

Table S1. The siRNA loci in Arabidopsis Genome^a

Chromosome	Total Loci	Retroelements ^b		Transposons ^b		5S rDNA		Pseudogene		Expressed gene		Hypothetical gene		IGR
		S ^c	AS ^c	S	AS	S	AS	S	AS	S	AS	S	AS	
1	1030	114	182	67	208	0	1	2	30	5	1	47	23	350
2	791	63	167	72	160	0	0	2	4	1	3	45	41	233
3	1487	115	187	72	167	215	406	2	2	5	8	20	15	273
4	844	79	183	46	125	28	39	2	3	0	1	18	17	303
5	1147	99	195	57	215	21	38	0	1	3	4	10	24	480
TOTAL	5299	470	914	314	875	264	484	8	40	14	17	140	120	1639

^asiRNAs that hit 18S and 25S rRNA loci are not included because the number of 18S and 25S rRNA loci is not given in the current genome sequence version.

^bPredicted using RepeatMasker program as indicated in the text.

^cS: Sense; AS: Antisense.

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Table S2. Cytosine Methylation of Arabidopsis *AtSN1*

<u>Genotype</u> ^a	<u>CpG</u> ^b	<u>CpNpG</u>	<u>CpHpH</u> ^c
Col-0	121/168 ^d (72.0%)	94/218 (43.1%)	287/1759 (16.3%)
<i>rdr2-1</i>	64/104 (61.5%)	35/142 (24.6%)	52/1168 (4.5%)
<i>dcl3-1</i>	76/89 (85.4%)	51/119 (42.9%)	70/915 (7.7%)
<i>La-er</i>	56/78 (71.8%)	45/100 (45.0%)	90/757 (11.9%)
<i>cmt3-7</i>	40/72 (55.6%)	2/88 (2.3%)	24/679 (3.5%)

^aEighteen to forty-seven clones were sequenced for each genotype.

^bCpGpG sites are counted as CpG sites, not as CpNpG.

^cH = A, T, or C.

^dNumber of methylated cytosines/total number of sites analyzed.