

## Supplementary data

**Figure S1.** Nucleotide sequence alignment of the four tandem repeats sequences of *AtNUC-L2* gene. The introns (I) 4 to 7 and exons (E) 4 to 7 are aligned separately to show the best sequence alignment.

**Figure S2.** Phylogenetic relation of different nucleolin and nucleolin-like proteins. Phylogenetic tree was generated with MEGA3.1 software (Kumar *et al.*, 2004), using Neighbour Joining method coupled with 1000 bootstrap tests. Numbers represent the percentage value of Bootstrap and PubMed accession number (<http://www.ncbi.nlm.nih.gov>) of proteins is available between brackets.

**Figure S3.** Gel filtration chromatographic analysis of the *AtNUC-L1* and *AtNUC-L2* in WT and *Atnuc-L1* plants respectively. The eluted fractions were analyzed by Western blot using the  $\alpha$ -NUC1 and  $\alpha$ -NUC2 antibodies. The numbered lanes correspond to size-fractionated protein fractions and arrows indicated the peak position of the Blue-dextran (2 Md), ferritin (440 kD) and alcohol dehydrogenase (158 kD).

**Figure S4.** Endoproteolytic analysis of *AtNUC-L1* in *A. thaliana*. This experiment shows that in flower extracts the ~83 kDa and the ~67 kDa polypeptides disappear and a ~46 kDa polypeptide becomes detectable after incubation (20 min at 25°C) with a diluted root fraction. The ~46 kDa polypeptide is not detected by Western blot in diluted root extracts and we therefore suspect that the ~46 kDa polypeptide in the treated flower extracts may correspond to endoproteolytically cleaved forms of the ~83 kDa and ~67 kDa proteins. Protein extracts from flowers alone (lane 1), incubated with a diluted extract from roots (lane 2) or 5x diluted extract from roots (lane 3, see undiluted extract in Figure 2C) were analysed. Note that in the root diluted fraction, the ~46 kDa polypeptide is not detected by Western blot. Black arrows indicate the ~82, ~67 and ~46 kDa immunorelated polypeptides detected by  $\alpha$ -NUC1 antibodies. the asterisk shows a major unrevealed polypeptide.

**Figure S5.** Immunofluorescent localization of AtNUC-L1 in wild type *A. thaliana* roots meristematic cells. The image represents a panorama showing AtNUC-L1 labelling throughout several layers of root cells. The bar corresponds to 20  $\mu\text{m}$ .

**Table S1.** Analysis of NORs by FISH in WT and *Atnuc-L1* background

Kumar, S., Tamura, K., and Nei, M. (2004). MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Brief Bioinform.* 5, 150-163.

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      *      20      *      40      *      60      *      80
14 : G|A|T|T|A|G|T|G|C|T|T|C|T|C|C|A|T|C|A|G|T|A|C|C|T|T|A|T|C|T|C|A|G|C|C|G|T|A|G|G|C|A|T|C|T|G|T|A|G|C|T|T|A|C|C|G|T|T|T|G|T|T|A|G| : 81
16 : G|T|A|T|C|A|G|T|T|A|C|T|T|C|A|T|C|A|T|T|A|G|T|A|C|A|C|C|T|T|A|A|C|T|C|A|A|G|C|T|T|A|G|A|T|G|A|A|T|G|T|T|G|T|A|G|C|T|T|G|T|T|A|G| : 83
15 : G|T|A|T|T|A|T|T|G|C|T|T|C|T|C|C|A|T|C|A|G|T|A|C|C|T|T|A|G|C|T|T|A|G|G|T|A|A|G|C|T|T|A|G|A|T|A|A|T|C|T|T|G|T|T|A|G|C|T|T|G|T|T|A|G| : 82
17 : G|T|A|C|A|G|T|T|A|T|G|T|T|A|-----C|A|G|A|T|G|T|A|G|C|T|C|A|A|T|T|T|C|A|C|A|C|T|A|A|A|A|A|A|T|T|C|C|T|T|A|G|C|T|T|T|A|A|A|A|A|A|A|A| : 75

      80      *      100      *      120      *      140      *      160
E 6 --G|A|A|T|T|C|C|C|C|T|G|A|A|G|A|G|C|A|C|C|A|C|G|T|C|C|T|T|G|A|G|A|C|C|T|A|A|A|T|A|G|A|C|A|C|C|A|C|T|C|T|C|G|A|C|G|T|C|T|C|T|C|G|A|C|C|G|A|C| : 90
E 7 --G|A|A|T|T|C|C|C|C|A|T|C|A|G|A|A|C|C|A|G|A|C|C|A|G|C|C|T|T|G|A|G|A|C|C|T|A|G|-----C|A|G|A|G|C|C|A|G|T|T|C|T|C|C|A|C|G|A|C|G|A|C|T|C|T|C|G|A|C|C|G|A|C| : 89
E 5 --G|A|A|T|T|C|C|C|C|C|T|G|A|A|G|A|G|C|A|C|C|A|C|A|G|T|C|C|T|T|G|A|G|A|C|C|T|A|A|C|T|A|G|A|C|A|C|C|A|C|T|C|T|C|G|A|C|G|T|C|T|C|T|C|G|A|C|C|G|A|C| : 90
E 4 --G|A|A|T|T|C|C|C|C|C|G|A|G|A|G|C|G|G|G|A|A|C|C|T|A|A|A|G|A|G|C|C|T|A|A|C|T|A|G|A|C|A|C|C|A|C|G|T|C|A|G|A|C|C|A|C|T|C|T|C|G|A|C|G|T|C|T|C|T|C|G|A|C|C|G|A|C| : 162

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FIGURE S1

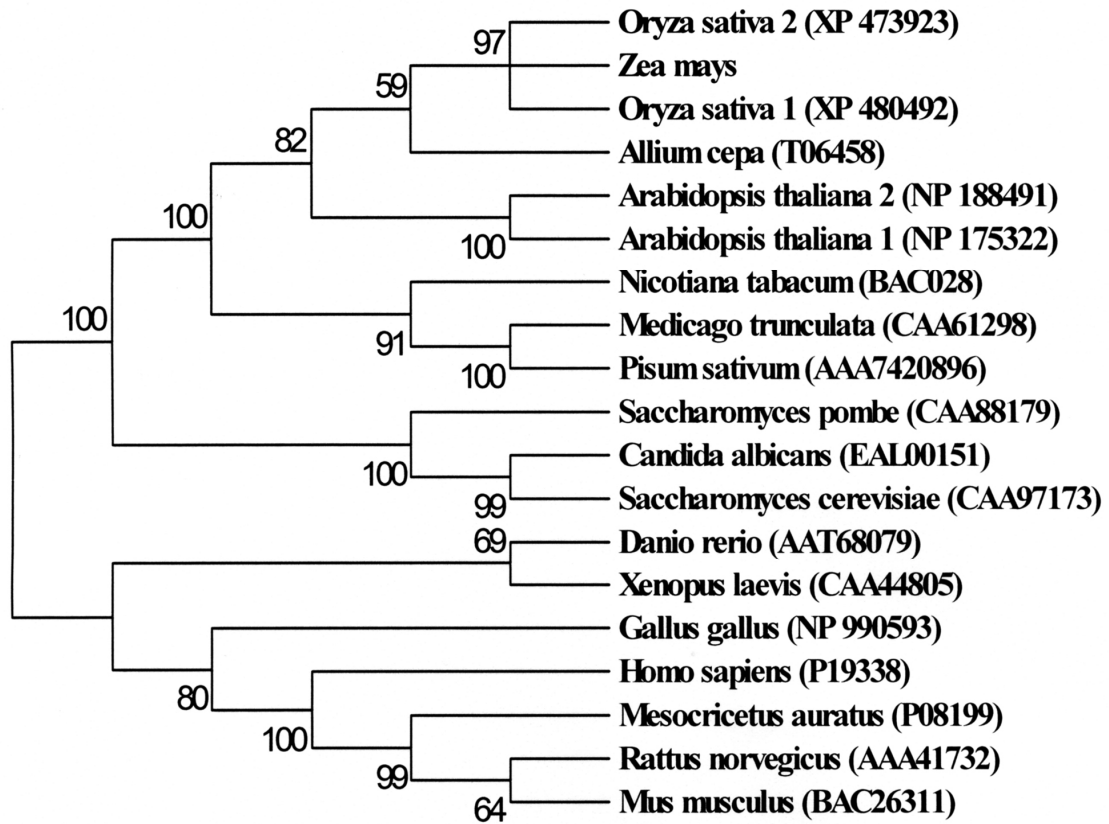


FIGURE S2

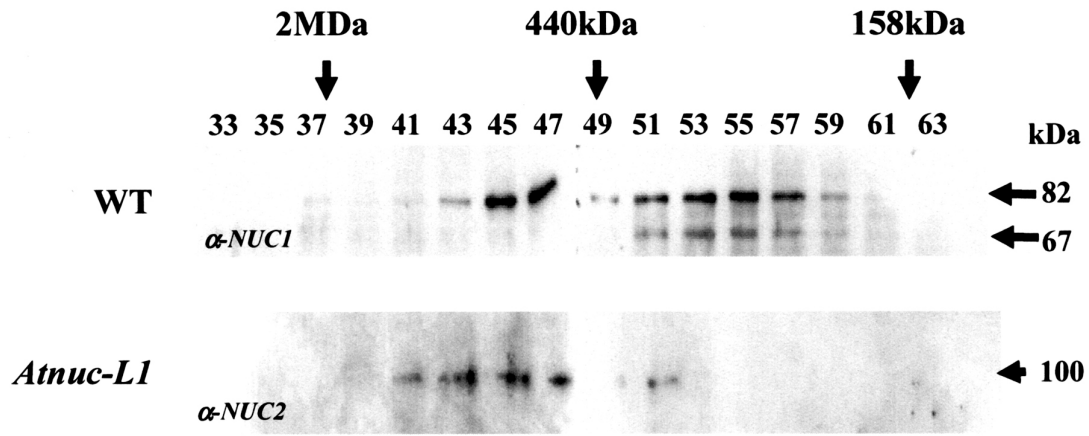


FIGURE S3

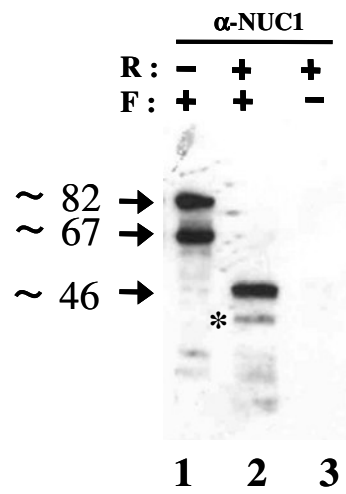


FIGURE S4

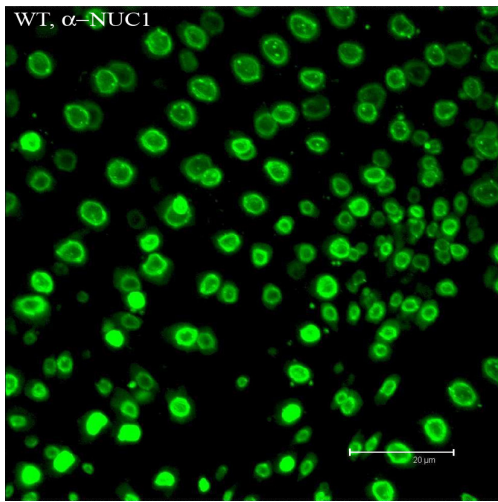


FIGURE S5

Genotype	Number of nuclei analyzed	Number of FISH signals per nucleus						
		1	2	3	4	5	6	>6
Wild-type	51	2%	12%	47%	29%	6%	2%	2%
<i>Atnuc-L1</i>	52	4%	10%	9%	26%	12%	17%	23%

Table S1