

Harr et al.

List of Supplemental materials:

Supplemental Figure S1: Schematic of genetic insertions for muscle-specific emerin DamID and controls for . muscle-specific EMR-1 DamID. (relates to Figure 1)

Supplemental Figure S2: Genes aberrantly tethered, or released from the nuclear periphery in LMN-Y59C are enriched for the binding consensus of the E2F homolog EFL-2. (relates to Figure 1)

Supplemental Figure S3: Loss of CEC-4 does not affect heterochromatin array localization in hypoderm, but releases it in early embryos (relates to Figure 3)

Supplemental Figure S4: Abnormal sarcomeres and junctions in *LMN-Y59C* mutants are suppressed by *cec-4Δ*, but not *lem2Δ* (relates to Figure 5)

Supplemental Figure S5: Heterochromatic array sequestration by the *LMN-Y59C* mutant is rescued by *cec-4Δ* or by the chromodomain deficient *cec-4-CD2YA* mutation (relates to Figure 5)

Supplemental Figure S6: Loss of CEC-4 significantly changes chromatin position in the *LMN-Y59C*, but not the *LMN-WT* background. (relates to Figure 6)

Supplemental Figure S7: Genes containing EFL-2 motifs that are aberrantly tethered or released from the INM in *LMN-Y59C* muscle are rescued by *LMN-Y59C*; *cec-4Δ* (relates to Figure 7).

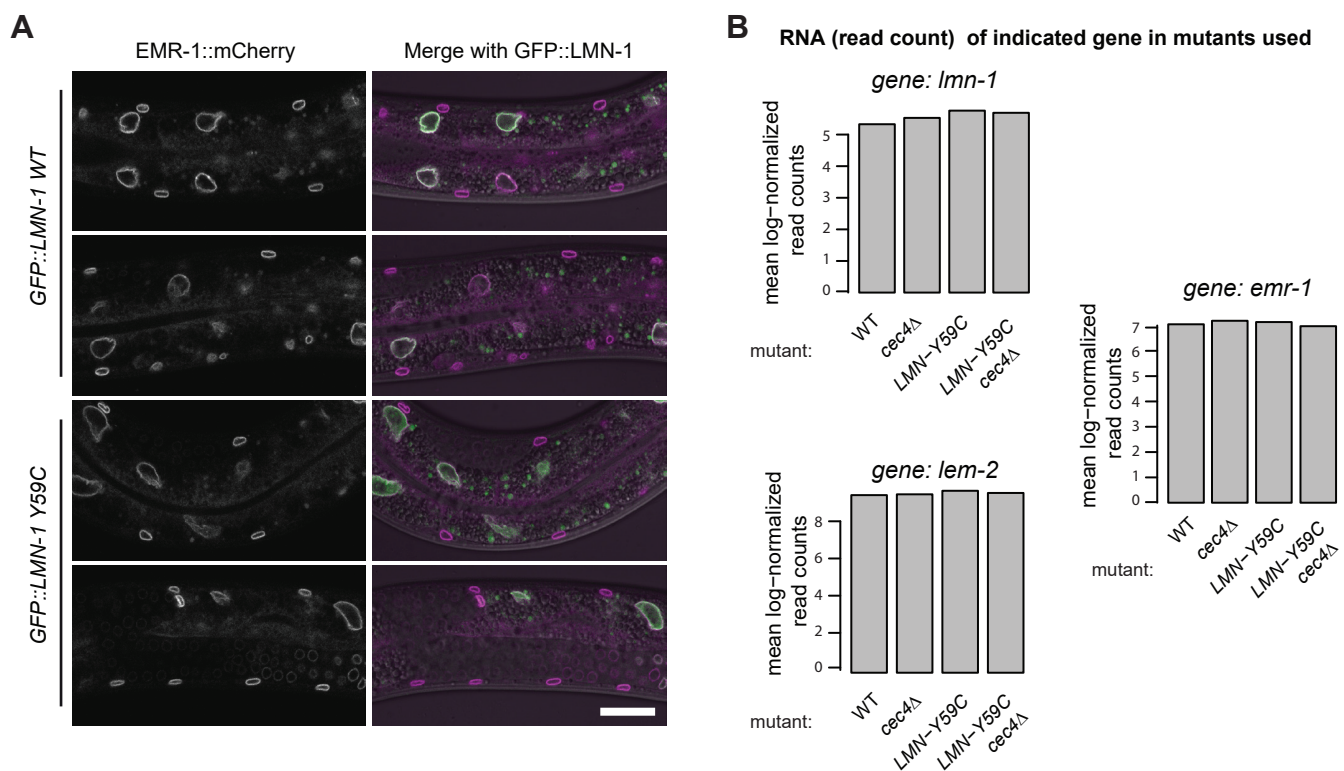
Supplemental Table S1: 97 genes with differential transcript abundance : '*LMN-Y59C*' vs 'WT'

Supplemental Table S2: 118 genes with differential transcript abundance : '*LMN-Y59C*; *cec-4*' vs '*LMN-Y59C*'

Supplemental Table S3: 8 genes with differential transcript abundance : '*cec-4Δ*' vs 'WT'

Supplemental Table S4: 27 genes with compensatory effects by *cec-4* deletion in the *LMN-Y59C* background

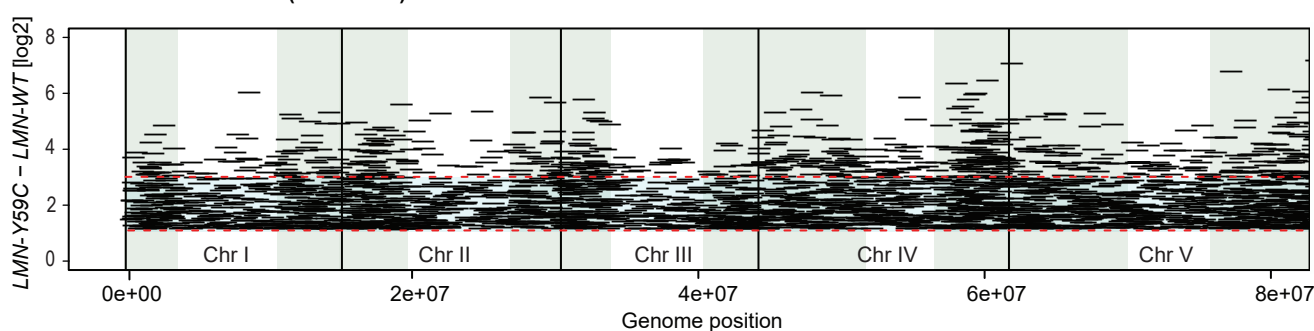
Supplemental Table S5: *C. elegans* strains used in the study



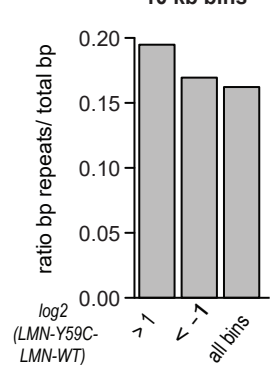
C 100 kb bins, absolute values of rolling means of 3 differential DamID log₂ ratios of LMN-Y59C - LMN-WT

DamID log ₂ ratios of LMN-Y59C - LMN-WT	Total # bins	% total	# bins in chr. arms	% in chr. arms	# bins in chr. core	% in chr. core
more peripheral (> 0.2 log ₂ [EMR-1/GFP])	235	28.5 %	212	90.2 %	23	9.7 %
no change (0.2 to -0.2 log ₂ [EMR-1/GFP])	420	50.8 %	230	54.7 %	190	45.2 %
more central (< -0.2 log ₂ [EMR-1/GFP])	171	20.7 %	71	41.5 %	100	58.4 %

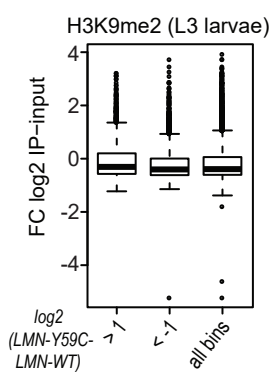
D EMR-1 DamID enrichment (10 kb bins) LMN-Y59C over LMN-WT



E Repeat element enrichment: 10 kb bins



F H3K9me enrichment: 10 kb bins



H3K9me enrichment: 10 kb bins

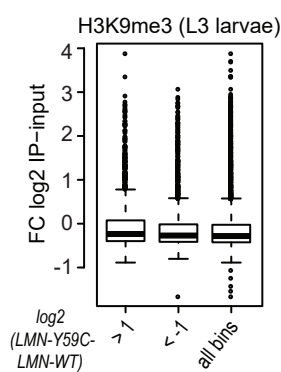


Figure S1: Controls for muscle-specific EMR-DamID A) Representative images of LMN-WT (BN403) and LMN-Y59C (BN404) containing strains showing unaltered NE association of emerin despite LMN mutation. Bar = 20 μ m. B) Mean log- normalized mRNA read counts from RNA-seq data of *lmn-1*, *emr-1* and *lem-2* in WT (N2), *cec-4* Δ (GW828), *LMN-Y59C* (GW653) and *LMN-Y59C; cec-4* Δ (GW1468) backgrounds. C) Tables of the absolute values of rolling means of 3 differential DamID log₂ ratios of *LMN-Y59C* - *LMN-WT* based on 100 kb bins. The table shows the percentage of bins in the arms and cores of chromosomes I-V. D) Graphs representing the position of 10 kb bins where the calculation $\log_2 (LMN-Y59C) - \log_2 (LMN-WT) = >1$. Red dotted lines indicate thresholds of $\log_2 (EMR-1/GFP) >1$ and >3 . E) Quantitation of repeat element enrichment in 10 kb regions of *LMN-Y59C* - *LMN-WT* ($\log_2[EMR-1/GFP] >1$ vs. all 10 kb bins. F) Enrichment levels of H3K9me2 or me3 based on whole L3 larval ChIP-seq in the 10 kb bins of *LMN-Y59C* - *LMN-WT* ($\log_2 [EMR-1/GFP] >1$ vs. all 10 kb bins.

A Transcription factor motif enrichment in genes in differentially positioned regions *LMN-Y59C* vs. *LMN-WT*

■ EFL-2 (E2F) [M0674_1.02d] ■ EFL-2 (E2F) [M0675_1.02d] ■ EFL-1 (E2F) [M2334_1.02d] ■ EFL-1 (E2F) [M4711_1.02d]

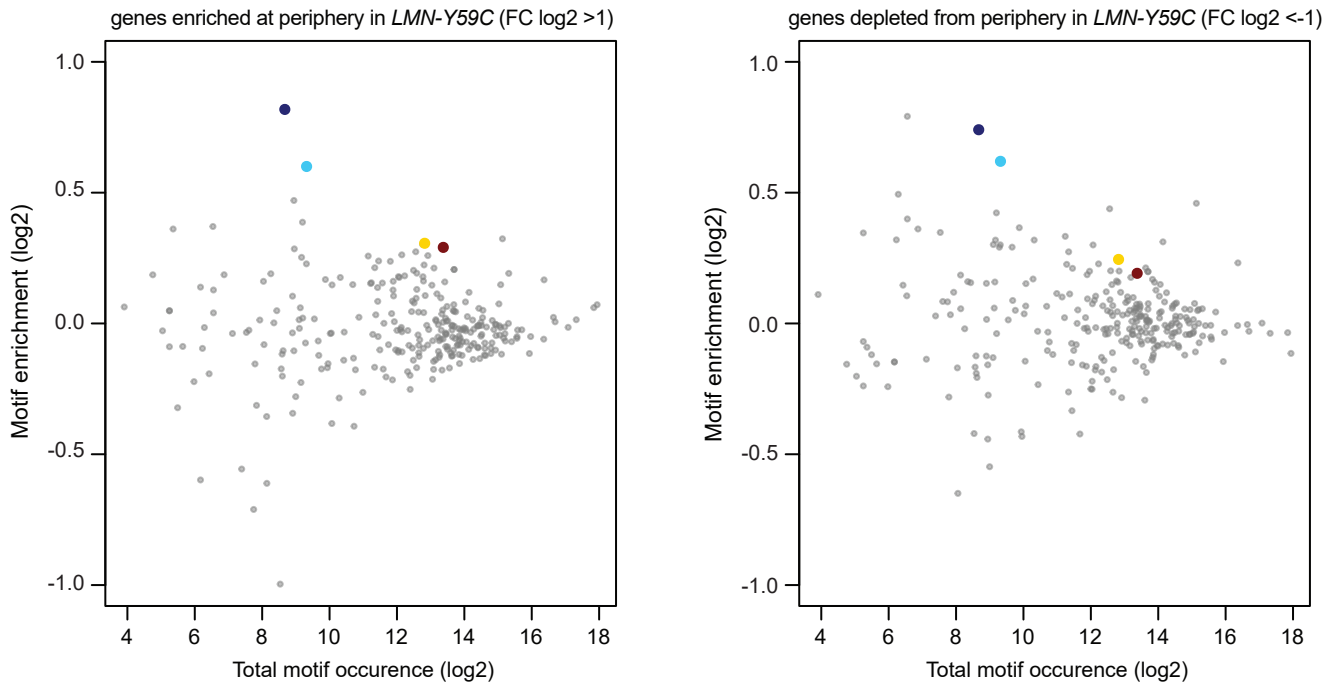
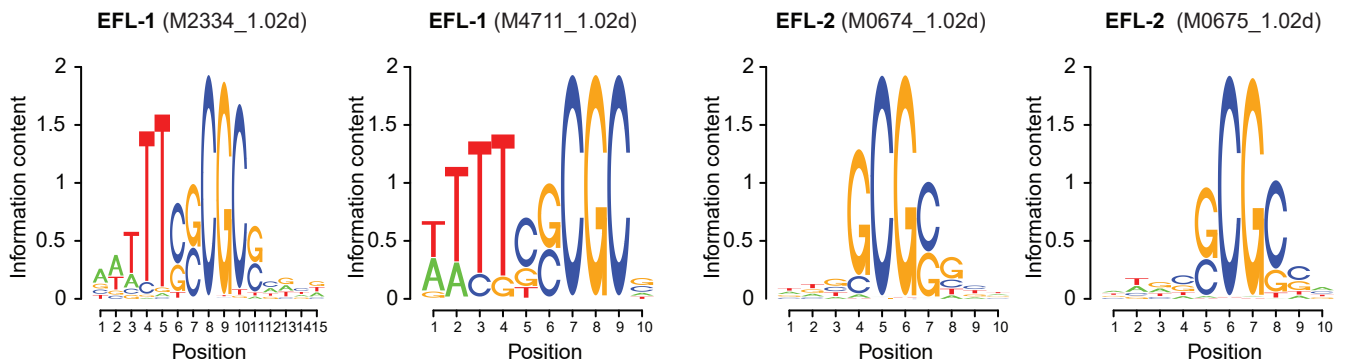
**B** Sequence logos of EFL-1 and EFL-2 motifs

Figure S2: Genes aberrantly tethered, or released from the nuclear periphery in *LMN-Y59C* are enriched for the binding consensus of the E2F homolog EFL-2. A) Plot showing enrichment of E2F transcription factor motifs in promoters of genes aberrantly tethered, or released from the nuclear periphery in the *LMN-Y59C* (>2 or <-2 fold change (FC) in log₂ [EMR-1/GFP] in *LMN-Y59C* over *LMN-WT* strains) versus occurrence in the whole genome. (B) Sequence logos showing the motifs recognized by the two E2F homologs, EFL-1 and EFL-2.

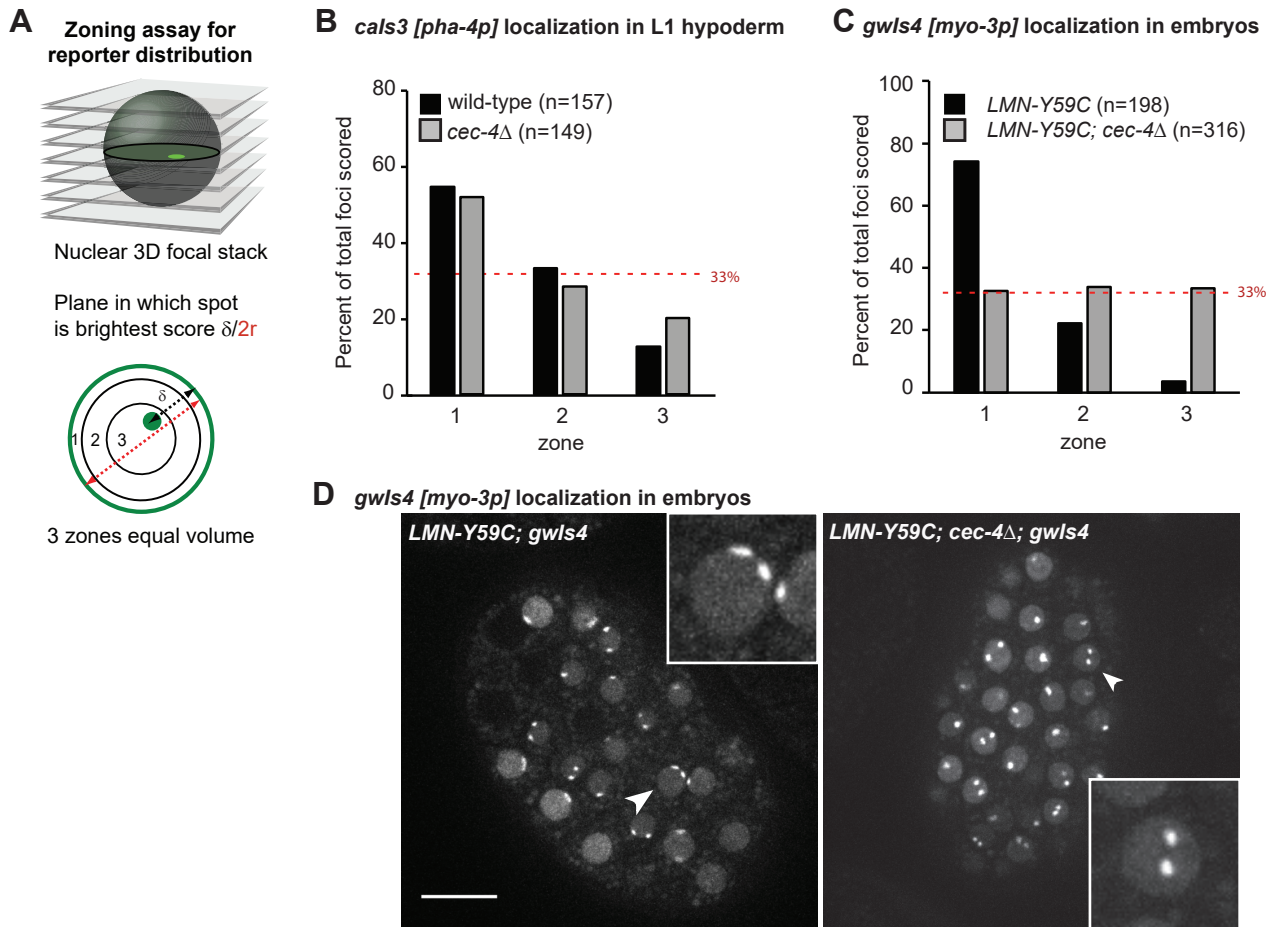
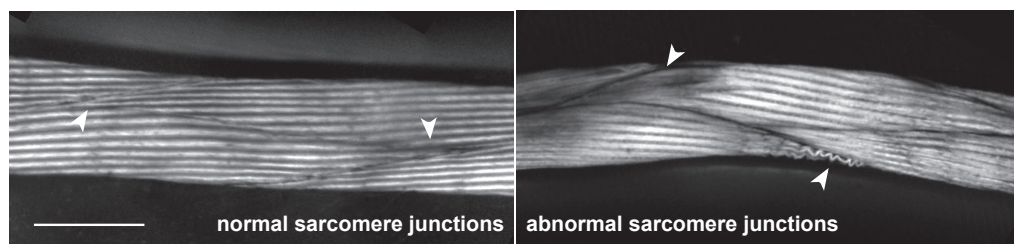
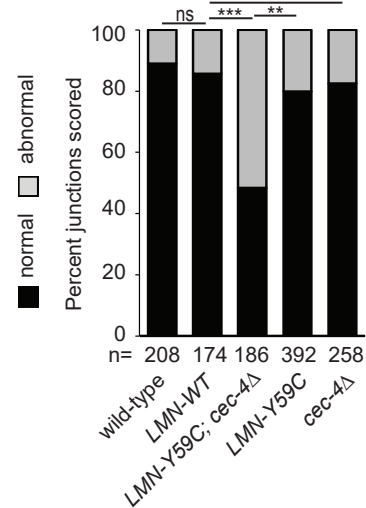


Figure S3: Loss of CEC-4 does not affect heterochromatin array localization in hypoderm, but releases it in early embryos. A) The zoning assay for subnuclear GFP-tagged reporter distribution in spherical cell types. B) Quantitation of the *cals3* (*pha-4p* reporter array) position using a zoning assay in hypoderm cells of wildtype or *cec-4*Δ L1 *C. elegans*. Data are from at least two biological replicas. Red dotted line is 33%, representing a random distribution in all three equal zones. C) as B, but quantitation of the *gwls4* *myo-3p* array position using the zoning assay in *C. elegans* early embryos expressing LMN-Y59C in wild type (GW654) or *cec-4*Δ (GW888) backgrounds. D) Confocal fluorescence microscopy of *C. elegans* early embryos (quantified in C) carrying the muscle-specific *gwls4* array and expressing LMN-Y59C in wild-type or *cec-4*Δ backgrounds. Bar = 10 μ m

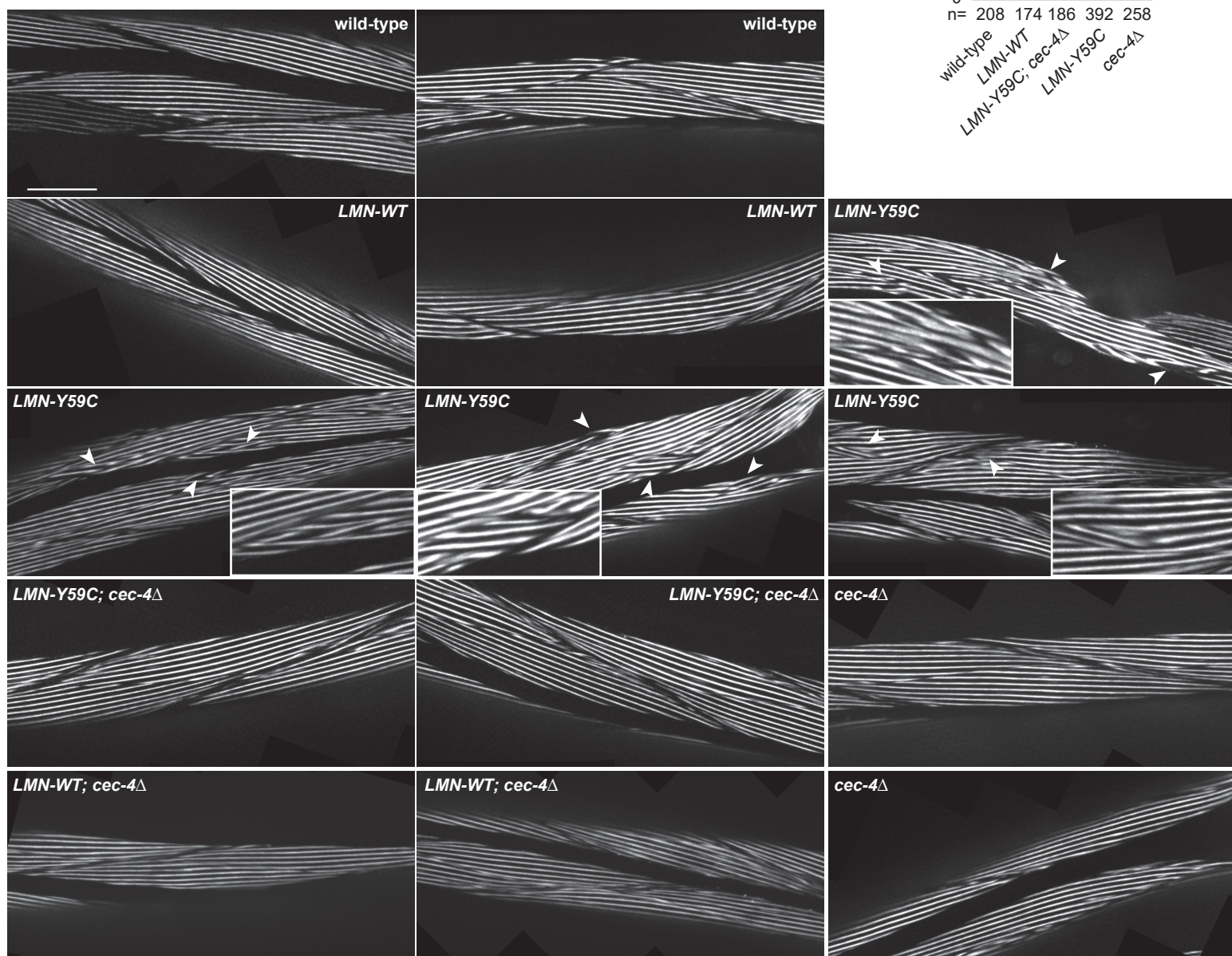
A Phalloidin-rhodamine labeling of actin



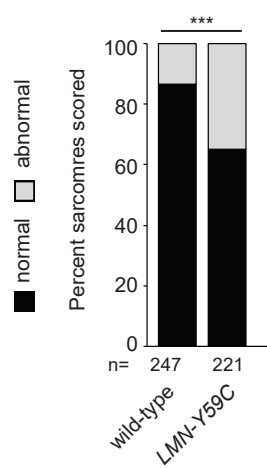
B Phalloidin-rhodamine labeling of actin



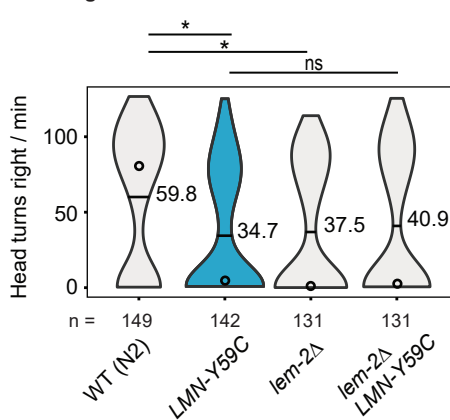
C GFP::MYO-3 live imaging



D GFP::MYO-3 live



E *C. elegans* L4 larval locomotion



F Phalloidin labeling of actin

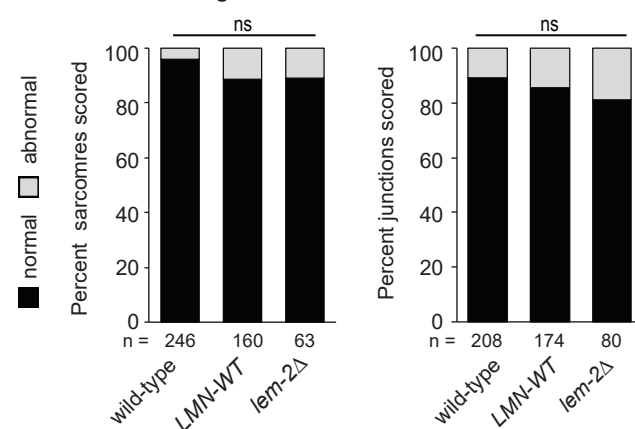


Figure S4: *LMN-Y59C*-induced abnormal sarcomeres and junctions are suppressed by *cec-4Δ*, but not *lem2Δ*. A) Representative images of phalloidin-rhodamine staining in L4/young adult *C. elegans*, showing normal and abnormal junctions between sarcomeres (see arrowheads). Bar= 20 μm. B) Quantitation of actin organization according to phalloidin-rhodamine staining in young adults of; wild-type (N2), *cec-4Δ* (GW828), *LMN-WT* (GW655), *LMN-Y59C* (GW653) and *LMN-Y59C; cec-4Δ* (GW1468), scoring for altered junctions between sarcomeres. Data from at least three biological replicas; n=total junctions scored. (***) p<0.001 and ns = non-significant (p>0.05), by Chi-squared test. C) Confocal fluorescence live imaging of L4/young adult *C. elegans* expressing GFP::MYO-3, in the following strains: wild-type (RW1596), *cec-4Δ* (GW1491), *LMN-WT* (GW1492), *LMN-WT; cec-4Δ* (GW1493), *LMN-Y59C* (GW1494) and *LMN-Y59C; cec-4Δ* (GW1495). Bar = 20 μm. D) Quantitation of GFP::MYO-3 organization in sarcomeres of L4/young adults. (***) p<0.0001, Chi-squared test. E) The deletion of *lem-2* causes defects in swimming assays that are epistatic with *LMN-Y59C*. L4 larvae from wild-type (N2), *LMN-Y59C* (GW653), *lem-2Δ* (GW1214), and *LMN-Y59C; lem-2Δ* (GW1226)) were transferred to liquid, and head bends to the right were counted as described in Materials and Methods. n= worms scored per genotype. Data are presented as violin plots where the horizontal bar indicates the mean and the empty dot indicates the median respectively. Values are taken from at least three independent assays with all genotypes quantified in parallel. (*) p<0.01 and ns = non-significant (>0.5), by Student's t test. F) Quantitation of sarcomere integrity and junction organization in muscle cells as in panel B, in the indicated strains: wild-type (N2), *LMN-Y59C* (GW653), *lem-2Δ* (GW1214). ns = non-significant by Chi-squared test.

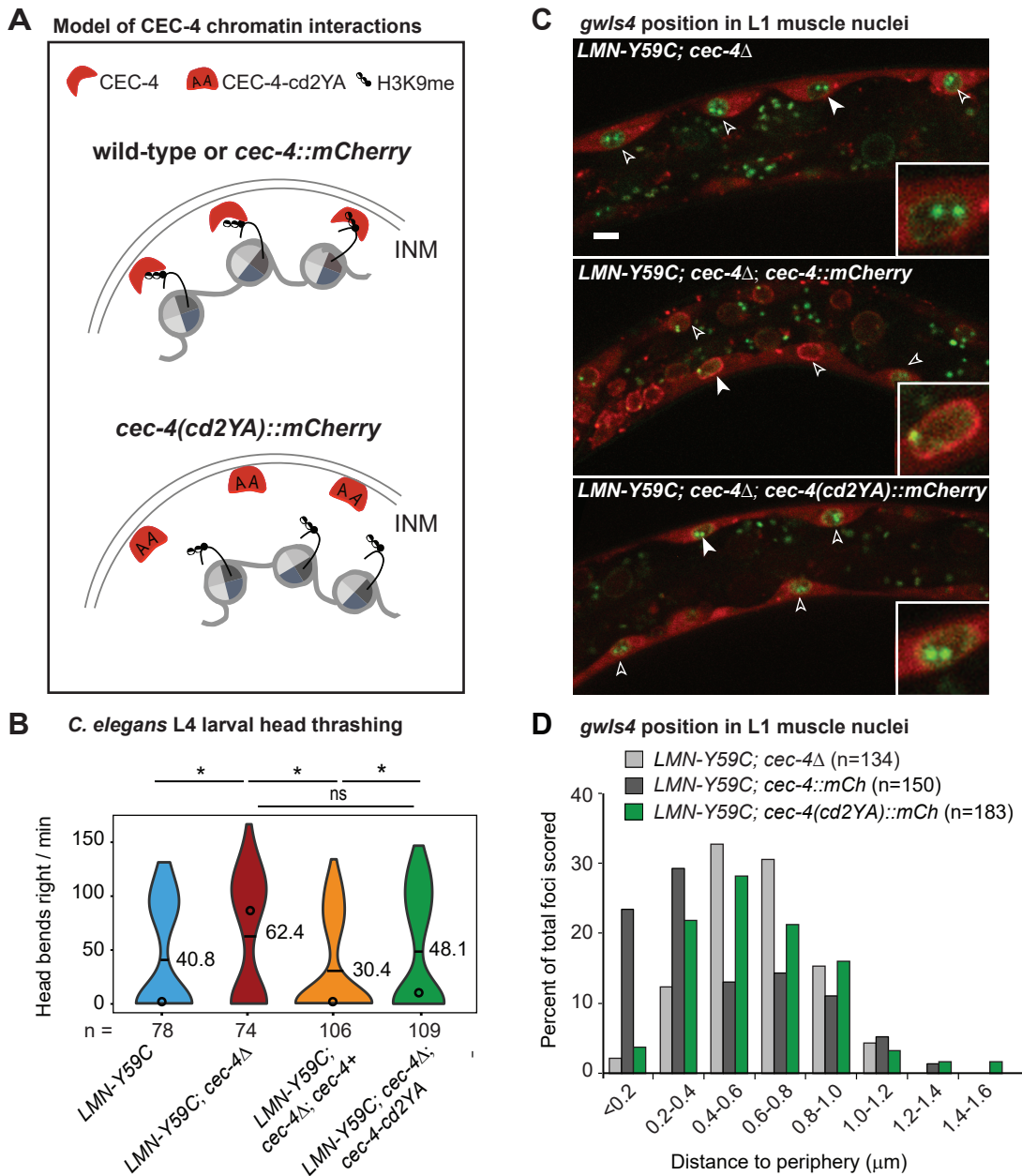


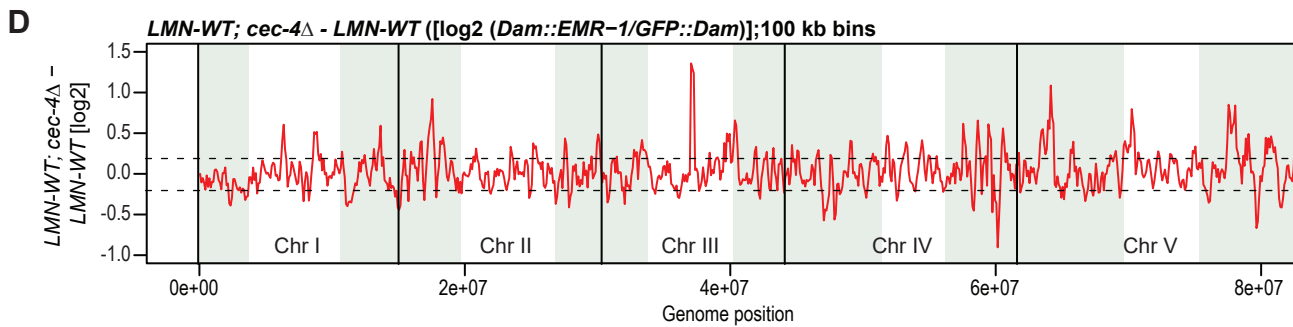
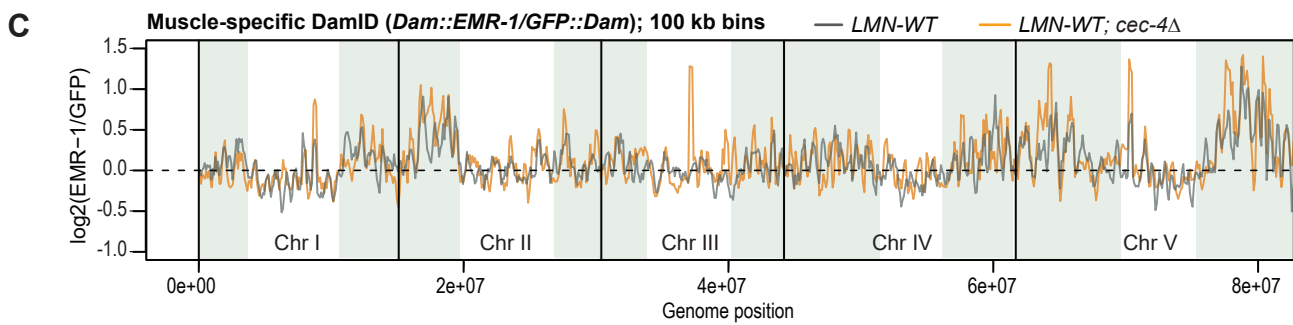
Figure S5: *LMN-Y59C* induced array sequestration is suppressed by *cec-4Δ* and by the chromodomain deficient *cec-4-CD2YA* mutant. A) Sketch of CEC-4 interacting with H3K9me^{1/2/3} marked chromatin (wild-type, top). The double point mutation (Y87A/Y111A) in the CEC-4 CD releases chromatin from the nuclear periphery (*cec-4-cd2YA::mCherry*, bottom (Gonzalez-Sandoval et al. 2015)). B) Quantitation of head thrashing in strains expressing *LMN-Y59C* and either *cec-4::mCherry* or *cec-4-cd2YA::mCherry*, (hereafter *mCh*) or no *cec-4*. *LMN-Y59C; gwlS4* (GW654), *cec-4Δ; gwlS4* (GW888), *LMN-Y59C; cec-4Δ; CEC-4::mCh*; *gwlS4* (GW1026) and *LMN-Y59C; cec-4Δ; CEC-4(cd2YA)::mCh; gwlS4* (GW1066). n = number of worms scored. (*) p < 0.01, ns = non-significant (p > 0.5), Student's t test. All genotypes were scored in parallel in three independent assays. C) Representative images of *C. elegans* L1 larvae bearing the muscle-specific *gwlS4* array, expressing *LMN-Y59C* in a *cec-4Δ* background (*LMN-Y59C; cec-4(ok3124); gwlS4* (GW888), to which either *cec-4::mCh* (*cec-4+*; GW1026) or *cec-4(cd2YA)::mCh* is restored (GW1066). Previous work showed that *cec-4::mCh* anchors arrays in embryos like CEC-4, while *cec-4(cd2YA)::mCh* does not (Gonzalez-Sandoval et al. 2015). Filled arrowheads indicate the muscle nuclei enlarged in insets. Images are a single focal plane. Bar = 10 μm. D) Quantitation of the *gwlS4* focus distance from the nuclear envelope (NE) in muscle cells of the strains shown in panel C. The distances measured as nearest radial distance from the focus to the NE. Probability values of *LMN-Y59C; cec-4Δ* vs *LMN-Y59C; cec-4Δ; cec-4::mCh* and *LMN-Y59C; cec-4Δ* vs *LMN-Y59C; cec-4Δ; cec-4(cd2YA)::mCh* are p < 0.0001 and ns (p > 0.05), respectively by Chi-squared tests.

A 100 kb bins, absolute values of rolling means of 3 differential DamID log₂ ratios of *LMN-Y59C;cec-4Δ* - *LMN-Y59C*

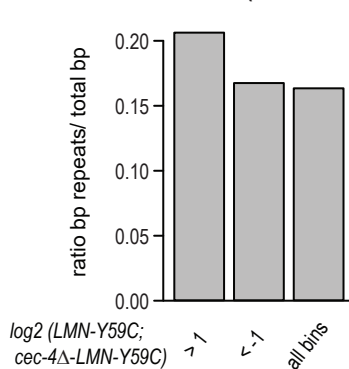
	total # bins	% total	# bins in chr. arms	% in chr. arms	# bins in chr. cores	% in chr. core
more peripheral (>0.2 log ₂ [EMR-1/Dam])	216	26.2 %	87	40.2%	129	59.7 %
no change (0.2 to -0.2 log ₂ [Emr-1/Dam])	405	49.0 %	236	58.2 %	169	41.7 %
more central (<-0.2 log ₂ [EMR-1/Dam])	205	24.8 %	190	92.6 %	15	7.3 %

B 100 kb bins, absolute values of rolling means of 3 differential DamID log₂ ratios of *LMN-WT;cec-4Δ* - *LMN-WT*

	total # bins	% total	# bins in chr. arms	% in chr. arms	# bins in chr. core	% in chr. core
more peripheral (>0.2 log ₂ [EMR-1/Dam])	166	20.1 %	111	66.8 %	55	33.1 %
no change (0.2 to -0.2 log ₂ [EMR-1/Dam])	558	67.6 %	320	57.3 %	238	42.6 %
more central (<-0.2 log ₂ [EMR-1/GFP])	102	12.3 %	82	80.3 %	20	19.6 %



E Repeat element enrichment: 10 kb bins (*EMR-1/GFP*)



F H3K9me modification enrichment: 10 kb bins (*EMR-1/GFP*)

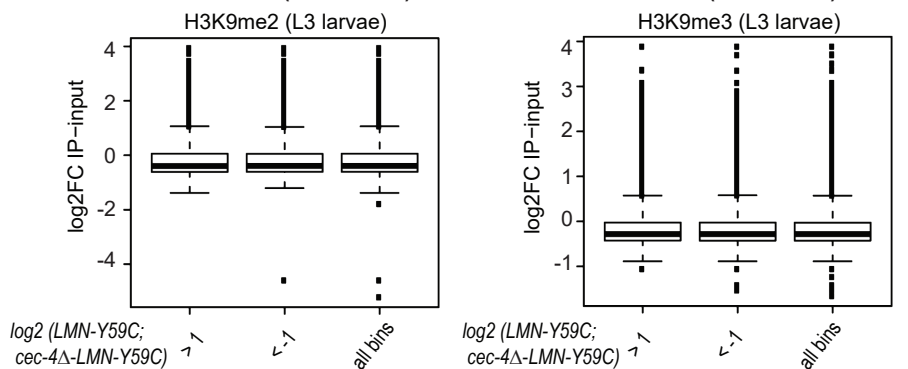
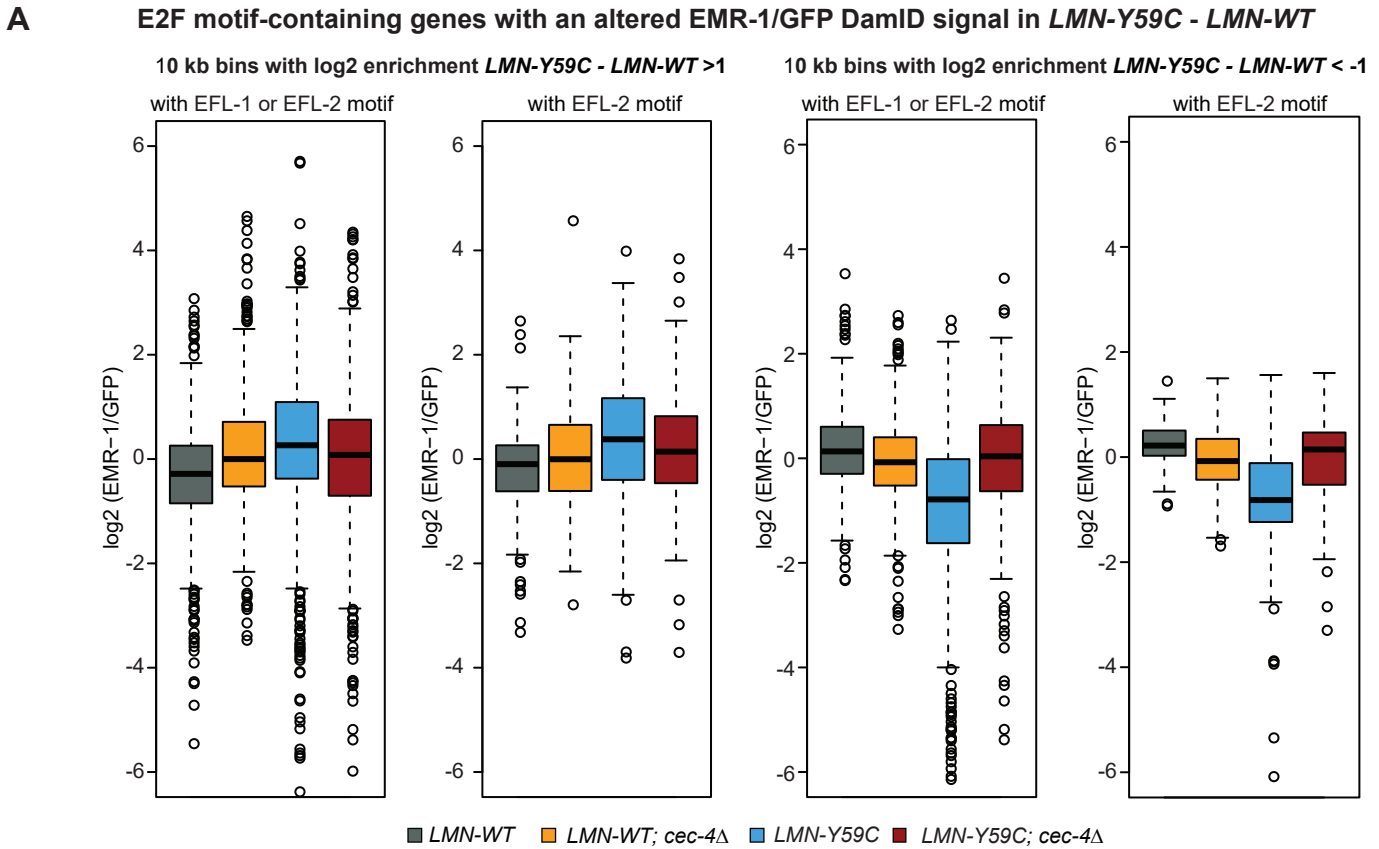
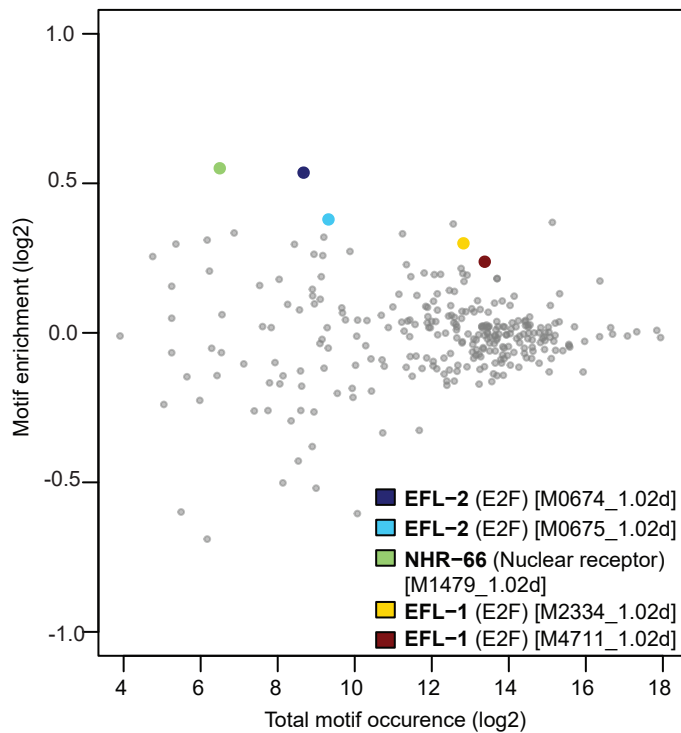


Figure S6: Loss of CEC-4 significantly changes chromatin position in the *LMN-Y59C*, but not the *LMN-WT* background. A) Table of 100 kb bins of the absolute values of rolling means of 3 differential DamID log₂ ratios of *LMN-Y59C; cec-4Δ* - *LMN-Y59C* showing the percent of bins in the arms and cores of chromosomes I-V. B) Table of 100 kb bins of the absolute values of rolling means of 3 differential DamID log₂ ratios of *LMN-WT; cec-4Δ* - *LMN-WT* showing the percent of bins in the arms and cores of chromosomes I-V. C) Line plot of log₂ (EMR-1::Dam/GFP::Dam) in *LMN-WT* and *LMN-WT; cec-4Δ*, L4/young adult *C. elegans* muscle for all autosomes. The signals are averaged over 3 sliding 100 kb windows. Chromosome arms are shaded in light green. Dotted line indicates zero log₂ ratio. D) Line plot of *LMN-WT; cec-4Δ* - *LMN-WT* (log₂) showing the differential association of EMR-1 in the *cec-4Δ* mutant strain compared to *LMN-WT*. Chromosome arms are shaded in light green. Dotted lines indicate 0.2 and -0.2 thresholds. E) Quantification of the number of base pair (bp) with a repetitive element over the total number of bp in each category (*LMN-Y59C* up [$>1 \log_2(\text{EMR-1/GFP})$], *LMN-Y59C* down [$<-1 \log_2(\text{EMR-1/GFP})$] and the whole genome. F) As Figure S1E for 10 kb bins of *LMN-Y59C; cec-4Δ* - *LMN-Y59C* ($\log_2 [\text{EMR-1/GFP}] \log_2 >1$ or <-1 vs. all 10 kb bins).



B TF motif enrichment *LMN-Y59C;cec-4*Δ - *LMN-Y59C*



C TF motif enrichment in muscle-expressed genes

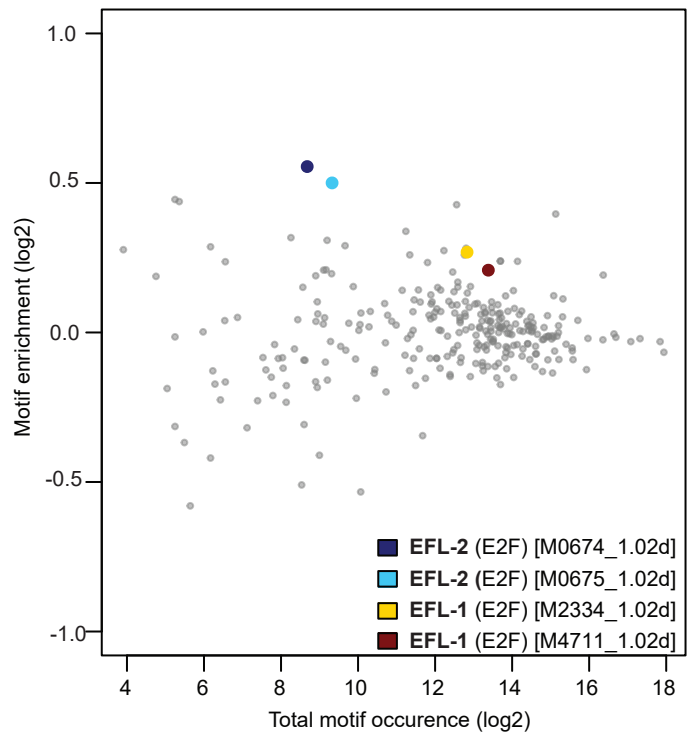


Figure S7: Genes containing EFL-2 motifs that are aberrantly tethered or released from the INM in *LMN-Y59C* muscle are rescued by *LMN-Y59C*; *cec-4Δ*. A) Boxplot showing the log₂ fold change (FC) in EMR-1/GFP based on 10 kb bins in the indicated genotypes for genes containing a EFL-2 motifs or either EFL-2 or EFL-1 motifs. Bins scored show enhanced tethering or release from the nuclear periphery in *LMN-Y59C* vs *LMN-WT* (log₂ >1 or <-1). B) Plot showing enrichment of E2F transcription factor motifs in promoters of genes from *cec-4* sensitive sequences (*LMN-Y59C*; *cec-4Δ* – *LMN-Y59C*, >0.2 or <-0.2 FC log₂ [EMR-1/GFP]) versus occurrence in the whole genome. C) Plot showing enrichment of E2F transcription factor motifs in promoters of muscle-expressed genes (i.e., genes expressed in *myo-2* and *myo-3* expressing cells) versus occurrence in the whole genome.

Table S1: 97 genes with differential transcript abundances : 'LMN-Y59C' vs 'WT'

Genes meeting significance criteria (FDR < 0.01) and (FC > 1.5), specified by the following five tab-delimited columns: Wormbase 'GeneID', the primary gene name or sequence name as extracted from Wormbase release 273 (Nov-1 2019) in 'gene name', the fold-changes of log₂ expression values of a first replicate sample pair in 'FC_log2_repl_a', the fold-changes of log₂ expression values of second replicate sample pair in 'FC_log2_repl_b' (Figure 7A), and the p-values for differential expression multiplicity corrected by the Benjamini-Hochberg method in 'FDR'.

#GeneID	gene name	FC_log2_repl_a	FC_log2_repl_b	FDR
WBGene00005016	sqt-1	-2.929635629	-1.607179923	3.30E-07
WBGene00015236	B0511.11	0.633438216	1.122141695	0.000416933
WBGene00015230	tag-344	1.113000491	0.914598375	0.008506665
WBGene00005017	sqt-2	-2.226775253	-1.496199671	4.18E-10
WBGene00044658	C01G10.17	0.70756948	0.748238635	0.006985979
WBGene00007231	C01G10.4	1.550408288	0.628462708	0.001360242
WBGene00015339	C02E7.6	-1.597870706	-1.038311007	0.000142131
WBGene00007404	best-5	-1.033740567	-0.980482313	1.59E-09
WBGene00004932	sod-3	1.28993283	0.668974716	0.007733759
WBGene00015642	C09E7.8	0.927714841	0.683926262	1.63E-05
WBGene00007484	C09G1.2	-1.678285516	-0.683286465	0.000907777
WBGene00000665	col-90	-2.625150205	-1.386176352	1.14E-08
WBGene00016667	C45E5.4	1.273016934	0.602318844	5.98E-09
WBGene00016970	C56E6.2	0.961299442	0.604204556	1.63E-06
WBGene00008390	D1086.3	-1.163989958	-0.917173549	0.000169926
WBGene00001864	him-5	-1.413766679	-0.655983632	3.51E-05
WBGene00008392	D1086.5	-1.333018636	-0.775010773	1.36E-08
WBGene00008425	D2045.8	-1.302448525	-0.690538447	6.73E-09
WBGene00001158	ech-9	-2.161196813	-0.792875419	0.000799176
WBGene00017305	ns pb-12	-1.909527393	-0.654624801	0.002770432
WBGene00000606	col-17	-2.694557575	-1.329917085	1.47E-07
WBGene00000649	col-73	-1.540711087	-1.439767633	4.50E-07
WBGene00000702	col-128	-1.101399436	-0.999362778	0.000383055
WBGene00045207	F13E9.14	1.279054602	0.949203904	1.27E-06
WBGene00008816	F14F8.8	1.750918948	0.970867683	1.48E-11
WBGene00003099	lys-10	0.746369523	0.904206337	0.007028456
WBGene00017717	F22F4.4	0.840488267	0.766576986	0.002352455
WBGene00005018	sqt-3	-2.440491213	-1.533413751	1.60E-12
WBGene00001067	dpy-5	-2.522815368	-1.959014444	2.61E-16
WBGene00003079	lsm-5	1.504614269	1.433013081	1.34E-76
WBGene00009222	fbxa-95	1.199188813	1.263198915	3.72E-10
WBGene00001074	dpy-13	-2.194050498	-1.108307233	2.17E-06
WBGene00017937	F30H5.3	-1.802625934	-1.168280929	1.36E-05
WBGene00009384	piit-1	1.436386638	0.761660059	5.98E-09

WBGene00009386	tag-290	1.157588536	0.679279411	2.50E-09
WBGene00018297	F41F3.3	-2.374655273	-0.864199413	4.72E-06
WBGene00018335	F42A9.6	0.651037168	0.598370511	0.006214941
WBGene00005702	sru-39	1.107344512	1.104066667	0.003224704
WBGene00009983	cut-2	-0.992976557	-0.937015371	0.004229825
WBGene00010125	dod-22	-0.7126715	-0.609028726	0.00897761
WBGene00000678	col-104	-1.299340145	-0.651850707	0.002839366
WBGene00000675	col-101	0.728558126	0.996653859	0.001864579
WBGene00003522	nas-3	-2.019947677	-1.14820081	1.52E-09
WBGene00019608	ani-2	1.596984618	1.291693261	2.56E-31
WBGene00006678	twk-25	1.766836774	0.641878327	3.69E-05
WBGene00006843	unc-119	0.861648662	0.842897625	7.90E-23
WBGene00000653	col-77	-1.604701959	-0.679425574	2.16E-06
WBGene00010958	ndfl-4	-1.169988455	-0.891981701	1.56E-10
WBGene00010996	R03G8.1	2.873251632	2.850023383	1.07E-23
WBGene00011105	R07E3.4	1.023470666	0.831912189	3.98E-10
WBGene00011107	R07E3.6	-1.214009935	-1.053741891	0.000615543
WBGene00011166	chil-22	0.59773076	0.594391248	0.000191214
WBGene00011244	R11D1.3	0.657647011	1.234335905	2.17E-06
WBGene00020033	R12E2.7	-1.42476644	-0.823948278	0.000136731
WBGene00011254	R12G8.1	1.049393674	0.65035201	0.00069061
WBGene00011262	pho-8	0.795999953	0.755644744	1.14E-07
WBGene00001703	grd-14	-1.426217871	-0.768858962	0.000871986
WBGene00004397	rol-6	-3.092764376	-2.232549737	2.07E-20
WBGene00011340	ugt-30	0.697002251	0.615555573	0.003733436
WBGene00006539	tbb-6	0.894755773	0.936588153	4.12E-07
WBGene00004264	qua-1	-0.667646359	-1.003289802	0.005848366
WBGene00011493	T05F1.8	1.117214378	0.708538509	0.001510308
WBGene00000618	col-41	-2.750996739	-2.793667973	2.29E-16
WBGene00000715	col-142	1.432092486	1.230422607	1.83E-06
WBGene00020550	T17H7.1	-1.709626613	-0.694429421	0.003968435
WBGene00020672	T22B7.3	0.626586302	1.159028666	0.001482062
WBGene00006580	tlp-1	1.480757271	1.397247769	2.38E-76
WBGene00012186	mlt-11	-2.86502476	-1.450413049	3.80E-07
WBGene00004156	pqn-74	-1.003963393	-0.68891031	6.47E-09
WBGene00001397	fat-5	1.291739256	1.119019514	3.89E-15
WBGene00001446	flp-3	0.929822671	0.92832234	1.54E-33
WBGene00022415	Y102A11A.5	-1.263161256	-0.923328151	0.001067267
WBGene00044213	Y102A5C.36	-1.120313175	-0.895801858	0.000878448
WBGene00013748	ssu-1	1.207688949	0.596238451	0.003194755
WBGene00044754	Y119C1B.12	2.004118858	0.877313069	2.16E-06
WBGene00021397	Y38C1AA.6	-1.014250211	-0.601172524	0.000509498
WBGene00012682	asp-16	1.635731338	1.850660605	2.88E-08

WBGene00000671	col-96	0.721791605	1.433285453	0.007088563
WBGene00012770	srt-47	-1.538976977	-1.00221045	0.002352455
WBGene00001066	dpy-4	-2.662614875	-1.721999398	2.18E-12
WBGene00012840	grsp-1	0.720219084	0.63526954	5.42E-05
WBGene00012910	Y46G5A.20	1.026196883	1.021682699	0.00058196
WBGene00002018	hsp-16.41	1.046641502	0.664935302	3.21E-13
WBGene00021624	Y47D7A.12	0.971227881	0.707848968	3.73E-05
WBGene00021731	Y49G5A.1	0.911907885	1.307236846	0.002584493
WBGene00013073	hmit-1.1	-1.109657576	-0.984678515	6.83E-11
WBGene00013074	hmit-1.2	-0.88659535	-0.678811568	0.000489083
WBGene00013146	Y53C12B.7	-1.115003697	-0.834937623	9.39E-10
WBGene00013207	zipt-2.3	0.959418241	0.625776275	0.001050618
WBGene00021977	Y58A7A.3	0.681909293	1.162287036	3.35E-06
WBGene00001725	grl-16	-2.332350454	-0.891931807	0.000148562
WBGene00022181	pho-9	-1.053053962	-0.630300176	1.85E-05
WBGene00045305	ZC250.4	1.087230462	0.60623385	4.74E-05
WBGene00000749	col-176	0.876720354	1.221856909	1.05E-07
WBGene00006956	wrt-10	-2.226775253	-0.814139956	0.000290943
WBGene00022679	ZK180.5	-1.900584944	-1.048806166	4.85E-08
WBGene00002087	ins-4	-0.953001316	-0.886647805	3.73E-05

Table S2: 118 genes with differential transcript abundance: 'LMN-Y59C; cec-4Δ' vs 'LMN-Y59C'

Genes meeting significance criteria (FDR < 0.01) and (FC > 1.5), specified by the following five tab-delimited columns: Wormbase 'GeneID', the primary gene name or sequence name as extracted from Wormbase release 273 (Nov-1 2019) in 'gene name', the fold-changes of log2 expression values of a first replicate sample pair in 'FC_log2_repl_a', the fold-changes of log2 expression values of second replicate sample pair in 'FC_log2_repl_b' (see Figure 7A), and the p-values for differential expression multiplicity corrected by the Benjamini-Hochberg method in 'FDR'

#GeneID	gene name	FC_log2_repl_a	FC_log2_repl_b	FDR
WBGene00005016	sqt-1	3.062803781	1.396039308	6.64E-05
WBGene00005017	sqt-2	2.285299011	1.488269169	2.31E-10
WBGene00044658	C01G10.17	-0.776487961	-0.934996607	0.000400198
WBGene00003096	lys-7	-1.588759491	-1.285905517	2.85E-51
WBGene00015399	cyp-35A1	0.811691313	0.903133717	0.006707422
WBGene00015479	wht-1	1.199979826	0.730397531	0.001619813
WBGene00007362	cyp-35C1	1.008099227	0.709733421	2.30E-07
WBGene00015574	irg-1	-1.085108631	-0.734399054	0.001855403
WBGene00003862	old-1	-0.593247921	-0.621785477	0.004232981
WBGene00015660	catp-3	-0.761131775	-0.687778832	1.35E-06
WBGene00002026	hsp-70	-1.065036156	-0.6411195	0.006754214
WBGene00015889	C17C3.3	1.770038948	1.13205584	1.29E-05
WBGene00007672	fbxa-136	-0.768759716	-0.820898567	0.00724604
WBGene00005832	srw-85	4.563936689	4.541186091	7.60E-253
WBGene00007876	dct-19	-1.320297252	-1.515979068	1.18E-14
WBGene00003528	nas-9	-0.727762797	-0.618964236	0.000165996
WBGene00016596	C42D4.3	-1.036783701	-1.142504058	3.94E-10
WBGene00016628	slc-36.5	0.626236347	0.618052307	3.21E-05
WBGene00016659	C45B2.2	-0.760261164	-0.71567167	0.00254962
WBGene00016782	phat-3	-0.783945402	-0.591504332	0.001114104
WBGene00000781	cpr-1	-0.84121641	-0.619840336	4.33E-16
WBGene00006310	sul-3	-0.6794118	-0.685366261	2.13E-05
WBGene00016943	acdh-1	3.16492565	3.160117765	2.14E-81
WBGene00004258	pyc-1	0.736688072	0.617452936	0.006754214
WBGene00008425	D2045.8	0.661674808	0.632749509	0.000237255
WBGene00017092	E02C12.6	-1.25045798	-0.587459183	0.002129484
WBGene00008477	clec-17	-0.807780028	-0.605022511	3.07E-06
WBGene00017128	E04F6.9	-0.739027352	-0.827622585	1.37E-07
WBGene00000704	col-130	-0.716172302	-1.214673276	0.001008521
WBGene00008584	irg-4	0.744883006	0.589163148	0.000410498
WBGene00008621	F09C8.1	-1.351618137	-1.107945992	6.14E-10
WBGene00000606	col-17	2.206529522	1.454346057	1.79E-08

WBGene00000649	col-73	0.998135474	1.090297863	0.000286311
WBGene00008816	F14F8.8	-1.515889622	-1.323529738	3.80E-10
WBGene00017469	F14F9.6	-0.929426678	-0.595372032	0.001285025
WBGene00000562	cng-1	-0.630623825	-0.694401408	0.00043877
WBGene00017501	pud-3	-1.474528558	-1.602509466	0.00043877
WBGene00008891	clec-42	-0.92834055	-0.849187089	7.64E-13
WBGene00008897	F16H6.7	-0.652658909	-1.254827546	0.004575406
WBGene00003099	lys-10	-1.148415596	-0.929076722	4.04E-05
WBGene00006733	ufd-1	0.603707993	0.719011971	7.99E-14
WBGene00008985	F20G2.1	-0.752607165	-0.666139399	0.00013768
WBGene00017658	F21C10.9	0.963882666	0.634290305	0.000239706
WBGene00017678	asp-12	0.925589649	0.706258452	6.19E-16
WBGene00005018	sqt-3	2.226578087	1.5849746	7.16E-12
WBGene00017784	F25E5.3	-0.736649458	-1.215785664	0.00849869
WBGene00001067	dpy-5	2.325929137	1.482561198	2.36E-09
WBGene00005003	spp-18	-0.915963028	-0.826082161	8.19E-12
WBGene00003079	lsm-5	-0.941982888	-1.088837959	9.53E-24
WBGene00009222	fbxa-95	-0.811447212	-0.928947721	1.28E-05
WBGene00017937	F30H5.3	1.845431479	1.359379139	4.15E-07
WBGene00017959	ugt-42	-0.999774395	-0.635113611	0.00711571
WBGene00000788	cpz-1	0.797605013	0.750065193	0.003626511
WBGene00017990	cec-4	-1.490054738	-1.432305099	2.60E-26
WBGene00009384	piit-1	-1.109261629	-1.169271692	2.72E-25
WBGene00009386	tag-290	-0.832454552	-0.708859532	4.67E-08
WBGene00002012	hsp-12.3	-1.203824122	-1.059612657	4.04E-05
WBGene00009628	tatn-1	-0.891886248	-0.774669169	4.48E-14
WBGene00018400	F43H9.4	-1.069221871	-0.762613727	8.56E-10
WBGene00009773	lipl-2	-0.667593154	-0.620745729	0.000216933
WBGene00018539	nhr-185	1.511048218	0.743602418	0.002818885
WBGene00009835	F47H4.2	-0.665674638	-0.66520501	0.008307174
WBGene00009855	clec-22	1.141698196	1.22302363	0.000508977
WBGene00018877	aman-1	-0.820602629	-0.965130755	0.000620576
WBGene00010124	F55G11.4	-1.008230936	-1.303721931	1.87E-28
WBGene00010181	F57A8.6	-1.382966959	-0.800449343	0.003330326
WBGene00019154	glf-1	1.244900534	1.699136363	0.002402181
WBGene00044109	K02E11.10	1.521129486	0.702499902	0.000811645
WBGene00000641	col-65	-0.905028879	-0.604072614	0.001346498
WBGene00019565	cyp-35A3	1.103848083	0.896002937	0.000102258
WBGene00010760	K10H10.4	-0.761932031	-0.96818578	0.004715514
WBGene00019730	asns-2	1.295798846	0.928181293	2.01E-15
WBGene00010931	M162.5	-1.07284764	-0.717334126	0.008646851
WBGene00010996	R03G8.1	1.708135074	1.073837095	3.95E-06
WBGene00019909	R06A10.1	-1.128661079	-0.767222612	0.000280175

WBGene00002270	lec-7	-0.732308909	-0.595224024	0.000165996
WBGene00019963	R08E5.3	-1.01189493	-0.830930011	1.93E-08
WBGene00019970	R08F11.7	-1.301791563	-1.029729018	4.31E-09
WBGene00044900	cnc-11	-1.187334549	-0.766177585	0.004766384
WBGene00004397	rol-6	2.700779222	1.862226069	4.48E-14
WBGene00011364	cest-1.2	1.125879038	0.860882529	4.33E-08
WBGene00020242	phat-5	-1.497173417	-0.830718437	8.12E-06
WBGene00011521	T06C12.14	-1.057213058	-0.678706913	5.03E-07
WBGene00011548	T06G6.6	0.805756904	0.702499902	0.008466948
WBGene00020309	T07D3.6	-0.925920525	-1.034083359	0.008466948
WBGene00000618	col-41	2.625518225	1.776511682	4.03E-12
WBGene00020593	ugt-11	0.76287649	0.626216362	0.006215034
WBGene00020672	T22B7.3	-0.8327133	-0.712575414	0.001205375
WBGene00020741	dlhd-1	-0.778435965	-0.589875907	0.002146601
WBGene00006580	tlp-1	-1.288926077	-1.428515348	1.66E-47
WBGene00012176	W01C9.2	-1.21964494	-1.070826542	2.93E-13
WBGene00012186	mlt-11	2.215830351	2.23358973	0.002590163
WBGene00012257	lpr-4	1.515457468	1.80623996	0.009711254
WBGene00021046	sedl-1	-0.712192687	-0.609003467	0.00047104
WBGene00001397	fat-5	-1.452723621	-1.297754583	7.81E-17
WBGene00022415	Y102A11A.5	0.805756904	0.99737207	0.00887945
WBGene00044754	Y119C1B.12	-1.587289173	-1.204331589	1.56E-15
WBGene00012591	nspe-1	-0.635750979	-0.798479971	1.26E-05
WBGene00012594	nspe-5	-1.37550176	-1.512783653	8.43E-07
WBGene00012604	nspe-2	-0.959758764	-0.862855831	0.002151654
WBGene00012664	Y39B6A.1	-1.36144743	-1.064815125	6.26E-22
WBGene00012682	asp-16	-1.856752051	-1.145877449	8.43E-07
WBGene00012686	Y39B6A.27	-0.641432197	-0.606921321	0.000165996
WBGene00012757	Y41C4A.11	-1.050935609	-0.624525608	2.07E-08
WBGene00001066	dpy-4	2.244278221	1.084974679	9.05E-06
WBGene00021625	Y47D7A.13	-0.661014897	-0.912068271	0.000506307
WBGene00013146	Y53C12B.7	-0.932944993	-0.859443248	8.54E-06
WBGene00001730	grl-21	-0.893335276	-1.649981022	1.11E-06
WBGene00000749	col-176	-1.616138911	-1.198710275	1.46E-19
WBGene00013875	cest-2.1	1.33554399	1.039928102	1.24E-10
WBGene00013901	ugt-16	0.819222034	0.65745035	3.80E-10
WBGene00004398	rol-8	1.487286437	0.889213287	0.006095695
WBGene00006956	wrt-10	1.478264212	1.997867599	0.007558535
WBGene00013935	ZK218.1	-0.628152473	-1.136345478	0.002590163
WBGene00004176	pqn-97	-0.815659757	-0.878289832	0.006755617
WBGene00004177	pqn-98	-1.326503874	-0.638783863	0.001302309
WBGene00013986	ZK512.7	-1.406384073	-1.287844334	5.62E-06
WBGene00014173	ZK970.7	-1.053655026	-0.63716855	0.002512822

Table S3: 8 genes with differential transcript abundances : ‘cec-4Δ’ vs ‘WT’

Genes meeting significance criteria (FDR < 0.01) and (FC > 1.5), specified by the following five tab-delimited columns: Wormbase ‘GeneID’, the primary gene name or sequence name as extracted from Wormbase release 273 (Nov-1 2019) in ‘gene name’, the fold-changes of log₂ expression values of a first replicate sample pair in ‘FC_log2_repl_a’, the fold-changes of log₂ expression values of second replicate sample pair in ‘FC_log2_repl_b’ (see Figure 7A), and the p-values for differential expression multiplicity corrected by the Benjamini-Hochberg method in ‘FDR’

#GeneID	gene name	FC_log2_repl_a	FC_log2_repl_b	FDR
WBGene00015642	C09E7.8	0.703518392	0.910599517	3.4546E- 3
WBGene00005832	srw-85	4.995608769	5.310109059	3.02E-261
WBGene00008652	F10D11.6	-0.720329215	-0.803017515	8.761E-3
WBGene00006733	ufd-1	0.766788026	0.779178976	2.80E-16
WBGene00017990	cec-4	-1.49582333	-1.334384792	1.49E-18
WBGene00000653	col-77	-1.59861625	-0.671500083	8.85E-05
WBGene00021625	Y47D7A.13	-1.23942259	-0.699298362	1.76E-05
WBGene00021977	Y58A7A.3	0.66690218	1.127006874	5.625E-05

Table S4: 27 genes with compensatory effects upon *cec-4* deletion in the *LMN-Y59C* background

Genes changing significantly in both the '*LMN-Y59C*' vs 'WT' and the '*LMN-Y59C; cec-4Δ*' vs '*LMN-Y59C*' comparisons were examined for compensatory effects upon *cec-4* deletion. This is defined as an opposing sign of the logFCs in the two comparisons.

Compensating genes specified by the following eight tab-delimited columns: Wormbase 'GeneID', the primary gene name or sequence name as extracted from Wormbase release 273 (Nov-1 2019) in 'gene name', and three columns each for the contrasts with the fold-changes of log2 expression values of a first replicate sample pair in 'FC_log2_repl_a', the fold-changes of log2 expression values of second replicate sample pair in 'FC_log2_repl_b' (see Figure 7A), and the p-values for differential expression multiplicity corrected by the Benjamini-Hochberg method in 'FDR'

#geneID	gene name	FC_log2_repl_a	FC_log2_repl_b	FDR	FC_log2_repl_a	FC_log2_repl_b	FDR
WBGene00044754	Y119C18.12	2.004118858	0.877313069	2.16E-06	-1.587289173	-1.204331589	1.56E-15
WBGene00044658	C01G10.17	0.70756948	0.748238635	0.00698598	-0.776487961	-0.934996607	0.000400198
WBGene00022415	Y102A11A.5	-1.263161256	-0.923328151	0.00106727	0.805756904	0.99737207	0.00887945
WBGene00020672	T22B7.3	0.626586302	1.159028666	0.00148206	-0.8327133	-0.712575414	0.001205375
WBGene00017937	F30H5.3	-1.802625934	-1.168280929	1.36E-05	1.845431479	1.359379139	4.15E-07
WBGene00012682	asp-16	1.635731338	1.850660605	2.88E-08	-1.856752051	-1.145877449	8.43E-07
WBGene00012186	mlt-11	-2.86502476	-1.450413049	3.80E-07	2.215830351	2.23358973	0.002590163
WBGene00009386	tag-290	1.157588536	0.679279411	2.50E-09	-0.832454552	-0.708859532	4.67E-08
WBGene00009384	piit-1	1.436386638	0.761660059	5.98E-09	-1.109261629	-1.169271692	2.72E-25
WBGene00009222	fbxa-95	1.199188813	1.263198915	3.72E-10	-0.811447212	-0.928947721	1.28E-05
WBGene00008816	F14F8.8	1.750918948	0.970867683	1.48E-11	-1.515889622	-1.323529738	3.80E-10
WBGene00008425	D2045.8	-1.302448525	-0.690538447	6.73E-09	0.661674808	0.632749509	0.000237255
WBGene00006956	wrt-10	-2.226775253	-0.814139956	0.00029094	1.478264212	1.997867599	0.007558535
WBGene00006580	tlp-1	1.480757271	1.397247769	2.38E-76	-1.288926077	-1.428515348	1.66E-47
WBGene00005018	sqt-3	-2.440491213	-1.533413751	1.60E-12	2.226578087	1.5849746	7.16E-12
WBGene00005017	sqt-2	-2.226775253	-1.496199671	4.18E-10	2.285299011	1.488269169	2.31E-10
WBGene00005016	sqt-1	-2.929635629	-1.607179923	3.30E-07	3.062803781	1.396039308	6.64E-05
WBGene00004397	rol-6	-3.092764376	-2.232549737	2.07E-20	2.700779222	1.862226069	4.48E-14
WBGene00003099	lys-10	0.746369523	0.904206337	0.00702846	-1.148415596	-0.929076722	4.04E-05
WBGene00003079	lsm-5	1.504614269	1.433013081	1.34E-76	-0.941982888	-1.088837959	9.53E-24
WBGene00001397	fat-5	1.291739256	1.119019514	3.89E-15	-1.452723621	-1.297754583	7.81E-17
WBGene00001067	dpy-5	-2.522815368	-1.959014444	2.61E-16	2.325929137	1.482561198	2.36E-09
WBGene00001066	dpy-4	-2.662614875	-1.721999398	2.18E-12	2.244278221	1.084974679	9.05E-06
WBGene00000749	col-176	0.876720354	1.221856909	1.05E-07	-1.616138911	-1.198710275	1.46E-19
WBGene00000649	col-73	-1.540711087	-1.439767633	4.50E-07	0.998135474	1.090297863	0.000286311
WBGene00000618	col-41	-2.750996739	-2.793667973	2.29E-16	2.625518225	1.776511682	4.03E-12
WBGene00000606	col-17	-2.694557575	-1.329917085	1.47E-07	2.206529522	1.454346057	1.79E-08

Strain	Genotype	Reference
N2	Wild-type Bristol isolate	
GW76	<i>gwls4 [myo-3::rfp baf-1::gfp-lacI let-858 3'UTR]X</i>	Meister et al. 2010
GW164	<i>emr-1(gk119); gwls4 [myo-3::rfp baf-1::gfp-lacI let-858 3'UTR]X</i>	
GW201	<i>lem-2 (tm1582); gwls4 [myo-3::rfp baf-1::gfp-lacI let-858 3'UTR]X</i>	
BN403	<i>Integrated Pemr-1::emr-1::mcherry::emr-1 3'UTR and GFP::LMN-1 wt. Made by crossing BN225 and YG301 or GW342; bqSi225[pBN34(unc-119(+)) Pemr-1::emr-1::mcherry] IV; ygls1[baf-1::gfp::lmn-1 unc119(+)]</i>	Mattout et al, 2011 for GW342
BN404	<i>Integrated Pemr-1::emr-1::mcherry::emr-1 3'UTR and GFP::LMN-1 Y59C. Made by crossing BN225 and YG117 or GW341; bqSi225[pBN34(unc-119(+)) Pemr-1::emr-1::mcherry] IV; ygls2[baf-1::gfp::lmn-1 Y59C unc119(+)]</i>	Mattout et al, 2011 for GW341
GW653	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3)</i>	Mattout et al. 2011
GW654	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119; gwls4 [myo-3::rfp baf-1::gfp-lacI let-858 3'UTR]X</i>	Mattout et al. 2011
GW656	<i>ygls1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3) gwls4[baf-1p::GFP-lacI::let-858 3'UTR; myo-3::rfp]</i>	Mattout et al. 2011
GW833	<i>cec-4 (ok3124) IV; gwls4[baf-1p::GFP-lacI::let-858 3'UTR; myo-3::rfp]</i>	Gonzalez-Sandoval et al. 2015
GW888	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; cec-4(ok3124), IV; gwls4 [baf-1::GFP-lacI let858 myo3::RFP] X.</i>	Gonzalez-Sandoval et al. 2015
GW1026	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)] II unc-119(ed3); gwSi17 [cec-4p::CEC-4-WmCherry::cec-4 3'UTR] II; cec-4(ok3124) IV; gwls4[myo-3::RFP baf-1::GFP lacI let-858] X.;</i>	Gonzalez-Sandoval et al. 2015
GW1066	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)] II unc-119(ed3), gwSi18 [cec-4p::CEC-4_Y87A_Y111A-WmCherry::cec-4 3'UTR] ttTi5605 II; cec-4(ok3124) IV; gwls4[myo-3::RFP baf-1::GFP lacI let-858] X.</i>	Gonzalez-Sandoval et al. 2015
GW1214	<i>lem-2 (tm1582)</i>	This study
GW1226	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3) lem-2(tm1582)</i>	This study
GW1340	<i>gwls4 X ; lem-2(tm1582) ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3)</i>	This study
GW1394	<i>bqSi225 [pBN34(unc-119(+)) Pemr-1::emr-1::mcherry] IV; gwls59 [pha-4::mCherry; unc-119(+); 256xLacO;4xLexA]; gwls39 [baf-1::GFP-LacI::let-858 3'UTR; vit-5::GFP]</i>	This study
GW1395	<i>bqSi225 [pBN34(unc-119(+)) Pemr-1::emr-1::mcherry] IV; gwls59 [pha-4::mCherry; unc-119(+); 256xLacO;4xLexA]; gwls39 [baf-1::GFP-LacI::let-858 3'UTR; vit-5::GFP]; cec-4 (ok3124) IV</i>	This study
GW1468	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3); cec-4(ok3124) IV</i>	This study
GW1480	<i>ygls1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3); Pmyo-3::FLP-D5 on chr IV.; bqsi433[pBN209(unc-119(+)); Phsp16.41::FRT::mCh::his-58::FRT::dam::emr-1] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study
GW1481	<i>ygls1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3); bqSi447[pBN181(unc-119(+)) Phsp16.41::FRT::mCh::his 58::FRT::gfp::dam] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV.; May carry unc-119(ed9) III.</i>	This study
GW1482	<i>cec-4(ok3124) IV; ygls[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3); Pmyo-3::FLP-D5 on chr IV.; bqsi433[pBN209(unc-119(+)) Phsp16.41::FRT::mCh::his-58::FRT::dam::emr-1] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study
GW1483	<i>cec-4(ok3124) IV; ygls1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3); bqSi447[pBN181(unc-119(+)) Phsp16.41::FRT::mCh::his-58::FRT::gfp::dam] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study
GW1485	<i>ygls2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3); bqSi447[pBN181(unc-119(+)) Phsp16.41::FRT::mCh::his-58::FRT::gfp::dam] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study

GW1486	<i>cec-4(ok3124) IV; yglS2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3); Pmyo-3::FLP-D5 on chr IV. bqsi433[pBN209(unc-119(+)) Phsp16.41::FRT::mCh::his-58::FRT::dam::emr-1] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study
GW1487	<i>cec-4(ok3124) IV; yglS2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3); bqSi447[pBN181(unc-119(+)); Phsp16.41::FRT::mCh::his-58::FRT::gfp::dam] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study
GW1491	<i>myo-3(st386) V. ; stEx30[Pmyo-3::GFP rol-6(su1006)]; cec-4(ok3124) IV</i>	This study
GW1492	<i>myo-3(st386) V. ; stEx30[Pmyo-3::GFP rol-6(su1006)]; yglS1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3)</i>	This study
GW1493	<i>myo-3(st386) V. ; stEx30[Pmyo-3::GFP rol-6(su1006)]; yglS1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3); cec-4(ok3124) IV</i>	This study
GW1494	<i>myo-3(st386) V. ; stEx30 [myo-3p::GFP::myo-3 + rol-6(su1006)] yglS2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3);</i>	This study
GW1495	<i>myo-3(st386) V. ; stEx30[Pmyo-3::GFP rol-6(su1006)]; yglS2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3); cec-4(ok3124) IV</i>	This study
GW1508	<i>yglS2[baf-1p::GFP-lmn-1 Y59C; unc-119(+)]; unc-119(ed-3); Pmyo-3::FLP-D5 on chr IV. bqsi433[pBN209(unc-119(+)) Phsp16.41::FRT::mCh::his-58::FRT::dam::emr-1] II; bqSi495[pBN260(unc-119(+)) Pmyo-3::FLP_D5] IV. May carry unc-119(ed9) III.</i>	This study
RW1596	<i>myo-3(st386) V. ; stEx30 [myo-3p::GFP::myo-3 + rol-6(su1006)]</i>	CGC
GW1754	<i>yglS1[baf-1p::GFP-lamin wt; unc-119(+)]; unc-119(ed-3) gwls4[baf-1p::GFP-lacI::let-858 3'UTR; myo-3::rfp]; cec-4(ok3124) IV</i>	This study

Table S5: *C. elegans* strains used in this study