				fe45	fe47
				Ochre	Opal
				A	
				Ť	Ť
Cel-SNA-1	1	MADKKDYAAIAEIEKQ	IADNAANFEKWKI	NANALQRGSADY	NAGVTRFTDWDRDLRTRL
Cbr-SNA-1	1	MADKKDYAAIVELEKQ	IADNASNFQKWKI	NANALQRGSVEY	NDGVTRFTDWDRDLRARL
Cre-SNA-1	1	MADKKDYVA IAELEKQ	IADNATNFOKWK	NANALQRGSIEY	NEGVTRFTDWDRDLRARL
HCO-SNA-1	1	MATAQSNAEV-USSMERQ	YAEQKAKFEKWK	IDNSRQIGTESY	NKYVQQFLQWEKEVFEKK
Asu-SNA-1	1	MADKIANITNALTNLERQ	YVEHKEKFEKWK	VDNIKORGSETY	NTYVERFHQWEMGVKEQQ
Bma-SNA-1	1	MADKITHITVALGRLEQQ	YVEHKEKFEKWK	LNNIAQCGTETY	NKYVEEFNEWEKGVKEQQ
LIO-SNA-1	1	MADKITHITVALGRLEQQ	YVEHKEKFEKWK	LNNIAQCGTETY	NKYVEEFNEWEKGVKEQQ
Cel-SNA-1	59	ASHOGINVESCER	STDAVILGEILLDK	VDGAGEAOAIOI	ANSADETEWETLOOEEHN
Cbr-SNA-1	59	AAHOGINVESGPK	SIDAVLDELLDK	VDLTGFAOAIOI	ANTADPTFYPSLNOGFLN
Cre-SNA-1	59	AAHOGINVESGPK	SIDAVLDELLDK	VDISGFAÕAIĤI	ANSADPTFYOSILLOGFON
HCO-SNA-1	60	AKVAALVOSPAAIAAGPA	NVDSILGOLLDD	VLPMEFLMALVT	VHMKDNTFLPCVIENFRK
Asu-SNA-1	61	ROLIEBRNNLAASS	DIDIALDSLLTR.	ISMKDFVLAVVT	MTSKDOSFFPALLSAFKR
Bma-SNA-1	61	ROLIEERNSLIAPO	DLDTTLDGLLAO	ISPKDFILAVVM	MTSKOPTFFPALLSALOK
Llo-SNA-1	61	RÕLIEERNSLIAPÕ	DLDTTLDGLLAO	ISPKDFILAVVM	MTSKOPTFFPALLSALÕK
Col CND 1	114		DDDDDVVDCTZ		
Cer-SNA-1	114	FKA-NPPOPVOM			SCRYAYAA DOWA
CDI-SNA-1	114	FRM-RFTRPVFQM			SCDVCVAADOCT
HCO SNA-1	120	ACT CELDOS KILV	ARIOF IFGFA		PUPOVVHPVOTASHA
ACU SNA-1	117	TOTNODUPOUCAUPSU	TETWYEDCTVHE	V 000VAG TA	VAUDAASHDVATTPOFTS
Bma GNA 1	117	FORVGERPORSTVORVAR	SAASVADAVNDO		I OTANDSHDVGA I DSDWI
Llo-SNA-1	117	VOAVDEAROASTVOAVAA	SAASVAPATNRO	VPSOTOVSSTKT	L BUSNDSHPYGAMPSDVL
HIO-BAR-I	11/	Vgalbeargabiiga	BARBIAFAIARQ.	IIBQIQIBBIKI	
Cel-SNA-1	148	SN-VPVYRPVLPTIITLP	'	KAVS	PVRDFQKK-TGAPFRDFS
Cbr-SNA-1	148	PPTVPVFRTIPSNIITLQ	!	RPVS	PVRDYOKK-TGAPFRDFS
Cre-SNA-1	148	VS-VPAYRPSVSSVVNVQ			PIRDYOKK-SGAPFRDFS
HCO-SNA-1	158	GLTLHTVPSTAVTWA	TTAAP	AGPKYRPPS	PVRDYKNPVASMPFRDFS
Asu-SNA-1	172	IGNGALKRPYESVAVASA	SSAVTAETNWKVI	EEPARKSYRPPS	PVKDYRNP-STLPFRDFS
Bma-SNA-1	177	I DVTKRSYDRLVGATT	GDELT	ARKNYRAPS	PVRDYRNP-STIPFRDFS
LIO-SNA-I	1//	IDVTKRSIDRLLGATK	GDELS		PVRDIANP-SHIPFRDFS
Cel-SNA-1	186	V -			
Cbr-SNA-1	187	V -			
Cre-SNA-1	186	<u>v</u> -			
Hco-SNA-1	205	Q			
Asu-SNA-1	231	Qт			
Bma-SNA-1	224	Qт			
llo-SNA-1	224	Qт			

Supplementary Figure 1. Multiple sequence alignment of SNA-1 homologues.

Arrows indicate the residues affected by the two *sna-1* mutations, and the nature of the resultant nonsense mutation. Residues conserved in more than 50% of the sequences are shaded (counter shading indicating identity and grey shading indicating similarity). Species key: Asu – *A. suum*; Bma – *B. malayi*; Cbr – *C. briggsae*; Cel – *C. elegans*; Cre – *C. remanei*; Hco – *H. contortus*; Llo – *L. loa*.

acggctcgattaaaattaaaattatcgaacggctcgattaaaattaaaattaaaattatcgaacggctcgattaaaattaaaattatcATGttttcaggaccggtagaaaaa **GCT**agtaaaggagaagaacttttcactggagttgtcccaattcttgttgaattagatggtga tgttaatgggcacaaattttctgtcagtggagagggtgaaggtgatgcaacatacggaaaac tt a ccctt a a atttatttg cact a ctg g a a a ctacctg tt ccatgg g t a a g t t t a a a catatatatactaaccaqattatttaaattttcaqccaacacttgtcactactttctgtta ${\tt tggtgttcaatgcttctcgagatacccagatcatatgaaacggcatgactttttcaagagtg}$ ccatgcccgaaggttatgtacaggaaagaactatatttttcaaagatgacgggaactacaag agtcaagtttgaaggtgatacccttgttaatagaatcgagttaaaaggtattgattttaaagaagatggaaacattcttggacacaaattggaatacaactataactcacacaatgtatacatc ctaatctgatttaaattttcagaacttcaaaattagacacaacattgaagatggaagcgttc aactagcagaccattatcaacaaaatactccaattggcgatggccctgtccttttaccagac aaccattacctgtccacacaatctgccctttcgaaagatcccaacgaaaagagagaccacat ggtccttcttgagtttgtaacagctgctgggattacacatggcatggatgaactatacaaat ag

Supplementary Figure 2. Sequence of the *gfp* **reporter gene with outron.** The original *gfp* start codon converted to GCT is shown in capital letters. The new ATG initiation codon is shown in red capital letters and is followed by a *trans*-splice site (underlined). Intron sequences are printed in grey. Arrows indicate positions of the primers for the detection of outron *gfp* mRNA (green) and of internal *gfp* mRNA sequence (blue).

Target	Primer 1	Primer 2
smn-1	<u>CCGCTCTAGAACTAGT</u> GCGACATGGA	CGGTGGATCCACTAGTCGGGAGGAATGGA
	GGTAGACGAT	GTGAGAA
smi-1	<u>CCGCTCTAGAACTAGT</u> GATCAAGAAG	CGGTGGATCCACTAGTAAAACAACGCGGA
	CCTGTCTCGG	GAAGGAG
icln-1	<u>CCGCTCTAGAACTAGT</u> TGAAGTCAGC	CGGTGGATCCACTAGTCACGGGTCAATAAC
	CAGCCAACT	AACATGGA
F23F1.5	<u>CCGCTCTAGAACTAGT</u> AAGCTGCAGA	CGGTGGATCCACTAGTACCCAAAACGGTCC
	ACAACAAGCA	AAAACT
snr-1	<u>CCGCTCTAGAACTAGT</u> TTCATGAGGC	CGGTGGATCCACTAGTATCTTACAGGGAAA
	CGAAGGTCACA	TCTCCGAAACC
snr-2	CCGCTCTAGAACTAGTCCAACGCCTC	CGGTGGATCCACTAGTCGAAGATTGGTGG
	AAGATGACTATC	GTGATGG
snr-3	<u>CCGCTCTAGAACTAGT</u> TAGAAAAATG	CGGTGGATCCACTAGTATTGAAGAAATTT
	AAGTTGGTCAGATTCC	ATAGAGATCAGAACG
snr-4	CCGCTCTAGAACTAGTAGCCAAACCC	CGGTGGATCCACTAGTCATTGAAACGAAAC
	CGTTCAGAGATG	AACAGGGTGAAC
snr-5	<u>CCGCTCTAGAACTAGT</u> AATGTCCGCA	CGGTGGATCCACTAGTGATAATTATAATT
	GTTCAACCAG	TATTGATTAAGAATGTGC
snr-6	<u>CCGCTCTAGAACTAGT</u> GAAAGCTCAA	CGGTGGATCCACTAGTTTAGGCTTCTTGTT
	CAAAGTGATGGTTCAG	GGGCGG
snr-7	CCGCTCTAGAACTAGTAAAATGAGTA	CGGTGGATCCACTAGTGAGTTTCCGCGAAT
	AGACACATCCACCAG	GACAG
lsm-1	CCGCTCTAGAACTAGTGCCCGATCCC	CGGTGGATCCACTAGTATTCATGCATCGTG
	TATTTACCC	TTCTTCTG
gut-2	<u>CCGCTCTAGAACTAGT</u> ATGCTGTTCT	CGGTGGATCCACTAGTCGTGGATTTACTGT
	ТСТСАТТСТТСА	TTTGCC
lsm-3	CCGCTCTAGAACTAGTGGCCACCGAA	CGGTGGATCCACTAGTAATGATGACGATG
	AAGAAAGAAG	AATTAGGATGC

lsm-4	CCGCTCTAGAACTAGTATGGTGTTGC	CGGTGGATCCACTAGTCGTCCTCCTCGTCC		
	CACTTTCTCTTCT	ACCA		
lsm-5	<u>CCGCTCTAGAACTAGT</u> CCATGGCAAC	CGGTGGATCCACTAGTTTAAATCTCTGGTC		
	СТСААСАТС	СТТСТССТС		
lsm-6	<u>CCGCTCTAGAACTAGT</u> GAAAATGAGC	CGGTGGATCCACTAGTTTATTTCGTCGATG		
	AAACGACAGAATC	TGGAGATGT		
lsm-7	CCGCTCTAGAACTAGTGAAAGACGAA	CGGTGGATCCACTAGTTTATTCTTCTTCCT		
	GGAAAACGAAAG	GGGTTGC		
lsm-8	<u>CCGCTCTAGAACTAGT</u> AATATGACTT	CGGTGGATCCACTAGTTGTGGAAATTATT		
	CAACTCTAGATGCGTA	GGGGAATC		
K07A1.15	CCGCTCTAGAACTAGTGACTCGAATC	CGGTGGATCCACTAGTCTGTTTCTGATCAA		
	TGGATGTGGTGC	GTCGCCG		
M142.5	CCGCTCTAGAACTAGTTTCGACACGA	CGGTGGATCCACTAGTGCCACAATAGCTCC		
	CTCGCAAGGTT	AATAGTGAAATC		
C48H3.4	CCGCTCTAGAACTAGTGAAGGGGTCG	CGGTGGATCCACTAGTGAACAGTTTCCGTA		
	AAGGAAATAGTG	ACATCTTTCATC		
Supplementary Table S1. Primers for the amplification of targets for RNAi feeding vector				
production. Sequences derived from pPD129.36 and included for In-Fusion cloning are				
underlined.				

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Target	Primers	Primer location ¹	Similarity to <i>E. coli</i> ^A	UPL probe	Amplicon	Efficiency ^B	R ²
				(sequence)	Length		
Outron <i>gfp</i> mRNA	TAAAATTATCATG TTTTCAGGAC	<i>gfp</i> reporter (supplementary Figure 2)	no primer binding sites	9 (TGGTGATG)	147 bp	1.982	0.957
	GTTGCATCACCTT CACCCTC	<i>gfp</i> reporter (supplementary Figure 2)	no primer binding sites				
Internal <i>gfp</i> mRNA	CCACATGGTCCTT CTTGAGTTT	<i>gfp</i> reporter (supplementary Figure 2)	no primer binding sites	3 (CTGCTGGG)	62 bp	1.969	0.955
	ATAGTTCATCCAT GCCATGTGTA	<i>gfp</i> reporter (supplementary Figure 2)	no primer binding sites				
Outron- <i>rps-3</i> mRNA	TATATTTCTTGTG TTTTGTTCGGATT	chrIII: 6206726-6206751	no primer binding sites	46 (ATGGCTGC)	140 bp C)	1.932	0.993
	ACGGCCTTCTTCT TCTTGGT	chrIII: 6206846-6206865	no primer binding sites				
Internal rps-3	TCCTTCCAAAGGA ACCACAC	chrIII: 6207842-6207861	no primer binding sites	63 (AGGAGGA)	62 bp	1.967	0.993
mRNA	TGCTGGGACTTGA ACATCCT	chrIII: 6207884-6207903	no primer binding sites				
Supplementary Table S2 . qPCR assays were designed using the Universal Probe Library Assay Design Centre (Roche). A BLAST searches were done at NCRL against <i>Caenorhabditis elegans</i> (tavid 6239). <i>Escherichia celi</i> K 12 (tavid 62322) and ORED (tavid 627012). No E-celi acquire converte >750/							
sequence id	lentity were found, ar	nd primers, and primer combination	tions, were specific for <i>gfp</i> and	<i>rps-3</i> mRNA. Each	primer pair v	was tested on a	serial
template dilutions. 10-fold serial dilutions of LP6 plasmid (covering a range from 0.1 ng/ μ l to 1 fg/ μ l) were used for primers detecting the <i>gfp</i>							
reporter mRNA, and 10-fold serial dilutions of N2 genomic DNA (covering a range from 70 ng/µl to 70 fg/µl) for primers detecting <i>rps-3</i> mRNA. Cq							
from the re	sulting slope accordin	In the equation: $E = (10^{[-1/slop]})$	^{e]}). R ² calculated for the linear r	e fitting. The qPCR] regression is also sh	ow.	ency (^{b)} was ca	iculated

PCR assays					
Target	Primers	Primer location	Amplicon Length		
			(genomic DNA/cDNA)		
act-1,	CGTGGTTACTCTT	chrV:11,081,709-11,081,735	<i>act-1</i> : 562/510 bp		
act-2,	TCACCACCACCGC	chrV:11,077,468-11,077,494	<i>act-2</i> : 561/510 bp		
act-3	Т	chrV:11,072,581-11,072,607	<i>act-3</i> : 563/509 bp		
	GGACTCGTCGTAT TCTTGCTTGGAGA T	chrV:11,082,244-11,082,270			
		chrV:11,076,934-11,076,959			
		chrV:11,072,045-11,072,071			
dab-1	TATGGACGCATT GGTTGGT	chrII:8,228,308-8,228,326	228/100 bp		
	CGACATGGAGTT CAGAGAAGC	chrII:8,228,515-8,228,535			
Supplementary Table S3 . PCR assays. The PCR assay for the detection of actin transcripts has been described elsewhere (1).					

REFERENCES

1. Keall,R., Whitelaw,S., Pettitt,J. and Müller,B. (2007) Histone gene expression and histone mRNA 3' end structure in *Caenorhabditis elegans. BMC Mol Biol.*, **8**, 51.