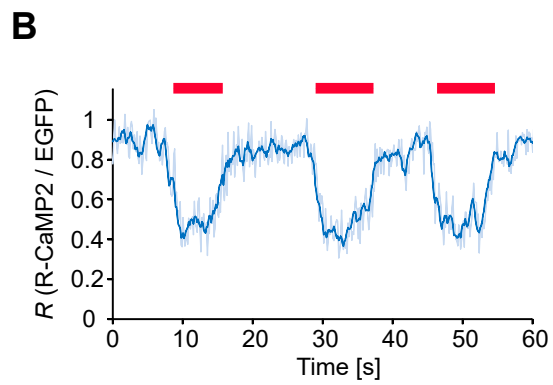
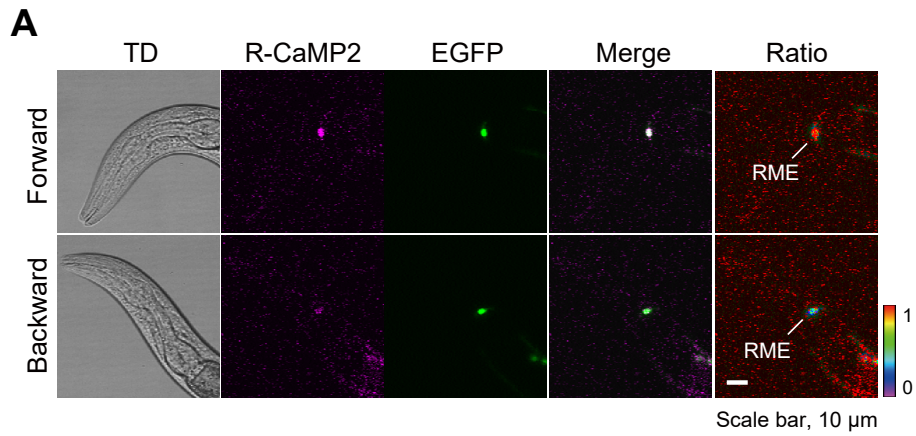
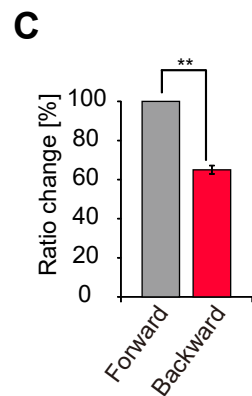


IR: infrared
 LSCM: laser-scanning confocal microscope



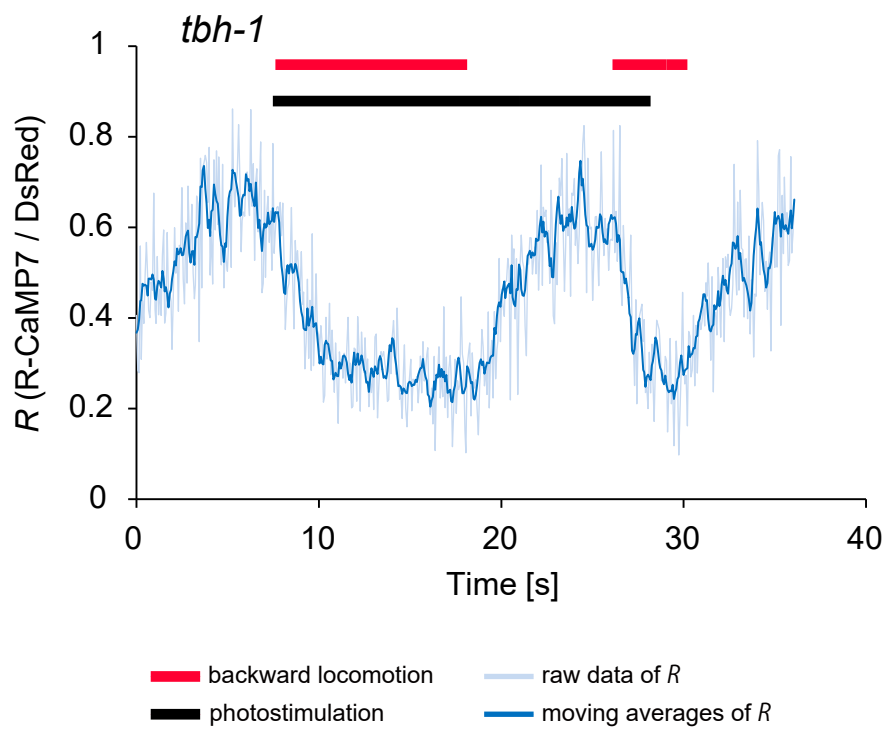
backward locomotion
 raw data of R
 moving averages of R across a 0.54 s window

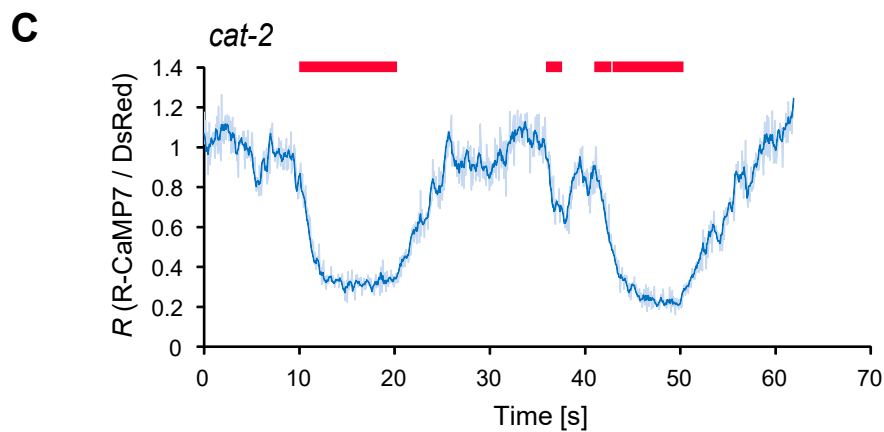
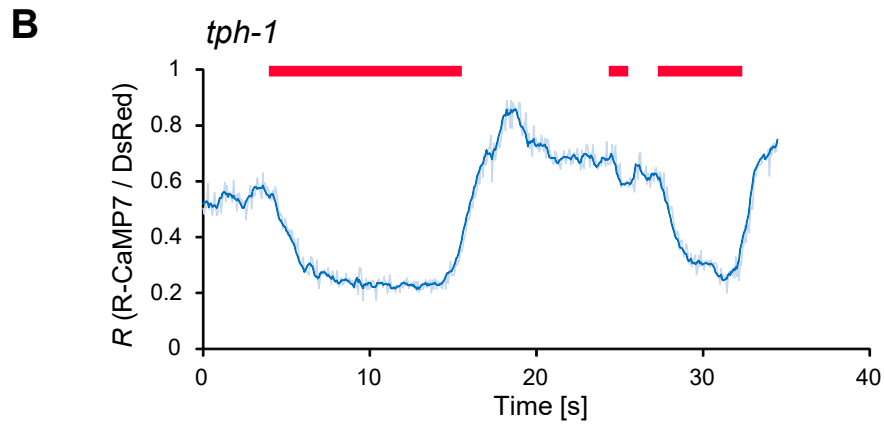
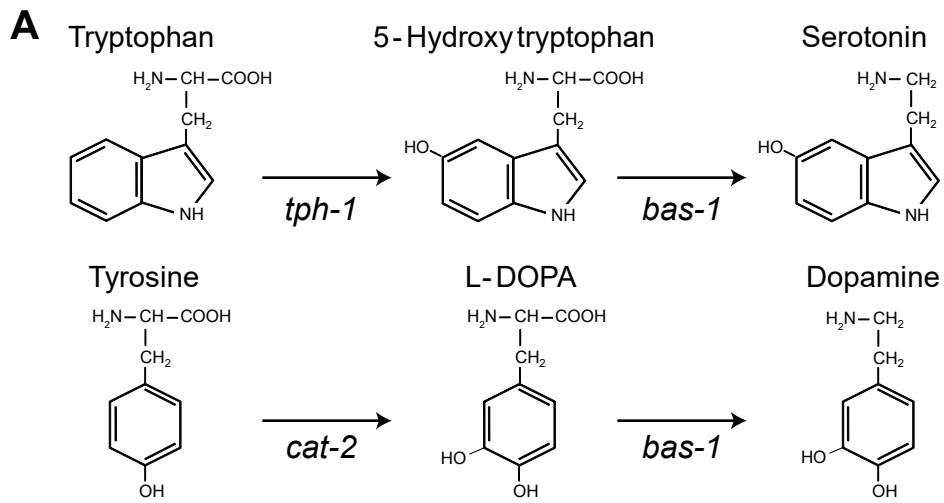


$n = 11$ from seven animals

** $P < 0.01$, Student' s two-tailed t-test.

Error bars, SEM.





█ backward locomotion
— raw data of R
— moving averages of R

Table S1 C. elegans strains used in this study

Strain	Genotype	Reference or Source
N2	wild type	Brenner, Genetics, 1974
RB993	<i>tdc-1 (ok914) II</i>	The C. elegans Deletion Mutant Consortium, G3, 2012. OMRF ^a
RB1161	<i>tbh-1 (ok1196) X</i>	The C. elegans Deletion Mutant Consortium, G3, 2012. OMRF ^a
RB1690	<i>ser-2 (ok2103) X</i>	The C. elegans Deletion Mutant Consortium, G3, 2012. OMRF ^a
VC125	<i>tyra-3 (ok325) X</i>	The C. elegans Deletion Mutant Consortium, G3, 2012. OMRF ^a
GR1321	<i>tph-1 (mg280) cam-1(vs166) II</i>	Sze JY et al., Nature, 2000
MT14680	<i>lgc-55 (n4331) V</i>	Ringstad N et al., Science, 2009
QJ6	<i>cat-2 (jq6) II</i>	Usami A, Ph.D. Thesis, 2012
QJ3063	<i>jqIs6</i>	This study
QJ3064	<i>jqIs71</i>	This study
QJ3065	<i>jqIs72</i>	This study
QJ3067	<i>jqIs75</i>	This study
QJ1412	<i>jqEx439</i>	This study
QJ4110	<i>tph-1 (mg280) II; jqIs6</i>	This study
QJ4111	<i>cat-2 (jq6) II; jqIs6</i>	This study
QJ1359	<i>ser-2 (ok2103) X; jqEx386</i>	This study
QJ1501	<i>ser-2 (ok2103) X; jqEx528</i>	This study
QJ1502	<i>ser-2 (ok2103) X; jqEx529</i>	This study
QJ1526	<i>ser-2 (ok2103) X; jqEx553</i>	This study
QJ1543	<i>ser-2 (ok2103) X; jqEx570</i>	This study
QJ1544	<i>ser-2 (ok2103) X; jqEx571</i>	This study
QJ4113	<i>jqIs73; jqIs75</i>	This study
QJ4114	<i>jqIs6; jqEx318</i>	This study
QJ1489	<i>jqIs75; jqEx516</i>	This study
QJ4116	<i>tdc-1 (ok914) II; jqIs6; jqEx318</i>	This study
QJ4117	<i>tbh-1 (ok1196) X; jqIs6; jqEx318</i>	This study
QJ4118	<i>ser-2 (ok2103) X; jqIs6; jqEx318</i>	This study
QJ4119	<i>lgc-55 (n4331) V; jqIs6; jqEx318</i>	This study
QJ4120	<i>tyra-3 (ok325) X; jqIs6; jqEx318</i>	This study
QJ4122	<i>ser-2 (ok2103) X; jqIs6; jqEx386</i>	This study
QJ4123	<i>ser-2 (ok2103) X; jqIs6; jqEx422</i>	This study
QJ4112	<i>ser-2 (ok2103) X; jqIs6; jqEx528</i>	This study

^aOMRF: Oklahoma Medical Research Foundation, The *C. elegans* Deletion Mutant Consortium

Table S2 Transgenic lines generated in this study

Transgenic array	DNA injected
<i>jqIs6</i>	<i>Punc-25::G-CaMP7</i> (100 ng/μl) <i>Punc-25::DsRedx</i> (50 ng/μl)
<i>jqIs71</i>	<i>Punc-25::G-CaMP7 (ce)</i> (50 ng/μl) <i>Punc-25::DsRedx</i> (50 ng/μl) <i>pBluescript II SK+</i> (100 ng/μl)
<i>jqIs72</i>	<i>Punc-25::G-CaMP7(ce)</i> (50 ng/μl) <i>Punc-25::DsRedx</i> (50 ng/μl) <i>pBluescript II SK+</i> (100 ng/μl)
<i>jqIs73</i>	<i>Punc-25::G-CaMP7(ce)</i> (50 ng/μl) <i>Punc-25::DsRedx</i> (50 ng/μl) <i>pBluescript II SK+</i> (100 ng/μl)
<i>jqIs75</i>	<i>Ptdc-1::G-CaMP7(ce)</i> (50 ng/μl) <i>Ptdc-1::DsRedx</i> (50 ng/μl) <i>Ptbh-1::EBFP2</i> (50 ng/μl) <i>pBluescript II SK+</i> (50 ng/μl)
<i>jqEx318</i>	<i>Psra-6::ChR2::mCherry</i> (100 ng/μl) <i>Punc-122::mCherry</i> (50 ng/μl) <i>pBluescript II SK+</i> (50 ng/μl)
<i>jqEx386</i>	<i>Punc-25::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (130 ng/μl)
<i>jqEx422</i>	<i>Punc-17::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (130 ng/μl)
<i>jqEx439</i>	<i>Punc-25::R-CaMP2</i> (50 ng/μl) <i>Punc-47::EGFP</i> (50 ng/μl) <i>pBluescript</i> (50 ng/μl)
<i>jqEx516</i>	<i>Punc-47::EGFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (150 ng/μl)
<i>jqEx528</i>	<i>Pser-2prom2::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (130 ng/μl)
<i>jqEx529</i>	<i>Pser-2prom2::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (130 ng/μl)
<i>jqEx553</i>	<i>Punc-25::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (110 ng/μl)
<i>jqEx570</i>	<i>Punc-30::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (130 ng/μl)
<i>jqEx571</i>	<i>Punc-30::ser-2 (+)</i> (20 ng/μl) <i>Punc-122::EYFP</i> (50 ng/μl) <i>pBluescript II SK+</i> (130 ng/μl)

Table S3 Mutations and primers for genotyping

Genotype	Mutation	Primer name	Sequence
<i>cat-2 (jq6) II</i>	320bp deletion + 9bp insertion	cat-2_jq6_forward	CTTCACACGACGTGCTCCTA
		cat-2_jq6_reverse1	GTTGTCTGGAAGACCCGAAA
		cat-2_jq6_reverse2	CTTGAACTCTAACGCCTGATC
<i>lgc-55 (n4331) V</i>	1986bp deletion	lgc-55_n4331_forward	CGGTGGTCAGTGGATAATTTTGTGC
		lgc-55_n4331_reverse1	GCGATTTGTGAATTGCAGAGCC
		lgc-55_n4331_reverse2	CGTCATCTATGAATTCGACCGTTG
<i>ser-2 (ok2103) X</i>	2043bp deletion	ser-2_ok2103_forward1	GTGATGGTACAAGCTTCACC
		ser-2_ok2103_reverse1	CTTCGTCATTTGTGGTTTCG
		ser-2_ok2103_forward2	CTCCATCATATTCTCCTGCC
<i>tbh-1 (ok1196) X</i>	981bp deletion	tbh-1_ok1196_forward	GGAAAGGACAATGGCACGTTGA
		tbh-1_ok1196_reverse1	AGGTGCTGAATTTGCCTGCC
		tbh-1_ok1196_reverse2	CGAAGGTCCAAGTATCAGCCAA
<i>tdc-1 (ok914) II</i>	629bp deletion	tdc-1_ok914_forward	GCTATGGCTTCATGTTGATGCTGC
		tdc-1_ok914_reverse1	GCCGTTATCAAAGGCGGAAACT
		tdc-1_ok914_reverse2	GCACATACACAGAAGCGGATCAC
<i>tph-1 (mg280) II</i>	1305bp deletion	tph-1_mg280_forward	GCAAAGACCCCTCTCAACCTCATT
		tph-1_mg280_reverse1	GGAAACCATTGAGAACCGTTGTC
		tph-1_mg280_reverse2	GCATGATGGCGAACGTATTGAGTG
<i>tyra-3 (ok325) X</i>	781bp deletion	tyra-3_ok325_forward1	GTTCTGAAACAGTTCACGGG
		tyra-3_ok325_forward2	GATTGCCTCATGAGAGCTTC
		tyra-3_ok325_reverse1	GGAGAAGAGTCCGTTTATCG

Table S4 Primers for molecular biology

No.	primer name	Sequence	Comments
1	G-CaMP7(CE)_NheI#F1	CTTACTAGTGCTAGCATGAGAGGAAGTCATCA TCA	1 and 2 were used to amplify the 1.4 kb codon-optimized G-CaMP7 cDNA for <i>C. elegans</i>
2	G-CaMP7(CE)_NheI#R1	TTTTTTTTGCTAGCTTATTGGCAGTCATCATC T	
3	R-CaMP2_Bgl#R1	TTTGTAGATCTCTATGGGTTGGACTCCACGT	3 and 4 were used to amplify the 1.5 kb R-CaMP2 cDNA
4	R-CaMP2_Not#F1	CTTACTAGTGCGGCCGCATGGGTTCTCATCAT CATCATC	
5	DsRedx_NheI#F1	CTTACTAGTGCTAGCATGGCTCCTCCGAGGA CGT	5 and 6 were used to amplify the 0.68 kb DsRed-Express-1 cDNA
6	DsRedx_NheI#R1	TTTTTTTTGCTAGCCTACAGGAACAGGTGGTG GC	
7	ser-2 cDNA Bgl#R1	TTTGTAGATCTCTAAGGTTGCGCACTCATTC	7 and 8 were used to amplify the 1.3 kb full-length <i>ser-2</i> cDNA
8	ser-2 cDNA Not#F1	CTTACTAGTGCGGCCGCATGTTCCGAAATTAC ACTGA	
9	ser-2prom2#F1	ATTGGCTGCAGATTTTATGACTTTCACTAGAA ATG	9 and 10 were used to amplify the 4.7 kb <i>ser-2prom2</i> promoter
10	ser-2prom2#R1	AGCTGGATCCTTTTGCAAATACTTGAGGCTG	
11	tbh-1 promoter#F1_Bam	AGCTGGATCCCCTTATGTATCTCATTGCTATTT	11 and 12 were used to amplify the 2.8 kb <i>tbh-1</i> promoter
12	tbh-1 promoter#R1_Not	CTTACTAGTGCGGCCGCTTCTGAAATCGTAT AGTAATGG	
13	tdc-1p_BamHI#R1	AGCTGGATCCTTGGGCGTCTGAAAAATG	13 and 14 were used to amplify the 4.4 kb <i>tdc-1</i> promoter
14	tdc-1p_HindIII#F1	TTTTTTTTAAGCTTAAGGGAGAGAGATTGCA GTGG	
15	unc-25p_BamHI#R1	AGCTGGATCCTCTTTTTGGCGGTGAACTG	15 and 16 were used to amplify the 1.9 kb <i>unc-25</i> promoter
16	unc-25p_HindIII#F1	TTTTTTTTAAGCTTTGTGCATGCAAAAAACACC C	
17	unc-30_SphI#F1	TTTTTTTTGCATGCTCGATGACACTTTTGTATG TGT	17 and 18 were used to amplify the 2.4 kb <i>unc-30</i> promoter
18	unc-30_BamHI#R1	AGCTGGATCCGTGTTGATCTTTGCCGGAG	
19	unc-54 3'#R1	GACTTAGAAGTCAGAGGCAC	19-25 were used to verify the sequences of DNA constructs
20	unc-86_UTR#R1	CAAAGCGAATTGCTAAACCC	
21	pFX#F1	GCAAGGCGATTAAGTTGGGT	
22	pPD49.26#F1	CGTTGGCCGATTCATTAATG	
23	ser-2#R2	GTAGACAACCCGCAACTATC	
24	ser-2 cDNA #F2	CATTGGGATTATAGTCACGC	
25	unc-25p#F1	CGGAATAGGGAAAAGCTCAG	