Fig. S1 C. elegans Argonautes and construction of in situ knockin strains. A. Phylogenetic 1 diagram of 20 potentially functional C. elegans Argonautes (AGO). The amino acid 2 3 sequences of AGO proteins were obtained from Wormbase (WS285) and subjected to 4 generate phylogenetic tree using Mega X with the Neighbor-Joining (NJ) method. Numbers above each node indicate the NJ bootstrap support values. Seven Argonaute genes are 5 annotated as pseudogenes. wago-5 is proven to be a pseudogene in this study. B. Diagram 6 showing in-frame GFP::3×FLAG, 3×FLAG, or 3×FLAG::GFP knockin (KI) individually 7 into the endogenous locus of 20 AGOs with CRISPR/Cas9 technology (left). For the inserted 8 tags, GFP and 3×FLAG encode 238 and 22 amino acids, respectively. Gel image of PCR 9 products from genotyping is shown (right), and the corresponding PCR products are 10 confirmed by Sanger sequencing. nt, nucleotide; bp, base pair; gDNA, genomic DNA. 11

12

Fig. S2 Proteins expressed as endogenous Argonaute fusions. A. Western blots revealing the 13 endogenous expressions of GFP::3×FLAG, 3×FLAG or 3×FLAG::GFP tagged AGO 14 proteins with the anti-FLAG antibody. Stars indicate unspecific bands (or maybe a minor 15 16 isoform with a lower molecular weight) for ALG-4, HRDE-1, NRDE-3, WAGO-1, and WAGO-4. For WAGO-10 and C04F12.1, the fusion protein levels were quite low in whole 17 worm lysate, but they were enriched in IP with anti-FLAG antibody. B. Western blots failed 18 19 to detect the expression of GFP::3×FLAG or 3×FLAG::GFP tagged WAGO-5 with the anti-FLAG antibody in both WWL and IP materials. For A and B, WWL, whole worm lysate; IP 20 21 immunoprecipitation; kDa, kilodaltons. Actin is a loading control for Western blotting.

22

Fig. S3 Characterization of Argonaute knockin strains. A. Longevity curves of indicated 23 animals (left). The detailed information, including the mean, S.E.M and p value, is indicated 24 (right). Survival curves are representative of three independent experiments. P values from 25 the log-rank test. **B**. Brood size of 19 KI strains and N2 worms (N = 10) at 20 °C. Error bars 26 indicate S.E.M from three independent experiments. P values from two-tailed Student's t 27 test. N.S., not significant. C. GFP Expression pattern of eight chosen tagged Argonautes. 28 HRDE-1, WAGO-4, and PRG-1 were imaged at young adult stage in germline; WAGO-1 29 30 and PPW-2 were imaged at L4 stage in germline; ALG-1 was imaged at L4 stage (head); NRDE-3 and ALG-2 were imaged at embryonic stage. Scale bar represents 20 µm. 31

32

Fig. S4 Comparison of our RIP-seq data to previous data. A. PCA plots of sRNA profiles 33 showing the clusters between our data and data from previous studies with four 34 endogenously expressed Argonautes, including ALG-5, PRG-1, CSR-1, and PPW-2. 35 Percentages represent variance captured by each principal component 1 and 2 in each 36 analysis. B. Hierarchical clustering of sRNA profiles from our data and previous data of the 37 38 four AGOs. C. Scatter plots of normalized reads for annotated piRNAs in Input and PRG-1 RIP samples. The dashed line shows the threshold at 2-fold enrichment normalized to Input. 39 Red plots represent significant enriched piRNAs bound by PRG-1 (RPM ≥10, Enrichment 40 \geq 2-fold relative to Input). 41

42

Fig. S5 General features of sRNAs bound to each *C. elegans* Argonaute. Bar graph showing
the first nucleotide and size distribution of normalized sRNA reads from Input and 19 AGO
RIP samples. Pie charts demonstrating the percentage of reads from Input and 19 AGO RIPs
according to the genomic origins of annotated transcripts.

47

Fig. S6 Argonaute-associated miRNAs. A. Hierarchical clustering of AGOs according to the associated miRNAs. Number of the associated miRNAs is indicated for each Argonaute. For PRG-1 associated miRNAs, 4 out of the 9 may actually be piRNAs (described later). Each blue line represents a single mature miRNA associated with AGOs. B. Bar graph demonstrating the first two nucleotides of miRNA reads from Input and the 10 AGO RIPseq. C. Sequence features of 4 mis-annotated "miRNAs" of PRG-1. Schematic illustration of classic genomic motifs upstream of the piRNA (21U-RNA) sequences is shown below.

55

Fig. S7 mRNA targets regulated by ALG-1 and ALG-2. A. Venn diagram showing the misregulated mRNAs in *alg-1* or *alg-2* mutants re-analyzed from GSE98935. B. GO analysis of 406 unique ALG-1 targeted mRNAs and 381 unique ALG-2 targeted mRNAs. The gene number of the corresponding GO term is included in the brackets.

60

Fig. S8 Sequence features of 22G-RNAs and 26G-RNAs. A. Motifs for 22G-RNAs from
Input and the 17 22G-RNA binding AGOs. B. Motifs for 26G-RNAs from Input and the 8
26G-RNA binding AGOs. C. Percentage of risiRNA (antisense ribosomal siRNA, a subclass
of 22G-RNAs) reads from Input and 17 22G-RNA binding AGOs. SAGO-1 and SAGO-2

exhibit the highest percentages (labeled in red) of risiRNAs.

66

Fig. S9 *C. elegans* argonaute targeted pseudogene transcripts and transposons. A. Hierarchical clustering of AGOs based on the associated 22G-RNAs and 26G-RNAs that targeted pseudogene transcripts. Antisense reads of siRNAs are counted for pseudogenes. B. Hierarchical clustering of AGOs based on the associated 22G-RNAs and 26G-RNAs that targeted transposons. Antisense reads of siRNAs are counted for transposons.

72

Fig. S10 Argonaute-associated 26G-RNA targeted mRNAs. Hierarchical clustering diagram
and Gene Ontology (GO) analysis of mRNAs targeted by AGOs associated 26G-RNAs.
26G-RNAs associated with specific argonaute are determined with the cutoff RPM ≥5 and
Enrichment ≥2-fold relative to Input. 26G-RNAs corresponding to 534 mRNAs are
identified in Input and RIP samples, and 19986 is the number of annotated mRNAs
according to Wormbase (WS285). Each red line represents a single mRNA targeted by the
AGO-bound 26G-RNAs. GO analysis is performed with Gorilla web-server.

80

Fig. S11 siRNAs targeted to lincRNAs. A. Venn diagram showing numbers of lincRNAs 81 82 targeted by 22G-RNAs and 26G-RNAs in Input. B. Expression levels of 55 lincRNAs targeted by siRNAs bound to AGOs in nine indicated developmental stages or groups of 83 worms from a previous study (GSE115324). YA, young adult. C. Violin plots revealing stage 84 specific score of lincRNAs targeted or untargeted by siRNAs bound to AGOs. Stage specific 85 score is defined by RPM^{max}/ Σ (RPM) (Wei et al., 2019). RPM^{max} indicates the maximum 86 RPM of the individual lincRNA among nine groups in B. P value is calculated by the Mann-87 Whitney U test. 88

89

Fig. S12 Uridylation of 22G-RNAs. A. Bar graph showing the first nucleotide and size distribution of sRNA reads with untemplated uridine from Input and 4 AGOs that bind uridylated sRNAs. The x axis represents read length of uridylated sRNAs after trimming U.
B. Venn diagrams demonstrating percentage of uridylated 22G-RNA and non-uridylated 22G-RNA molecules from Input, and CSR-1, HRDE-1, PPW-2 and WAGO-4 RIP. C. Pie chart demonstrating the percentage of mRNAs targeted by CSR-1 associated non-uridylated and uridylated 22G-RNAs. D. GO analysis of 491 CSR-1 associated mRNAs with non-

- 97 uridylated 22G-RNAs and 2642 CSR-1 associated mRNAs with uridylated 22G-RNAs. The 98 gene number of the corresponding GO term is included in the brackets. **E**. Knockdown 99 efficiency of feeding RNAi for *cde-1*, *csr-1*, *hrde-1*, and *wago-4*. Actin mRNA was the 100 endogenous control. Error bars indicate SEM from three independent experiments. **p < 101 0.01; ***p < 0.001; ****p < 0.0001 by two-tailed Student's t test.
- 102
- 103Fig. S13 PPW-1 binds sRNAs with *E. coli* origin. First nucleotide and size distribution of104PPW-1 bound sRNAs derived from *E. coli* lacI/lacZ region (A) and hdeA/hdeB/hdeD region105(B). Only sRNAs (\geq 20-nt) are analyzed and aligned to the *E. coli* genome. Peaks of PPW-1106associated sRNAs corresponding to *E. coli* genomic loci were also presented. Red and black107peaks, respectively, represent sense and antisense strand reads mapping to *E. coli* genome
- 108 (NC_000913.3).

Fig. S1





Insertion

Fig. S2

А



В



gfp::3×flag::wago-5

wago-5::3×flag::gfp



		Mean surviva (days)	al S.E.M	P_value
•	N2	18.23	0.56	
•	3xflag::csr-1	19.26	0.56	0.317
•	c04f12.1::3xflag::gf	d 17.43	0.64	0.379
•	gfp::3xflag::nrde-3	18.76	0.56	0.603
•	gfp::3xflag::wago-1	0 18.36	0.55	0.864
•	gfp::3xflag::hrde-1	18.63	0.55	0.704
•	gfp::3xflag::wago-1	18.59	0.52	0.797
•	gfp::3xflag::wago-4	18.29	0.62	0.963
•	gfp::3xflag::ppw-2	18.54	0.59	0.756
•-	gfp::3xflag::sago-1	18.61	0.50	0.906
•-	gfp::3xflag::sago-2	17.50	0.50	0.196
•	ppw-1::3xflag::gfp	19.20	0.57	0.336
•	gfp::3xflag::rde-1	19.18	0.51	0.387
•	ergo-1::3xflag::gfp	17.59	0.40	0.113
•	gfp:3xflag::alg-1	18.20	0.52	0.691
•	gfp::3xflag::alg-2	17.65	0.66	0.495
•	alg-3::3xflag::gfp	17.73	0.53	0.442
•	alg-4::3xflag::gfp	18.86	0.58	0.440
•	gfp::3xflag::alg-5	18.47	0.52	0.996
•	gfp::3xflag::prg-1	18.54	0.46	0.901





Fig. S4









Four mis-annotated "miRNAs"

miR-78 AATAAAATATATTGTTTCATAGTGTCCGTAAAATAA TATTGGAGG miR-4936 TATCGAGATAATAA CAT miR-5549 GGGGGAGAGAT miR-8202 AAATAATTTCTA CGG GGTAATT

A/T rich

A/T rich

~20nt spacer

21U RNA

Fig. S7

Fig. S9

Α

Fig. S12

60

60 60

60

<

Normalized reads (RPM)

E. coli

В

Sense strand reads

Antisense strand reads

<

<

А

0.1kb

Table S1. List of *C. elegans* strains used in this study.

C. elegans	C. elegans strains			
Strain	Allele name	Genotype		
GSH410	hzhCR175	wago-10(hzhCR175[gfp::3xflag::wago-10]) V		
GSH411	hzhCR176	hrde-1(hzhCR176[gfp::3xflag::hrde-1]) III		
GSH412	hzhCR177	nrde-3(hzhCR177[gfp::3xflag::nrde-3]) X		
GSH413	hzhCR178	csr-1(hzhCR178[3xflag::csr-1]) IV		
GSH414	hzhCR179	c04f12.1(hzhCR179[c04f12.1::3xflag::gfp]) I		
GSH415	hzhCR180	<pre>sago-1(hzhCR180[gfp::3xflag::sago-1]) V</pre>		
GSH416	hzhCR181	sago-2(hzhCR181[gfp::3xflag::sago-2]) I		
GSH417	hzhCR182	ppw-1(hzhCR182[ppw-1::3xflag::gfp]) I		
GSH418	hzhCR183	wago-1(hzhCR183[gfp::3xflag::wago-1]) I		
GSH419	hzhCR184	wago-4(hzhCR184[gfp::3xflag::wago-4]) II		
GSH420	hzhCR185	wago-5(hzhCR185[gfp::3xflag::wago-5]) II		
GSH421	hzhCR186	wago-5(hzhCR186[wago-5::3xflag::gfp]) II		
GSH422	hzhCR187	ppw-2(hzhCR187[gfp::3xflag::ppw-2]) I		
GSH423	hzhCR188	alg-3(hzhCR188[alg-3::3xflag::gfp]) IV		
GSH424	hzhCR189	alg-4(hzhCR189[alg-4::3xflag::gfp]) III		
GSH425	hzhCR190	alg-1(hzhCR190[gfp:3xflag::alg-1]) X		
GSH426	hzhCR191	alg-2(hzhCR191[gfp::3xflag::alg-2]) II		
GSH427	hzhCR192	alg-5(hzhCR192[gfp::3xflag::alg-5]) I		
GSH428	hzhCR193	ergo-1(hzhCR193[ergo-1::3xflag::gfp]) V		
GSH429	hzhCR194	rde-1(hzhCR194[gfp::3xflag::rde-1]) V		
GSH430	hzhCR195	prg-1(hzhCR195[gfp::3xflag::prg-1]) I		
GSH431	hzhCR196	ppw-2(hzhCR196) I		
GSH432	hzhCR197	ppw-1(hzhCR197) I		
	hzhCR196;	ppw-2(hzhCR196) I;		
GSH433	ustIs45	ustIs45[mex-5p::GFP::his-58::tbb-2utr]		
SHG366	ustIs45	ustIs45[mex-5p::GFP::his-58::tbb-2utr]		
E. coli strains				
Strain	Allele name	Genotype		
HT115	-	-		
OP50	-	-		
OP50 ^{nanCM}	-	OP50/∆nanCM		

 Table S2. List of all oligonucleotide sequences used in this study.

sgRNA for <i>C. elegans</i> Knockin			
	sequence 5'-3'	Description	
wago-10 KI	CACGTGGATACTCTGATTAA	sgRNA	
hrde-1 KI	GTCATCGTCTGTTCCAGCAA	sgRNA	
nrde-3 KI sgRNA	ACTACTCCGGGCTCACAGCA	sgRNA	
csr-1 KI sgRNA	CATCGATCGTCAGCACAATA	sgRNA	
c04f12.1 C-terminal KI	TCGTTTGGAAGCAGAGAATT	sgRNA	
sago-1 KI sgRNA	TGCAGAGAAAAAACCAAAAG	sgRNA	
sago-2 KI sgRNA	AAGACGAGAAATGAGGAGTG	sgRNA	
ppw-1 C-terminal KI	GCGGCTACCAACAGTGCATA	sgRNA	
wago-1 KI	CCACCAGTCACTGCTCCACC	sgRNA	
wago-4 KI sgRNA	TCCGACTCAACCGTTAAGAT	sgRNA	
wago-5 N-terminal KI	GCCAACCGAACCGGGAACAT	sgRNA	
wago-5 C-terminal KI	ATACCATGAAGAGCATCTCA	sgRNA	
ppw-2 KI sgRNA	ATGCCACCAGTGCCACCAGT	sgRNA	
alg-3 C-terminal KI	AATCCTTCAGGACTGCGTCT	sgRNA	
alg-4 C-terminal KI	AGACACAGTCTTGAAGGATT	sgRNA	
alg-1 KI sgRNA	ACCTCACACGAACAACCTGT	sgRNA	
alg-2 KI sgRNA	GCTCGGCTCACGGAGCAATT	sgRNA	
alg-5 KI sgRNA	TGGTCGAAAAGTTAAAAGTG	sgRNA	
ergo-1 C-terminal KI	GACGAAGACCTGAAACGTCT	sgRNA	
rde-1 KI sgRNA	AAATGGCTTGCGAGGCCCAC	sgRNA	
prg-1 KI sgRNA	ATCGAACAACAGTGGAGGAA	sgRNA	
Homologous Recombination	primers for <i>C. elegans</i> Knockin		
wago-10-HRL-F	TGTAGGAGTTTCTTCTTTTG	Homologous	
wago-10-HRL-R	CATAACTTGAACACAGTTTC	Recombination	
wago-10-HRR-F	CCGACTACCGTCCAAAATCC	Homologous	
wago-10-HRR-R	AAGCTCTCGGCGTTTTTTGT	Recombination	
hrde-1-HRL-F	AGTATATGGAAGACTTGTCG	Homologous	
hrde-1-HRL-R	AGAGAACATTGGTGCTGAAA	Recombination	
hrde-1-HRR-F	ACTCCGAAGTCAACAACACC	Homologous	
hrde-1-HRR-R	CTCGGAGAGTAGTCCGCTCC	Recombination	
nrde-3-HRL-F	GGAAGTTTCAATTCCGGCAA	Homologous	
nrde-3-HRL-R	TGGTGTGGATGACGCAGATGT	Recombination	
nrde-3-HRR-F	CGTACAAATGTTTGGGGGCAC	Homologous	
nrde-3-HRR-R	GGATTTGTCTTGATGCGAAT	Recombination	
csr-1-FLAG-HRL–F	CGCACCTGTGATTTTTCGGG	Homologous	
csr-1-FLAG-HRL–R	CATGTCAGAGTTAAGTCCTG	Recombination	
csr-1-FLAG-HRR-F	AATCAGAAGCAAAATCCAAG	Homologous	
csr-1-FLAG-HRR–R	TCCGTCTGAACGAATGACGG	Recombination	

c04f12.1-C-HRL-F	ATACGAATGTCCCACCGTTG	Homologous
c04f12.1-C-HRL-R	AGCAATTCTCTTATTTTTGA	Recombination
c04f12.1-C-HRR-F	TAAATTAACGTTTTAAACTT	Homologous
c04f12.1-C-HRR-R	ACAAATCACATTTCTTAGCT	Recombination
sago-1-HRL–F	ATTGTTGTCTTTTTCAAACTG	Homologous
sago-1-HRL–R	TTGGGTGATATTGGACATGG	Recombination
sago-1-HRR–F	GTCACCAGCAGCATGGCTTC	Homologous
sago-1-HRR–R	CCTTCACCCGTGATGCTTCG	Recombination
sago-2-HRL–F	GAAATTCACCGTCGTTTTTCACG	Homologous
sago-2-HRL–R	TTTTAGTTGTTTTTCCATAG	Recombination
sago-2-HRR–F	GCTATGTCCGTCTCGGACAA	Homologous
sago-2-HRR–R	CTCCAGTTGGGTCGATGAGG	Recombination
ppw-1-C-HRL-F	ATTCAGTGCCCGAGTGAAGG	Homologous
ppw-1-C-HRL-R	TGCATTGAAACGAGTGGTGA	Recombination
ppw-1-C-HRR-F	TAATTATCTGTACTCCTCCG	Homologous
ppw-1-C-HRR-R	TTCTCACAGATCGCATCGTC	Recombination
wago-1-HRL-F	GTACTTTTTACAGTCACGTCG	Homologous
wago-1-HRL-R	TGGTGGATGAGGAGACATCT	Recombination
wago-1-HRR-F	CAACCGCATCCACCGATGCC	Homologous
wago-1-HRR-R	ACCCTCGATGAATTGAATCG	Recombination
wago-4-HRL–F	TGGGCAACACGTCATTTC	Homologous
wago-4-HRL–R	CATCCTTCTCGATTTTGTAA	Recombination
wago-4-HRR-F	CCAGCTCTTCCTCCAGTCTA	Homologous
wago-4-HRR-R	CCCATCCCCAACGTCCACAA	Recombination
wago-5-N-HRL–F	CGTTGCAACATGTGGCCAAC	Homologous
wago-5-N-HRL-R	GACAACGCCAGTATTCATTCAG	Recombination
wago-5-N-HRR-F	CTGTTGGATCAAAATGATCA	Homologous
wago-5-N-HRR–R	GAAATATACTTTTCCATGCT	Recombination
wago-5-C-HRL-F	GAGATGAATCGCAATACTTT	Homologous
wago-5-C-HRL-R	AGCATTGATGCGAGTCTTGT	Recombination
wago-5-C-HRR-F	TAGATTGCCAACGGTGCATC	Homologous
wago-5-C-HRR-R	CCATGCTGATAACTGCCCCA	Recombination
ppw-1-HRL-F	GACATTGGGAACTAGTGAAC	Homologous
ppw-1-HRL-R	AACCGGTGTAGCAGGCATTG	Recombination
ppw-1-HRR–F	CCACCGGTAACAATGCCACC	Homologous
ppw-1-HRR–R	TAGCGAGATCGAGAATCTG	Recombination
alg-3-C-HRL–F	GGTTGGAAAGGCAAAGAATG	Homologous
alg-3-C-HRL–R	AATGAAGTACATACGACTCT	Recombination
alg-3-C-HRR–F	TGAAGACTCTTCATGCAGAC	Homologous
alg-3-C-HRR–R	TTTGGCACGTATGCTTCCCA	Recombination
alg-4-C-HRL–F	ACTTCCGTCCACCCATCACC	Homologous
alg-4-C-HRL–R	AATGAAGTACATACGACTCT	Recombination

alg-4-C-HRR–F	TGAGCACTCTTCACTCTGTC	Homologous
alg-4-C-HRR-R	AGCTTGAATGGGTCCGATGT	Recombination
alg-1-HRL–F	TAGTGATTAAATAAGTGATT	Homologous
alg-1-HRL–R	TTGCGGCCCGCCGGACATTG	Recombination
alg-1-HRR–F	TATTTGCCAGGAGTCATGAA	Homologous
alg-1-HRR–R	GTAAACAGGGCGAATATTAG	Recombination
alg-2-HRL–F	GCCCCCAAAACTGTGTCTG	Homologous
alg-2-HRL–R	CAGCGAATCGCCGGGCATTT	Recombination
alg-2-HRR–F	ACATCGTCGTCTTTCATGCC	Homologous
alg-2-HRR–R	CCCGCGTGTACATGTTACGC	Recombination
alg-5-HRL–F	GCCTTTTCCTCCCTTTCCAC	Homologous
alg-5-HRL–R	CAACCATTGGTCTTCCATAC	Recombination
alg-5-HRR-F	CTGTCGGCAATTTATGATGA	Homologous
alg-5-HRR–R	CAAACTTCTCGTCCAACTCC	Recombination
ergo-1-C-HRL-F	CCGTCCAACTCATTACTATG	Homologous
ergo-1-C-HRL-R	GACAAATGTCATTCCTTCGA	Recombination
ergo-1-C-HRR-F	TAATATGTTTCTTAATGATT	Homologous
ergo-1-C-HRR-R	TCGCTCGTGTCGAGACCCGG	Recombination
rde-1-HRL-F	ATTGACATGTGAAAAATAC	Homologous
rde-1-HRL-R	GGGAAAATTCGAGGACATGT	Recombination
rde-1-HRR-F	GAATTGGAAAAAGGATTTTA	Homologous
rde-1-HRR-R	CAGGTTCACCATCGAACAAT	Recombination
prg-1-HRL-F	GTTGATCAATACTCACCATC	Homologous
prg-1-HRL-R	CATTATTACCTGAAAAATAT	Recombination
prg-1-HRR–F	GCATCTGGAAGTGGTCGCGG	Homologous
prg-1-HRR-R	GCGATCTCCTTCATCATCTT	Recombination
check primers for C. elegans	Knockin	
wago-10-check-F	GTGGGTCCAAAAACACTCGC	Genotyping
wago-10-check-R	GTTCGGAGACTGGTTGAGCA	
hrde-1-check-F	ATTATGGGAAGTTCGTCTTC	Genotyping
hrde-1-check-R	CGGGCTCATCTTGTTGACCT	
nrde-3-check-F	ACTAATCATGGATCTCCTAG	Genotyping
nrde-3-check-R	CAGTCGTCTTCATTGGTAAC	
csr-1-check-F	GTGGATCGACCCAAACCACT	Genotyping
csr-1-check-R	CATTTGCACAACATGCCGGA	
c04f12.1-check-F	GGCAAAGGCTCCGTCTTTTG	Genotyping
c04f12.1-check-R	CGGCAAATTTTTCTGAACTTTGT	
sago-1-check-F	ACCTGCCCACTGTGTTTTCA	Genotyping
sago-1-check-R	TGCAAGTGGTTGATGTCCGA	
sago-2-check-F	CGGCAGTGTTTGCCCACATC	Genotyping
sago-2-check-R	TCATTGTAAACGTTCTGGCA	
ppw-1-check-F	GTTCTTGCCGCCAATCAAGG	Genotyping
ppw-1-check-R	TTACACATCGGAGTCGCACC	

wago-1-check-F	-check-F AGCTTCGACAGTTGGCATGT		
wago-1-check-R	TGCCCATTTTTCCAGGTTCG		
wago-4-check-F	ACCCAGAATTTTAGGATGAC	Genotyping	
wago-4-check-R	TTACTCCGTCCTCTGCCGTA		
wago-5-N-check-F	TACAATTGCCGATTTGGGCG	Genotyping	
wago-5-N-check-R	ATCTGTGAACTGTTGTTTCC		
wago-5-C-check-F	GGCTTCGCTTCAAATGCTGT	Genotyping	
wago-5-C-check-R	CGAACTTCCTTCCAGAAAAA		
ppw-2-check-F	CTCGCCAATCGCATTTTCGA	Genotyping	
ppw-2-check-R	GTTTCCCATCTCCAACTTCC		
alg-3-check-F	TGTGACACCAACTCGCTCTC	Genotyping	
alg-3-check-R	-check-R ATCCGCAAACAAAGCACGA		
alg-4-check-F	-check-F CGCTCTTCAACGCTTGCTTC		
alg-4-check-R	CGGAAAAACCGCCCGAAAAA		
alg-1-check-F	TTTCTGTTGACCCTCCTGGC	Genotyping	
alg-1-check-R	TTCTAGATCATTTTGGAGCG		
alg-2-check-F	TACCGCAGAGTTATGACGGC	Genotyping	
alg-2-check-R	TAAGTTTCCCAGTTCTGGGC		
alg-5-check-F	GTTGGGTTCGGTGGTTGTTG	Genotyping	
alg-5-check-R	CCTATCAATTTGAATGGCTC		
ergo-1-check-F	GGAGACCTCTGCGAAGTCAA	Genotyping	
ergo-1-check-R	CGTGTCGAGACCCGGAAAA		
rde-1-check-F	GAGTGGTTCTGCAAACACGG	Genotyping	
rde-1-check-R	TTCCCGCTGTTTCGTTGACT		
prg-1-check-F	CACCTTTTCTAAGTGGACTGT	Genotyping	
prg-1-check-R	ATCGGTGACGTTATTATCAC		
sgRNA for <i>C. elegans</i> Knock	out		
ppw-1 KO sgRNA1	CAAATCAGCGAGTTGGTTAC	2171bp deletion between	
ppw-1 KO sgRNA2	TCACGCATCGATATTTTTTG	two sgRNA sites	
ppw-2 KO sgRNA1	TCATTCTCTCTTCTGTGAAT	1445 bp deletion between	
ppw-2 KO sgRNA2	TAGCACTGCACTTCTCATGG	two sgRNA sites	
check primers for <i>C. elegans</i> Knockout			
ppw-1-KO-check-F	GCCGCACAACCACATATCAG	Genotyping	
ppw-1-KO-check-R	TCAAGCTCGTCGAGTAGTGTC		
ppw-2-KO-check-F	GAGAGTAATCATCGACGGTA	Genotyping	
ppw-2-KO-check-R	TTTCCAGTTGGAATTCCTTC		
C. elegans RNAi assay			
act-1-qPCR-F	ACGACGAGTCCGGCCCATCC	qPCR	
act-1-qPCR-R	GAAAGCTGGTGGTGACGATGGTT		
hrde-1-qPCR-F CCGGATACCGTCCACATCTC		qPCR	
hrde-1-qPCR-R	ACGGACGAACGGTACCAATAA		
csr-1-qPCR-F	ACAGAGTGCCATTAGAAGCGAAAG qPCR		
csr-1-qPCR-R	GTACTGAGTCGATTGAGGATCGAG		

wago-4-qPCR-F	ACGTCGCTTCCAACTCCATT	qPCR	
wago-4-qPCR-R	TCATGCGTTGACACGACGAC		
16s-qPCR-F	CGAGGTCGCTTCTCTTTG	qPCR	
16s-qPCR-R	GGAGACTGCCAGTGATAAAC		
nanCM-qPCR-F	TTTGTACACAACGGCAAGGC	qPCR	
nanCM-qPCR-R	TTCGCCAGCGTAACTCCATT		
Bacteria assay associated olig	gos		
pKD46-check-F	TACTGGCTCTTCTCGCTA	PCR primers for	
pKD46-check-R	TTGCTTGATCTCAGTTTCAG	Transformation verification	
nanCM-ko-HR-F	TCTCAGGCTGCGACACTGGACGTAC		
	GTGGTGGATATCGTAGTGGAAGCCA		
	CGCCTATGAGTCCTCCTTAGTTCCTA		
	TTCC	Homologous	
nanCM-ko-HR-R	AAATACGGCATCCGTTCGCAATCCT	Recombination	
	GGTTTGGCTTCGCCATTAATAAGCCA		
	GGTTTTATCGTGTAGGCTGGAGCTG		
	CTTC		
pCP20-check-F	GAACACTGCCAGCGCATCAA	PCR primers for	
pCP20-check-R	GAGCTTTGTTGTAGGTGGACC	Transformation verification	
nanCM-ko-check-F	CTGGCGTATTATTACTGTGC	Genotyping	
nanCM-ko-check-R	GCGCATAGTTCTTACCGTTC		
T08E11.1-qPCR-F	TTGCCTACAAAGGCTCAAGTC	qPCR	
T08E11.1-qPCR-R	TGTTTTCCAGGTGGGGTTGT		
Adapters sequence for Library construction			
3' DNA adapter	rAppAGATCGGAAGAGCACACGTCT	-	
	GAACTCCAGTCA/3ddC/		
5' RNA adapter	rArCrArCrUrCrUrUrUrCrCrCrUrArCrAr	-	
	CrGrArCrGrCrUrCrUrUrCrCrGrArUrCr		
	U		