**SUPPLEMENTARY TEXT S1**

**Isolation of nuclei**

Selected root segments were isolated and submerged in freshly prepared Isolation Medium pH 7.8 (IM; 2% arabic gum, 1.25% ficoll, 2.5% dextran, 0.01% BSA, 0.5 mM EDTA, 50 mM magnesium acetate, 8 mM β-mercaptoethanol, 4 mM n-octanol, 25 mM TRIS, 7 mM diethylypyrocarbonate, 30% glycerol) containing 1% protease inhibitor cocktail (Sigma-Aldrich). The pieces of tissue were incubated in vacuum on ice for 15 min and then homogenized 3x 20 s with an Ultra-Turrax homogenizer IKA T25 digital with dispersor IKA S25-10G at 20,000 rpm. Next, the homogenate was filtrated through a set of 100, 50 and 30 µm nylon sheets. The homogenization and filtration was repeated three times and each batch was collected separately. The homogenates were centrifuged at 2,500 rpm, for 15 min at 4°C. The supernatants containing the cytoplasmic fractions were transferred to a fresh centrifuge tube, precipitated with 10% v/v trichloroacetic acid (TCA) for 1 h on ice, centrifuged 5 min at 12,000 rpm and mixed with Laemmli Buffer 2x or Lysis Buffer (LysB). The pellets containing the nuclei were washed with Isolation Medium containing 0.1% protease inhibitor cocktail (Sigma-Aldrich). The purity and integrity of isolated nuclei were controlled using a light microscope after methyl green staining (Sigma-Aldrich M8884).

**Isolation of the nucleoskeleton**

The isolation of the NSK fraction was obtained after sequential extraction of nuclei with non-ionic detergent, DNase and high salt buffer. Freshly isolated nuclei were incubated for 5 minutes with cytoskeleton buffer (CSKB; 10 mM PIPES pH 6.8, 100 mM KCl, 300 mM sucrose, 3 mM MgCl2, 20 mM DTT, 1 mM EGTA) containing 1% protease inhibitor cocktail (P9599, Sigma-Aldrich) and 0.5% Tx-100. Next, soluble and membrane associated nuclear proteins were removed by centrifugation at 3000 rpm for 10 min at 4 °C and collected in supernatant (S1). The pellet containing nuclear insoluble fraction (F1) was next digested with 75 U of Benzonase (P9599 Sigma-Aldrich) in Digestion Buffer (DB; 10 mM PIPES pH 6.8, 50 mM KCl, 50 mM NaCl, 300 mM sucrose, 3 mM MgCl2, 20 mM DTT, 1 mM EGTA, 1% protease inhibitor coctail, 0.5% Tx-100) for 1h. Then 1 M (NH4)2SO4 was added slowly to a final concentration of 0.25 M to remove the DNA and DNA-associated proteins (S2), then the sample was incubated for 15 minutes and centrifuged. To the pellet (F2) containing loosely bound proteins 4 M NaCl was added to a final concentration of 2 M, incubated for 5 minutes and centrifuged. This step released proteins bound to the NSK (S3) and revealed the insoluble NSK fraction. All steps were performed at 4 °C.

**Flow cytometry analysis**

For estimation of DNA content by flow cytometry, the different root segments were isolated and fixed for 30 min at 4 °C in 2% (w/v) FA in TRIS buffer (10 mM TRIS pH 7.5, 10 mM EDTA, 100 mM NaCl) containing 0.1% Tx-100. Then samples were washed 3x with TRIS buffer and homogenized in lysis
buffer (15 mM TRIS pH 7.5, 2 mM EDTA, 80 mM KCl, 20 mM NaCl, 0.1% Tx-100) with an Ultra-Turrax T-25. Next, homogenates were filtered through a 30 µm nylon-mesh. The nuclear suspensions were centrifuged at 2,500 rpm for 20 minutes at 4 ºC and resuspended in 300 µl of lysis buffer. Before the analysis the nuclei were incubated with RNaseA (Boehringer-Mannheim) at concentration 30 µg/ml for 30 minutes and stained with propidium iodide (Sigma-Aldrich) at concentration 20 µg/ml. After 10 min flow-cytometry analysis was performed with an EPICS XL analyzer (Coulter) equipped with an argon laser tuned at 488 nm, and fluorescent signals from propidium iodide-labelled nuclei collected by a 620 nm band-pass filter.

**Immunofluorescence**

Nuclear or nucleoskeleton fractions were fixed in freshly prepared 2% formaldehyde (FA) in PBS buffer (pH 7.4) containing 0.5% Tx-100 for 30 minutes, then centrifuged at 2,500 rpm for 15 min and washed in the same buffer for 30 min. Pellets were re-suspended in 20 mM glycine and incubated for 30 min, then blocked in 2% BSA in PBS with 0.05% Tween-20 for 30 min. Next, the anti-AcNMCP1 antibody was added to the blocking solution to a final dilution 1:100, incubated overnight at 4 ºC and washed 3x 15 min in PBS with 0.05% Tween-20. Pellets were incubated with A488-coupled secondary antibody (Molecular Probes) at 1:100 for 45 min at room temperature, washed 2x 15 min and stained with 1 µg/ml 4’,6’ diamidino-2-phenylindole (DAPI) to counterstain DNA in the nuclei. Pellets were washed again 3x 15min. All steps were performed at room temperature and in constant shaking if not stated differently. The labelled fractions were layered onto 0.1% poly-L-lysine coated multi-wells slides, air dried and mounted with Vectashield (Vector). Negative controls were prepared by omitting the primary antibody. Samples were examined in a Confocal Microscope Leica TCS-SP2-AOBS, using the Leica-confocal software.
Supplementary Figure SL. AcNMCP1 sequence and sequence similarity. Protein sequence alignment of AcNMCP1 and NMCPI. The NMCPI sequences from Oryza sativa (OsM1; LOC. Os02g68810), Ipomoea batatas (AgNMCP1; BA187715.1), Daucus carota (DaNMCP1; BA260047) and, Aristolochia thaliana (LINC1; NP_176892.1) were aligned with that of AcNMCP1 (BAM10899.1) using ClustalW2 (Larkin et al., 2007) and edited in Jalview (Waterhouse et al., 2009). The coiled-coil segments predicted using MARCOIL (Delorme and Speed, 2002) are shaded in gray, the cdk1 consensus sequences in pink, the predicted NLS in green and the NMCPI-specific conserved regions in blue and brown, the stretch of acidic amino acids in red. The degree of conservation is represented by yellow and brown bars beneath the alignment (generated by Jalview) and the region used for antibody production is contained in a red box.
| NAME     | SPECIES                | GENE ID                  | SOURCE (GENOME PROJECT) |
|----------|------------------------|--------------------------|-------------------------|
| Aly3     | Arabidopsis lyrata     | gene 47806               | JGI release v1.0         |
| Luc1     | Zea mays silvestris    | gene U10003075.g          | BGI v1.0 on assembly v1.0 |
| Luc2     | Zea mays silvestris    | gene U10003257.g          |                          |
| Luc3     | Zea mays silvestris    | gene U30034265.g          |                          |
| Psu1     | Phaseolus vulgaris     | gene Phve001032159m.g     | JGI annotation v0.95 on assembly v0.9 using published ESTs, and JGI RNAseq |
| Psu2     | Phaseolus vulgaris     | gene Phve001034579m.g     |                          |
| Mbo2     | Malus domestica        | gene MDP000012171.g       | GDR prediction v1.0 on Malus x domestica assembly v1.0 |
| Mbo3     | Malus domestica        | gene MDP000020564.g       |                          |
| Mbo1     | Malus domestica        | gene MDP0000112257        |                          |
| Cru1     | Capsella rubella       | gene Carv000119639m.g     |                          |
| Cru2     | Capsella rubella       | gene Carv000125809m.g     |                          |
| Bra1     | Brassica rapa          | gene Bra29402             | Annotation v1.2 on assembly v1.1 from brassicadb.org |
| Bra2     | Brassica rapa          | gene Bra294099            |                          |
| Tha3     | Thellungiella halophila| gene Thalv00006021m.g      | JGI annotation v1.0 on assembly v1 |
| Tha2     | Thellungiella halophila| gene Thalv00007287m.g      |                          |
| Tha1     | Thellungiella halophila| gene Thalv00018144m.g      |                          |
| Mes1     | Marchantia excelsa     | gene cassaw1_000510m.g    | Assembly version 4, JGI annotation v4.1 |
| Mes3     | Marchantia excelsa     | gene cassaw1_000491m.g    |                          |
| Cua1     | Cuscuta australis      | gene C usca1.25180        | Roche 454-XR assembly and JGI v1.0 annotation |
| Cua3     | Cuscuta australis      | gene C usca1.28080        |                          |
| Cua2     | Cuscuta australis      | gene C usca1.30490        |                          |
| Ppe1     | Prunus persica         | gene ppa003199m.g         | JGI release v1.0         |
| Ppe2     | Prunus persica         | gene ppa003195m.g         |                          |
| Cpa1     | Carica papaya          | gene evm.TU.supercontig_179.33 | ASGPR release of 2007 |
| Cpa2     | Carica papaya          | gene evm.TU.supercontig_1.235 |                          |
| Cu1      | Cucurnicaca           | gene orange1.1:086975m.g  | JGI v1.1 annotation on v1 assembly |
| Cu3      | Cucurnicaca           | gene orange1.1:089874m.g  |                          |
| Cu2      | Cucurnicaca           | gene orange1.1:091326m.g  |                          |
| Ccl1     | Citrus limon          | gene clementin1.0:026300m.g | JGI v0.9 assembly and annotation |
| Ccl2     | Citrus limon          | gene clementin1.0:028880m.g |                          |
| Egr1     | Eucalyptus grandis    | gene egrandis_v1.0:001076m.g | JGI assembly v1.0, annotation v1.1 |
| Egr2     | Eucalyptus grandis    | gene egrandis_v1.0:001127m.g |                          |
| Vv1      | Vitis vinifera        | gene GSVIVG010119720001   | March 2020 12X assembly and annotation from Genoscope |
| Vv3      | Vitis vinifera        | gene GSVIVG0101295001     |                          |
| Vv2      | Vitis vinifera        | gene GSVIVG010128620001   |                          |
| Mgj1     | Microtus guttatus     | gene mgj10004342m.g       | JGI 7X assembly release v1.0 of strain INM2, annotation v1.0 |
| Mgj2     | Microtus guttatus     | gene mgj10004519m.g       |                          |
| Aco1     | Apis mellifera        | gene AcoGoldSmith_v1.000268m.g | JGI BX assembly v1.0, annotation v1.1 |
| Aco2     | Apis mellifera        | gene AcoGoldSmith_v1.001172m.g |                          |
| Sbi1     | Streptomyces lividans  | gene Sbi100120240         | Sbi1.4 models from MPS/PSA on v1.0 assembly |
| Sbi2     | Streptomyces lividans  | gene Sbi100130570         |                          |
| Zma1     | Zebrafish             | gene ZGR002105087         | 5b.6b annotation (filtered set) of the major "B73" genome v2 produced by the Maize Genome Project |
| Zma2     | Zebrafish             | gene ZGR002105087         |                          |
| Sst1     | Stentor coeruleus     | gene Sst1001647m.g        | JGI 8.3K chromosome-scale assembly release 2.0, annotation version 2.0 |
| Sst2     | Stentor coeruleus     | gene Sst100171m.g         |                          |
| Osa1     | Oryza sativa          | gene Osa101146100         | MSU Release 7.0 of the Rice Genome Annotation |
| Osa2     | Oryza sativa          | gene Osa101156140         |                          |
| Bbi1     | Brachypodium distachyon| gene Bra21g13500         | JGI Be assembly release v1.0 of strain BBI2 with JGI/MPS PSA A annotation v1.2 |
| Ppy1     | Pyrus communis        | gene Ppy117b3102         | JGI assembly release v1.0 and COSMOS2015 annotation v1.6 |
| Ppy2     | Pyrus communis        | gene Ppy1120014A         |                          |

**SUPPLEMENTARY TABLE S1**

| ACCESSION NUMBER | NAME                  | SPECIES                        |
|------------------|-----------------------|--------------------------------|
| DQ4601.1         | Drosophila casei       | GenBank/EMBL/DDBI              |
| DQ14501.9        | Drosophila casei       | GenBank/EMBL/DDBI              |
| AB14501.6        | Apis mellifera        | GenBank/EMBL/DDBI              |
| AB14507.1        | Apis mellifera        | GenBank/EMBL/DDBI              |
| MA10550.2        | Arabidopsis thaliana  | GenBank/EMBL/DDBI              |
| MA101104.2       | Arabidopsis thaliana  | GenBank/EMBL/DDBI              |
| MA105501.2       | Arabidopsis thaliana  | GenBank/EMBL/DDBI              |
| MA125745.1       | Arabidopsis thaliana  | GenBank/EMBL/DDBI              |
| AB310204.1       | Arbutus unedo         | GenBank/EMBL/DDBI              |
| AB110035.1       | Arbutus unedo         | GenBank/EMBL/DDBI              |