| sample	Sequencer	Total useful reads*	rRNAs sense	rRNAs anti-sense	tRNAs sense	tRNAs anti-sense	snRNAs sense	snRNAs anti-sense	Mitochond rial genome	Used for analysis	Data used for Fig.
Twi1p-IP	GAII	34959335	1133041	5622	771751	1473	13178	159	69643	32964468	1
TWI1_KO_3h	GAII	24967491	915849	1947	749782	836	4306	145	151125	23143501	2,3
HA-Twi1p IP	HiSeq2000	41322677	32721	2400	27154	1324	475	198	1359	41260968	2F
HA-Twi1p-hAGO2Lmut IP	HiSeq2000	39352231	215056	2819	27318	1083	483	163	2022	39107352	2F

*longer than 18 nt, did not match to the mixed phiX174 phage DNA, and no non-ACGT bases in the first 25 nt

Table S1. Basic analysis of sequence reads from small RNA cDNA libraries

Table S1
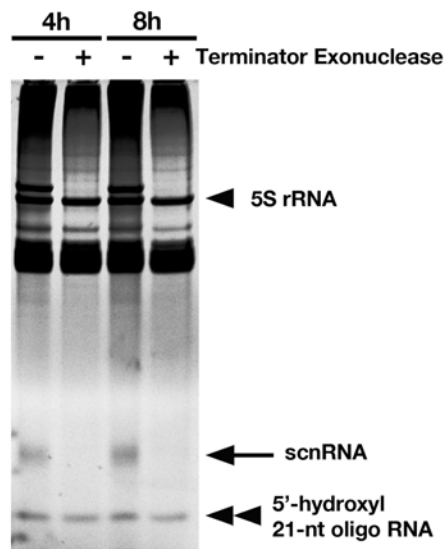
Supplementary Figure S1. Treatment of total RNA with the terminator 5'-monophosphate specific exonuclease.

Total RNA from the wild-type cells at 4 h or 8 h post-mixing was combined with a 21-nt oligoribonucleotide possessing a 5'-hydroxyl and was incubated with (+) or without (-) Terminator Exonuclease. Positions of the scnRNA, the 5S rRNA (possessing a 5'-triphosphate), and the 21-nt oligoribonucleotide are marked with an arrow, a single arrowhead, and double arrowheads, respectively.

Figure S1
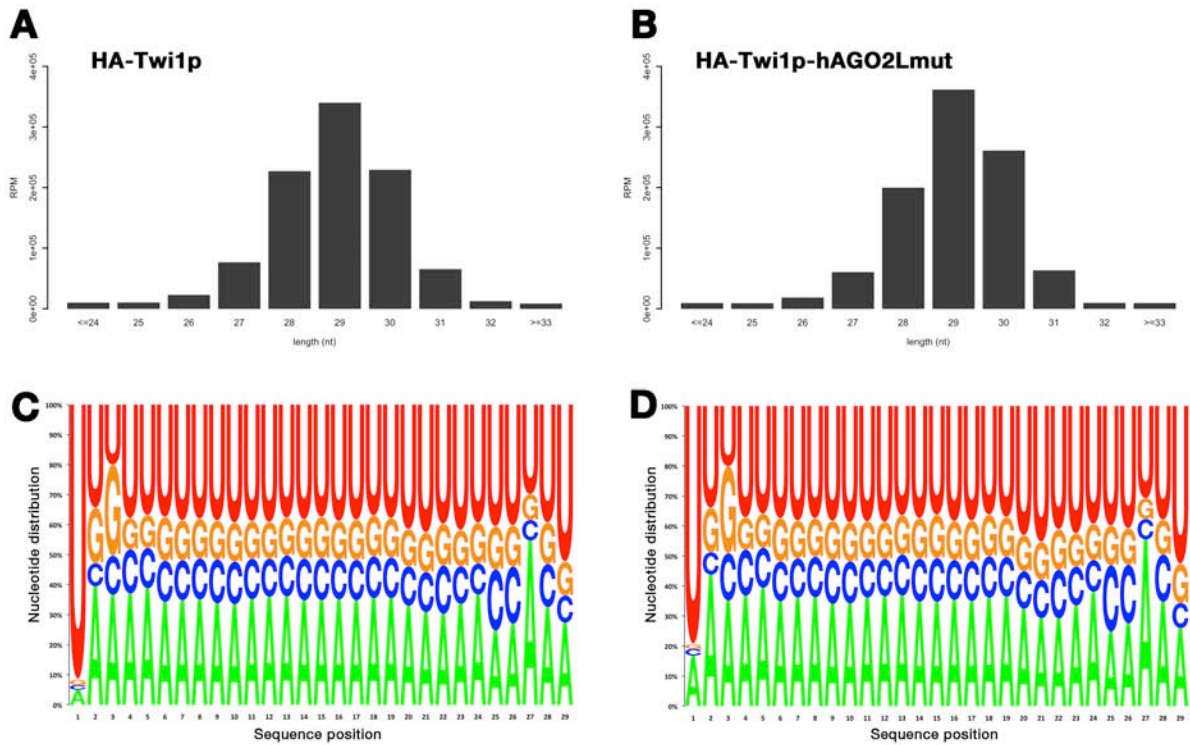
Supplementary Figure S2. Comparison of HA-Twi1p-associated and HA-Twi1p-hAGO2Lmut-associated small RNAs

(A, B) Size distribution of the HA-Twi1p-associated (A) and Twi1p-hAGO2Lmut-associated (B) small RNAs. The number of sequenced small RNAs (reads per million sequences (RPM)) of each size is shown.
(C, D) Base composition of the HA-Twi1p-associated (C) and Twi1p-hAGO2Lmut-associated (C) 29-nt RNAs.

Figure S2