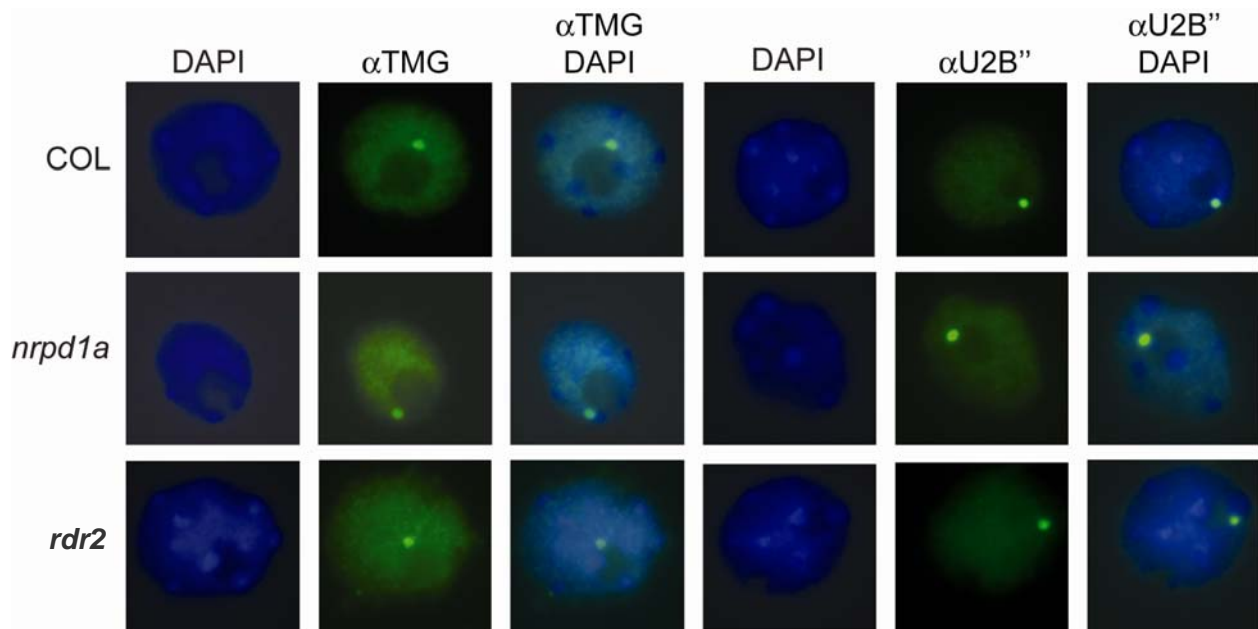


Supplemental Data

An ARGONAUTE4-Containing Nuclear  
Processing Center Colocalized with  
Cajal Bodies in *Arabidopsis thaliana*

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**Figure S1. Fluorescence Microscopy Analysis Showing Wild-Type Localizations of TMG and U2B'' in *nrpd1a* and *rdr2* Mutant Nuclei**

**Table S1. Nuclei Counts for the Characterization of the Nucleolar Dot**

	Frequency of localization displayed in figure images	Total nuclei examined (n)
AGO4 nucleolar dot localization	97%	173
Two or more AGO4 nucleolar dots	8%	168*
H3K9me2 and AGO4	100%	>40*
H3K27me3 and AGO4	100%	53*
DRM2 localization	96%	50
NRPD1a and AGO4	100%	52*
NRPD1b and AGO4	23%	51* <sup>#</sup>
SmD3 and AGO4	96%	54*
U2B'' and AGO4	95%	135*
TMG and AGO4	100%	41*
SmD3 and TMG	98%	56
SmD3 and U2B''	96%	55
TMG in <i>nRPD1a</i> mutant	100%	54
U2B'' in <i>nRPD1a</i> mutant	100%	51
TMG in <i>rdr2</i> mutant	100%	56
U2B'' in <i>rdr2</i> mutant	100%	50

\*Nuclei containing a visible AGO4 body were examined.

<sup>#</sup>NRPD1b AGO4 colocalization was most clearly seen in nuclei with the strongest AGO4 dot staining (23%, n=51), while other weaker AGO4 staining nuclei did not reveal any distinct NRPD1b localization (77%, n=51). This lack of NRPD1b immunostaining is probably attributable to differences in antibody detection limits, since the NRPD1b signals were much lower than those of myc-AGO4. However, we cannot rule out the possibility of a tissue specific or cell cycle specific effect.

**Table S2. Nuclei Counts for DNA-FISH Analyses**

	No colocalization	Partial colocalization	Perfect colocalization	Total nuclei examined (n)
<i>CENs</i> and AGO4	81%	19%	0%	57
<i>NORs</i> and AGO4	74%	26%	0%	141
5S rDNA loci and AGO4	63%	37%	0%	61

**Table S3. Nuclei Counts for AGO4 Localization in Mutants**

	<b>Percent with WT AGO4 localization</b>	<b>Percent with AGO4 mislocalization</b>	<b>Total nuclei examined (n)</b>
AGO4 in WT (segregated from the <i>dcl3 rdr2</i> cross)	94%	6%	63
AGO4 in <i>dcl3</i>	39%	61%	70
AGO4 in <i>rdr2</i>	0%	100%	>50
AGO4 in <i>dcl3 rdr2</i>	0%	100%	>40
AGO4 in WT (segregated from the <i>drm2</i> cross)	95%	5%	35
AGO4 in <i>drm2</i>	97%	3%	42
AGO4 in WT (segregated from the <i>npr1a</i> cross)	93%	7%	70
AGO4 in <i>npr1a</i>	0%	100%	61
AGO4 in WT (segregated from the <i>npr1b</i> cross)	91%	9%	64
AGO4 in <i>npr1b</i>	94%	6%	67