Supplemental Material and Methods:

IP-TRAP (Immunoprecipitation-Telomere Repeat Amplification Protocol)
For IP-TRAP, 7-day-old seedlings of Columbia 0 WT and complemented *nuc1* mutant plants that contain the transgene pNUC1:NUC1-FLAG and expressed the NUC1 flagged protein under its own promoter (Pontvianne et al., 2010) were used. The seedlings were grown on half-strength Murashige and Skoog plates under the conditions of 16 h light (100 µmol/m2.s-1), 21 °C and 8 h dark, 19 °C, homogenized in liquid nitrogen, dissolved in buffer W (50 mM Tris acetate, pH 7.5; 5 mM MgCl; 100 mM potassium glutamate; 20 mM EGTA; 1 mM DTT; 0.1 mM phenylmethylsulfonyl fluoride; 0.6 mM vanadyl ribonucleoside complex; pepstatin (1 µg/ml); leupeptin (2 µg/ml)), filtrated through 3 layers of miracloth and centrifuged at 15 000 g for 15 min at 4 °C. The supernatant was incubated with ANTI-FLAG® M2 Magnetic Beads (Sigma Aldrich) for 2 hours at 4 °C and after removing the unbound faction two washes by buffer W were performed finally leaving the beads in W buffer. Activity of telomerase in fractions collected from all steps was analyzed by the TRAP assay as described in (Fajkus et al., 1998). Briefly, 1 µl of 10 µM TS21 substrate primer (GACAATCCGTCGAGCAGAGTT) was mixed with 1 µl of the analyzed fraction and extension of the primer by telomerase run in 25 µl of the reaction buffer for 45 min at 26 °C. Then, telomerase was inactivated at 95 °C for 5 minutes and 1 µl of 10 µM TELPR reverse primer (CCGAATTCAACCCTAAACCCTAAACCCTAAACCC) was added together with 2 units of DyNAzymeII DNA polymerase (Finnzymes). PCR proceeded for 32 cycles of 94 °C / 30 sec, 65 °C / 30 sec, and 72 °C / 30 sec. Products of TRAP were analyzed by vertical gel electrophoresis (12.5 % (w/v) polyacrylamide gel in 0.5xTBE buffer), stained with GelStar Nucleic Acid Gel Stain (LONZA) and visualized by LAS3000 (Fujifilm) instrument. Telomerase activity was assessed from the intensity of a ladder formed by products of extension of substrate primer by telomerase.

Supplemental Figure legends:

Figure S1, related to figure 2: Chromatin states description and the link with gene expression
A. Table describing the characteristics of the nine chromatin states defined in (Sequeira-Mendes et al., 2014). B. Box plot representing the relative expression of genes present in each category of chromatin state.

Figure S2, related to figure 3: NAD-tRNA distribution on the genome
Distribution of all or NAD-tRNA along all five chromosomes of *A. thaliana*.

Figure S3, related to figure 4: nuclear distribution of centromeres in WT and *nuc1*
Six nuclei images of WT and *nuc1* are presented in this panel. DAPI-stained DNA is shown blue, and the green signal represent the fluorescence obtained from the anti-cenH3 antibody.

figure S4, related to figure 5: NAD-genes and TEs reactivation in *nuc1* mutant.
A-B. Genome browser screenshot showing examples of NAD-genes in Col-0 whom nucleolus association is lost in *nuc1* and is accompanied by a significant increase of their expression. Specific regions are zoom in to allow a better visual analyses of the data. RNA deep sequencing in triplicates (dark blue) and NAD position (light blue) correspond to Col-0 data, while RNA deep sequencing in triplicates (red) and NAD position (orange) correspond to *nuc1* data.

Figure S5, related to figure 6: nuclear distribution of telomeres in WT and *nuc1*
A-B. DNA-FISH analyses using a telomere specific probe (red signal) on DAPI-stained nuclei (Blue) from WT Col-0 or from *nuc1* plants. For each images, the proportion of nucleolar associated TEL signals are specified. In B, the green signal represent the signal emitted by the nucleolar marker Fibrillarin fused to YFP. Scale bar is 5μm.

Supplemental data 1, related to figure 1: NAD-TEs in Col-0
List of NAD-TEs identified in the Wild-type Col-0 with their fold-change No/N ratio and the associated *p* value.

Supplemental data 2, related to figure 1: NAD-genes in Col-0
List of NAD-genes identified in the Wild-type Col-0 with their fold-change No/N ratio and the associated *p* value.

Supplemental data 3, related to figure 4: NAD-TEs in *nuc1*
List of NAD-TEs identified in the mutant *nuc1* with their fold-change No/N ratio and the associated *p* value.

Supplemental data 4, related to figure 4: NAD-genes in *nuc1*
List of NAD-genes identified in the mutant *nuc1* with their fold-change No/N ratio and the associated *p* value.

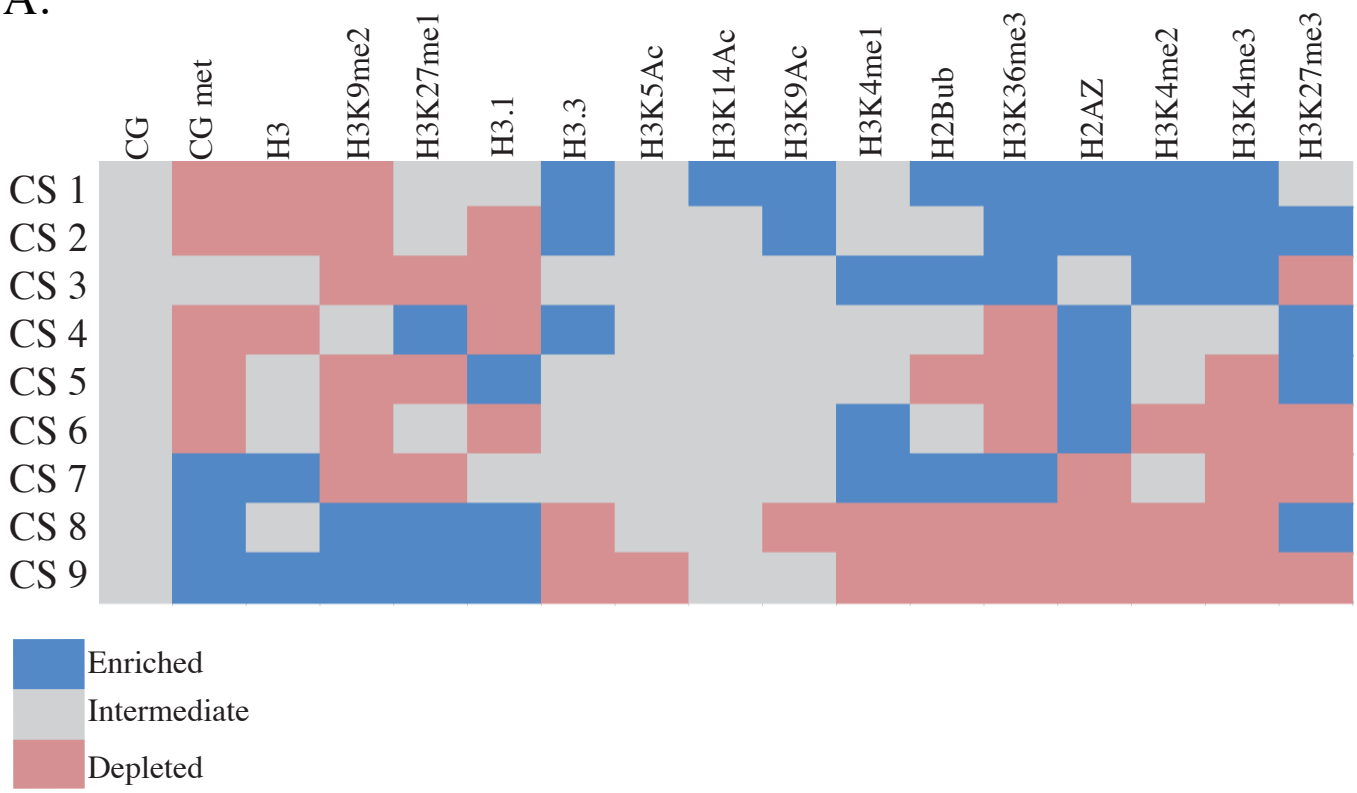
Supplemental data 5, related to figure 1: NADs identification in Col-0 and in *nuc1*
Table listing the reads number per 100kb windows along all 5 chromosomes in Col-0 and in *nuc1*.

References

Fajkus, J., Fulneckova, J., Hulanova, M., Berkova, K., Riha, K., Matyasek, R., 1998. Plant cells express telomerase activity upon transfer to callus culture, without extensively changing telomere lengths. Mol. Gen. Genet. MGG 260, 470–474.

Sequeira-Mendes, J., Araguez, I., Peiro, R., Mendez-Giraldez, R., Zhang, X., Jacobsen, S.E., Bastolla, U., Gutierrez, C., 2014. The Functional Topography of the Arabidopsis Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States. Plant Cell 26, 2351–2366. doi:10.1105/tpc.114.124578

A.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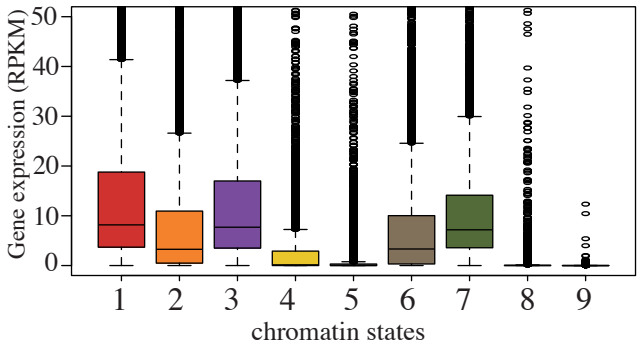
CG met
H3
H3K9me2
H3K27me1
H3.1
H3.3
H3K5Ac
H3K14Ac
H3K9Ac
H3K4me1
H2Bub
H3K36me3
H2AZ
H3K4me2
H3K4me3
H3K27me3
CS 1
CS 2
CS 3
CS 4
CS 5
CS 6
CS 7
CS 8
CS 9
Enriched
Intermediate
Depleted

B.


Gene expression (RPKM)
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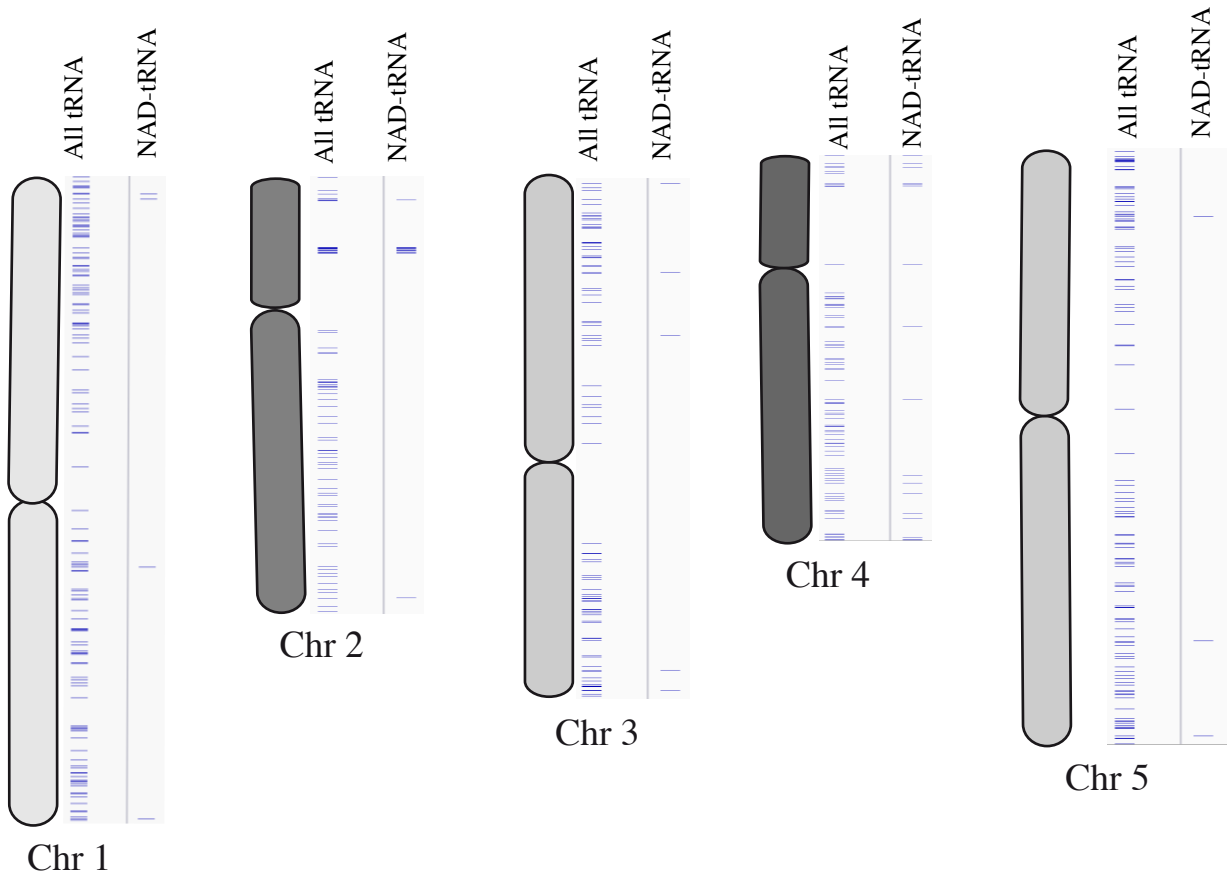
40
30
20
10
0
1
2
3
4
5
6
7
8
9
chromatin states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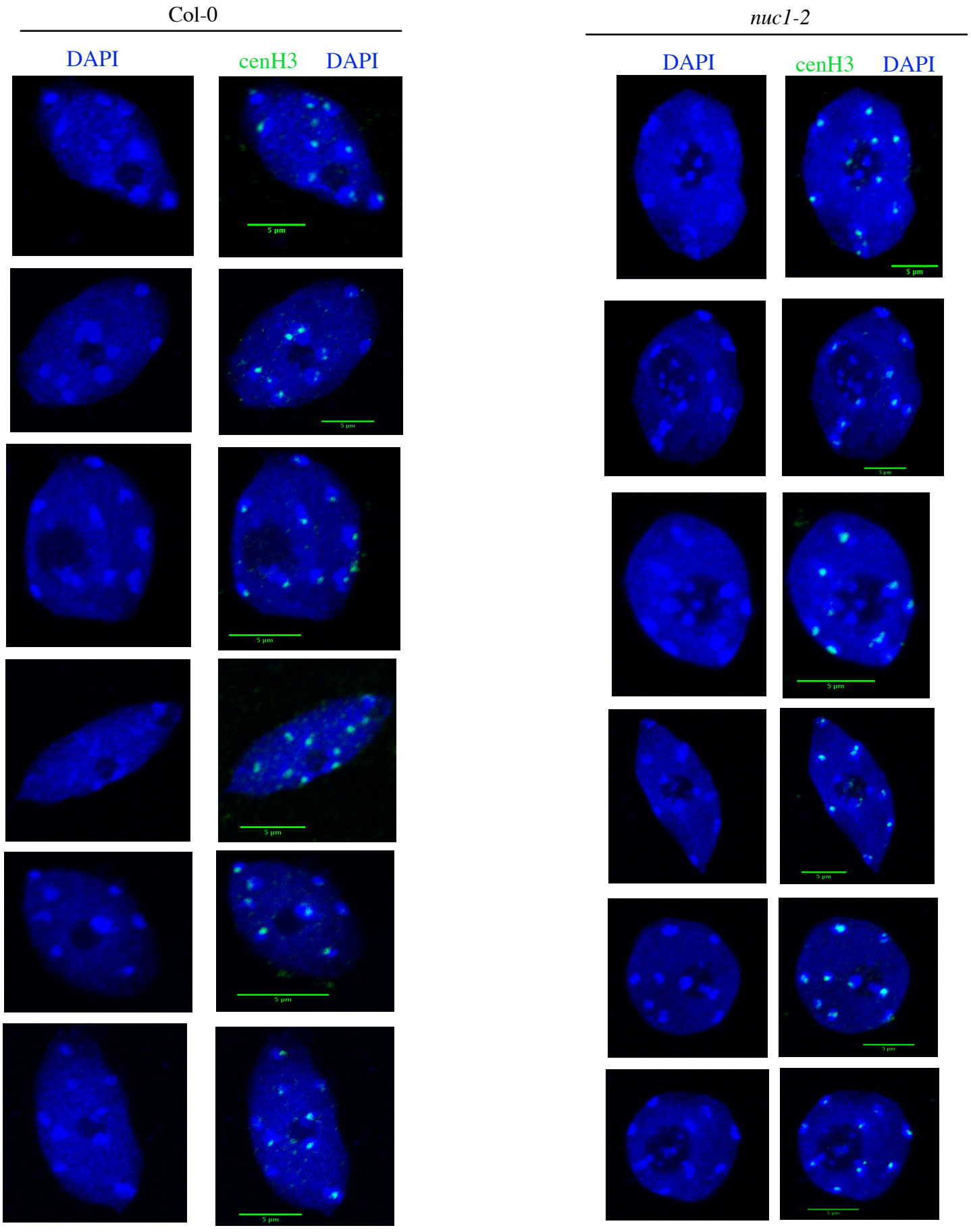
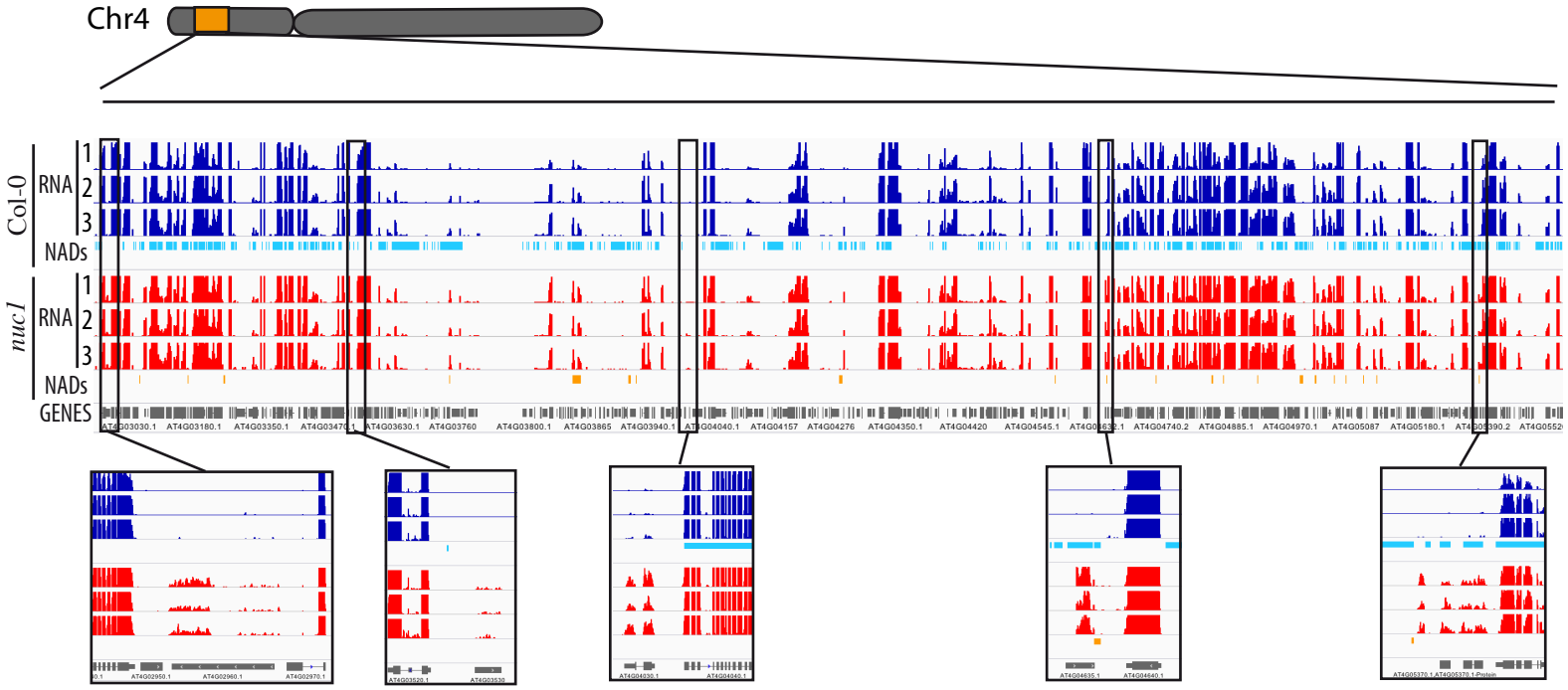
NAD-tRNA
Chr 1
Chr 2
Chr 3
Chr 4
Chr 5


Col-0
DAPI
cenH3
DAPI
nuc1-2
DAPI
cenH3
DAPI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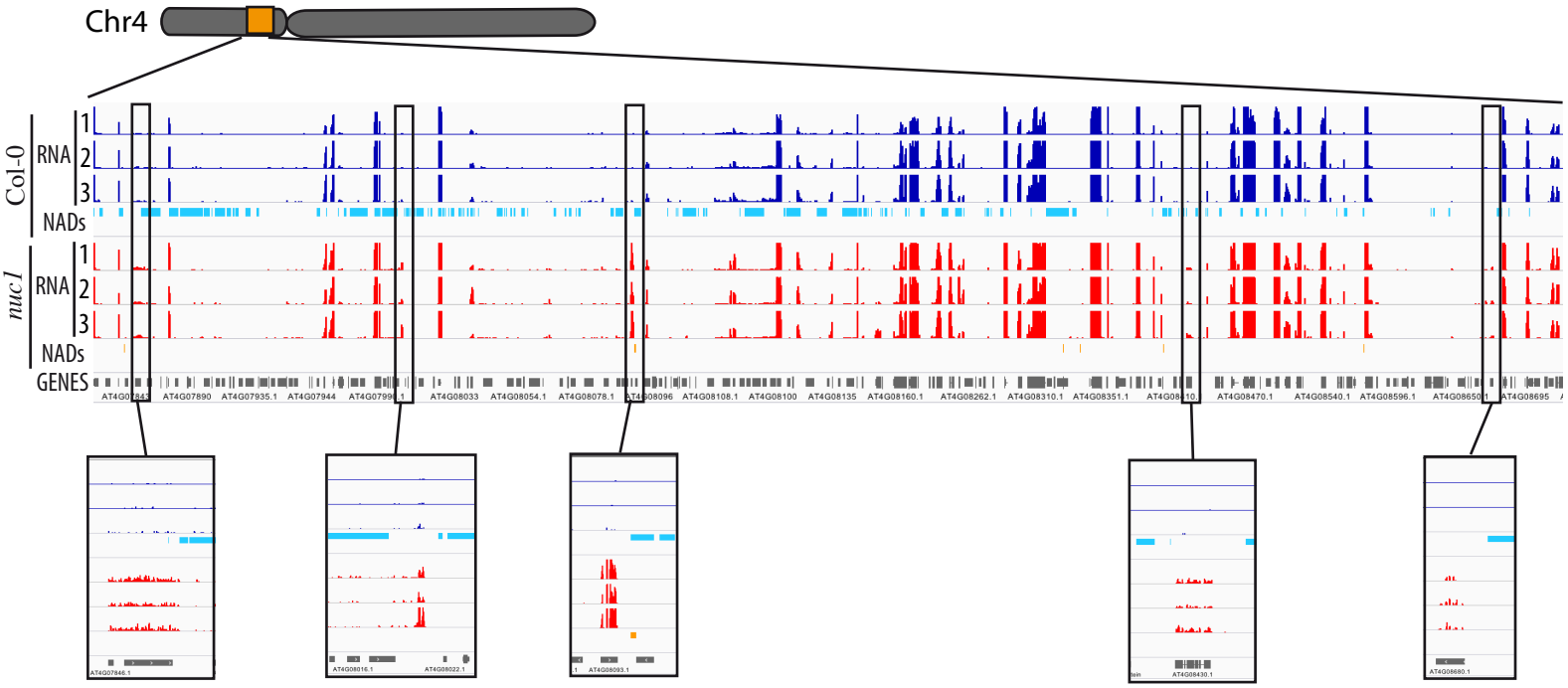
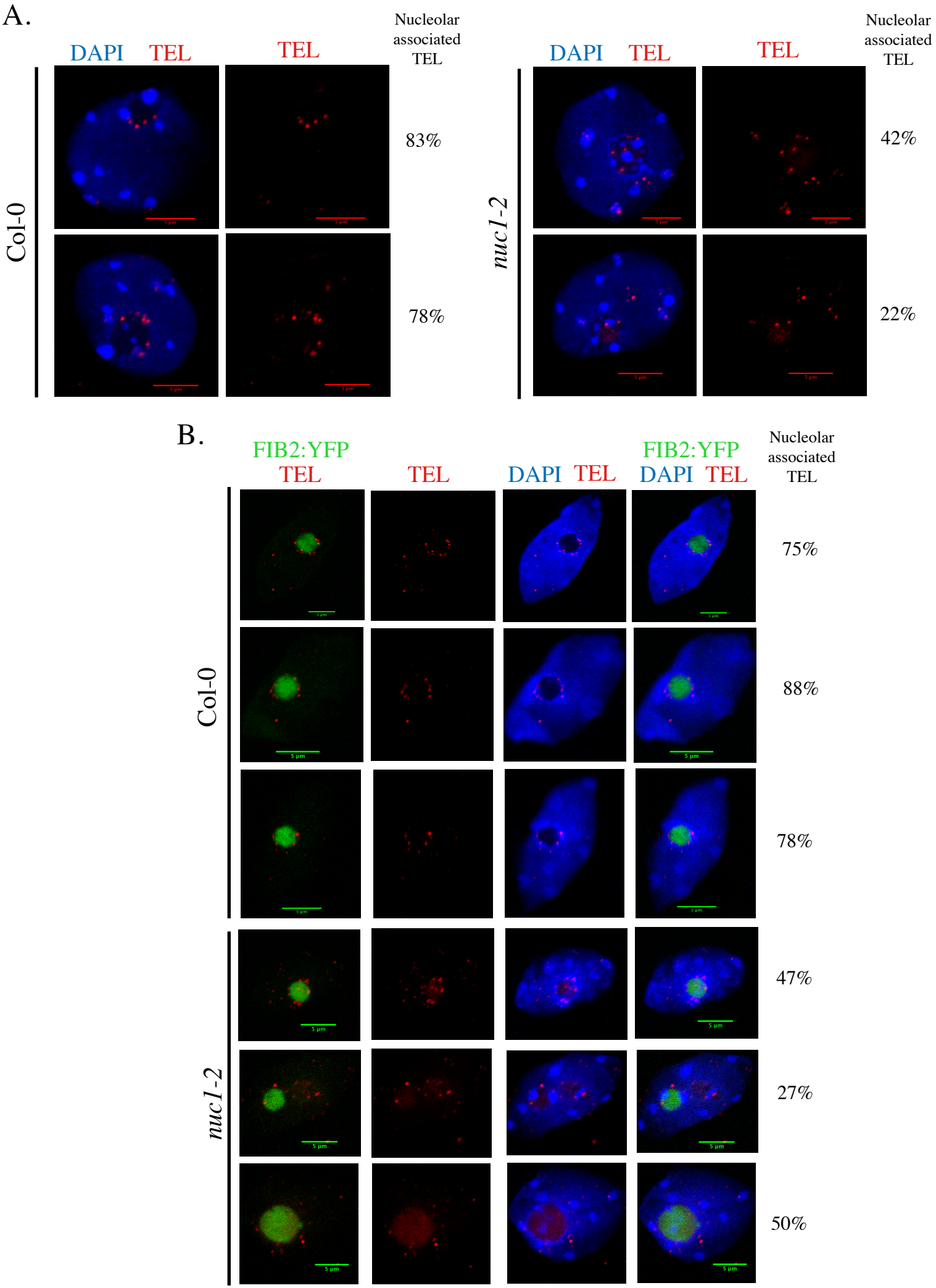
Col-0
RNA
1
2
3
NADs
nuc1
RNA
1
2
3
NADs
GENES


Chr4
Col-0
RNA
1
2
3
NADs
nuc1
RNA
1
2
3
NADs
GENES


A.
DAPI TEL
TEL
Nucleolar associated TEL
Col-0
83%
78%
nuc1-2
42%
22%
B.
FIB2:YFP TEL
TEL
DAPI TEL
FIB2:YFP DAPI TEL
Nucleolar associated TEL
Col-0
75%
88%
78%
nuc1-2
47%
27%
50%