

stage	state	feature	count	enrichment	p-value
ee	Enhancer	intergenic	59	0.6778360552	0.00048
ee	Enhancer	intron	55	-0.1570874597	0.3279272727
ee	Gene body	intergenic	57	-0.4570613948	0.0006
ee	Gene body	intron	209	-0.3705784898	0.0066857143
ee	Heterochromatin	intergenic	34	-0.0892991405	0.3279272727
ee	Heterochromatin	intron	119	1.2496763643	0.0075
ee	Low signal	intergenic	182	0.0156254583	0.4227130435
ee	Low signal	intron	227	-0.449121839	0.0075
ee	Polycomb	intergenic	52	1.1496090691	0.0003
ee	Polycomb	intron	160	2.1278433535	0.0003
ee	Promoter	intergenic	2	-3.1452021959	0.0003
ee	Promoter	intron	9	-1.2488723695	0.0219789474
l3	Enhancer	intergenic	98	0.9958072399	0.0003
l3	Enhancer	intron	66	-0.4703345716	0.19668
l3	Gene body	intergenic	22	-2.0003681619	0.0003
l3	Gene body	intron	214	-0.4505126037	0.0051692308
l3	Heterochromatin	intergenic	46	-0.0289542175	0.4245
l3	Heterochromatin	intron	172	1.1047287454	0.0168
l3	Low signal	intergenic	102	-0.5127075469	0.0006
l3	Low signal	intron	97	-1.0541539975	0.00048
l3	Polycomb	intergenic	116	2.0772017409	0.0003
l3	Polycomb	intron	228	2.1816948244	0.0003
l3	Promoter	intergenic	2	-2.4362512894	0.0003

I3	Promoter	intron	2	-2.4225137827	0.0196
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Table S1. Chromatin state enrichment for ITS sites based on simulations

gene name			ITS present		
<i>C. elegans</i>	<i>C. briggsae</i>	<i>C.remanei</i>	<i>C. elegans</i>	<i>C. briggsae</i>	<i>C.remanei</i>
ego-2	Cbr-ego-2	Cre-ego-2	1	1	0
sri-54	Cbr-sri-54	WBGene00068079	1	1	0
sri-54	CBG30920	WBGene00068079	1	1	0
tsr-1	Cbr-tsr-1		1	1	0
best-8	Cbr-best-8	WBGene00056079	1	1	0
usp-39	Cbr-usp-39	WBGene00068095	1	1	0
F54A3.2	CBG21459	WBGene00067022	1	1	0
cutl-20	Cbr-cutl-20	Cre-cutl-20	1	1	0
pmt-2	Cbr-pmt-2	Cre-pmt-2	1	1	0
fmil-1	Cbr-fmil-1	WBGene00059166	1	1	0
Y94H6A.5	CBG13909	WBGene00071875	1	1	0
srab-25	Cbr-srab-25	Cre-srab-25	1	1	0
srab-25	Cbr-srab-25	WBGene00063629	1	1	0
aat-9	Cbr-aat-9	WBGene00072979	1	0	1
cmk-1	Cbr-cmk-1	Cre-cmk-1	1	0	1
fat-5	Cbr-fat-5	Cre-fat-5	1	0	1
pqn-48	Cbr-pqn-48	Cre-pqn-48	1	0	1
rhgf-2	Cbr-rhgf-2	Cre-rhgf-2	1	0	1
twk-33	Cbr-twk-33	Cre-twk-33	1	0	1
kcnl-1	Cbr-kcnl-1	WBGene00065967	1	0	1
F56G4.6	CBG08045	WBGene00069984	1	0	1
F30B5.4	CBG05349	WBGene00080036	1	0	1
F30B5.4	CBG24006	WBGene00080036	1	0	1

lin-42	Cbr-lin-42	Cre-lin-42	1	0	1
K07D4.5		WBGene00064962	1	0	1
T06A4.1	CBG18554	WBGene00060957	1	0	1
Y50D4B.1	CBG01105	WBGene00061109	1	0	1
mlt-7	Cbr-mlt-7	Cre-mlt-7	1	0	1
abu-14	Cbr-abu-14	Cre-pqn-95	0	1	1
F33H1.4	CBG00931	WBGene00072743	0	1	1
ipla-1	Cbr-ipla-1	Cre-ipla-1	0	1	1
vps-18	Cbr-vps-18	Cre-vps-18	0	1	1
vha-19	Cbr-vha-19	Cre-vha-19	0	1	1
Y54H5A.2	CBG21315	WBGene00071936	0	1	1
Y32B12B.2	CBG23974	WBGene00067598	0	1	1

Table S2. Genes which contain ITS sites in more than one species

sample_id	mismatches	freq
gu_2009A_WAGO_1_input_CIPPNK_seq_prb_s7	0	1
gu_2009A_WAGO_1_input_CIPPNK_seq_prb_s7	1	6
gu_2009A_WAGO_1_input_CIPPNK_seq_prb_s7	2	17
gu_2009A_WAGO_1_input_CIPPNK_seq_prb_s7	3	49
gu_2009A_WAGO_1_IP_CIPPNK_seq_prb_s6	1	10
gu_2009A_WAGO_1_IP_CIPPNK_seq_prb_s6	2	49
gu_2009A_WAGO_1_IP_CIPPNK_seq_prb_s6	3	125
phillips_2015_FLAGHRDE-1_input	0	3
phillips_2015_FLAGHRDE-1_input	1	1
phillips_2015_FLAGHRDE-1_input	2	31
phillips_2015_FLAGHRDE-1_input	3	147
phillips_2015_FLAGHRDE-1_IP	1	5
phillips_2015_FLAGHRDE-1_IP	2	40
phillips_2015_FLAGHRDE-1_IP	3	138
phillips_2015_FLAGHRDE-1_prg- 1_male_herm_input	0	1
phillips_2015_FLAGHRDE-1_prg- 1_male_herm_input	1	2
phillips_2015_FLAGHRDE-1_prg- 1_male_herm_input	2	7
phillips_2015_FLAGHRDE-1_prg- 1_male_herm_input	3	12
phillips_2015_FLAGHRDE-1_prg-1_male_herm_IP	3	15

phillips_2015_FLAGHRDE-1_prg-1_male_input	0	2
phillips_2015_FLAGHRDE-1_prg-1_male_input	1	9
phillips_2015_FLAGHRDE-1_prg-1_male_input	2	32
phillips_2015_FLAGHRDE-1_prg-1_male_input	3	62
phillips_2015_FLAGHRDE-1_prg-1_male_IP	0	1
phillips_2015_FLAGHRDE-1_prg-1_male_IP	1	9
phillips_2015_FLAGHRDE-1_prg-1_male_IP	2	47
phillips_2015_FLAGHRDE-1_prg-1_male_IP	3	82
sapetsching_2015_hrde_1_HRDE_1RIP	3	3
sapetsching_2015_WT_HRDE_1RIP	2	2
sapetsching_2015_WT_HRDE_1RIP	3	19
seth_2013_CSR_1_IP_gfp	0	2
seth_2013_CSR_1_IP_gfp	2	8
seth_2013_CSR_1_IP_gfp	3	15
seth_2013_CSR_1_IP_oma_1gfp	2	10
seth_2013_CSR_1_IP_oma_1gfp	3	24
seth_2013_input_for_CSR_1_IP_gfp	0	2
seth_2013_input_for_CSR_1_IP_gfp	2	13
seth_2013_input_for_CSR_1_IP_gfp	3	31
seth_2013_input_for_CSR_1_IP_oma_1gfp	1	1
seth_2013_input_for_CSR_1_IP_oma_1gfp	2	2
seth_2013_input_for_CSR_1_IP_oma_1gfp	3	19
seth_2013_total_oma_1gfp	2	6
seth_2013_total_oma_1gfp	3	41

seth_2013_total_oma_1gfp_csr_1	1	2
seth_2013_total_oma_1gfp_csr_1	2	7
seth_2013_total_oma_1gfp_csr_1	3	20
seth_2013_total_oma_1gfp_rde_3	2	2

Table S3. Total telomere sRNAs from input and IP datasets.

sample_id	sequence	fre q	lengt h
gu_2009A_WAGO_1_input_CIPPNK_seq_pr			
b_s7	TTAGGCTTAGGCTTAGGCTT AGGCTTAGGCTTAGGCTTAG	1	20
phillips_2015_FLAGHRDE-1_input	G	2	21
phillips_2015_FLAGHRDE-1_input	CTTAGGCTTAGGCTTAGGC	1	19
phillips_2015_FLAGHRDE-1_prg-	CTAAGCCTAAGCCTAAGCCT		
1_male_herm_input	AAG	1	23
phillips_2015_FLAGHRDE-1_prg-	AAGCCTAAGCCTAAGCCTAA		
1_male_input	G	1	21
phillips_2015_FLAGHRDE-1_prg-	TAAGCCTAAGCCTAAGCCTA		
1_male_input	AGC TTAGGCTTAGGCTTAGGCTTA	1	23
phillips_2015_FLAGHRDE-1_prg-1_male_IP	GG CTAAGCCTAAGCCTAAGCCT	1	23
seth_2013_CSR_1_IP_gfpcdk_1	AAG	2	23
seth_2013_input_for_CSR_1_IP_gfpcdk_1	CTAAGCCTAAGCCTAAGC	2	18

Table S4. Perfect telomeric sRNAs from input and IP datasets.

sample_id	0	1	2	3
miwi2HET_E165_Testis_smallRNA	36	7	10	59
miwi2HET_P10_Testis_smallRNA	2	1	2	37
miwi2KO_E165_Testis_smallRNA	91	13	11	70
BmTdrd12_IP	0	0	0	3
HA_BmTdrd12_IP	0	0	0	7
MILI_IP	0	1	2	9
MILI_IP_	0	2	3	6
TDRD12_IP_	0	4	1	9
Total_small_RNA_14_40_nt_rep1	0	0	1	37
Total_small_RNA_14_40_nt_rep2	0	0	1	43
trimmed_10_dpp	1	0	1	0
trimmed_15_dpp	2	2	4	3
trimmed_18_dpp	0	0	1	1
trimmed_40_dpp	2	3	3	9
trimmed_6_dpp	2	0	0	1
trimmed_Input_Miwi_ADH__1	1	0	0	0
trimmed_LZ	1	0	0	0
trimmed_MIWI_IP_Miwi__1	1	0	0	0
trimmed_MIWI_IP_Miwi__2	2	0	0	1
trimmed_MIWI_IP_Miwi__2	0	0	0	1
trimmed_MIWI_IP_Miwi_ADH__1	0	0	1	0
trimmed_Miwi__late_sc_rep1	0	0	0	1

MVH__adultMILI_IPlonger_RNAs	0	0	0	1
MVH__adultMILI_IPpiRNAs	0	0	0	1
MVH__adultMIWI_IPlonger_RNAs	0	0	0	10
MVH__adultMIWI_IPpiRNAs	0	0	0	23
MVH_adultMVH_IPlonger_RNAs	2	0	1	20
MVH_adultMVH_IPpiRNAs	0	1	0	15
MVH_KladultMILI_IPlonger_RNAs	0	0	0	1
MVH_KladultMILI_IPpiRNAs	0	0	0	2
MVH_KladultMVH_IPlonger_RNAsrep1	0	0	0	3
MVH_KladultMVH_IPlonger_RNAsrep3	0	0	1	3
MVH_KladultMVH_IPpiRNAsrep1	1	0	0	3
MVH_KladultMVH_IPpiRNAsrep2	0	0	0	1
MVH__KIP0MILI_IPlonger_RNAs	0	0	1	6
MVH_KIP0MILI_IPlonger_RNAs	0	0	1	5
MVH__KIP0MILI_IPpiRNAs	2	1	3	14
MVH_KIP0MILI_IPpiRNAs	0	2	3	25
MVH_KIP0MIWI2_IPlonger_RNAs	0	0	1	32
MVH_KIP0MIWI2_IPpiRNAs	0	1	3	129
MVH__P0MILI_IPpiRNAs	0	1	0	12
MVH__P0MIWI2_IPlonger_RNAs	0	0	2	16
MVH__P0MIWI2_IPpiRNAs	0	2	0	32
Rosa26_pi_reporterMVH__KIP0MILI_IPlonger_RNAs	0	0	0	5
Rosa26_pi_reporterMVH_KIP0MILI_IPlonger_RNAs	1	0	0	4

Rosa26_pi_reporterMVH__KIP0MILI_IPpiRNAs	2	5	3	32
Rosa26_pi_reporterMVH_KIP0MILI_IPpiRNAs	2	3	4	40
Rosa26_pi_reporterMVH___P0MILI_IPlonger_RNA s	1	1	5	8
Rosa26_pi_reporterMVH__P0MILI_IPlonger_RNAs	0	0	1	10
Rosa26_pi_reporterMVH___P0MILI_IPpiRNAs	1	2	5	53
Rosa26_pi_reporterMVH__P0MILI_IPpiRNAs	3	3	7	22
Tdrd9_KIKIP0MILI_IPpiRNAs	0	1	0	3
Tdrd9_KIKIP0MIWI2_IPpiRNAs	0	0	1	14
Tdrd9_KIP0MILI_IPpiRNAs	0	0	2	5
Tdrd9_KIP0MIWI2_IPpiRNAs	0	0	1	6
Tdrd9___P0MILI_IPpiRNAs	0	0	0	1
Tdrd9___P0MIWI2_IPpiRNAs	0	0	2	6

Table S5. Telomeric reads from 77 small RNA libraries from mouse with 0, 1, 2 or 3 mismatches.

name	dataset	total_mappe d	telo_read s
6_dpp	watanabe_2014	965453	3
MIWI_IP_Miwi___2	watanabe_2014	1951904	3
Miwi___early_RS_rep2	watanabe_2014	17939	0
MIWI_IP_Miwi_ADH___1	watanabe_2014	582024	1
Miwi___early_RS_rep2	watanabe_2014	12284	0
early_P	watanabe_2014	5329	0
15_dpp	watanabe_2014	2258599	11
40_dpp	watanabe_2014	2532418	17
Input_Miwi_ADH___1	watanabe_2014	171962	1
Input_Miwi___1	watanabe_2014	228486	0
22_dpp	watanabe_2014	275686	0
MIWI_IP_Miwi_ADH___2	watanabe_2014	747319	0
Input_Miwi___2	watanabe_2014	169922	0
Miwi___early_RS_rep1	watanabe_2014	22573	0
late_PD	watanabe_2014	16586	0
MIWI_IP_Miwi___2	watanabe_2014	1440884	1
Miwi___late_sc_rep1	watanabe_2014	163379	1
10_dpp	watanabe_2014	529654	2
Input_Miwi_ADH___2	watanabe_2014	46804	0
Miwi___early_RS_rep1	watanabe_2014	18688	0
18_dpp	watanabe_2014	540617	2
Miwi___early_RS_rep3	watanabe_2014	18883	0
mid_P	watanabe_2014	24147	0
Miwi___early_RS_rep3	watanabe_2014	18864	0
LZ	watanabe_2014	12885	1

MIWI_IP_Miwi___1	watanabe_2014	959010	1
Miwi__late_sc_rep1	watanabe_2014	103609	0
Input_Miwi___2	watanabe_2014	407209	0
28_dpp	watanabe_2014	641072	0
Input_Miwi___1	watanabe_2014	156467	0
MIWI_IP_Miwi___1	watanabe_2014	884287	0
MILI_IP_	pandey_2013	17659714	11
BmTdrd12_IP	pandey_2013	25859314	3
Total_small_RNA_14_40_nt_rep2	pandey_2013	21771414	44
TDRD12_IP_	pandey_2013	11657018	14
Total_small_RNA_14_40_nt_rep1	pandey_2013	15775465	38
HA_BmTdrd12_IP	pandey_2013	25035732	7
MILI_IP	pandey_2013	16782336	12
MVH__P0MIWI2_IPpiRNAs	wenda_2017	13084791	34
MVH__P0MILI_IPpiRNAs	wenda_2017	14351656	13
Rosa26_pi_reporterMVH_KIP0MILI_IPpiRNAs	wenda_2017	22398538	49
MVH__adultMILI_IPpiRNAs	wenda_2017	29317491	1
MVH_KladultMILI_IPpiRNAs	wenda_2017	20743492	2
MVH__KIP0MILI_IPlonger_RNAs	wenda_2017	5908535	7
MVH_KladultMVH_IPlonger_RNAsrep3	wenda_2017	33749110	4
MVH_KIP0MIWI2_IPlonger_RNAs	wenda_2017	3136830	33
MVH__adultMIWI_IPpiRNAs	wenda_2017	24360585	23
Tdrd9__P0MILI_IPpiRNAs	wenda_2017	10302314	1
MVH__adultMILI_IPlonger_RNAs	wenda_2017	19677190	1
Rosa26_pi_reporterMVH__KIP0MILI_IPpiRNAs	wenda_2017	14466903	42
MVH_KladultMILI_IPlonger_RNAs	wenda_2017	11187973	1
MVH_KIP0MILI_IPlonger_RNAs	wenda_2017	4254928	6
Tdrd9_KIKIP0MIWI2_IPpiRNAs	wenda_2017	10382704	15

Tdrd9_KIKIP0MILI_IPpiRNAs	wenda_2017	9434523	4
MVH_adultMVH_IPpiRNAs	wenda_2017	7508372	16
MVH_KladultMVH_IPpiRNAsrep1	wenda_2017	16375488	4
Tdrd9_KIP0MILI_IPpiRNAs	wenda_2017	8232034	7
MVH_KIP0MIWI2_IPpiRNAs	wenda_2017	9100669	133
Rosa26_pi_reporterMVH__P0MILI_IPpiRNAs	wenda_2017	16236562	35
Rosa26_pi_reporterMVH__KIP0MILI_IPlonger_RNAs	wenda_2017	2204031	5
MVH__P0MIWI2_IPlonger_RNAs	wenda_2017	7613869	18
Tdrd9_KIP0MIWI2_IPpiRNAs	wenda_2017	12678748	7
MVH_KladultMVH_IPlonger_RNAsrep1	wenda_2017	11915289	3
MVH_KladultMVH_IPpiRNAsrep2	wenda_2017	15206654	1
MVH__KIP0MILI_IPpiRNAs	wenda_2017	11313520	20
Rosa26_pi_reporterMVH_KIP0MILI_IPlonger_RNAs	wenda_2017	4210652	5
MVH_KIP0MILI_IPpiRNAs	wenda_2017	11715236	30
Rosa26_pi_reporterMVH__P0MILI_IPlonger_RNAs	wenda_2017	5375843	15
Rosa26_pi_reporterMVH__P0MILI_IPlonger_RNAs	wenda_2017	3850038	11
MVH__adultMIWI_IPlonger_RNAs	wenda_2017	16844161	10
Rosa26_pi_reporterMVH__P0MILI_IPpiRNAs	wenda_2017	22267409	61
MVH_adultMVH_IPlonger_RNAs	wenda_2017	12500461	23
Tdrd9__P0MIWI2_IPpiRNAs	wenda_2017	8456563	8
miwi2KO_E165_Testis_smallRNA	manakov_2015	17357284	185
miwi2HET_P10_Testis_smallRNA	manakov_2015	15540073	42
miwi2KO_P10_Testis_smallRNA	manakov_2015	989182	0
miwi2HET_E165_Testis_smallRNA	manakov_2015	14841295	112

Table S6. Sample information for mouse small RNA analysis.

sequence	length	freq
GTTAGGGTTAGGGTTAGGG	19	77
GTTAGGGTTAGGGTTAGGGTTAG	23	10
TTAGGGTTAGGGTTAGGGTTAG	22	5
GGGTTAGGGTTAGGGTTAG	19	4
GGTTAGGGTTAGGGTTAGGGTT	22	3
GTTAGGGTTAGGGTTAGGGTT	21	3
GTTAGGGTTAGGGTTAGGGTTA	22	3
TAGGGTTAGGGTTAGGGTTAG	21	3
AGGGTTAGGGTTAGGGTTAG	20	2
GTTAGGGTTAGGGTTAGGGTTAGG	24	2
TAGGGTTAGGGTTAGGGTTAGG	22	2
AGGGTTAGGGTTAGGGTTA	19	1
AGGGTTAGGGTTAGGGTTAGGGTTAGGGTT	30	1
GGGTTAGGGTTAGGGTTAGGGTTAG	25	1
GGTTAGGGTTAGGGTTAG	18	1
GGTTAGGGTTAGGGTTAGG	19	1
GGTTAGGGTTAGGGTTAGGG	20	1
GGTTAGGGTTAGGGTTAGGGT	21	1
GTTAGGGTTAGGGTTAGGGT	20	1
GTTAGGGTTAGGGTTAGGGTTAGGG	25	1
GTTAGGGTTAGGGTTAGGGTTAGGGTT	27	1
GTTAGGGTTAGGGTTAGGGTTAGGGTTAG	29	1

TAGGGTTAGGGTTAGGGTTA	20	1
TAGGGTTAGGGTTAGGGTTAGGGTTAGGGT	30	1
TTAGGGTTAGGGTTAGGG	18	1
TTAGGGTTAGGGTTAGGGTT	20	1
TTAGGGTTAGGGTTAGGGTTAGGGTTAGG	29	1

Table S7. Perfect G-rich telomeric sRNAs from mouse small RNA datasets.

sequence	length	freq
TAACCCTAACCCCTAACCCCTAACCC	24	4
TAACCCTAACCCCTAACCCCTAACCCCTAACCC	30	4
TAACCCTAACCCCTAACCCCTAACCCCTAAC	28	3
TAACCCTAACCCCTAACCCCTAAC	22	2
AACCCTAACCCCTAACCCCTAACCCCT	24	1
AACCCTAACCCCTAACCCCTAACCCCTAAC	27	1
AACCCTAACCCCTAACCCCTAACCCCTAACCCCT	30	1
ACCCTAACCCCTAACCCCTAACCC	22	1
ACCCTAACCCCTAACCCCTAACCCCTAACCCCT	29	1
CCCTAACCCCTAACCCCTAAC	19	1
CCCTAACCCCTAACCCCTAACCCCTAACCC	27	1
CCTAACCCCTAACCCCTAACCCCTAACCCCTA	28	1
CTAACCCCTAACCCCTAACCCCTA	21	1
CTAACCCCTAACCCCTAACCCCTAAC	23	1
CTAACCCCTAACCCCTAACCCCTAACCCCT	26	1
TAACCCTAACCCCTAACCCCTAACCCCT	25	1
TAACCCTAACCCCTAACCCCTAACCCCTAACCC	29	1

Table S8. Perfect C-rich telomeric sRNAs from mouse small RNA datasets.

Dataset	GEO accession	PMID
Wanatabe (2014)	GSE42004	25480952
Pandey (2013)	GSE50544	24067652
Wenda (2017)	GSE95580	28633017
Manakov (2015)	GSE70731	26279574
Fischer (2011)	GSE32366	22102828
Gent (2010)	GSE19414	20116306
Gu (2009)	GSE18215	19800275
Phillips (2014)	GSE54320	24684932
Phillips (2015)	GSE63114	26279487
Sapetsching (2015)	GSE66344	25811365
Seth (2013)	GSE49532	24360782
McMurchy (2017)	GSE87524	28294943
Zeller (2017)	NA	27668659

Table S9. Accession numbers for data sets analyzed in this study. Top 4 for mouse sRNAs and bottom 9 for *C. elegans* sRNAs.

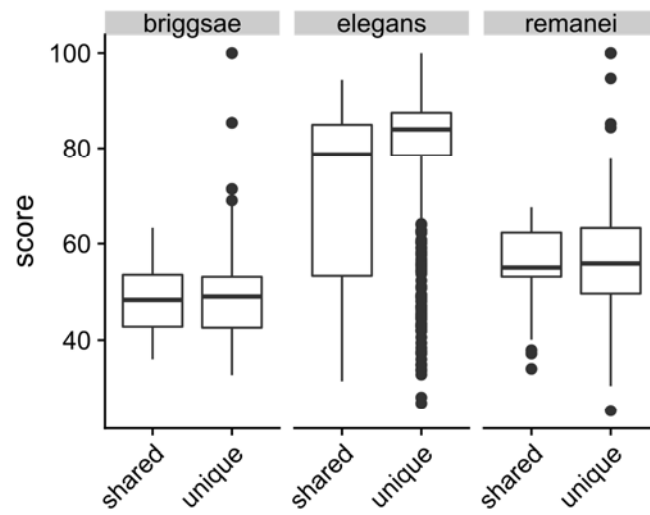


Figure S1: Telomere homology scores for intronic ITS sites broke down by whether or not a homologue of the gene containing the ITS site also contains an ITS site in another species (“shared” versus “unique” respectively).