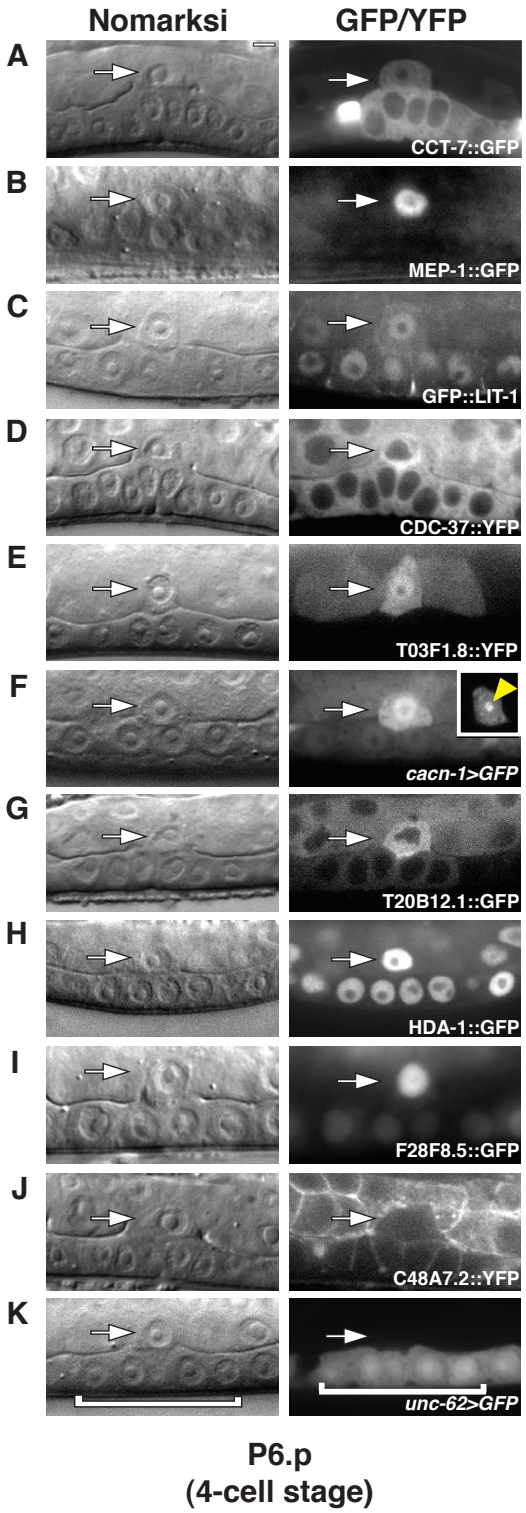

Figure S4. Transgene reporter localization of newly identified pro-invasive genes at the P6.p 4-cell stage of VPC division. Nomarksi, left; corresponding fluorescence, right. All images are confocal z-slices except (C) and (D), which are wide-field fluorescence images. (**A** to **J**) Translational (::) and transcriptional (>) reporter constructs for the *cct* complex [as shown by *cct-7::GFP* in (J)] and nine of the remaining 11 newly identified pro-invasive genes showed AC-enriched (arrow) GFP localization in a variety of subcellular compartments prior to and during AC invasion. (**I**) A transcriptional reporter for *cacn-1* (*cacn-1>GFP*), is up-regulated in the AC. A translational CACN-1::GFP fusion (*cdh-3>cacn-1::GFP*) is localized throughout the AC, and is enriched in the nucleolus (inset; yellow arrowhead). (**K**) A transcriptional reporter for *unc-62* (*unc-62>GFP*) shows VPC expression (white brackets).

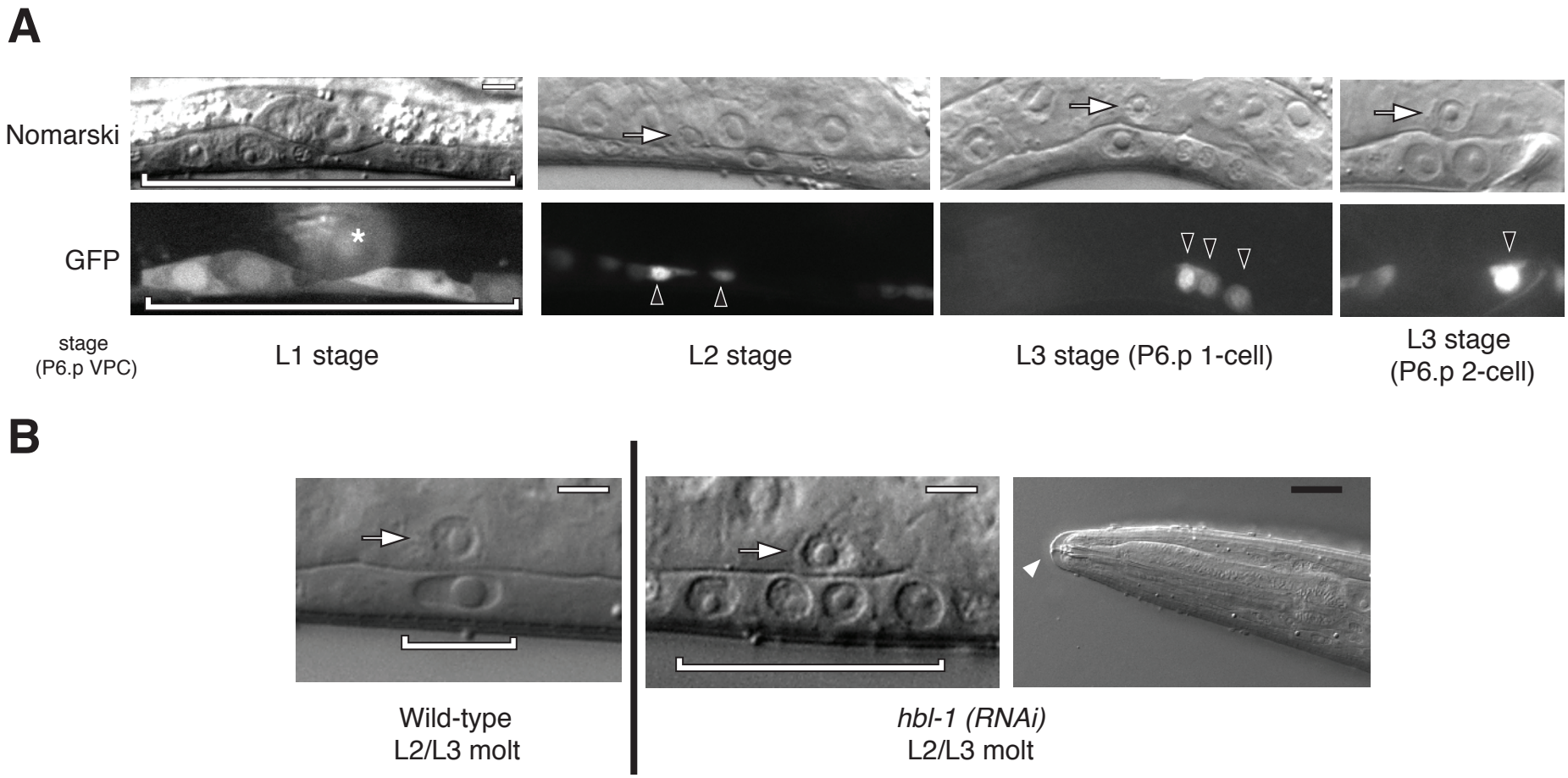

Figure S5. *hbl-1* functions in VPC specification to promote AC invasion. (**A**) Nomarski image (top) and corresponding confocal z-slice fluorescence image (bottom). At the L1 larval stage (left), HBL-1::GFP is localized to the Pn.p cells (white bar) along the ventral surface. Asterisk denotes weak out of focus expression in coelomocytes. During the L2 stage (second panel), HBL-1::GFP is only found in the cell bodies of the ventral nerve cord (VNC; black arrowheads). This VNC expression persists throughout the time of AC invasion during the L3 stage (third and fourth panels). (**B**) *hbl-1(RNAi)* treatment results in precocious vulval precursor cell (VPC) division. At the time of the L2/L3 molt, approximately six hours before AC invasion, the P6.p VPC (white bars) has not undergone cell division in wild-type animals (left). In *hbl-1* RNAi depleted animals at the L2/L3 molt as evidenced by loosening of pharyngeal cuticle at the anterior (white arrowhead; right), P6.p has undergone two precocious rounds of division (middle; P6.p 4-cell stage), but the AC has not invaded. White scale bar represents 5 µm; black scale bar represents 50 µm.

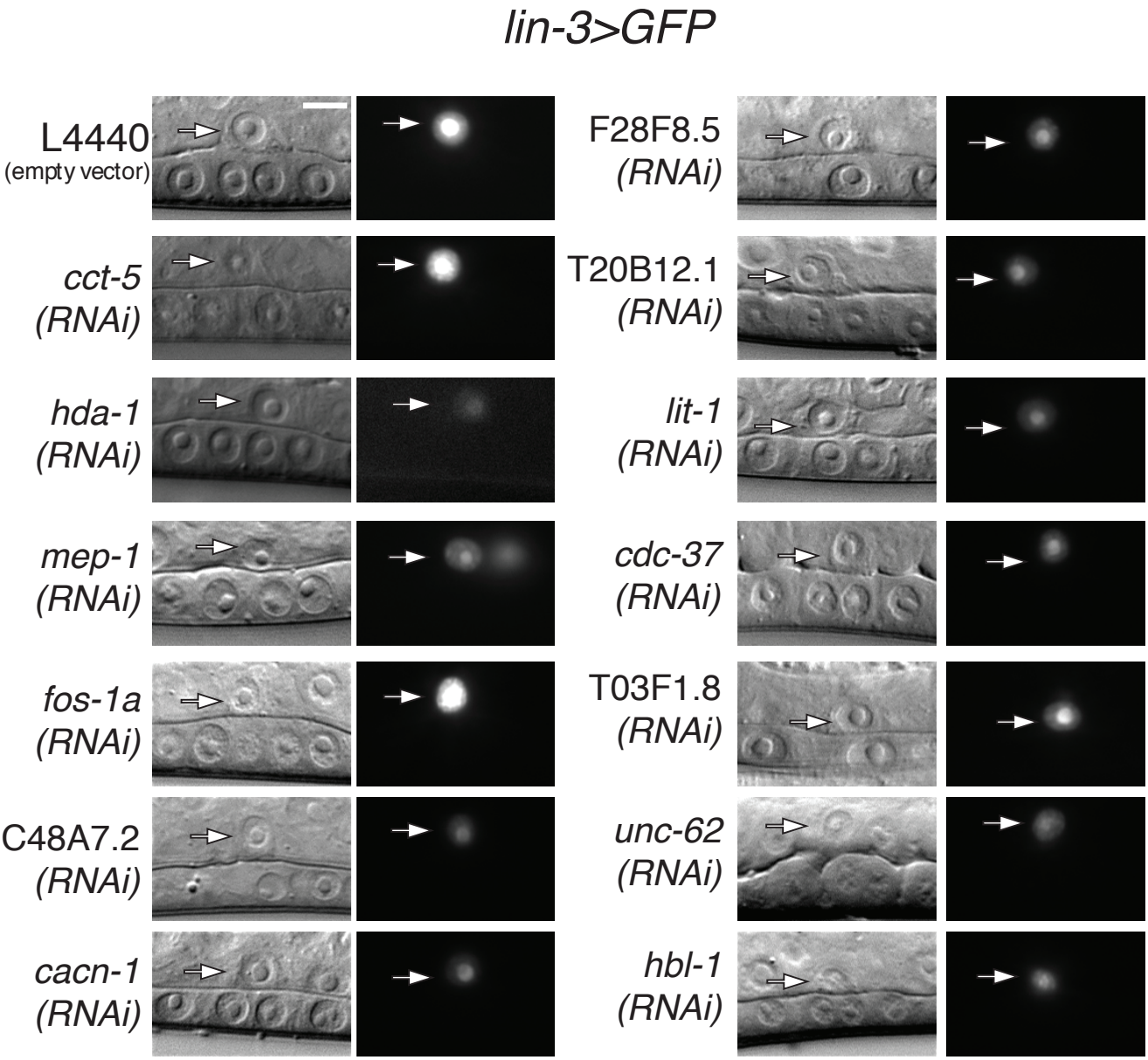

Figure S6. The AC is correctly specified, as shown by *lin-3>GFP*, following RNAi depletion of the newly identified regulators of AC invasion. White arrow, AC; Nomarski image, left; corresponding fluorescence image, right.

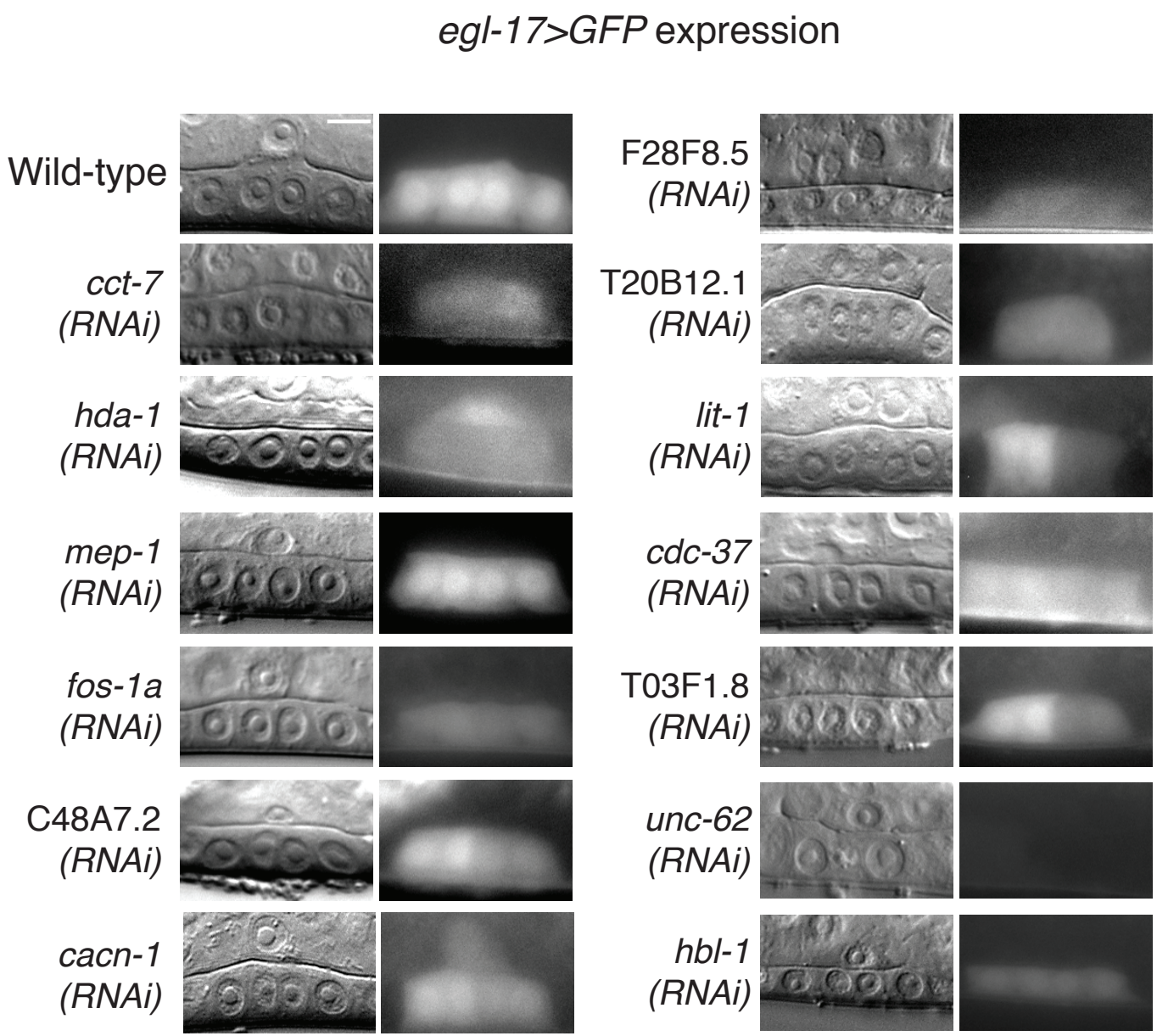

Figure S7. 1° VPC specification following RNAi depletion of newly identified AC invasion genes. Nomarski image, left; corresponding fluorescence image, right. *egl-17>GFP* is expressed in the 1° VPCs at the time of invasion following RNAi treatment in all cases except *unc-62(RNAi)*. *hbl-1(RNAi)*- treated animals show early expression of *egl-17>GFP* and precocious specification of VPCs (fig. S5).

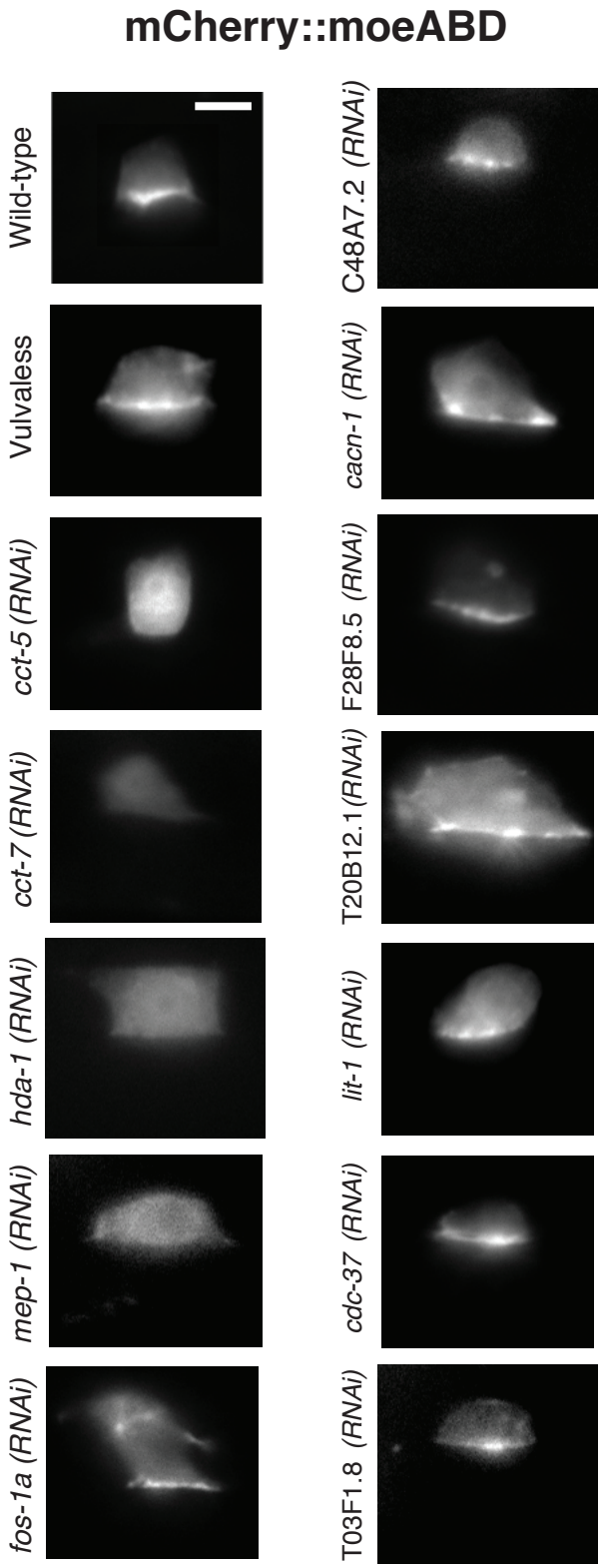

Figure S8. Identification of regulators of invasive membrane formation. The top left micrograph shows invasion of wild-type ACs, whereas all other wide-field fluorescence images are of ACs that failed to invade. An F-actin probe (mCherry::moeABD) was utilized as a marker of the invasive membrane following RNAi directed against the newly identified AC invasion regulators. In both wild-type (during normal invasion) and in Vulvaless (Vul) *(lin-3(n1059)/lin-3(n378))* animals with AC (white arrow) invasion defects, F-actin was polarized to the invasive membrane of the AC. RNAi depletion of members of the *cct* complex (as shown by *cct-5* and *cct-7*), *hda-1*, and *mep-1* resulted in a complete loss of F-actin polarization at the invasive membrane. RNAi targeting the remaining eight genes did not affect F-actin polarization at the invasive membrane. See Fig. 3B for data quantification.

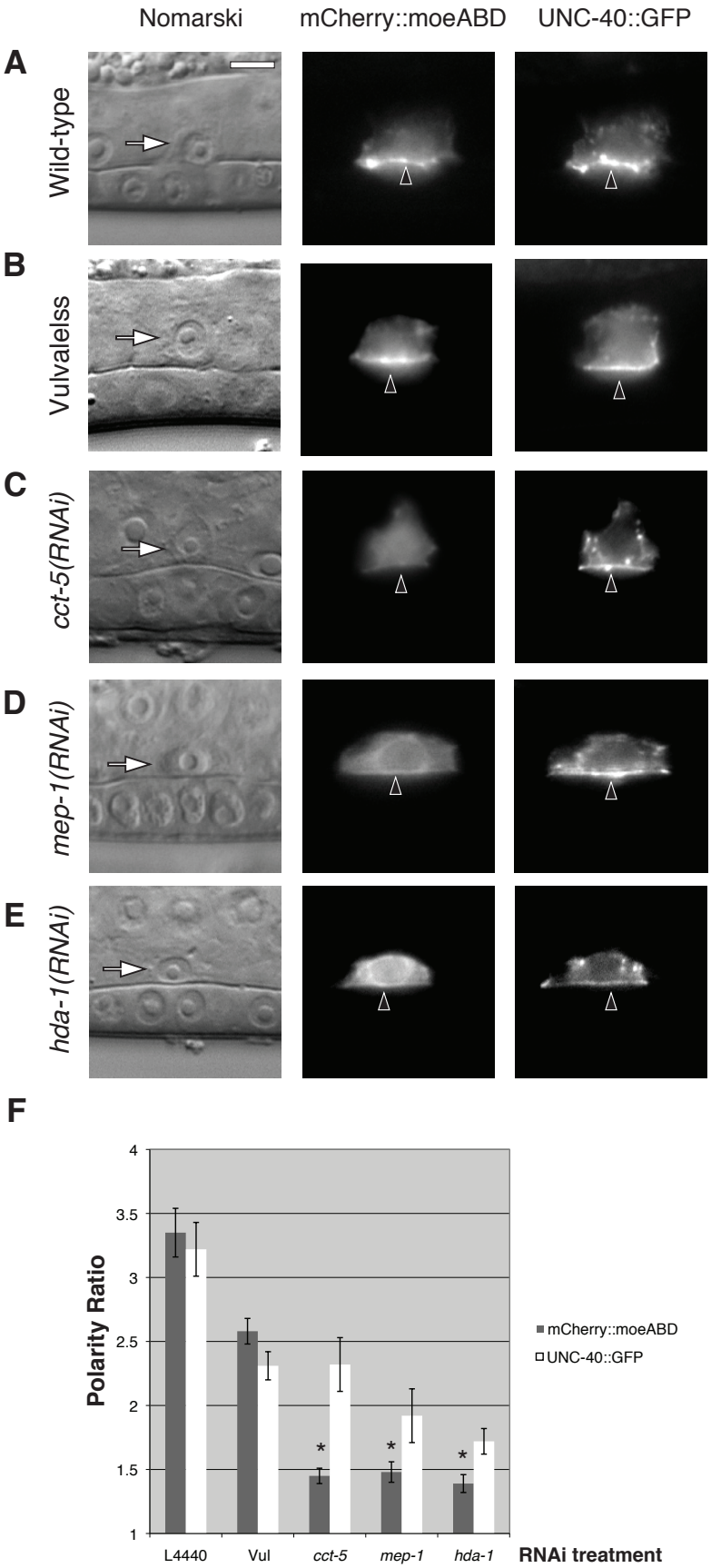

Figure S9. Regulators of invasive membrane formation function independently of netrin receptor localization. (**A** to **E**) Nomarski, left; corresponding confocal z-slice fluorescence; mCherry::moeABD, middle, and UNC-40::GFP, right. (**A** and **B**) in both wild-type, during (**A**) normal invasion and in (**B**) Vulvaless (Vul) (*lin-3(n1059)/lin-3(n378)*) animals with AC (white arrow) invasion defects, both an F-actin probe and UNC-40::GFP polarize to the invasive membrane (black arrowheads). (**C** to **E**) Although animals treated with RNAi directed against *cct-5, mep-1,* or *hda-1* show loss of F-actin at the invasive membrane (middle), UNC-40::GFP (right) is still polarized. (**F**) Quantification of F-actin and UNC-40::GFP polarity in wild-type and Vul controls as well as following RNAi depletions directed against *mep-1, hda-1*, and *cct-5*. *, $P < 0.05$ (Tukey's post hoc test; $n > 10$). Error bars report the SEM.

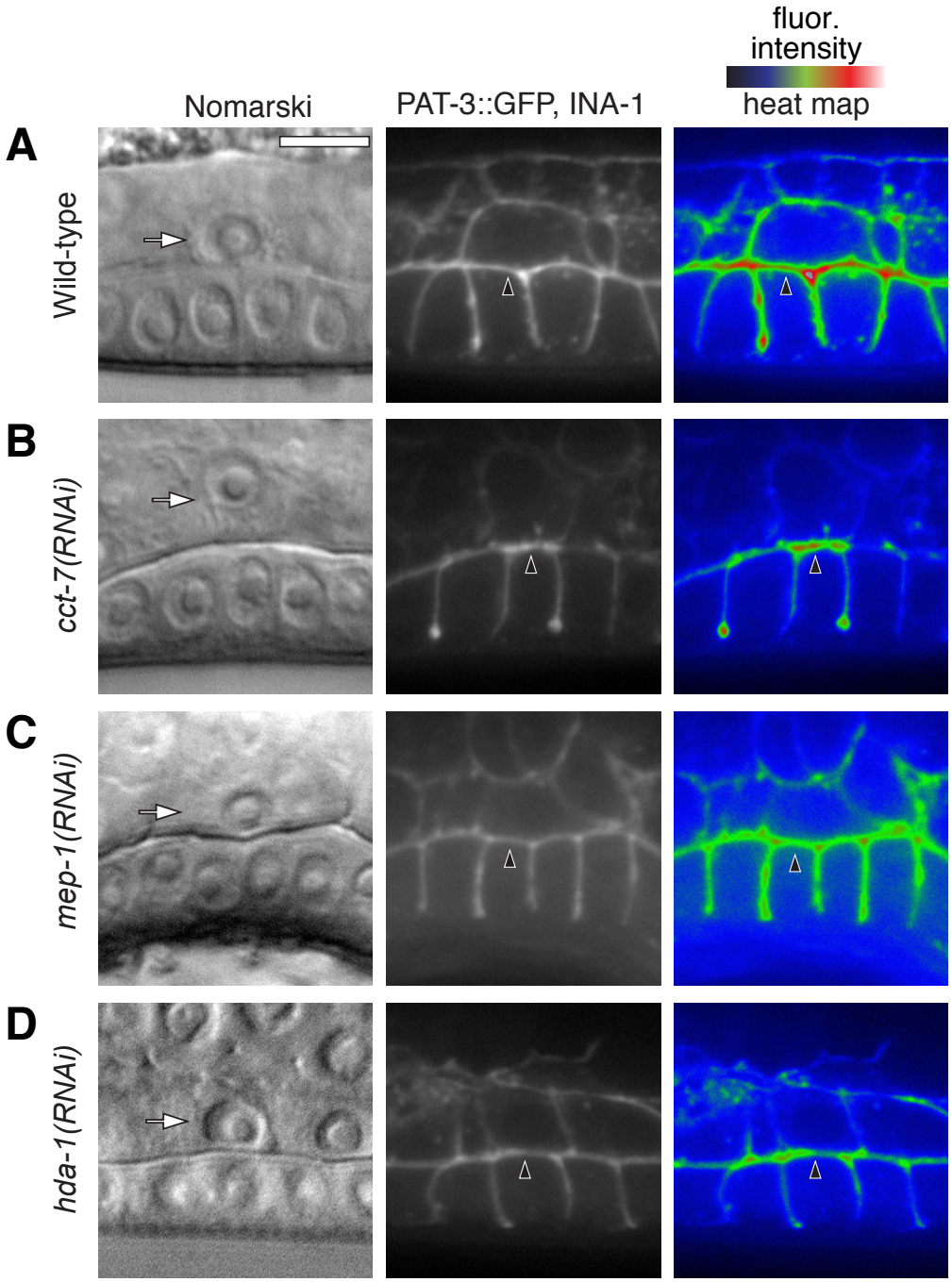

Figure S10. Regulators of invasive membrane formation function independently of integrin receptor localization. Nomarski, left; corresponding confocal z-slice fluorescence (PAT-3::GFP, INA-1; middle), and spectral representation of the fluorescence intensity, right. (**A** to **D**) In wild-type animals, during normal invasion and after RNAi depletion of *cct*, *mep-1*, and *hda-1*, the ß integrin subunit PAT-3::GFP shows AC (white arrow) surface localization and is concentrated at the invasive cell membrane (black arrowhead), when cotransformed with the α integrin subunit *ina-1*.

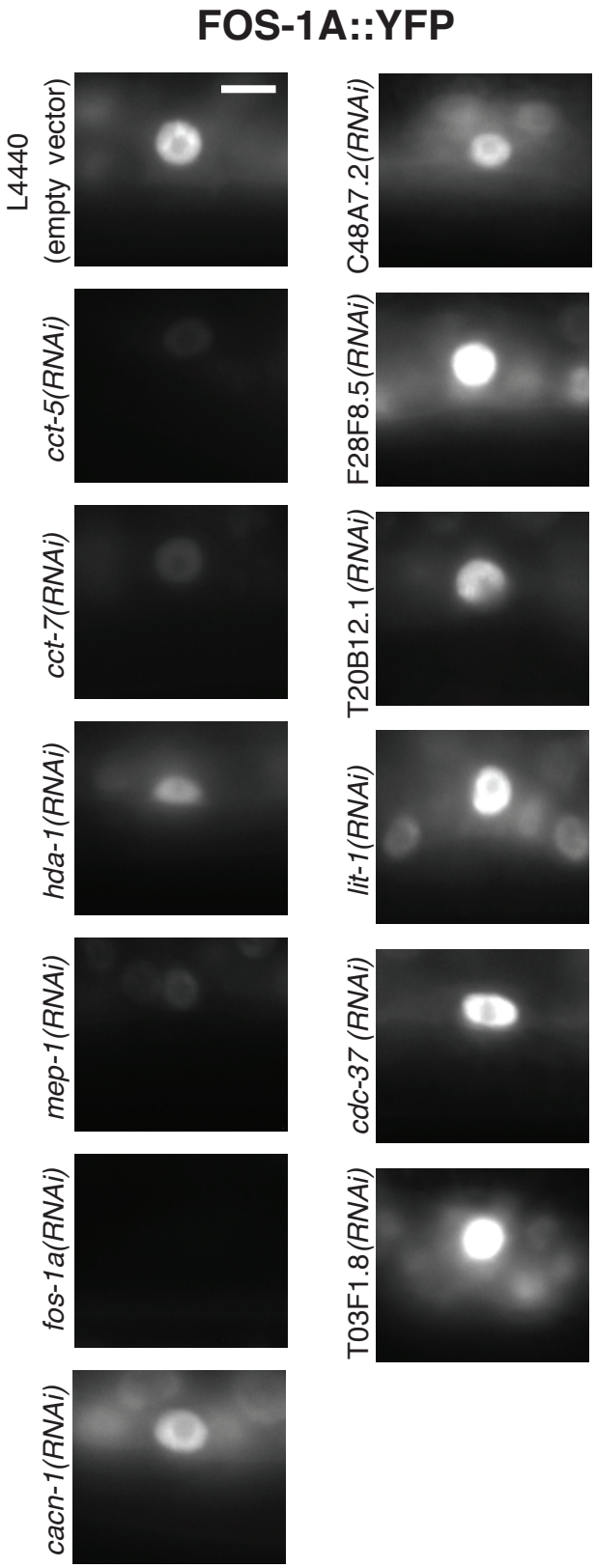

Figure S11. Identification of regulators of the *fos-1a* pathway. All wide-field fluorescence images except empty vector control (L4440) are of ACs that have failed to invade. A translational reporter, *fos-1a::YFP*, was utilized to determine whether any of the newly identified AC invasion regulators act upstream of FOS-1A during invasion. In wild-type animals, the *fos-1a* reporter (*fos-1a::YFP*) was up-regulated in the AC nucleus at the time of invasion. RNAi depeletion of the *cct* complex, *hda-1*, and *mep-1* down-regulated FOS-1A::YFP in the AC nucleus. *fos-1a(RNAi)* effectively knocked down FOS-1A::YFP. RNAi depletion of the remaining seven genes did not decrease FOS-1A::YFP abundance in the AC. See Fig. 3C for data quantification.

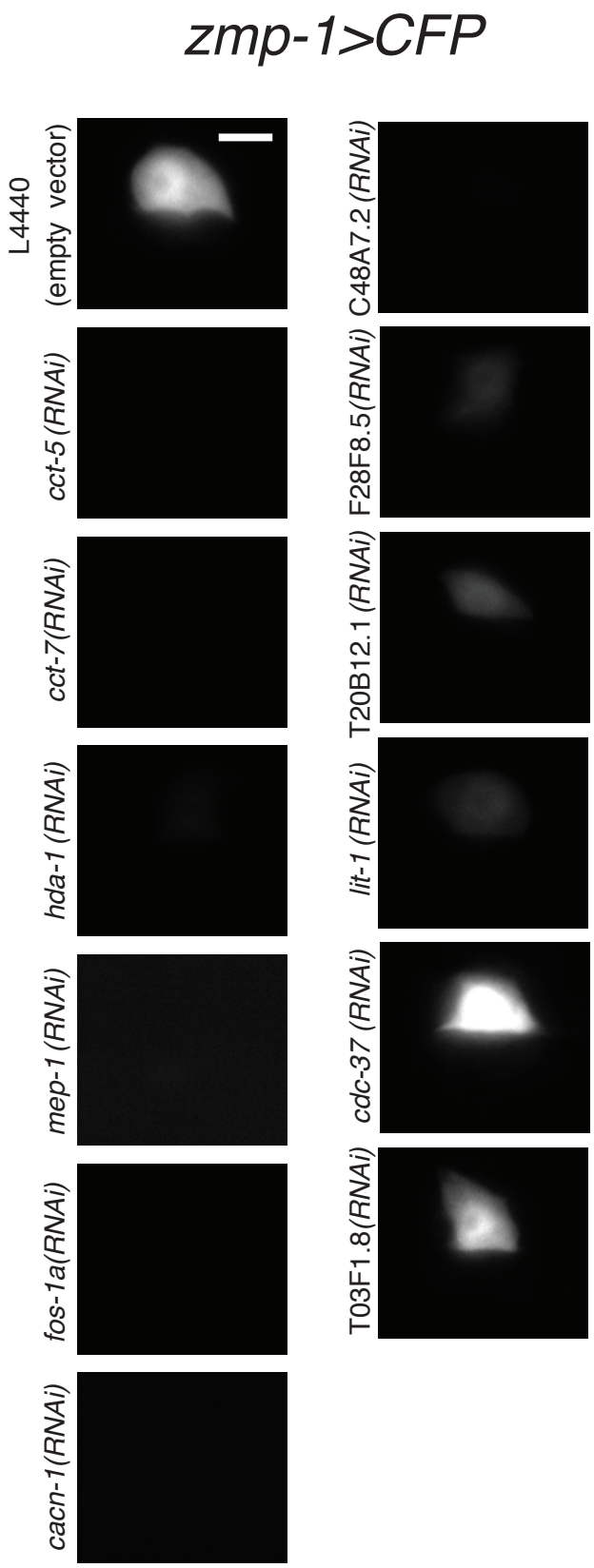

Figure S12. Identification of genes that act within or parallel to the *fos-1a* pathway. All wide-field fluorescence images except empty vector control (L4440) are of ACs that have failed to invade. A transcriptional reporter for a target of the *fos-1a* pathway, *zmp-1>CFP*, was utilized to determine if any of the newly identified AC invasion regulators act within or parallel to the *fos-1a* pathway. RNAi targeting 10/12 genes down-regulated *zmp-1>CFP* in the AC following a defect in AC invasion, while *cdc-37* and T03F1.8 RNAi treated animals did not show significant down-regulation of the *zmp-1>CFP* reporter as compared to empty vector (L4440) controls. See Fig. 3C for data quantification.

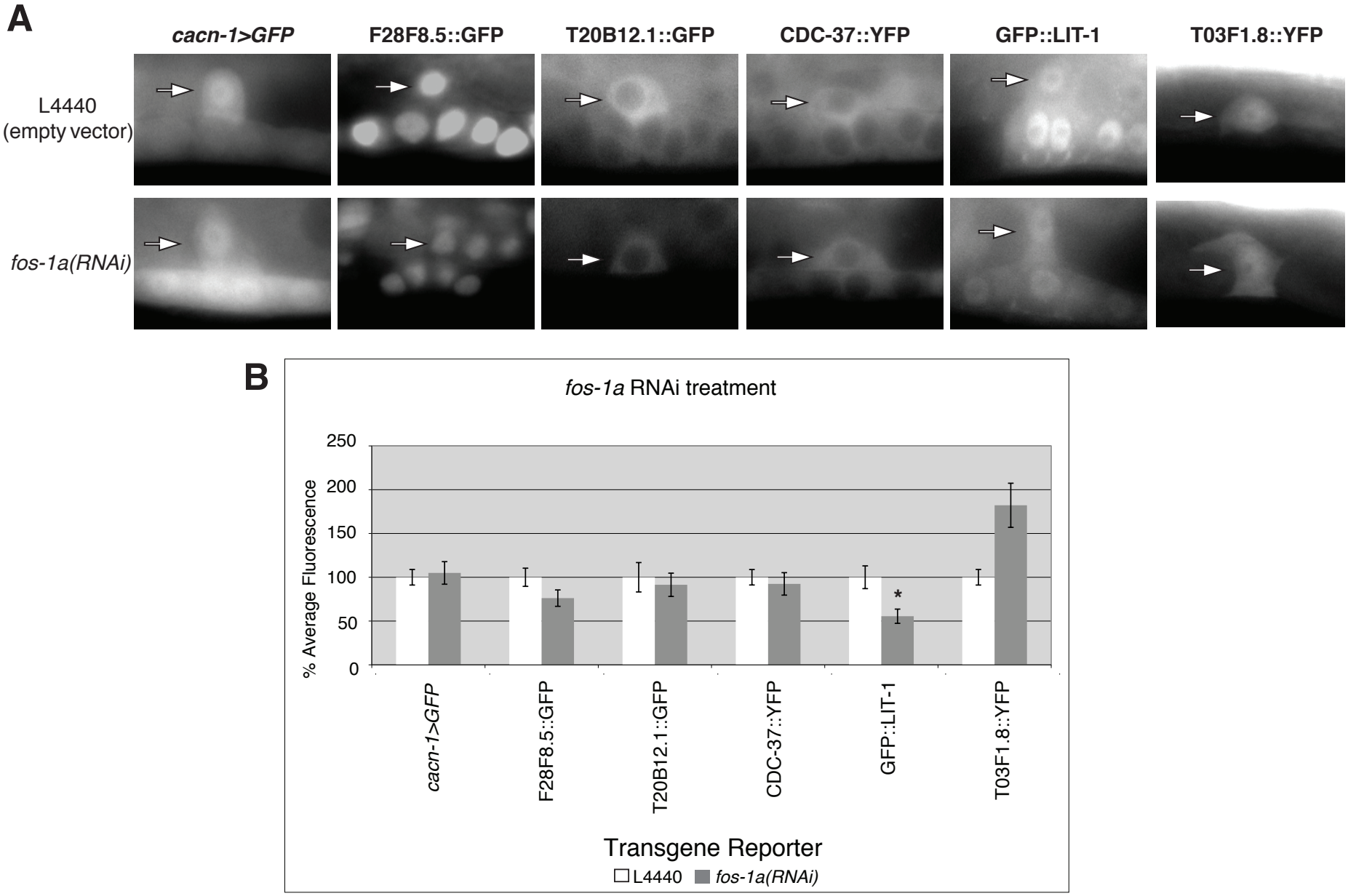

Figure S13. *fos-1a* RNAi depletion identifies *lit-1* as a new member of the *fos-1a* pathway. (**A**) Wide-field fluorescence image (top) of empty vector control (L4440) shows invasion and reporter expression in wild-type animals. Fluorescence image (bottom) shows corresponding expression following failed AC invasion. (**B**) Quantification of expression of six reporters in the AC of wild-type (L4440) and *fos-1a* RNAi depleted animals. *, $P = 0.01$ (Student's t-test; $n > 10$). Error bars report SEM.

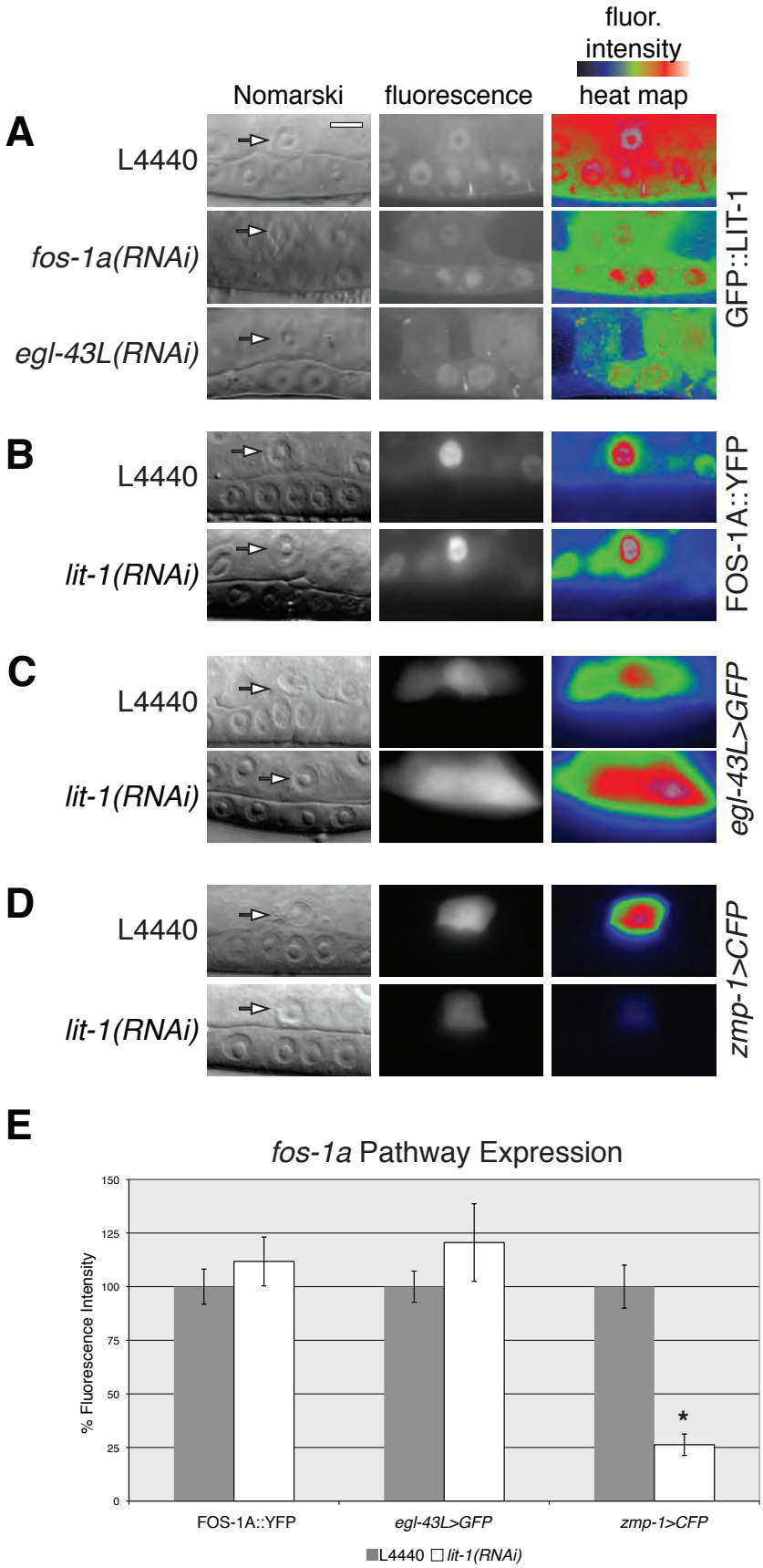

Figure S14. *lit-1* functions downstream of *fos-1a* and *egl-43L* during AC invasion. Nomarski, left; corresponding fluorescence, middle; and corresponding spectral representation of the fluorescence intensity, right. (**A**) Both *fos-1a* and *egl-43L* RNAi down-regulated the abundance of GFP::LIT-1 in the AC in animals with a failure in invasion. (**B** and **C**) *lit-1* RNAi depletion did not down-regulate FOS-1A::YFP (B) or *egl-43L>GFP* (C). (**D**) *lit-1* RNAi down-regulated *zmp-1>CFP* in the AC. (**E**) Quantification of FOS-1A::YFP, *egl-43L>GFP*, and *zmp-1>CFP* in wild-type (L4440) and *lit-1* RNAi depleted animals. * $P < 0.05$ (Tukey's post hoc test; $n > 10$). Error bars report the SEM.

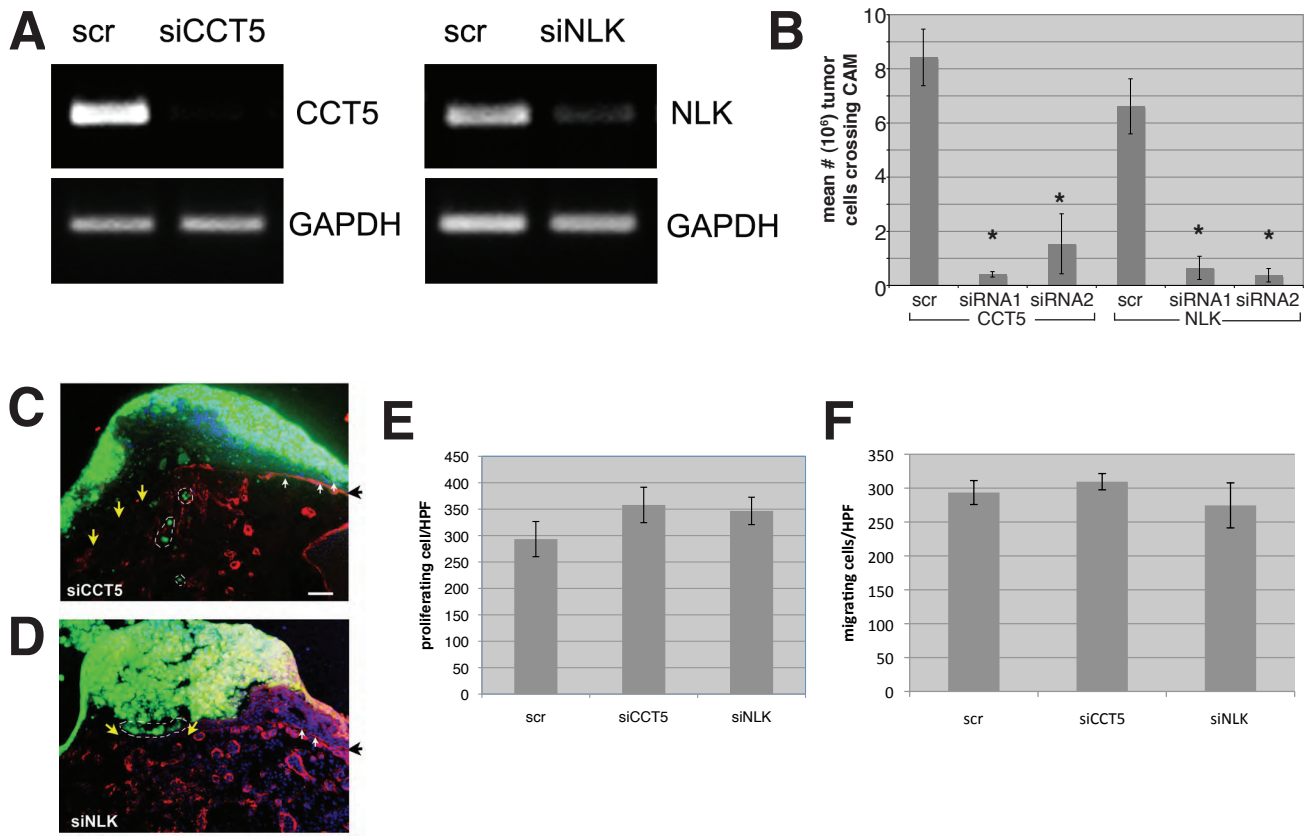

Figure S15. CCT5 and NLK siRNA-mediated knockdown specifically affect BM transmigration activity. (**A**) CCT5 and NLK expression in each of the MDA-MB-231 transfectants was examined by RT-PCR. (**B**) The BM-invasive activity of MDA-MB-231 cells transfected with either of two independent single siRNA oligonucleotides targeting CCT5 or NLK is inhibited significantly. Invasion is quantified as the number of tumor cells (10^6) that cross the CAM surface (mean Inv ± SEM of three or more experiments) following siRNA knockdown of CCT5 and NLK (*$P < 0.001$) compared to control (Scr) siRNA treatment, using a single factor ANOVA followed by Tukey's post hoc test for significance. (**C** and **D**) Following electroporation with siRNA directed against CCT5 (C) or NLK (D), small populations of MDA-MB-231 cells continue to express BM-invasive activity, likely as a consequence of incomplete target gene silencing or the stochastic activation of alternate invasion programs. In these instances, small numbers of invading cells (outlined with white dashed lines) breach the underlying BM (areas demarcated with yellow arrows). Areas of intact BM are marked with white arrows and the CAM surface is indicated by the black arrows to the right of each panel. Scale bar represents 100 µm. (**E**) Proliferation (ki67) and (**F**) migratory activity of MDA-MB-231 cells were unaffected by siRNA-dependent silencing of CCT5 ($P = 0.08$ (E); 0.20 (F)) or NLK ($P = 0.10$ (E); 0.27 (F)) (mean ± SEM of 3 experiments). Apoptosis (TUNEL) was less than 1 cell/hpf in scrambled-, CCT5-, or NLK-siRNA-treated cells.

Table S1. 539 Pvl and Egl genes targeted by RNAi for AC invasion defects. For each RNAi clone tested, the corresponding genetic sequence name, public name, and KOG descriptor from www.wormbase.org is given. The asterisk denotes that *cct-4* and *cct-8* were confirmed as hits following the initial RNAi screen.

Sequence Name (Gene)	Gene Public Name	KOG Info (merged)
B0025.2	csn-2	[KOG1464] COP9 signalosome, subunit CSN2
B0207.4	air-2	[KOG0580] Serine/threonine protein kinase
B0207.6	B0207.6	[KOG1533] Predicted GTPase
B0286.5	fkh-6	[KOG2294] Transcription factor of the Forkhead/HNF3 family
B0336.2	arf-1.2	[KOG0070] GTP-binding ADP-ribosylation factor Arf1
B0336.6	abi-1	[KOG2546] Abl interactor ABI-1, contains SH3 domain
B0379.4	scpl-1	[KOG1605] TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)
B0393.1	rps-0	[KOG0830] 40S ribosomal protein SA (P40)/Laminin receptor 1
B0464.5	spk-1	[KOG1290] Serine/threonine protein kinase
B0511.10	eif-3.E	[KOG2758] Translation initiation factor 3, subunit e (eIF-3e)
B0511.8	tag-264	[KOG4461] Mitochondrial 28S ribosomal protein S30
C01F1.3	C01F1.3	[KOG0747] Putative NAD+-dependent epimerases
C01G6.8	cam-1	
C01H6.5	nhr-23	[KOG4216] Steroid hormone nuclear receptor
C02B8.4	hlh-8	[KOG4447] Transcription factor TWIST
C02F5.1	knl-1	
C02F5.2	C02F5.2	[LSE0940] Unnamed protein
C02F5.9	pbs-6	[KOG0179] 20S proteasome, regulatory subunit beta type PSMB1/PRE7
C03C10.3	rnr-2	[KOG1567] Ribonucleotide reductase, beta subunit
C03D6.1	C03D6.1	[KOG1041] Translation initiation factor 2C (eIF-2C) and related proteins
C03D6.8	rpl-24.2	[KOG1723] 60s ribosomal protein L30 isolog
C04A2.3	egl-27	[KOG2133] Transcriptional corepressor Atrophin-1/DRPLA
C04F6.4	unc-78	[KOG0318] WD40 repeat stress protein/actin interacting protein
C04H5.6	mog-4	[KOG0923] mRNA splicing factor ATP-dependent RNA helicase
C05C8.2	C05C8.2	[KOG2874] rRNA processing protein
C05D11.3	tag-170	[KOG1672] ATP binding protein
C06A5.1	C06A5.1	[KOG4596] Uncharacterized conserved protein
C06A5.3	C06A5.3	[KOG1904] Transcription coactivator
C06E4.6	C06E4.6	[KOG0725] Reductases with broad range of substrate specificities
C06E7.1	C06E7.1	[KOG1506] S-adenosylmethionine synthetase
C06E7.3	C06E7.3	[KOG1506] S-adenosylmethionine synthetase
C06G1.4	ain-1	[LSE0932] Unnamed protein
C06G3.10	cogc-2	[KOG2307] Low density lipoprotein receptor
C07A9.2	C07A9.2	[KOG3404] G10 protein/predicted nuclear transcription regulator
C07G2.3	cct-5	[KOG0357] Chaperonin complex component, TCP-1 epsilon subunit (CCT5)
C07H6.5	cgh-1	[KOG0326] ATP-dependent RNA helicase
C07H6.7	lin-39	[KOG0489] Transcription factor zerknullt and related HOX domain proteins
C08B11.1	zyg-11	[KOG3665] ZYG-11-like serine/threonine protein kinases
C08B11.3	C08B11.3	[KOG2312] Predicted transcriptional regulator, contains ARID domain
C08B11.5	sap-49	[KOG0131] Splicing factor 3b, subunit 4
C08C3.1	egl-5	[KOG0489] Transcription factor zerknullt and related HOX domain proteins
C08F8.1	pfd-1	[KOG3501] Molecular chaperone Prefoldin, subunit 1
C08F8.8	nhr-67	[KOG3575] Hormone receptors
C08H9.2	C08H9.2	[KOG2208] Vigilin
C09F5.1	C09F5.1	[LSE0919] Unnamed protein
C09H10.2	rpl-41	[KOG3464] 60S ribosomal protein L44
C09H10.6	nasp-1	[KOG4563] Cell cycle-regulated histone H1-binding protein
C09H10.7	C09H10.7	
C09H10.8	glb-4	[KOG3378] Globins and related hemoproteins
C11H1.3	C11H1.3	[KOG4265] Predicted E3 ubiquitin ligase
C14B9.4	plk-1	[KOG0575] Polo-like serine/threonine protein kinase
C14F5.5	sem-5	[KOG3601] Adaptor protein GRB2, contains SH2 and SH3 domains
C15C6.3	C15C6.3	
C15C6.4	C15C6.4	[KOG4046] RNase MRP and P, subunit POP4/p29
C15H7.4	C15H7.4	[LSE0915] Unnamed protein
C16A3.3	let-716	[KOG1070] rRNA processing protein Rrp5
C17G10.2	C17G10.2	[KOG0551] Hsp90 co-chaperone CNS1 (contains TPR repeats)
C18A3.3	C18A3.3	[KOG3080] Nucleolar protein-like/EBNA1-binding protein
C18E3.5	C18E3.5	[KOG0265] U5 snRNP-specific protein-like factor and related proteins
C18H2.1	C18H2.1	
C23G10.8	C23G10.8	[LSE1050] Unnamed protein
C23H3.5	C23H3.5	
C24A11.9	coq-1	[KOG0776] Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase
C25A1.9	rsa-1	[KOG2562] Protein phosphatase 2 regulatory subunit
C25A11.1	C25A11.1	
C25A11.2	C25A11.2	[LSE0895] Unnamed protein
C25D7.6	mcm-3	[KOG0479] DNA replication licensing factor, MCM3 component
C26B9.3	C26B9.3	
C26C6.1	pbrm-1	[KOG1827] Chromatin remodeling complex RSC, subunit RSC1/Polybromo and related proteins
C26C6.2	goa-1	[KOG0082] G-protein alpha subunit (small G protein superfamily)
C26C6.5	dcp-66	[KOG3740] Uncharacterized conserved protein
C26D10.1	ran-3	[KOG1426] RCC1 domain
C26D10.5	eff-1	[LSE1047] Unnamed protein
C26E6.8	ula-1	[KOG2016] NEDD8-activating complex, APP-BP1/UBA5 component
C27A2.6	dsh-2	
C27D11.1	egl-45	[KOG2072] Translation initiation factor 3, subunit a (eIF-3a)
C27H6.2	ruvb-1	[KOG1942] DNA helicase, TBP-interacting protein
C28A5.3	nex-3	[KOG0819] Annexin
C29E4.2	kle-2	[KOG2359] Uncharacterized conserved protein
C29E4.7	gsto-1	[KOG0406] Glutathione S-transferase
C29H12.5	C29H12.5	
C30A5.7	unc-86	[KOG1168] Transcription factor ACJ6/BRN-3, contains POU and HOX domains
C30C11.4	C30C11.4	[KOG0103] Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily
C30F12.1	C30F12.1	
C30G7.1	hil-1	[KOG4012] Histone H1
C30H7.2	C30H7.2	[KOG0912] Thiol-disulfide isomerase and thioredoxin
C31C9.4	fbxa-168	
C31H2.2	dpy-8	[KOG3544] Collagens (type IV and type XIII), and related proteins
C32A3.1	sel-8	[LSE4012] Unnamed protein
C32F10.2	lin-35	[KOG1010] Rb (Retinoblastoma tumor suppressor)-related protein
C32F10.5	hmg-3	[KOG0526] Nucleosome-binding factor SPN, POB3 subunit
C33H5.7	C33H5.7	[KOG1446] Histone H3 (Lys4) methyltransferase complex and RNA cleavage factor II complex, subunit SWD2
C33H5.9	sec-10	[KOG3745] Exocyst subunit - Sec10p
C34B2.7	sdha-2	[KOG2403] Succinate dehydrogenase, flavoprotein subunit
C34E10.2	gop-2	[KOG1532] GTPase XAB1, interacts with DNA repair protein XPA
C35C5.1	sdc-2	[LSE0878] Unnamed protein
C36B1.1	cle-1	[KOG3546] Collagens (type XV)
C36B1.5	prp-4	[KOG0272] U4/U6 small nuclear ribonucleoprotein Prp4 (contains WD40 repeats)
C36E6.5	mlc-2	[KOG0031] Myosin regulatory light chain, EF-Hand protein superfamily
C37A2.4	cye-1	[KOG0655] G1/S-specific cyclin E
C37C3.6	ppn-1	[KOG4597] Serine proteinase inhibitor (KU family) with thrombospondin repeats
C37F5.1	lin-1	[KOG3806] Predicted transcription factor
C37H5.5	C37H5.5	[KOG2153] Protein involved in the nuclear export of pre-ribosomes
C37H5.6	C37H5.6	[KOG1355] Adenylosuccinate synthase
C38C3.5	unc-60	[KOG1735] Actin depolymerizing factor
C39B10.1	C39B10.1	[LSE0772] Unnamed protein
C39E9.13	rfc-3	[KOG2035] Replication factor C, subunit RFC3
C39E9.14	dli-1	[KOG3905] Dynein light intermediate chain
C41C4.6	ulp-4	[KOG0779] Protease, Ulp1 family
C42D4.8	rpc-1	[KOG0261] RNA polymerase III, large subunit
C43E11.9	C43E11.9	[KOG3492] Ribosome biogenesis protein NIP7
C43G2.2	bicd-1	[KOG0999] Microtubule-associated protein Bicaudal-D
C43H8.1	C43H8.1	[KOG4528] Uncharacterized conserved protein

C44B7.3	aff-1	
C44E4.4	C44E4.4	[KOG4213] RNA-binding protein La
C45G3.1	aspm-1	[KOG0165] Microtubule-associated protein Asp
C46A5.4	C46A5.4	[KOG2408] Peroxidase/oxygenase
C46A5.5	C46A5.5	
C46C2.1	wnk-1	[KOG0584] Serine/threonine protein kinase
C46H11.6	C46H11.6	[KOG3528] PDZ domain
C47C12.3	ref-2	[KOG1721] Zn-finger
C47D12.1	trr-1	[KOG0889] Histone acetyltransferase SAGA, TRRAP/TRA1 component, PI-3 kinase superfamily
C48A7.1	egl-19	[KOG2301] Voltage-gated Ca2+ channels, alpha1 subunits
C48A7.2	C48A7.2	[KOG2493] Na+/Pi symporter
C48B6.2	C48B6.2	[KOG4655] U3 small nucleolar ribonucleoprotein (snoRNP) component
C48B6.6	smg-1	[KOG0891] DNA-dependent protein kinase
C49H3.8	C49H3.8	
C50A2.2	C50A2.2	[LSE0984] Unnamed protein
C50C3.6	prp-8	[KOG1795] U5 snRNP spliceosome subunit
C50F4.11	mdf-1	
C50F4.13	his-35	[KOG1756] Histone 2A
C52A11.2	glb-12	[KOG3378] Globins and related hemoproteins
C53A5.3	hda-1	[KOG1342] Histone deacetylase complex, catalytic component RPD3
C53B4.7	bre-1	[KOG1372] GDP-mannose 4,6 dehydratase
C53H9.2	C53H9.2	
C54D1.6	bar-1	[KOG4203] Armadillo/beta-Catenin/plakoglobin
C54G4.8	cyc-1	[KOG3052] Cytochrome c1
C55A6.9	C55A6.9	[KOG2478] Putative RNA polymerase II regulator
C55B7.5	uri-1	[KOG3130] Uncharacterized conserved protein
C56C10.13	dnj-8	[KOG0714] Molecular chaperone (DnaJ superfamily)
C56C10.8	icd-1	[KOG2240] RNA polymerase II general transcription factor BTF3 and related proteins
D1046.2	D1046.2	[LSE0537] C2H2-type Zn-finger
D1069.3	D1069.3	[KOG4688] Putative beta-catenin-Tcf/Lef signaling pathway component DRCTNNB1A
D2013.7	eif-3.F	[KOG2975] Translation initiation factor 3, subunit f (eIF-3f)
D2021.1	utx-1	[KOG1124] TPR repeat I [KOG1246] DNA-binding protein jumonji/RBP2/SMCY, contains JmjC domain
D2030.9	wdr-23	[KOG0266] WD40 repeat-containing protein
D2045.9	D2045.9	[KOG4179] Lysyl hydrolase/glycosyltransferase family 25
D2085.3	D2085.3	[KOG1461] Translation initiation factor 2B, epsilon subunit (eIF-2Bepsilon/GCD6)
D2096.8	D2096.8	[KOG1507] Nucleosome assembly protein NAP-1
E01A2.2	E01A2.2	[KOG2295] C2H2 Zn-finger protein
E02D9.1	E02D9.1	[KOG0581] Mitogen-activated protein kinase kinase (MAP2K)
E04A4.5	E04A4.5	[KOG1652] Mitochondrial import inner membrane translocase, subunit TIM17
F01F1.12	F01F1.12	[KOG1557] Fructose-biphosphate aldolase
F01F1.8	cct-6	[KOG0359] Chaperonin complex component, TCP-1 zeta subunit (CCT6)
F01G4.2	ard-1	[KOG1199] Short-chain alcohol dehydrogenase/3-hydroxyacyl-CoA dehydrogenase
F01G4.6	F01G4.6	[KOG0767] Mitochondrial phosphate carrier protein
F07A5.7	unc-15	[KOG0161] Myosin class II heavy chain
F07E5.5	F07E5.5	[KOG4400] E3 ubiquitin ligase interacting with arginine methyltransferase
F08B4.5	F08B4.5	[KOG3818] DNA polymerase epsilon, subunit B
F09D1.1	F09D1.1	[KOG2026] Spindle pole body protein - Sad1p
F09E5.1	pkc-3	[KOG0695] Serine/threonine protein kinase
F09F7.2	mlc-3	[KOG0030] Myosin essential light chain, EF-Hand protein superfamily
F10B5.6	emb-27	[KOG1173] Anaphase-promoting complex (APC), Cdc16 subunit
F10C1.5	dmd-5	[KOG3815] Transcription factor Doublesex
F10C5.1	mat-3	[KOG1155] Anaphase-promoting complex (APC), Cdc23 subunit
F10E9.5	F10E9.5	
F10E9.6	mig-10	[KOG3751] Growth factor receptor-bound proteins (GRB7, GRB10, GRB14)
F10G7.4	scc-1	[KOG1213] Sister chromatid cohesion complex Cohesin, subunit RAD21/SCC1
F10G8.3	npp-17	[KOG0647] mRNA export protein (contains WD40 repeats)
F11A3.2	F11A3.2	[KOG1467] Translation initiation factor 2B, delta subunit (eIF-2Bdelta/GCD2)
F11C1.6	nhr-25	[KOG4218] Nuclear hormone receptor betaFTZ-F1
F12F6.7	F12F6.7	[KOG2732] DNA polymerase delta, regulatory subunit 55
F13D11.2	hbl-1	[KOG1721] Zn-finger
F13E6.4	F13E6.4	[KOG0940] Ubiquitin protein ligase RSP5/NEDD4
F14B4.3	F14B4.3	[KOG0216] RNA polymerase I, second largest subunit
F14D12.2	unc-97	[KOG2272] Focal adhesion protein PINCH-1, contains LIM domains
F15C11.1	sem-4	[KOG1074] Transcriptional repressor SALM
F15D3.7	F15D3.7	[KOG3324] Mitochondrial import inner membrane translocase, subunit TIM23
F15G9.4	him-4	[KOG4475] Immunoglobin and related proteins
F16D3.4	F16D3.4	[KOG1943] Beta-tubulin folding cofactor D
F17E9.13	his-33	[KOG1756] Histone 2A
F18E2.2	abcf-1	[KOG0066] eIF2-interacting protein ABC50 (ABC superfamily)
F18E2.3	scc-3	[KOG2011] Sister chromatid cohesion complex Cohesin, subunit STAG/IRR1/SCC3
F18G5.2	pes-8	
F18H3.5	cdk-4	[KOG0594] Protein kinase PCTAIRE and related kinases
F19B6.1	F19B6.1	[KOG4203] Armadillo/beta-Catenin/plakoglobin
F19H6.1	nekl-3	[KOG0591] NIMA (never in mitosis)-related G2-specific serine/threonine protein kinase
F20B6.3	mrp-6	[KOG0054] Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily
F20G4.3	nmy-2	[KOG0161] Myosin class II heavy chain
F20H11.2	nsh-1	[KOG1513] Nuclear helicase MOP-3/SNO (DEAD-box superfamily)
F20H11.6	F20H11.6	
F21C3.5	pfd-6	[KOG3478] Prefoldin subunit 6, KE2 family
F21H12.4	ptc-2	[KOG1935] Membrane protein Patched/PTCH
F22B3.1	his-64	[KOG3467] Histone H4
F22B5.1	evl-20	[KOG0073] GTP-binding ADP-ribosylation factor-like protein ARL2
F22B5.7	zyg-9	[KOG1820] Microtubule-associated protein
F22D3.5	F22D3.5	
F22F4.1	F22F4.1	
F23F1.1	nfyc-1	[KOG1657] CCAAT-binding factor, subunit C (HAP5)
F25B5.2	F25B5.2	
F25D7.3	blmp-1	[KOG2461] Transcription factor BLIMP-1/PRDI-BF1, contains C2H2-type Zn-finger and SET domains
F25H2.5	F25H2.5	[KOG0888] Nucleoside diphosphate kinase
F25H5.4	eft-2	[KOG0469] Elongation factor 2
F25H8.2	F25H8.2	[KOG2236] Uncharacterized conserved protein
F25H8.3	gon-1	
F26A3.2	ncbp-2	[KOG0121] Nuclear cap-binding protein complex, subunit CBP20 (RRM superfamily)
F26B1.7	let-381	[KOG2294] Transcription factor of the Forkhead/HNF3 family
F26D11.11	let-413	
F26E4.1	sur-6	[KOG1354] Serine/threonine protein phosphatase 2A, regulatory subunit
F26F4.11	rpb-8	[KOG3400] RNA polymerase subunit 8
F26H11.1	kbp-3	
F27C1.6	F27C1.6	[KOG2172] Uncharacterized conserved protein
F27E5.2	pax-3	[KOG0849] Transcription factor PRD and related proteins, contain PAX and HOX domains
F28B3.7	him-1	
F28D1.10	gex-3	[KOG1917] Membrane-associated hematopoietic protein
F28D1.7	rps-23	[KOG1749] 40S ribosomal protein S23
F28F8.5	F28F8.5	
F29A7.6	F29A7.6	[KOG4531] M phase phosphoprotein 6
F29B9.6	ubc-9	[KOG0424] Ubiquitin-protein ligase
F29G9.4	fos-1	[KOG1414] Transcriptional activator FOSB/c-Fos and related bZIP transcription factors
F30A10.10	F30A10.10	[KOG1863] Ubiquitin carboxyl-terminal hydrolase
F31C3.5	F31C3.5	[KOG4071] Uncharacterized conserved protein
F31E3.1	ceh-20	[KOG0774] Transcription factor PBX and related HOX domain proteins
F31E3.2	F31E3.2	[KOG0694] Serine/threonine protein kinase
F32D1.10	mcm-7	[KOG0482] DNA replication licensing factor, MCM7 component
F32E10.1	nol-10	[KOG2321] WD40 repeat protein
F32H2.1	gei-11	[KOG0049] Transcription factor, Myb superfamily
F33H2.2	F33H2.2	[KOG3707] Uncharacterized conserved protein
F33H2.5	F33H2.5	[KOG1798] DNA polymerase epsilon, catalytic subunit A
F35G12.8	smc-4	[KOG0996] Structural maintenance of chromosome protein 4 (chromosome condensation complex Condensin, subunit C)
F35H10.4	vha-5	[KOG2189] Vacuolar H+-ATPase V0 sector, subunit a
F36A2.3	F36A2.3	[TWOG0224] Predicted malate dehydrogenase

F36H1.2	tag-144	
F36H2.1	tat-5	[KOG0210] P-type ATPase
F37A4.8	isw-1	[KOG0385] Chromatin remodeling complex WSTF-ISWI, small subunit
F37B12.1	F37B12.1	
F37E3.1	ncbp-1	[KOG1104] Nuclear cap-binding complex, subunit NCBP1/CBP80
F39B2.4	sur-2	[KOG1883] Cofactor required for Sp1 transcriptional activation, subunit 3
F41B4.2	F41B4.2	[LSE0721] Unnamed protein
F41E6.4	smk-1	[KOG2229] Protein required for actin cytoskeleton organization and cell cycle progression
F42E11.4	tni-1	[KOG3977] Troponin I
F43C1.2	mpk-1	[KOG0660] Mitogen-activated protein kinase
F43D2.1	F43D2.1	
F43G9.1	F43G9.1	[KOG0785] Isocitrate dehydrogenase, alpha subunit
F43G9.12	F43G9.12	[KOG2136] Transcriptional regulators binding to the GC-rich sequences
F44C4.4	gon-14	
F45E12.3	cul-4	[KOG2167] Cullins
F45H11.2	ned-8	[KOG0005] Ubiquitin-like protein
F46A9.4	skr-2	[KOG1724] SCF ubiquitin ligase, Skp1 component
F46A9.5	skr-1	[KOG1724] SCF ubiquitin ligase, Skp1 component
F46C8.6	dpy-7	[KOG3544] Collagens (type IV and type XIII), and related proteins
F46E10.9	dpy-11	[KOG0913] Thiol-disulfide isomerase and thioredoxin
F47A4.2	dpy-22	[KOG3598] Thyroid hormone receptor-associated protein complex, subunit TRAP230
F47D12.4	hmg-1.2	[KOG0381] HMG box-containing protein
F47F6.1	lin-42	[KOG3753] Circadian clock protein period
F48C1.4	F48C1.4	
F48F7.1	alg-1	[KOG1041] Translation initiation factor 2C (eIF-2C) and related proteins
F52B5.6	rpl-25.2	[KOG1751] 60s ribosomal protein L23
F52C6.12	F52C6.12	
F52C6.13	F52C6.13	
F52E10.5	ifa-3	[KOG0977] Nuclear envelope protein lamin, intermediate filament superfamily
F53A2.4	nud-1	[KOG2265] Nuclear distribution protein NUDC
F53B3.1	tra-4	[KOG1721] Zn-finger
F53F10.5	npp-11	[KOG0845] Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116) I [KOG2196] Nuclear porin
F53F4.11	F53F4.11	[KOG1685] Uncharacterized conserved protein
F53H1.1	F53H1.1	[KOG0334] RNA helicase
F54C8.2	cpar-1	[KOG1745] Histones H3 and H4
F54C8.3	emb-30	
F54C9.1	iff-2	[KOG3271] Translation initiation factor 5A (eIF-5A)
F54C9.5	rpl-5	[KOG0875] 60S ribosomal protein L5
F54C9.9	F54C9.9	[KOG2409] KRR1-interacting protein involved in 40S ribosome biogenesis
F54D8.1	dpy-17	[KOG3544] Collagens (type IV and type XIII), and related proteins
F54E7.3	par-3	[LSE4030] Unnamed protein
F54F2.1	pat-2	[KOG3637] Vitronectin receptor, alpha subunit
F54F2.2	zfp-1	[KOG0956] PHD finger protein AF10
F54G8.3	ina-1	[KOG3637] Vitronectin receptor, alpha subunit
F54H12.1	aco-2	[KOG0453] Aconitase/homoaconitase (aconitase superfamily)
F55A12.8	F55A12.8	[KOG2036] Predicted P-loop ATPase fused to an acetyltransferase
F55C5.4	F55C5.4	[KOG1949] Uncharacterized conserved protein
F55C5.8	F55C5.8	[KOG2460] Signal recognition particle, subunit Srp68
F55C7.7	unc-73	[KOG0689] Guanine nucleotide exchange factor for Rho and Rac GTPases
F55F8.4	cir-1	[KOG3794] CBF1-interacting corepressor CIR and related proteins
F55F8.5	tag-345	[KOG0313] Microtubule binding protein YTM1 (contains WD40 repeats)
F56A11.1	gex-2	[KOG3534] p53 inducible protein PIR121
F56B3.4	F56B3.4	
F56C9.1	gsp-2	[KOG0374] Serine/threonine specific protein phosphatase PP1, catalytic subunit
F56D1.4	clr-1	[KOG4228] Protein tyrosine phosphatase
F56F3.5	rps-1	[KOG1628] 40S ribosomal protein S3A
F56F3.6	ins-17	[LSE0996] Unnamed protein
F56H11.1	fbl-1	[KOG1217] Fibrillins and related proteins containing Ca2+-binding EGF-like domains
F56H6.5	gmd-2	[KOG1372] GDP-mannose 4,6 dehydratase
F57B10.1	let-607	[KOG0709] CREB/ATF family transcription factor
F57B10.3	F57B10.3	[KOG4513] Phosphoglycerate mutase
F57B9.5	byn-1	[KOG3871] Cell adhesion complex protein bystin
F58A3.1	ldb-1	[KOG2181] LIM domain binding protein LDB1/NLI/CLIM
F58A3.2	egl-15	[KOG0200] Fibroblast/platelet-derived growth factor receptor and related receptor tyrosine kinases
F58A4.3	hcp-3	[KOG1745] Histones H3 and H4
F58A4.8	tbg-1	[KOG1374] Gamma tubulin
F58B6.3	par-2	[LSE4021] Unnamed protein
F58D5.1	hrp-2	[KOG0117] Heterogeneous nuclear ribonucleoprotein R (RRM superfamily)
F59A2.1	npp-9	[KOG0864] Ran-binding protein RANBP1 and related RanBD domain proteins
F59B10.1	pqn-47	[KOG3661] Uncharacterized conserved protein
F59E10.1	orc-2	[KOG2928] Origin recognition complex, subunit 2
H02I12.6	his-66	[KOG1744] Histone H2B
H24G06.1	H24G06.1	[KOG1408] WD40 repeat protein
H27M09.2	rpb-5	[KOG3218] RNA polymerase, 25-kDa subunit (common to polymerases I, II and III)
H37N21.1	H37N21.1	
H38K22.1	evl-14	[KOG1525] Sister chromatid cohesion complex Cohesin, subunit PDS5
H38K22.2	dcn-1	[KOG3077] Uncharacterized conserved protein
H39E23.1	par-1	[KOG0586] Serine/threonine protein kinase
H41C03.1	H41C03.1	[KOG1471] Phosphatidylinositol transfer protein SEC14 and related proteins
JC8.6	lin-54	[KOG1171] Metallothionein-like protein
K01C8.9	nst-1	[KOG2484] GTPase
K01C8.10*	cct-4	[KOG0358] Chaperonin complex component, TCP-1 delta subunit (CCT4)
K02F2.3	tag-203	[KOG1898] Splicing factor 3b, subunit 3
K03A1.6	his-38	[KOG3467] Histone H4
K03H1.10	K03H1.10	[KOG1778] CREB binding protein/P300 and related TAZ Zn-finger proteins
K04C2.2	K04C2.2	[KOG1926] Predicted regulator of rRNA gene transcription (MYB-binding protein)
K04D7.1	rack-1	[KOG0279] G protein beta subunit-like protein
K04G2.1	iftb-1	[KOG2768] Translation initiation factor 2, beta subunit (eIF-2beta)
K04G7.10	rnp-7	[KOG0113] U1 small nuclear ribonucleoprotein (RRM superfamily)
K04G7.11	K04G7.11	
K06H7.6	apc-2	
K07A1.11	rba-1	[KOG0264] Nucleosome remodeling factor, subunit CAF1/NURF55/MSI1
K07A1.12	lin-53	[KOG0264] Nucleosome remodeling factor, subunit CAF1/NURF55/MSI1
K07C5.4	K07C5.4	[KOG2573] Ribosome biogenesis protein - Nop56p/Sik1p
K07E12.1	dig-1	
K07F5.14	K07F5.14	[KOG4365] Uncharacterized conserved protein
K08A8.2	sox-2	[KOG0527] HMG-box transcription factor
K08B4.1	lag-1	[KOG3743] Recombination signal binding protein-J kappa(CBF1, Su(H), HS2NF5)
K08E3.6	cyk-4	[KOG3564] GTPase-activating protein
K08E4.1	spt-5	[KOG1999] RNA polymerase II transcription elongation factor DSIF/SUPT5H/SPT5
K09B11.3	K09B11.3	
K10B2.1	lin-23	[KOG0281] Beta-TrCP (transducin repeats containing)/Slimb proteins
K10G6.1	lin-31	[KOG3562] Forkhead/HNF-3-related transcription factor
K10G9.2	K10G9.2	
K12C11.2	smo-1	[KOG1769] Ubiquitin-like proteins
K12H4.3	K12H4.3	[KOG2971] RNA-binding protein required for biogenesis of the ribosomal 60S subunit
K12H4.8	dcr-1	[KOG0701] dsRNA-specific nuclease Dicer and related ribonucleases
M01D7.7	egl-30	[KOG0085] G protein subunit Galphaq/Galphay, small G protein superfamily
M03F4.6	M03F4.6	[KOG1218] Proteins containing Ca2+-binding EGF-like domains
M04B2.1	mep-1	[TWOG0702] Unnamed protein
M04F3.1	rpa-2	[KOG3108] Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit
M05B5.5	hlh-2	[KOG3910] Helix loop helix transcription factor
M7.1	let-70	[KOG0417] Ubiquitin-protein ligase
PAR2.4	mig-22	[KOG3708] Uncharacterized conserved protein
R02D3.5	R02D3.5	[KOG0530] Protein farnesyltransferase, alpha subunit/protein geranylgeranyltransferase type I, alpha subunit
R05D11.7	R05D11.7	[KOG3263] Nucleic acid binding protein
R05D3.11	met-2	
R05D3.4	rfp-1	[KOG0978] E3 ubiquitin ligase involved in syntaxin degradation
R06A10.2	gsa-1	[KOG0099] G protein subunit Galphas, small G protein superfamily

R06C1.3	wve-1	[KOG1830] Wiskott Aldrich syndrome proteins
R06C7.5	R06C7.5	[KOG2700] Adenylosuccinate lyase
R06C7.8	bub-1	[KOG1166] Mitotic checkpoint serine/threonine protein kinase I [LSE0746] Unnamed protein
R06F6.1	cdl-1	[KOG3934] Histone mRNA stem-loop binding protein
R07E5.10	pdcd-2	[KOG2061] Uncharacterized MYND Zn-finger protein
R07E5.14	rnp-4	[KOG0130] RNA-binding protein RBM8/Tsunagi (RRM superfamily)
R07E5.3	R07E5.3	[KOG1649] SWI-SNF chromatin remodeling complex, Snf5 subunit
R07G3.1	cdc-42	[KOG0393] Ras-related small GTPase, Rho type
R08C7.10	wapl-1	[KOG2152] Sister chromatid cohesion protein
R08D7.2	R08D7.2	[KOG4780] Uncharacterized conserved protein
R08D7.3	eif-3.D	[KOG2479] Translation initiation factor 3, subunit d (eIF-3d)
R09B3.4	ubc-12	[KOG0420] Ubiquitin-protein ligase
R107.8	lin-12	[KOG1217] Fibrillins and related proteins containing Ca2+-binding EGF-like domains
R13A5.12	lpd-7	[KOG2481] Protein required for normal rRNA processing
R13G10.1	dpy-27	[KOG0996] Structural maintenance of chromosome protein 4 (chromosome condensation complex Condensin, subunit C)
R151.9	pfd-5	[KOG3048] Molecular chaperone Prefoldin, subunit 5
R31.1	sma-1	[KOG0517] Beta-spectrin
R53.3	egl-43	[KOG1721] Zn-finger
R53.4	R53.4	[KOG4092] Mitochondrial F1F0-ATP synthase, subunit f
R53.6	R53.6	[KOG3303] Predicted alpha-helical protein, potentially involved in replication/repair
R53.7	R53.7	[KOG1764] 5'-AMP-activated protein kinase, gamma subunit
T01B7.5	T01B7.5	[KOG3118] Disrupter of silencing SAS10
T01B7.7	rol-6	[KOG3544] Collagens (type IV and type XIII), and related proteins
T01C3.1	T01C3.1	
T01D1.2	etr-1	[KOG0144] RNA-binding protein CUGBP1/BRUNO (RRM superfamily)
T01G9.4	npp-2	[KOG2271] Nuclear pore complex component (sc Nup85)
T01G9.6	kin-10	[KOG3092] Casein kinase II, beta subunit
T01H8.5	gon-2	[KOG3614] Ca2+/Mg2+-permeable cation channels (LTRPC family)
T02C12.2	T02C12.2	[KOG2664] Small nuclear RNA activating protein complex - 50kD subunit (SNAP50)
T03F1.8	T03F1.8	[KOG0707] Guanylate kinase
T04A8.6	T04A8.6	[KOG4208] Nucleolar RNA-binding protein NIFK
T04G9.3	ile-2	[KOG3839] Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans
T05C12.6	mig-5	[KOG3571] Dishevelled 3 and related proteins
T05C12.7	cct-1	[KOG0360] Chaperonin complex component, TCP-1 alpha subunit (CCT1)
T05D4.4	osm-7	[LSE0781] Unnamed protein
T05E8.3	T05E8.3	[KOG0922] DEAH-box RNA helicase
T05G5.2	hlh-4	[KOG4029] Transcription factor HAND2/Transcription factor TAL1/TAL2/LYL1
T05G5.3	cdk-1	[KOG0594] Protein kinase PCTAIRE and related kinases
T06E6.1	T06E6.1	[KOG3881] Uncharacterized conserved protein
T06E6.2	cyb-3	[KOG0653] Cyclin B and related kinase-activating proteins
T06G6.11	T06G6.11	
T06G6.9	pfd-3	[KOG3313] Molecular chaperone Prefoldin, subunit 3
T07D3.7	alg-2	
T08A11.2	T08A11.2	[KOG0213] Splicing factor 3b, subunit 1
T09A5.9	T09A5.9	[KOG0531] Protein phosphatase 1, regulatory subunit, and related proteins
T10B5.5	cct-7	[KOG0361] Chaperonin complex component, TCP-1 eta subunit (CCT7)
T10B5.6	knl-3	
T10F2.4	T10F2.4	[KOG0289] mRNA splicing factor
T12F5.4	lin-59	[KOG1083] Putative transcription factor ASH1/LIN-59
T13A10.11	tag-32	[KOG1506] S-adenosylmethionine synthetase
T13H5.4	T13H5.4	[KOG2636] Splicing factor 3a, subunit 3
T14D7.2	oac-46	[KOG3700] Predicted acyltransferase
T14F9.4	peb-1	
T16G12.5	ekl-6	[KOG4653] Uncharacterized conserved protein
T19A6.2	ngp-1	[KOG2423] Nucleolar GTPase
T19B4.7	unc-40	[KOG4221] Receptor mediating netrin-dependent axon guidance
T19E10.1	ect-2	[KOG3524] Predicted guanine nucleotide exchange factor (PEBBLE)
T19E7.3	bec-1	[KOG2751] Beclin-like protein
T20B12.1	T20B12.1	
T20B12.8	hmg-4	[KOG0526] Nucleosome-binding factor SPN, POB3 subunit
T20G5.6	unc-47	[KOG4303] Vesicular inhibitory amino acid transporter
T21B10.3	T21B10.3	[LSE1138] Unnamed protein
T21B10.7	cct-2	[KOG0363] Chaperonin complex component, TCP-1 beta subunit (CCT2)
T21G5.4	T21G5.4	[KOG3528] PDZ domain
T21G5.5	asd-2	[KOG1588] RNA-binding protein Sam68 and related KH domain proteins
T22B7.1	egl-13	[KOG0528] HMG-box transcription factor SOX5
T22D1.10	ruvb-2	[KOG2680] DNA helicase TIP49, TBP-interacting protein
T22D2.1	vab-19	[KOG0514] Ankyrin repeat protein
T22F3.4	rpl-11.1	[KOG0397] 60S ribosomal protein L11
T23D8.1	mom-5	[KOG3577] Smoothened and related G-protein-coupled receptors
T23D8.5	his-67	[KOG3467] Histone H4
T23D8.6	his-68	[KOG1756] Histone 2A
T23D8.9	sys-1	[LSE4038] Unnamed protein
T23F2.1	bus-8	[KOG0853] Glycosyltransferase
T23G5.1	rnr-1	[KOG1112] Ribonucleotide reductase, alpha subunit
T25C12.1	lin-14	[LSE4059] Unnamed protein
T26A5.9	dlc-1	[KOG3430] Dynein light chain type 1
T26A8.4	T26A8.4	[KOG1040] Polyadenylation factor I complex, subunit, Yth1 (CPSF subunit)
T26G10.1	T26G10.1	[KOG0330] ATP-dependent RNA helicase
T27A3.2	T27A3.2	[KOG0944] Ubiquitin-specific protease UBP14
T27C4.4	lin-40	[KOG3554] Histone deacetylase complex, MTA1 component
T27F2.1	skp-1	[KOG2441] mRNA splicing factor/probable chromatin binding snw family nuclear protein
T28F12.2	unc-62	[KOG0773] Transcription factor MEIS1 and related HOX domain proteins
T28F2.5	ccb-1	
W01B11.3	nol-5	[KOG2572] Ribosome biogenesis protein - Nop58p/Nop5p
W01B6.9	ndc-80	[KOG0995] Centromere-associated protein HEC1
W01G7.3	rpb-11	[KOG4392] RNA polymerase, subunit L
W02A11.1	W02A11.1	[KOG2915] tRNA(1-methyladenosine) methyltransferase, subunit GCD14
W02A11.4	uba-2	
W02D7.7	sel-9	[KOG1692] Putative cargo transport protein EMP24 (p24 protein family)
W02D9.1	pri-2	[KOG2267] Eukaryotic-type DNA primase, large subunit
W03C9.4	lin-29	[KOG1721] Zn-finger
W03H9.4	cacn-1	[KOG2370] Cactin
W04A4.5	W04A4.5	[KOG2259] Uncharacterized conserved protein
W04A8.2	W04A8.2	
W04A8.7	taf-1	
W04D2.6	W04D2.6	[KOG2253] U1 snRNP complex, subunit SNU71 and related PWI-motif proteins
W06B11.2	puf-9	[KOG1488] Translational repressor Pumilio/PUF3 and related RNA-binding proteins (Puf superfamily)
W06F12.1	lit-1	[KOG0664] Nemo-like MAPK-related serine/threonine protein kinase
W07A12.6	oac-54	
W07B3.2	gei-4	[LSE0738] Unnamed protein
W07E6.4	prp-21	[KOG0007] Splicing factor 3a, subunit 1
W08F4.8	cdc-37	[KOG2260] Cell division cycle 37 protein, CDC37
W09C2.1	elt-1	
W09C5.1	W09C5.1	[KOG3163] Uncharacterized conserved protein related to ribosomal protein S8E
W09C5.2	unc-59	[KOG2655] Septin family protein (P-loop GTPase)
W09C5.6	rpl-31	[KOG0893] 60S ribosomal protein L31
W10D5.3	gei-17	
W10G6.1	W10G6.1	[LSE0136] Uncharacterized protein, contains BRCT, WSN domains and ankyrin repeats
Y106G6E.6	csnk-1	[KOG1165] Casein kinase (serine/threonine/tyrosine protein kinase)
Y106G6H.7	sec-8	[KOG3691] Exocyst complex subunit Sec8
Y113G7B.18	mdt-17	
Y116A8C.3	Y116A8C.3	
Y11D7A.9	Y11D7A.9	[KOG3979] FGF receptor activating protein 1
Y17G7B.5	mcm-2	[KOG0477] DNA replication licensing factor, MCM2 component
Y23H5B.5	Y23H5B.5	
Y34D9A.3	Y34D9A.3	
Y34D9A.4	spd-1	
Y37D8A.1	arx-5	[KOG3155] Actin-related protein Arp2/3 complex, subunit ARPC3

Y38F2AL.4	vha-3	[KOG0232] Vacuolar H+-ATPase V0 sector, subunits c/c'
Y39A1A.13	Y39A1A.13	
Y40B1A.4	sptf-3	
Y41D4B.11	Y41D4B.11	
Y44F5A.1	Y44F5A.1	[KOG2444] WD40 repeat protein
Y45F10D.9	sas-6	
Y47D3A.26	smc-3	[KOG0964] Structural maintenance of chromosome protein 3 (sister chromatid cohesion complex Cohesin, subunit SMC3)
Y47D3B.1	Y47D3B.1	[KOG4735] Extracellular protein with conserved cysteines
Y47G6A.15	Y47G6A.15	
Y47G6A.20	rnp-6	[KOG0124] Polypyrimidine tract-binding protein PUF60 (RRM superfamily)
Y48A6B.11	rsa-2	
Y48A6C.5	pha-1	[LSE0017] Uncharacterized protein
Y48B6A.1	Y48B6A.1	[KOG0650] WD40 repeat nucleolar protein Bop1, involved in ribosome biogenesis
Y49E10.20	Y49E10.20	[KOG3776] Plasma membrane glycoprotein CD36 and related membrane receptors
Y49E10.21	Y49E10.21	
Y50D7A.11	Y50D7A.11	
Y51A2D.15	Y51A2D.15	[KOG4643] Uncharacterized coiled-coil protein
Y51H7C.6	cogc-4	[KOG0412] Golgi transport complex COD1 protein
Y53C10A.12	hsf-1	[KOG0627] Heat shock transcription factor
Y53C12B.2	Y53C12B.2	[KOG3273] Predicted RNA-binding protein Pno1p interacting with Nob1p and involved in 26S proteasome assembly
Y53H1C.2	ego-2	[KOG2220] Predicted signal transduction protein
Y54E10A.15	cdt-1	
Y54E10A.16	Y54E10A.16	
Y54E2A.1	Y54E2A.1	[KOG3656] 7 transmembrane receptor
Y54E5A.4	npp-4	[KOG0845] Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)
Y54E5B.3	let-49	[KOG0570] Transcriptional coactivator
Y55F3AR.3*	cct-8	[KOG0362] Chaperonin complex component, TCP-1 theta subunit (CCT8)
Y56A3A.6	Y56A3A.6	
Y57E12AL.1	Y57E12AL.1	[KOG2592] Tumor differentially expressed (TDE) protein
Y66A7A.5	Y66A7A.5	[LSE4116] Unnamed protein
Y73F8A.24	Y73F8A.24	[KOG3471] RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB2
Y75B8A.7	Y75B8A.7	[KOG2600] U3 small nucleolar ribonucleoprotein (snoRNP) subunit - Mpp10p
Y77E11A.7	Y77E11A.7	
Y87G2A.1	Y87G2A.1	
Y87G2A.4	aex-6	[KOG0081] GTPase Rab27, small G protein superfamily
Y92C3B.2	uaf-1	[KOG0120] Splicing factor U2AF, large subunit (RRM superfamily)
ZC123.3	ZC123.3	[KOG1146] Homeobox protein
ZC168.3	ZC168.3	[KOG2543] Origin recognition complex, subunit 5
ZC395.3	toc-1	[KOG1484] Putative Zn2+ transporter MSC2 (cation diffusion facilitator superfamily)
ZC504.4	mig-15	[KOG0587] Traf2- and Nck-interacting kinase and related germinal center kinase (GCK) family protein kinases
ZK1098.1	ZK1098.1	[KOG0152] Spliceosomal protein FBP11/Splicing factor PRP40
ZK1098.7	ZK1098.7	[TWOG0854] Unnamed protein
ZK1127.5	ZK1127.5	[KOG3980] RNA 3'-terminal phosphate cyclase
ZK1128.3	ZK1128.3	
ZK1128.5	tag-246	[KOG2570] SWI/SNF transcription activation complex subunit
ZK1151.1	vab-10	[KOG0516] Dystonin, GAS (Growth-arrest-specific protein), and related proteins
ZK1251.9	ZK1251.9	[KOG1832] HIV-1 Vpr-binding protein
ZK131.1	his-26	[KOG3467] Histone H4
ZK177.6	fzy-1	[KOG0305] Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits
ZK262.8	ZK262.8	
ZK265.6	ZK265.6	[KOG4706] Uncharacterized conserved protein
ZK287.5	rbx-1	[KOG2930] SCF ubiquitin ligase, Rbx1 component
ZK430.7	ZK430.7	[KOG0268] Sof1-like rRNA processing protein (contains WD40 repeats)
ZK507.6	ZK507.6	[KOG0654] G2/Mitotic-specific cyclin A
ZK546.1	zyg-12	
ZK546.13	mdt-4	[KOG4552] Vitamin-D-receptor interacting protein complex component
ZK632.13	lin-52	[KOG4402] Uncharacterized conserved protein
ZK632.2	ZK632.2	[KOG1881] Anion exchanger adaptor protein Kanadaptin, contains FHA domain
ZK637.7	lin-9	[KOG1019] Retinoblastoma pathway protein LIN-9/chromatin-associated protein Aly
ZK637.8	unc-32	[KOG2189] Vacuolar H+-ATPase V0 sector, subunit a
ZK675.1	ptc-1	
ZK686.1	ZK686.1	
ZK770.3	inx-12	[TWOG0193] Innexin-type channels
ZK856.10	ZK856.10	[KOG3297] DNA-directed RNA polymerase subunit E'
ZK858.1	ZK858.1	
ZK867.1	syd-9	[KOG1721] Zn-finger
ZK909.2	kin-1	[KOG0616] cAMP-dependent protein kinase catalytic subunit (PKA)
ZK930.3	ZK930.3	
ZK970.3	mdt-22	[KOG3304] Surfeit family protein 5

Table S2. Identification of 99 regulators of AC invasion. AC invasion was scored at the P6.p 4-cell and 8-cell stage of 1° VPC division. Data is shown for each individual RNAi experiment, as well as the % AC invasion defect averaged across multiple trials. Genes denoted with an asterisk have been previously identified as regulators of AC invasion. Genes in bold were further characterized. All genes above the double line have an AC invasion defect of greater than 30% at the P6.p 4-cell stage.

Gene Public Name	Sequence Name	TRIAL 1				TRIAL 2				TRIAL 3				TRIAL 4				TRIAL 5				%AC invasion defect		Homolog Description
		4-cell		8-cell		4-cell		8-cell		4-cell		8-cell		4-cell		8-cell		4-cell		8-cell		P6.p 4 cell	P6.p 8-cell	
		inv.	total	inv.	total	inv.	total	inv.	total	inv.	total	inv.	total	inv.	total	inv.	total	inv.	total	inv.	total			
cct-1	**T05C12.7**	1	11	0	14	2	11	0	7	2	20	8	25									88.10	82.61	T-complex protein 1 subunit alpha
tag-203	K02F2.3	2	15	3	9																	86.67	66.67	
cct-5	**C07G2.3**	0	10	0	12	4	13	7	7													82.61	63.16	T-complex protein 1 subunit epsilon
cct-4	**K01C8.10**	4	21	14	21	2	12	5	10													81.82	38.71	T-complex protein 1 subunit delta
cct-8	**Y55F3AR.3**	4	21	16	24	2	12	6	12													81.82	38.89	T-complex protein 1 subunit theta
cct-2	**T21B10.7**	2	10	2	4	1	11	2	7	5	20	10	20									80.49	54.84	T-complex protein 1 subunit beta
cct-7	**T10B5.5**	3	12	6	10	2	12	5	15													79.17	56.00	T-complex protein 1 subunit eta
cct-6	**F01F1.8**	4	20	8	15	1	4	6	16													79.17	54.84	T-complex protein 1 subunit zeta
cdt-1	Y54E10A.15	3	14	3	3	3	15	6	10	4	14	5	15									76.74	50.00	
C48B6.2	C48B6.2	1	7	1	8	4	14	5	13													76.19	71.43	U3 small nucleolar ribonucleoprotein protein IMP3
C48A7.2	**C48A7.2**	1	12	3	11	6	16	16	18	11	16	2	11	2	16	14	16	11	16	23	32	59.21	34.09	Sodium-dependent phosphate transporter 1
**unc-40*	T19B4.7	12	16	13	16	10	26	19	23	5	23	25	26									58.46	12.31	Netrin receptor DCC precursor
unc-60	C38C3.5	5	19	6	7	9	14	5	14													57.58	47.62	Cofilin-2
hda-1	**C53A5.3**	3	13	4	8	5	8	7	7	8	16	10	16									56.76	32.26	Histone deacetylase 1
fzy-1	ZK177.6	7	15	7	7																	53.33	0.00	Cell division cycle protein 20 homolog
dnj-8	C56C10.13	8	16	8	14																	50.00	42.86	Isoform 1 of DnaJ homolog subfamily C member 16 precursor
mcm-7	F32D1.10	1	2	6	16	7	13	4	4													46.67	50.00	Isoform 1 of DNA replication licensing factor MCM7
K03H1.10	K03H1.10	5	21	10	22	16	18	6	7													46.15	44.83	CREB-binding protein
K07F5.14	K07F5.14	1	2	10	14	1	1	2	4	4	13	12	13	7	8	3	4					45.83	22.86	
**fos-1a*	F29G9.4	8	14	7	25	4	15	9	24	18	26	16	19									45.45	52.94	
T20B12.1	**T20B12.1**	6	12	11	11	6	16	15	15	7	12	40	41	10	13	5	5					45.28	1.39	
mep-1	**M04B2.1**	15	15	13	13	10	13	16	20	8	15	17	28	3	13	14	36	2	13	22	33	44.93	36.92	
R06C7.5	R06C7.5	6	18	17	19	15	20	17	19													44.74	10.53	Isoform 1 of Adenylosuccinate lyase
cdc-37	**W08F4.8**	13	24	11	12	8	15	27	30	13	22	34	37									44.26	8.86	Hsp90 co-chaperone Cdc37
hbl-1	**F13D11.2**	8	12	6	7	9	12	16	20	1	7	22	22									41.94	10.20	Isoform 2 of Zinc finger protein 124
T03F1.8	**T03F1.8**	1	16	9	41	0	8	10	21	6	13	38	53	22	23	67	67	18	19	20	20	40.51	28.71	Guanylate kinase
let-49	Y54E5B.3	8	13	12	12																	38.46	0.00	Mediator of RNA polymerase II transcription subunit 7
C06E4.6	C06E4.6	5	8	10	13																	37.50	23.08	17-beta-hydroxysteroid dehydrogenase 14
C50A2.2	C50A2.2	4	5	6	6	6	11	8	8													37.50	0.00	
T02C12.2	T02C12.2	12	19	22	34																	36.84	35.29	snRNA-activating protein complex subunit 3
unc-62	**T28F12.2**	10	10	9	9	1	7	3	6													35.29	20.00	Isoform Meis2C of Homeobox protein Meis2
smc-4	F35G12.8	10	15	11	13	15	23	5	9													34.21	27.27	Isoform 1 of Structural maintenance of chromosomes protein 4
mdt-4	ZK546.13	6	14	6	8	12	14	1	6	9	13											34.15	50.00	Mediator of RNA polymerase II transcription subunit 4
mog-4	C04H5.6	11	16	12	13	5	8	17	17													33.33	3.33	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
C06E7.3	C06E7.3	8	12	0	0																	33.33	0.00	S-adenosylmethionine synthetase isoform type-2
R07E5.3	R07E5.3	8	12	9	9																	33.33	0.00	
**egl-43L*	R53.3	16	18	13	16	0	6	1	9													33.33	44.00	
cacn-1	**W03H9.4**	15	18	15	16	10	12	3	3	9	20	9	15									32.00	20.59	Isoform 2 of Uncharacterized protein C19orf29
gon-14	F44C4.4	15	20	26	36	18	28	13	15	15	17	20	24	7	17	27	32	13	17	54	54	31.31	13.04	
iff-2	F54C9.1	8	15	10	10	14	17	19	19													31.25	0.00	Isoform 2 of Eukaryotic translation initiation factor 5A-1
mpk-1	F43C1.2	13	16	10	12	7	13	4	4													31.03	12.50	Mitogen-activated protein kinase 1
lit-1	**W06F12.1**	11	15	5	5	14	21	36	36													30.56	0.00	nemo-like kinase
**ina-1*	F54G8.3	6	11	9	13	11	17	25	25	15	18	40	40									30.43	5.13	Isoform Alpha-6X1A of Integrin alpha-6 precursor
F28F8.5	**F28F8.5**	6	10	28	30	8	13	18	21	5	12	13	13	27	31							30.30	7.81	
D2096.8	D2096.8	5	7	1	1																	28.57	0.00	Nucleosome assembly protein 1-like 1
ceh-20	F31E3.1	5	7	0	0																	28.57	0.00	Pre-B-cell leukemia transcription factor 2
nsh-1	F20H11.2	14	15	25	25	8	15	45	49	16	16	31	31	7	16	19	19					27.42	3.23	Isoform 2 of Protein strawberry notch homolog 2
T13H5.4	T13H5.4	5	13	9	13	17	17	5	5													26.67	22.22	Splicing factor 3A subunit 3
rnp-7	K04G7.10	8	16	8	12	16	18	6	7	12	15	13	17									26.53	25.00	Isoform 1 of U1 small nuclear ribonucleoprotein 70 kDa
F53F4.11	F53F4.11	10	14	10	10	8	10	4	4													25.00	0.00	
F55C5.4	F55C5.4	6	12	18	22	18	20															25.00	18.18	CDNA FLJ20311 fis, clone HEP07319
T08A11.2	T08A11.2	9	10	7	7	3	6	13	18													25.00	20.00	
T26G10.1	T26G10.1	13	15	1	1	12	14	8	8	19	29	15	15									24.14	0.00	Probable ATP-dependent RNA helicase DDX47
F43G9.1	F43G9.1	16	21																			23.81	0.00	Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor
Y53C12B.2	Y53C12B.2	12	19	18	21	13	13	6	6	17	23	13	15									23.64	11.90	RNA-binding protein PNO1
mdf-1	C50F4.11	17	23	17	22	21	25	15	17	10	14	16	17									22.58	14.29	
lin-59	T12F5.4	7	9	6	11																	22.22	45.45	Probable histone-lysine N-methyltransferase ASH1L
rnr-1	T23G5.1	8	13	7	11	10	10	6	6													21.74	23.53	Ribonucleoside-diphosphate reductase large subunit
F01F1.12	F01F1.12	14	20	12	13	9	9															20.69	7.69	Fructose-bisphosphate aldolase A
Y44F5A.1	Y44F5A.1	12	13	3	4	11	15	21	21	12	16	11	11	11	14	25	26					20.69	3.23	
npp-9	F59A2.1	14	18	4	4	17	21	6	6													20.51	0.00	E3 SUMO-protein ligase RanBP2
bus-8	T23F2.1	12	15	30	34																	20.00	11.76	Isoform 1 of Alpha-1,3-mannosyltransferase ALG2
tag-144	F36H1.2	11	11	16	16	4	15	19	19	23	24	30	30	21	25	20	20	18	21	32	33	19.79	0.85	Isoform 1 of Ankyrin repeat-rich membrane spanning protein

T01C3.1	T01C3.1	13	19	27	33	16	17	20	20											19.44	11.32	
C06A5.1	C06A5.1	8	13	27	27	4	5	18	18	13	13	20	20							19.35	0.00	
rpl-31	W09C5.6	18	22	20	20															18.18	0.00	60S ribosomal protein L31
cdc-42	R07G3.1	14	17	15	15															17.65	0.00	Isoform 2 of Cell division control protein 42 homolog precursor
Y11D7A.9	Y11D7A.9	14	17	26	26															17.65	0.00	
F52C6.12	F52C6.12	13	17	31	31	12	13	15	15											16.67	0.00	
npp-4	Y54E5A.4	10	12	28	29															16.67	3.45	
apc-2	K06H7.6	8	10	11	13	11	11	10	12	14	17	18	22	8	11	12	14	6	7	13	13	16.07	13.51	
rsa-1	C25A1.9	7	8	15	15	22	29	44	46	14	14	11	12									15.69	4.11	Isoform 1 of Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma
mp-6	Y47G6A.20	17	19	8	8	10	13	17	18													15.63	3.85	
emb-27	F10B5.6	3	4	4	4	0	3	0	3	20	20	13	13									14.81	15.00	CDC16 protein
gon-2	T01H8.5	13	18	21	23	16	16	6	6													14.71	6.90	
C09H10.7	C09H10.7	3	7	6	8	17	17	16	16	13	13	12	12	5	9	10	10	23	25	30	30	14.08	2.63	
sec-10	C33H5.9	11	15	14	14	22	23	20	20	22	25	15	16									12.70	2.00	
smo-1	K12C11.2	9	13	20	20	13	13	6	6	18	21	20	20	18	19	30	30	14	15	15	15	11.11	0.00	
rsa-2	Y48A6B.11	15	15	10	10	9	13	14	14	10	11	14	15	15	15	16	19	7	9			11.11	6.90	
scc-3	F18E2.3	15	17	0	0	13	14	16	16													9.68	0.00	Isoform 1 of Cohesin subunit SA-3
C23G10.8	C23G10.8	17	19	12	12	13	16	17	17	8	9	20	20	19	19	31	31					9.52	0.00	
mdt-17	Y113G7B.18	14	17	11	11	15	15	25	27													9.38	5.26	
cdk-4	F18H3.5	11	11	10	10	9	13	5	5	19	19	16	17									9.30	3.13	Cell division protein kinase 6
gei-17	W10D5.3	10	10	16	16	12	14	12	12	18	20	13	13									9.09	0.00	E3 SUMO-protein ligase PIAS1
D2085.3	D2085.3	21	23	18	18																	8.70	0.00	Translation initiation factor eIF-2B subunit epsilon
npp-17	F10G8.3	15	18	30	30	27	27	31	31	22	25	25	25									8.57	0.00	mRNA export factor
F30A10.10	F30A10.10	34	38	18	19	14	14															7.69	5.26	
nol-10	F32E10.1	9	14	37	46	26	26	25	25	13	13	12	12	19	19	25	25					6.94	8.33	Isoform 1 of Nucleolar protein 10
dcn-1	H38K22.2	9	10	6	6	14	17	20	20	20	20	13	13	16	16	13	13					6.35	0.00	DCN1-like protein 1
dpy-11	F46E10.9	22	26	17	17	23	23	20	20	16	16	15	15									6.15	0.00	Thioredoxin domain-containing protein 1 precursor
C43H8.1	C43H8.1	5	7	5	5	12	12	20	20	16	16	20	20									5.71	0.00	cDNA FLJ75987, highly similar to H. sapiens zinc finger and BTB domain containing 8 opposite strand (ZBTB8OS)
F52C6.13	F52C6.13	23	25	12	12	45	47	23	23													5.56	0.00	
sur-2	F39B2.4	19	19	31	31	19	21	34	34													5.00	0.00	Isoform 1 of Mediator of RNA polymerase II transcription subunit 23
T27A3.2	T27A3.2	15	18	17	17	18	18	19	19	25	25	18	18									4.92	0.00	Isoform Long of Ubiquitin carboxyl-terminal hydrolase 5
Y87G2A.1	Y87G2A.1	20	20	8	8	8	10	8	8	18	18	5	5									4.17	0.00	
lin-40	T27C4.4	23	23	9	9	16	18	18	18	35	36	57	57									3.90	0.00	
nekl-3	F19H6.1	21	23	23	23	12	14	49	54	13	13	15	15	24	24	19	19	33	33	21	21	3.74	3.79	Serine/threonine-protein kinase Nek7
mat-3	F10C5.1	9	9	19	19	13	15	19	29	13	13	14	15	16	16	13	13	15	15	21	23	2.94	13.13	
cdk-1	T05G5.3	4	4	4	7	8	8	5	5													0.00	25.00	Cell division control protein 2 homolog
L4440	empty vector	30	30	30	30	25	25	25	25	20	20	20	20									0	0	empty vector dsRNA control

Table S3. RNAi depletion of 99 genes results in an AC invasion defect. Genes are listed by public name (3 letter abbreviation) and genetic sequence name from www.wormbase.org. The 99 genes were categorized by gene ontology or molecular function search. Where available, the orthologous or homologous human protein with the best BLASTP e-value is given for each gene. Genes in bold have been previously implicated in metastasis or cell invasion. Genes denoted with an asterisk have been previously implicated in AC invasion. The double asterisk (**) denotes that *cct-4* and *cct-8* were confirmed as hits following the initial RNAi screen.

Gene Public Name	Sequence Name (Gene)	CDS Description	Homolog BLASTP evalue	Homologous Protein	Homolog Description
Transcriptional Regulation / DNA Binding					
mog-4	C04H5.6	Helicases conserved C-terminal domain	5.30E-286	ENSEMBL:ENSP00000365625	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
scc-3	F18E2.3		2.90E-143	ENSEMBL:ENSP00000319318	Isoform 1 of Cohesin subunit SA-3
nsh-1	F20H11.2		1.40E-245	ENSEMBL:ENSP00000250872	Isoform 2 of Protein strawberry notch homolog 2
mcm-7[1]	**F32D1.10**	**cell division control protein**	**3.50E-186**	**ENSEMBL:ENSP00000307288**	**Isoform 1 of DNA replication licensing factor MCM7**
tag-144	F36H1.2	ankyrin like	1.00E-181	ENSEMBL:ENSP00000256707	Isoform 1 of Ankyrin repeat-rich membrane spanning protein
sur-2	F39B2.4	SUR-2 PROTEIN	2.40E-37	ENSEMBL:ENSP00000357047	Isoform 1 of Mediator of RNA polymerase II transcription subunit 23
tag-203	K02F2.3		5.50E-94	ENSEMBL:ENSP00000311296	Splicing factor 3B subunit 3
K03H1.10[2]	**K03H1.10**		**2.00E-55**	**ENSEMBL:ENSP00000262367**	**CREB-binding protein**
rnp-7	K04G7.10	SN-RNP U1	1.00E-60	ENSEMBL:ENSP00000221448	Isoform 1 of U1 small nuclear ribonucleoprotein 70 kDa
T02C12.2	T02C12.2		2.60E-19	ENSEMBL:ENSP00000370191	snRNA-activating protein complex subunit 3
T08A11.2	T08A11.2		1.70E-09	ENSEMBL:ENSP00000324804	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (PP2A, subunit A, PR65-alpha isoform)
lin-59	T12F5.4		1.20E-50	ENSEMBL:ENSP00000357330	Probable histone-lysine N-methyltransferase ASH1L
T13H5.4	T13H5.4	PRP9 like protein	6.50E-146	ENSEMBL:ENSP00000362110	Splicing factor 3A subunit 3
T26G10.1	T26G10.1	RNA helicase	2.80E-154	ENSEMBL:ENSP00000350698	Probable ATP-dependent RNA helicase DDX47
skp-1	T27F2.1	Drosophila puff specific protein BX42 like	1.50E-153	ENSEMBL:ENSP00000261531	SNW domain-containing protein 1
mdt-17	Y113G7B.18		7.40E-24	ENSEMBL:ENSP00000251871	mediator complex subunit 17
rnp-6	Y47G6A.20	RNA-binding protein	4.41E-108	VG:OTTHUMP00000178419	Isoform 2 of Poly(U)-binding-splicing factor PUF60
let-49	Y54E5B.3		6.20E-31	ENSEMBL:ENSP00000286317	Mediator of RNA polymerase II transcription subunit 7
mdt-4	ZK546.13		3.70E-24	ENSEMBL:ENSP00000258648	Mediator of RNA polymerase II transcription subunit 4
Transcription Factors					
hbl-1	F13D11.2	C2H2-type zinc finger	1.10E-20	ENSEMBL:ENSP00000340749	Isoform 2 of Zinc finger protein 124
****fos-1a***[3-6]	**F29G9.4**	**BZIP transcription factor**	**0.000000017**	**VG:OTTHUMP00000200848**	**FOS-like antigen 2**
ceh-20[7-8]	**F31E3.1**		**9.90E-95**	**ENSEMBL:ENSP00000364190**	**Pre-B-cell leukemia transcription factor 2**
mep-1	M04B2.1	C2H2-type zinc-finger			
****egl-43L***[9]	**R53.3**	**Zinc finger, C2H2 type (4 domains)**	**9.10E-47**	**ENSEMBL:ENSP00000367643**	**PR domain zinc finger protein 16 (PR domain-containing protein 16)(Transcription factor MEL1)**
lin-40[10]	**T27C4.4**		**4.10E-71**	**VG:OTTHUMP00000197385**	**MTA3 metastasis-associated gene 3**
unc-62	T28F12.2		7.10E-79	ENSEMBL:ENSP00000326296	Isoform Meis2C of Homeobox protein Meis2
gei-17	W10D5.3		1.30E-51	ENSEMBL:ENSP00000249636	E3 SUMO-protein ligase PIAS1
Chromatin remodification and architecture					
C50A2.2	C50A2.2		0.0000041	VG:OTTHUMP00000182120	Probable E3 ubiquitin-protein ligase MARCH10
hda-1[11-14]	**C53A5.3**	**Yeast RPD3 protein like**	**2.80E-170**	**ENSEMBL:ENSP00000362649**	**Histone deacetylase 1**
D2096.8	D2096.8		2.90E-63	ENSEMBL:ENSP00000261182	Nucleosome assembly protein 1-like 1
smc-4	F35G12.8	chromosome segregation protein	9.29E-115	ENSEMBL:ENSP00000341382	Isoform 1 of Structural maintenance of chromosomes protein 4
R07E5.3[15]	**R07E5.3**	**Snf5 (yeast)**	**1.70E-97**	**VG:OTTHUMP00000198411**	**SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1**
RNA Processing and regulation					
C48B6.2	C48B6.2	ribosomal protein	4.30E-46	ENSEMBL:ENSP00000326981	U3 small nucleolar ribonucleoprotein protein IMP3
npp-17	F10G8.3	polyA RNA export protein	5.90E-97	ENSEMBL:ENSP00000360286	mRNA export factor
Y53C12B.2	Y53C12B.2		6.10E-63	ENSEMBL:ENSP00000263657	RNA-binding protein PNO1
Protein synthesis / degradation / folding					
cct-5	C07G2.3	TCP-1 like chaperonin	1.90E-203	ENSEMBL:ENSP00000280326	T-complex protein 1 subunit epsilon
dnj-8	C56C10.13		1.10E-73	ENSEMBL:ENSP00000365007	Isoform 1 of DnaJ homolog subfamily C member 16 precursor
D2085.3	D2085.3	translation initiation factor (EIF)	2.90E-31	ENSEMBL:ENSP00000273783	Translation initiation factor eIF-2B subunit epsilon
cct-6	F01F1.8		6.81E-183	ENSEMBL:ENSP00000275603	T-complex protein 1 subunit zeta
F30A10.10	F30A10.10	ubiquitin carboxyl-termianl hydrolase	1.60E-42	ENSEMBL:ENSP00000383157	ubiquitin specific peptidase 48
dpy-11	F46E10.9	thioredoxin	1.80E-54	ENSEMBL:ENSP00000267434	Thioredoxin domain-containing protein 1 precursor
F52C6.12	F52C6.12		3.00E-22	ENSEMBL:ENSP00000222402	Ubiquitin-conjugating enzyme E2 D4
F53F4.11	F53F4.11		7.90E-15	ENSEMBL:ENSP00000379760	Ribosomal L1 domain-containing protein 1
iff-2	F54C9.1	initiation factor 5A	8.70E-48	ENSEMBL:ENSP00000336702	Isoform 2 of Eukaryotic translation initiation factor 5A-1
dcn-1	H38K22.2		6.00E-51	ENSEMBL:ENSP00000292782	DCN1-like protein 1
*cct-4***	K01C8.10	TCP-1 like chaperonin	4.30E-179	ENSEMBL:ENSP00000377958	T-complex protein 1 subunit delta
apc-2	K06H7.6		5.00E-54	ENSEMBL:ENSP00000314004	Anaphase-promoting complex subunit 2 (APC2)
smo-1	K12C11.2		4.10E-25	ENSEMBL:ENSP00000376076	Small ubiquitin-related modifier 1 Precursor (SUMO-1)
cct-1	T05C12.7	TCP-1 like chaperonin	3.00E-196	ENSEMBL:ENSP00000317334	T-complex protein 1 subunit alpha
cct-7	T10B5.5	TCP-1 like chaperonin	7.10E-188	ENSEMBL:ENSP00000258091	T-complex protein 1 subunit eta
cct-2	T21B10.7	TCP-1 like chaperonin	4.20E-183	ENSEMBL:ENSP00000299300	T-complex protein 1 subunit beta
T27A3.2	T27A3.2	ubiquitin carboxyl-terminal hydrolase	3.90E-137	ENSEMBL:ENSP00000229268	Isoform Long of Ubiquitin carboxyl-terminal hydrolase 5
cdc-37[16,17]	**W08F4.8**		**2.00E-73**	**ENSEMBL:ENSP00000222005**	**Hsp90 co-chaperone Cdc37**
rpl-31	W09C5.6	Ribosomal protein L31e	8.60E-41	ENSEMBL:ENSP00000264258	60S ribosomal protein L31
*cct-8***	Y55F3AR.3	TCP-1 like chaperonin	3.60E-166	ENSEMBL:ENSP00000286788	T-complex protein 1 subunit theta
Signaling and membrane trafficking					
sec-10	C33H5.9		1.80E-118	VG:OTTHUMP00000028003	Exocyst complex component 5
cdk-4	F18H3.5	serine/threonine kinase (CDC2/CDKX subfamily)	7.20E-60	ENSEMBL:ENSP00000265734	Cell division protein kinase 6
nekl-3	F19H6.1	serine/threonine kinase	9.91E-111	ENSEMBL:ENSP00000356355	Serine/threonine-protein kinase Nek7
mpk-1[18]	**F43C1.2**	**serine/threonine kinase (CDC2/CDC28 subfamily)**	**2.80E-154**	**ENSEMBL:ENSP00000215832**	**Mitogen-activated protein kinase 1**
****ina-1***[19]	**F54G8.3**	**Integrin alpha chain**	**2.00E-83**	**ENSEMBL:ENSP00000264107**	**Isoform Alpha-6X1A of Integrin alpha-6 precursor**
gon-2	T01H8.5		1.20E-274	ENSEMBL:ENSP00000366314	Transient receptor potential cation channel subfamily M member 3
cdk-1[20]	**T05G5.3**	**serine/threonine kinase (CDC2/CDKX subfamily)**	**4.80E-102**	**ENSEMBL:ENSP00000306043**	**Cell division control protein 2 homolog (Cyclin-dependent kinase 1)**
****unc-40***[21]	**T19B4.7**	**membrane protein**	**1.30E-164**	**ENSEMBL:ENSP00000304146**	**Netrin receptor DCC precursor**
lit-1	W06F12.1	serine/threonine kinase (CDC2/CDC28 subfamily)	2.50E-144	ENSEMBL:ENSP00000262393	nemo-like kinase
Y11D7A.9	Y11D7A.9		0.000000047	ENSEMBL:ENSP00000300730	Post-GPI attachment to proteins factor 2
Metabolism					
C06E4.6	C06E4.6	dehydrogenase	2.00E-25	ENSEMBL:ENSP00000263278	17-beta-hydroxysteroid dehydrogenase 14
C06E7.3	C06E7.3	S-adenosylmethionine synthetase	4.40E-156	ENSEMBL:ENSP00000303147	S-adenosylmethionine synthetase isoform type-2
C48A7.2	C48A7.2	phosphate permease	1.90E-105	ENSEMBL:ENSP00000272542	Sodium-dependent phosphate transporter 1
F01F1.12	F01F1.12	Fructose-biphosphate aldolase	2.70E-117	ENSEMBL:ENSP00000336927	Fructose-bisphosphate aldolase A
F43G9.1	F43G9.1	isocitrate dehydrogenase	4.30E-126	ENSEMBL:ENSP00000299518	Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor
R06C7.5	R06C7.5	adenylosuccinate lyase	7.80E-111	ENSEMBL:ENSP00000216194	Isoform 1 of Adenylosuccinate lyase
T01C3.1[22]	**T01C3.1**	**WD domain, G-beta repeats**	**3.60E-29**	**ENSEMBL:ENSP00000355958**	**Isoform 1 of Denticleless protein homolog**
T03F1.8	T03F1.8	guanylate kinase	1.30E-51	ENSEMBL:ENSP00000317659	Guanylate kinase

bus-8	T23F2.1	glycosyltransferase	4.90E-38	ENSEMBL:ENSP00000238477	Isoform 1 of Alpha-1,3-mannosyltransferase ALG2
rnr-1	T23G5.1	Ribonucleoside-disphosphate reductase large chain	0	ENSEMBL:ENSP00000300738	Ribonucleoside-diphosphate reductase large subunit
Cell Cycle / Cell Division					
rsa-1	C25A1.9		5.20E-15	ENSEMBL:ENSP00000261475	Isoform 1 of Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma
mdf-1	C50F4.11		5.60E-09	VG:OTTHUMP00000200098	MAD1 mitotic arrest deficient-like 1
emb-27	F10B5.6	cell division control protein	1.20E-39	ENSEMBL:ENSP00000364457	CDC16 protein
mat-3	F10C5.1		4.20E-80	ENSEMBL:ENSP00000378350	Cell division cycle protein 23 homolog
rsa-2	Y48A6B.11		2.50E-06	ENSEMBL:ENSP00000354486	Isoform 1 of Golgin subfamily A member 4
cdt-1	Y54E10A.15		6.30E-20	ENSEMBL:ENSP00000301019	DNA replication factor Cdt1
fzy-1	ZK177.6	CDC20	3.50E-26	ENSEMBL:ENSP00000308450	Cell division cycle protein 20 homolog
Nuclear import / export					
npp-9	F59A2.1	Nucleoporin	2.60E-63	ENSEMBL:ENSP00000283195	E3 SUMO-protein ligase RanBP2
npp-4	Y54E5A.4		1.80E-16	ENSEMBL:ENSP00000380202	Nuclear pore complex protein Nup98-Nup96 Precursor
Cytoskeletal Regulation					
unc-60[23]	**C38C3.5**	**actin depolymerizing factor**	**4.00E-11**	**ENSEMBL:ENSP00000298159**	**Cofilin-2**
cdc-42[24]	**R07G3.1**	**RAS protein**	**8.30E-91**	**ENSEMBL:ENSP00000337669**	**Isoform 2 of Cell division control protein 42 homolog precursor**
Nematode-specific gene with unknown function					
C09H10.7	C09H10.7				
F28F8.5	F28F8.5				
gon-14	F44C4.4	hAT family dimerisation domain			
F52C6.13	F52C6.13				
Y87G2A.1	Y87G2A.1				
Uncharacterized conserved genes					
C06A5.1	C06A5.1		2.70E-20	VG:OTTHUMP00000200036	integrator complex subunit 1
C23G10.8	C23G10.8	S. pombe adenylyl cyclase-associated protein (weak)	0.0000026	VG:OTTHUMP00000076919	
C43H8.1	C43H8.1		6.60E-34	ENSEMBL:ENSP00000362605	cDNA FLJ75987, highly similar to Homo sapiens zinc finger and BTB domain containing 8 opposite strand (ZBTB8OS), mRNA
nol-10	F32E10.1		6.61E-137	ENSEMBL:ENSP00000371101	Isoform 1 of Nucleolar protein 10
F55C5.4	F55C5.4		2.50E-16	ENSEMBL:ENSP00000275830	CDNA FLJ20311 fis, clone HEP07319
K07F5.14	K07F5.14		4.20E-18	VG:OTTHUMP00000021645	NOL8 nucleolar protein 8
T20B12.1	T20B12.1		1.30E-90	ENSEMBL:ENSP00000313953	tetratricopeptide repeat domain 27, TTC27
Y44F5A.1	Y44F5A.1		4.30E-19	ENSEMBL:ENSP00000351100	WD repeat-containing protein 55
cacn-1	W03H9.4		4.10E-112	ENSEMBL:ENSP00000221899	Isoform 2 of Uncharacterized protein C19orf29

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Table S4 Timing and degree of AC invasion into the vulval epithelium: mutant analysis and off-target RNAi controls.

Genotype / Treatment	ACs showing full, partial, or no invasion							
	P6.p 4-cell stage (mid-to-late L3 stage)				**P6.p 8-cell stage (early L4 stage)**			
	% Full invasion	**% Partial invasion**	**% No invasion**	**n=**	**% Full invasion**	**% Partial invasion**	**% No invasion**	**n=**
wild-type (N2)	100	0	0	> 100	100	0	0	> 100
hda-1(e1795)	77%	0%	23%	30	71%	16%	14%	51
hda-1(ok1595)	17%	0%	83%	24	10%	0%	90%	21
C48A7.2*(ok2116)*	0%	0%	100%	27	35%	4%	61%	23
mep-1(q660)	36%	0%	64%	28	33%	0%	67%	21
mep-1(ok421)	14%	6%	80%	35	30%	0%	70%	20
mep-1(n3702)	90%	0%	10%	20	97%	0%	3%	36
cacn-1(tm3126)	100%	0%	0%	51	100%	0%	0%	60
cct-2(ok3438)[a]	-	-	-		-	-	-	
cct-6(ok2904)[b]	-	-	-		0%	0%	100%	1
lit-1(ok649)[c]	-	-	-		-	-	-	
cacn-1(tm3042)[d]	-	-	-		-	-	-	
unc-62(e644)[e]	100%	0%	0%	25	100%	0%	0%	50
unc-62(mu232)[f]	100%	0%	0%	20	100%	0%	0%	20
hbl-1(mg285)	60%	0%	40%	20	95%	0%	5%	20
hbl-1(ve18)	22%	7%	70%	27	75%	13%	13%	40
off-target RNAi control experiment:								
rrf-3(pk1426)*; *lam-1::GFP								
L4440	100%	0%	0%	50				
cct-5(RNAi)[g]	42%	0%	58%	12				
cct-7(RNAi)[g]	83%	0%	17%	18				
cacn-1(RNAi)[g]	89%	7%	4%	28				
F28F8.5*(RNAi)*[i]	62%	0%	38%	13				
F28F8.5*(RNAi)*[j]	62%	8%	31%	13				
T20B12.1*(RNAi)*[g]	92%	0%	8%	12				
lit-1(RNAi)[g]	90%	0%	10%	10				
cdc-37(RNAi)[h]	50%	10%	40%	10				
cdc-37(RNAi)[i]	60%	0%	40%	10				
unc-62(RNAi)[h]	70%	0%	30%	10				
unc-62(RNAi)[j]	55%	9%	36%	11				
eri-1(mg366); lin-15B(n744)								
L4440	100%	0%	0%	50				
T03F1.8*(RNAi)*[g]	80%	0%	20%	10				

[a] Animals do not survive to the time of AC invasion (L1 arrest, n=6, L2 arrest n=24)
[b] A majority of animals do not survive to the time of AC invasion (L2 arrest n=32), 1 animal survived and exhibited an P.6.p 8-cell stage AC invasion defect
[c] Unable to distinguish homozygous null animals, no AC invasion defect observed (n=25)
[d] in frame deletion
[e] molecular information unknown
[f] missense mutation
[g] 100bp dsRNA construct designed to minimize off target affects
[h] ORF dsRNA clone from Vidal RNAi library
[i] genomic dsRNA clone from Ahringer RNAi library
[j] ORF dsRNA clone

Table S5. Timing and degree of AC invasion into the vulval epithelium: uterine-specific RNAi. While RNAi targeting all genes tested had an AC invasion defect in *rrf-3(pk1426)* animals (RNAi sensitive background), only those genes that showed AC transgene localization (Fig. 2, fig. S3 and fig. S4) had invasion defects in *rde-1(ne219); fos-1a>rde-1; rrf-3(pk1426)*; a background where only the uterine cells are sensitive to RNAi.

Genotype / Treatment	ACs showing full, partial, or no invasion			
	P6.p 4-cell stage (mid-to-late L3 stage)			
	% Full invasion	**% Partial invasion**	**% No invasion**	**n=**
Site of action:				
(general RNAi sensitivity)				
rrf-3(pk1426);				
L4440	100%	0%	0%	27
cct-5(RNAi)	17%	0%	83%	23
cct-7(RNAi)	21%	0%	79%	24
hda-1(RNAi)	43%	0%	57%	37
mep-1(RNAi)	55%	0%	45%	69
fos-1a(RNAi)	55%	0%	45%	55
C48A7.2*(RNAi)*	48%	0%	52%	76
cacn-1(RNAi)	68%	0%	32%	50
F28F8.5*(RNAi)*	54%	0%	46%	66
T20B12.1*(RNAi)*	55%	0%	45%	53
lit-1(RNAi)	69%	0%	31%	36
cdc-37(RNAi)	56%	0%	44%	61
T03F1.8*(RNAi)*	59%	0%	41%	79
unc-62(RNAi)	71%	0%	29%	31
hbl-1(RNAi)	73%	0%	27%	17
(uterine specific RNAi sensitivity)				
rde-1(ne219); fos-1a>*RDE-1;*rrf-3(pk1426);				
L4440	100%	0%	0%	15
cct-5(RNAi)	36%	0%	64%	28
cct-7(RNAi)	65%	0%	35%	31
hda-1(RNAi)	54%	0%	46%	35
mep-1(RNAi)	56%	0%	44%	32
fos-1a(RNAi)	43%	0%	57%	42
C48A7.2*(RNAi)*	89%	0%	11%	35
cacn-1(RNAi)	82%	0%	18%	49
F28F8.5*(RNAi)*	91%	0%	9%	45
T20B12.1*(RNAi)*	81%	0%	19%	37
lit-1(RNAi)	74%	0%	26%	27
cdc-37(RNAi)	78%	0%	22%	41
T03F1.8*(RNAi)*	86%	0%	14%	32
unc-62(RNAi)	100%	0%	0%	55
hbl-1(RNAi)	100%	0%	0%	56

Table S6. Extrachromosomal array and integrated strain generation.

***Ex* Strain Designation**	***Ex* Designation**	**Construct**	**Co-injection marker**
NK839	*qyEx171*	*cct-7::GFP*	*unc-119+*
***Is* Strain Designation**	***Is* Designation**	**Construct**	**Co-injection marker**
NK370	*qyIs49*	*T03F1.8::YFP*	*unc-119+*
NK448	*qyIs69*	*C48A7.2::YFP*	*unc-119+*
NK451	*qyIs72*	*cdc-37::YFP*	*unc-119+*
NK556 NK557	*qyIs90* *qyIs91*	*egl-43L>GFP*	*unc-119+*
NK558 NK559	*qyIs92* *qyIs93*	*hda-1::GFP*	*unc-119+*
NK598 NK599	*qyIs96* *qyIs97*	*cacn-1>GFP*	*unc-119+*
NK607	*qyIs99*	*unc-62>GFP*	*unc-119+*
NK624	*qyIs100*	*T20B12.1::GFP*	*unc-119+*
NK671	*qyIs114*	*cdh-3>cacn-1::GFP*	*unc-119+*

Table S7. Primer sequences and templates used for PCR fusions and restriction enzyme cloning.

Primer sequence	**Primer Type**	**Amplicon**	**Template**
5'TAATGTGAGTTAGCTCACTC ATTAGG 3'	Forward	*cdh-3* promoter	*cdh-3>*, pPD107.94/mk62-63
5'AACGATGGATACGCTAACAA CTTGG 3'	Forward nested	*cdh-3* promoter	*cdh-3>*, pPD107.94/mk62-63
5'TTTCTGAGCTCGGTACCCTC CAAG 3'	reverse	*cdh-3* promoter	*cdh-3>*, pPD107.94/mk62-63
5'ATGAGTAAAGGAGAAGAACT TTTCAC 3'	forward	GFP	pPD95.81 (GFP)
5'CTCGCGCGTTTCGGTGATGA CGGTGA 3'	reverse	GFP	pPD95.81 (GFP)
5'CTACTAGTCGGCCGTACGG GCCCTT 3'	reverse nested	GFP	pPD95.81 (GFP)
5'ATGAGTAAAGGAGAAGAACT TTTC 3'	forward	YFP	pDRS64(*cdh-3>*FOS-1A::YFP)
5'TCTACCGTAAGAAGGAAGAG AGCTCCAG 3'	reverse	YFP	pDRS64(*cdh-3>*FOS-1A::YFP)
5'AGCTTGCATGCCTGCAGGTC GACTC 3'	forward	GFP for *egl-43L>*GFP	pPD95.81
5'AAGATTTTCAAGGAGAATGA CTGATCC 3'	forward	*T03F1.8::YFP*	Cosmid T03F1
5'ACTGGTCGATAGCCAACTTG	forward	*T03F1.8::YFP*	Cosmid T03F1

TTGAGGG 3’	nested		
5’AGTGAAAAGTTCTTCTCCTTTACTCATTTTTTTGGAGGTTTTTTCGAGATCATC 3’	reverse YFP extension	*T03F1.8::YFP*	Cosmid T03F1
5’AGACCATAGCAGTTCAGAAGAGAC 3’	forward	*C48A7.2::YFP*	Cosmid T12B3
5’ACCCTTTCTGCGTTTTCGGTAATC 3’	forward nested	*C48A7.2::YFP*	Cosmid T12B3
5’GAAAAGTTCTTCTCCTTTACTCATGAAGAAGAGCTGGAGGATAGAATC 3’	reverse YFP extension	*C48A7.2::YFP*	Cosmid T12B3
5’TGTACACGTGGGACTCGAACTGTC 3’	forward	*cdc-37::YFP*	Cosmid W08F4
5’TTCGCGAGTTTTCAAGAGGGACAG 3’	forward nested	*cdc-37::YFP*	Cosmid W08F4
5’gaaaagttcttctcctttactcatGGAGCTGGTTGTTGGCTCTTCCTC 3’	reverse YFP extension	*cdc-37::YFP*	Cosmid W08F4
5’GCACATCATGTGTCAAGTGATG 3’	forward	*egl-43L>GFP*	Cosmid W02B7
5’agtcgacctgcaggcatgcaagctGTCTGTGTCGATGCTCATCCTG	reverse GFP extension	*egl-43L>GFP*	Cosmid W02B7
5’CGGCTCCTTTGACTGTCTCG 3’	forward	*hda-1::GFP*	Cosmid C35A5
5’TCAAAGAGCTTTCCTACGACC 3’	forward nested	*hda-1::GFP*	Cosmid C35A5
5’aagttcttctcctttactcatCTCTGTCTTCTGACGCTTTTCACCA 3’	reverse GFP extension	*hda-1::GFP*	Cosmid C35A5
5’ATGCTGTCATCAATAACCTCAAAACGCG 3’	forward	*cacn-1>GFP*	N2 gDNA
5’CAGTTCGTAATCTGGTTGACAGAGCAAG 3’	forward nested	*cacn-1>GFP*	N2 gDNA
5’aagttcttctcctttactcatATGCTTTTTGGAATCTTTTCCCATAGT 3’	reverse GFP extension	*cacn-1>GFP*	N2 gDNA
5’ATGTAGCTGCCAGCCATGGATACC 3’	forward	*unc-62>GFP*	N2 gDNA
5’ATGCAAATCAGGTTGGGATGTTG 3’	forward nested	*unc-62>GFP*	N2 gDNA
5’cccacacttttgagtcgccgctcatGTTCCTGCAAGAGAGAAATATTAAATTTTG 3’	reverse GFP extension	*unc-62>GFP*	N2 gDNA
5’CAGTCAATTTAAGTGTTCCGAACGCCAAATG 3’	Forward	*T20B12.1::GFP*	N2 gDNA
5’CAACATAAACTCCCGGGAATTGGAGCTCAG 3’	forward nested	*T20B12.1::GFP*	N2 gDNA
5’agttcttctcctttactcatAATTGCCACACTATCCAGAAGAC 3’	reverse GFP extension	*T20B12.1::GFP*	N2 gDNA
5’cttggagggtaccgagctcagaaaATGGGAAAAGATTCC 3’	forward with reverse *cdh-3* extension	*cdh-3>cacn-1:GFP*	CACN-1::GFP plasmid
5’aactgcagATGGGAAAAGATTCCAAAAA 3’	forward (PstI)	*cacn-1::GFP*	N2 cDNA
5’aaggtaccCGACGACGATAGC	reverse (KpnI)	*cacn-1::GFP*	N2 cDNA

GATATTTCT 3’			
5’aatctagaCCGATATGGAAACACCATGG 3’	forward (XbaI)	C48A7.2 100bp dsRNA	N2 gDNA
5’aaaagcttTCTCCGACAGTGTAGATGAC 3’	reverse (HindIII)	C48A7.2 100bp dsRNA	N2 gDNA
5’aatctagaAGACTGGATTCGACTGGAAT 3’	forward (XbaI)	*cacn-1* 100bp dsRNA	N2 gDNA
5’aaaagcttGGGTAGAAGATATTAAACTT 3’	reverse (HindIII)	*cacn-1* 100bp dsRNA	N2 gDNA
5’aatctagaTTTGAGACAATGATTCGACA 3’	forward (XbaI)	*cct-5* 100bp dsRNA	N2 gDNA
5’aaaagcttCATTTGCTTGCAGAAGATGA 3’	reverse (HindIII)	*cct-5* 100bp dsRNA	N2 gDNA
5’aatctagaTCAGGCATGTACGCTTCTTC 3’	forward (XbaI)	*cct-7* 100bp dsRNA	N2 gDNA
5’aaaagcttCTTGGCACGACGAACAATCA 3’	reverse (HindIII)	*cct-7* 100bp dsRNA	N2 gDNA
5’aatctagaTCGAGAAGAAGCTTGCCGCA 3’	forward (XbaI)	*cdc-37* 100bp dsRNA	N2 gDNA
5’aagggcccTCCTTCTTGCGCCAGGCTTC 3’	reverse (ApaI)	*cdc-37* 100bp dsRNA	N2 gDNA
5’aatctagaTCACATCGAGTCGTCGAATG 3’	forward (XbaI)	*hda-1* 100bp dsRNA	N2 gDNA
5’aaaagcttAACAAAAGTGAGCTGCTCGA 3’	reverse (HindIII)	*hda-1* 100bp dsRNA	N2 gDNA
5’aatctagaAACCTGGGACCAACGTGACC 3’	forward (XbaI)	*lit-1* 100bp dsRNA	N2 gDNA
5’aaaagcttTCCCGTATACCTTCGCGCGC 3’	reverse (HindIII)	*lit-1* 100bp dsRNA	N2 gDNA
5’aatctagaTGATGCTGCATCTACATCGG 3’	forward (XbaI)	*mep-1* 100bp dsRNA	N2 gDNA
5’aaaagcttGTCTTGTTCAATCTCAGATG 3’	reverse (HindIII)	*mep-1* 100bp dsRNA	N2 gDNA
5’aatctagaAATAGCGGAAAGATCTGCGT 3’	forward (XbaI)	T03F1.8 100bp dsRNA	N2 gDNA
5’aaaagcttATGGGGCACGGATCAGAATG 3’	reverse (HindIII)	T03F1.8 100bp dsRNA	N2 gDNA
5’aatctagaGCTGCCTACATTCGACATGG 3’	forward (XbaI)	T20B12.1 100bp dsRNA	N2 gDNA
5’aaaagcttTATAGTTCTCCCATACATTC 3’	reverse (HindIII)	T20B12.1 100bp dsRNA	N2 gDNA
5’aatctagaATGTTCGAGGAATTGGATGC 3’	forward (XbaI)	F28F8.5 ORF dsRNA	N2 cDNA
5’aaaagcttTTAAGTGGTAAAATGTTTCC 3’	reverse (HindIII)	F28F8.5 ORF dsRNA	N2 cDNA
5’TGATTTCTGATTTCTCACGCTCTG 3’	forward	*cct-7::GFP*	N2 gDNA
5’GATCCTAGCTGCTTTGGTCCT 3’	forward nested	*cct-7::GFP*	N2 gDNA
5’aagttcttctcctttactcatTTGCCCGGGAAGTCCTGG 3’	reverse GFP extension	*cct-7::GFP*	N2 gDNA