Additional file 5

Figure S1. Different accessions express either rDNA-2 or rDNA-4, or both. The mean proportion of RNA-seq reads expressing a particular reporter variant (y-axis) against the proportion of DNA-seq reads accounting for the existence of the same variant (x-axis) for five natural inbred lines: Edi-0 (7111), Ws-0 (7396), Wu-0 (7415), Can-0 (7063), Hi-0 (8304), Ler-0 (7213) and Zu-0 (7417). Error bars represent standard deviations of 3 biological replicates. Notice that no variants Can-0 rDNA-4-specific passed the threshold (present in > 5% of copies within an individual) presumably due to the small size of that rDNA cluster. The dashed line indicates the one-to-one ratio between DNA and RNA.

Figure S2. The pattern of rRNA expression is consistent across replicate lines. (A) The proportion of RNA-seq reads expressing a particular reporter variant (y-axis) against the proportion of DNA-seq reads accounting for the existence of the same variant (x-axis) for MAGIC lines 18, 303 and 319. These MAGIC lines inherited the same genotypes at both rDNA loci after undergoing independent pedigrees. (B) Similar to (A), but for a different combination of genotypes at rDNA loci in MAGIC lines 81 and 117. (C) Similar to (A), but for MAGIC lines 67 and 188 that inherited both rDNA clusters from founder accession Col-0. (D) Similar to (C), but for MAGIC lines 96 and 120 that inherited both rDNA clusters from founder accession No-0. For all subfigures, error bars represent standard deviations of 2 biological replicates, and the dashed line indicates the one-to-one ratio between DNA and RNA.

Figure S3. Expression of Bur-0 rDNA-4 when used as a mother in an F1 cross. (A) The mean proportion of RNA-seq reads expressing a particular reporter variant (y-axis) against the proportion of DNA-seq reads accounting for the existence of the same variant (x-axis) for F1: ♀ Col-0 x ♂ Sf-2. (B) Similar to (A), but for F1: ♀ Bur-0 x ♂ Col-0. Contrary to the reciprocal cross ♀ Col-0 x ♂ Bur-0, we detected expression of Bur-0 rDNA-4. This discrepancy suggests that the onset of nucleolar dominance may be impacted by a maternal control.

Figure S4. Cvi-0 expresses rDNA-4. The mean proportion of RNA-seq reads expressing a particular reporter variant (y-axis) against the proportion of DNA-seq reads accounting for the existence of the same variant (x-axis) for accession Cvi-0 (6911). Error bars represent standard deviations of five biological replicates. The dashed line indicates the one-to-one ratio between DNA and RNA. For both subfigures, error bars represent standard deviations of 4 biological replicates. The dashed line indicates the one-to-one ratio between DNA and RNA.

Figure S5. Col-0 rDNA-2 is not reactivated in mutants of the RdDM pathway. RT-PCR analysis of rRNA gene 3’ variants — VAR1-4, first described by Pontvianne et al. (2010) — in WT Col-0 (lanes 2-4), dcl2/3/4 triple (lanes 5-7) and nrpd1a-3 single (lanes 8-10) mutant plants. Recently, Chandrasekhar et al., (2016) mapped VAR1 to rDNA-2 in Col-0. Amplification of Actin-2 mRNA (ACT2) was used as a control of total amount of RNA in each sample. Genomic DNA for all assays was loaded in lane 1. RT-PCR without the reverse transcriptase gave no PCR product (-RT panels).
Figure S1

Proportion of DNA-seq reads supporting a particular variant

Proportion of RNA-seq reads expressing a particular variant
Figure S2

A

MAGIC.18

MAGIC.303

MAGIC.319

B

MAGIC.81

MAGIC.117

C

MAGIC.67

MAGIC.188

D

MAGIC.96

MAGIC.120

Proportion of DNA-seq reads supporting a particular variant
Figure S4
Figure S5

[Image of gel electrophoresis patterns for VAR1, VAR4, VAR2, VAR3, and ACT2 under WT, dcl2/3/4, and nrpd1a-3 conditions with RT and -RT treatments.]

rRNA gene 3' variable region

ACT2