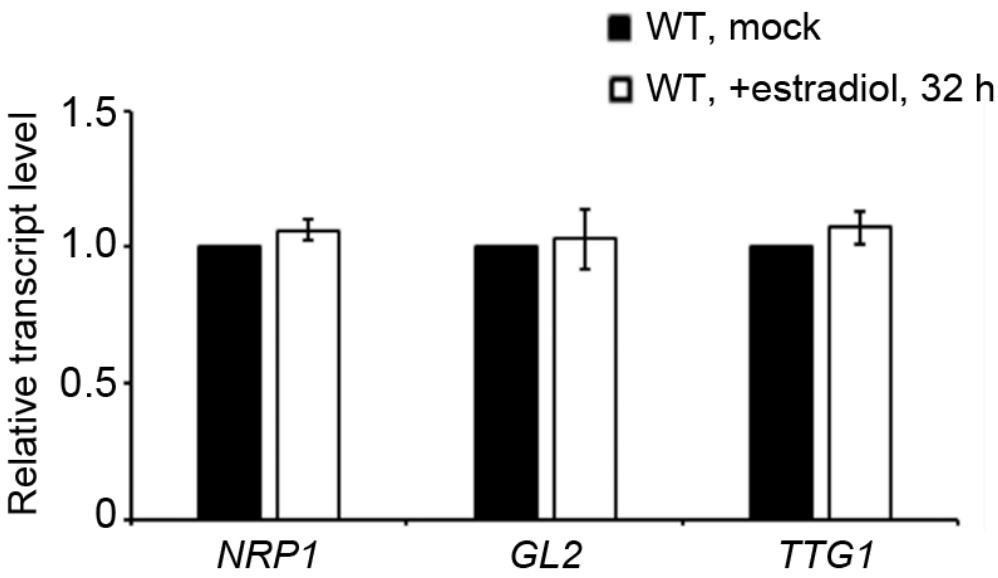
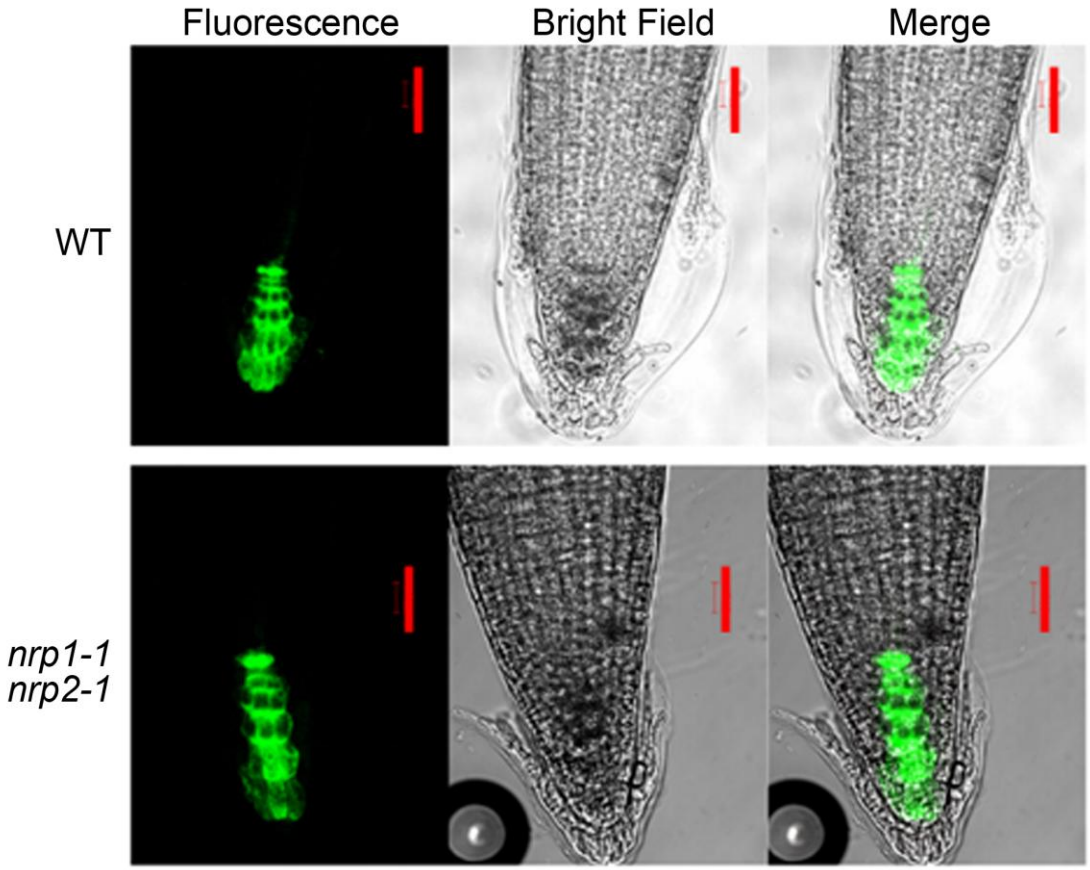


Supplemental Figure 1. Transcript Levels of Examined Genes in Roots of Wild Type (WT).

(**Supports Figure 1.**)

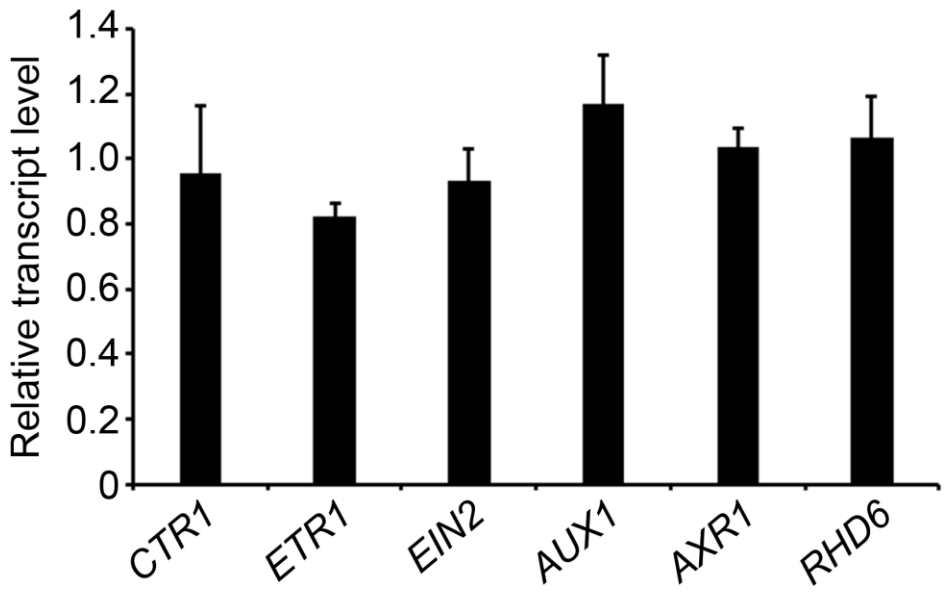
WT plants at 12 days after germination (DAG) were treated with or without 4 μM estradiol for 32 hours, and the roots were collected for RNA isolation and quantitative RT-PCR analysis. Values are normalized to *ACTIN2*. Error bars show standard deviation from three biological replicates. Mean values of relative gene expression levels treated with estradiol compared to those without estradiol (set as 1) are shown with error bars.



Supplemental Figure 2. Auxin Reporter *DR5:GFP* Reveals Similar Auxin Distribution in Roots of Wild Type (WT) and *nrp1-1 nrp2-1*.

(**Supports Figure 2.**)

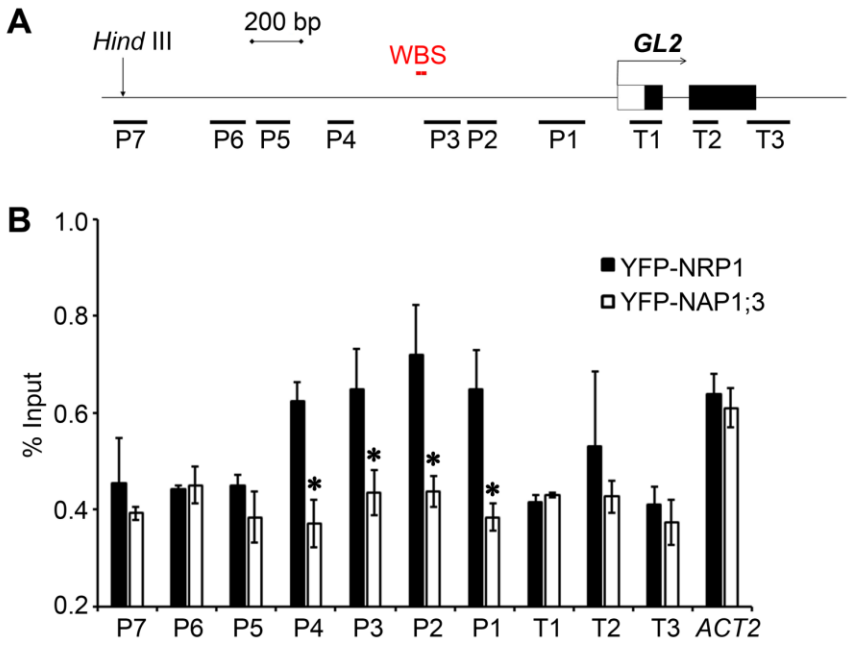
WT and *nrp1-1 nrp2-1* double mutant plants harboring the reporter *DR5:GFP* were grown vertically in culture medium. GFP fluorescence (in green) and bright field images of root tips are shown. Bar = 50 μm.



Supplemental Figure 3. Similar Transcript Levels of Ethylene/Auxin-Related Genes and *RHD6* in Wild Type (WT) and *nrp1-1 nrp2-1*.

(**Supports Figure 2.**)

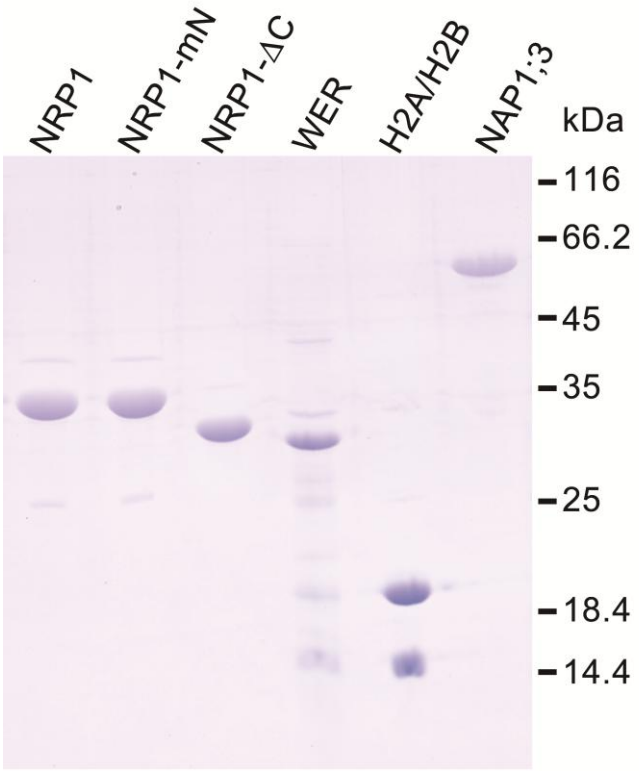
Relative transcription levels of ethylene/auxin-related genes (Masucci and Schiefelbein, 1996) in *nrp1-1 nrp2-1*. Roots of WT and *nrp1-1 nrp2-1* were collected at 12 DAG for RNA isolation and quantitative RT-PCR. Values are normalized to *ACTIN2*. Error bars show standard deviation from three biological replicates. Mean values of relative gene expression levels in *nrp1-1 nrp2-1* compared to those in WT (set as 1) are shown with error bars.



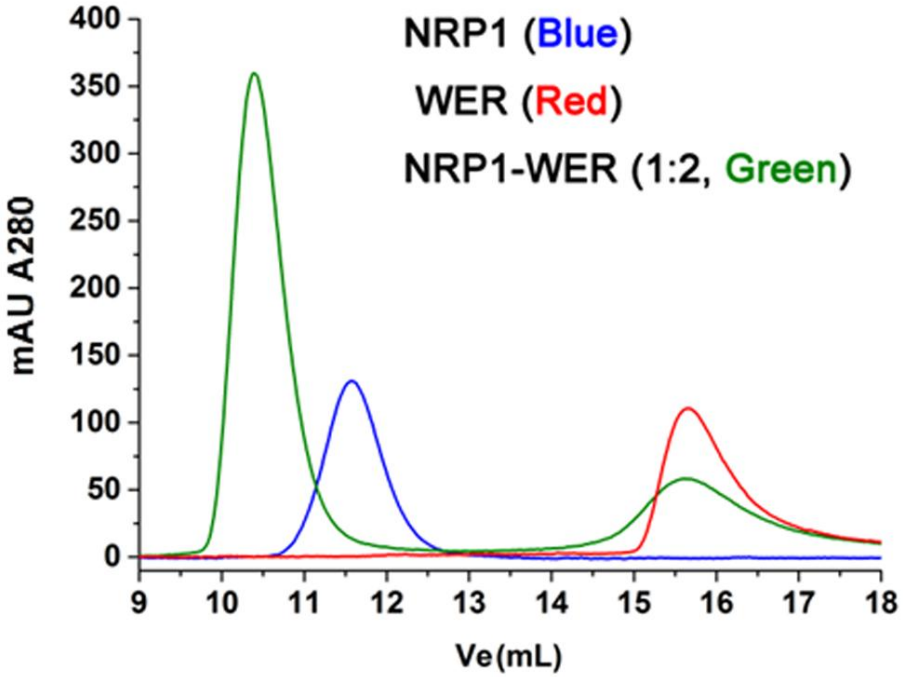
Supplemental Figure 4. YFP-NAP1;3 Is Not Enriched at the *GL2* Promoter. (**Supports Figure 3.**)

(A) Schematic representation of the *GL2* promoter and first two exons.

(B) Transgenic plants harboring *35S:YFP-NAP1;3* were grown vertically until 12 days after germination. Roots were used for ChIP-PCR analysis using polyclonal anti-GFP antibody. Note that ChIP-PCR data of YFP-NRP1 (Figure 3) are included here for visual comparison. Error bars show standard deviation from three biological replicates. Asterisks indicate statistically significant difference of enrichment at *GL2* and *ACTIN2* (*ACT2*) between YFP-NAP1;3 and YFP-NRP1 ($p < 0.01$).



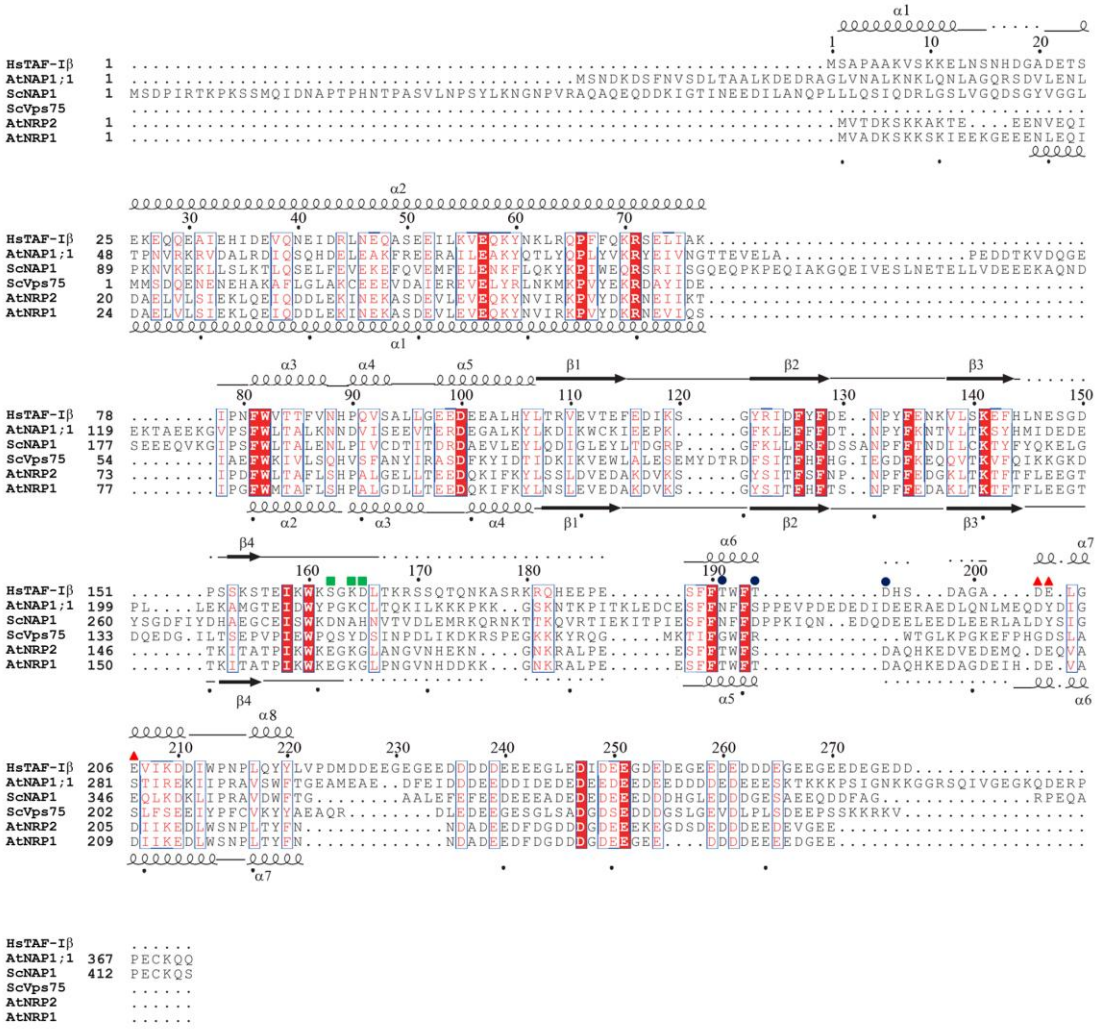
Supplemental Figure 5. Purified Recombinant Proteins used in This Study. (**Supports Figure 4,6.**)



Supplemental Figure 6. Size exclusion chromatography of NRP1 and WER mixture.

(**Supports Figure 4.**)

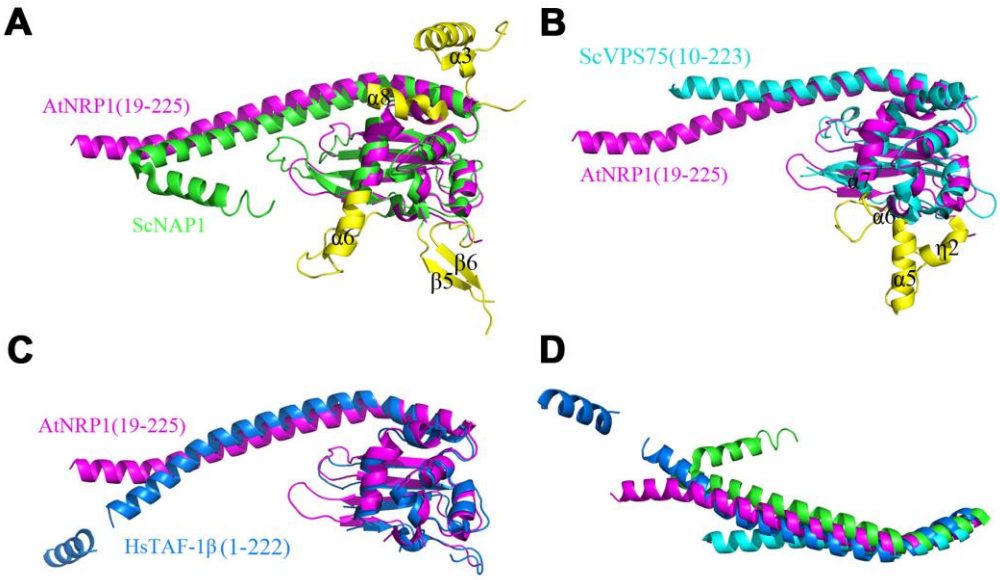
Size exclusion chromatography profiles (Superdex 200 10/300 GL) of NRP1 (blue) and WER (red), as well as their mixture at a molar ratio of 1:2 (green).



Supplemental Figure 7. Protein Sequence Alignment of NAP1 Family Members.

(**Supports Figure 5.**)

Amino acid sequence alignment of NAP1 family members including HsTAF-Iβ, AtNAP1;1, ScNAP1, ScVps75, AtNRP1, and AtNRP2 was generated by CLUSTALW (Sc, *Saccharomyces cerevisiae*; Hs, *Homo sapiens*; At, *Arabidopsis thaliana*). Secondary structure alignment of HsTAF-Iβ and AtNRP1 is shown (dashed lines: disordered regions; black dots: intervals for 10 amino acids). The amino acids within N (S162/K164/D165), O (T191/T194/D195) and P (D202/E203/E206) of HsTAF-Iβ are indicated by green, blue, and red marks, respectively.

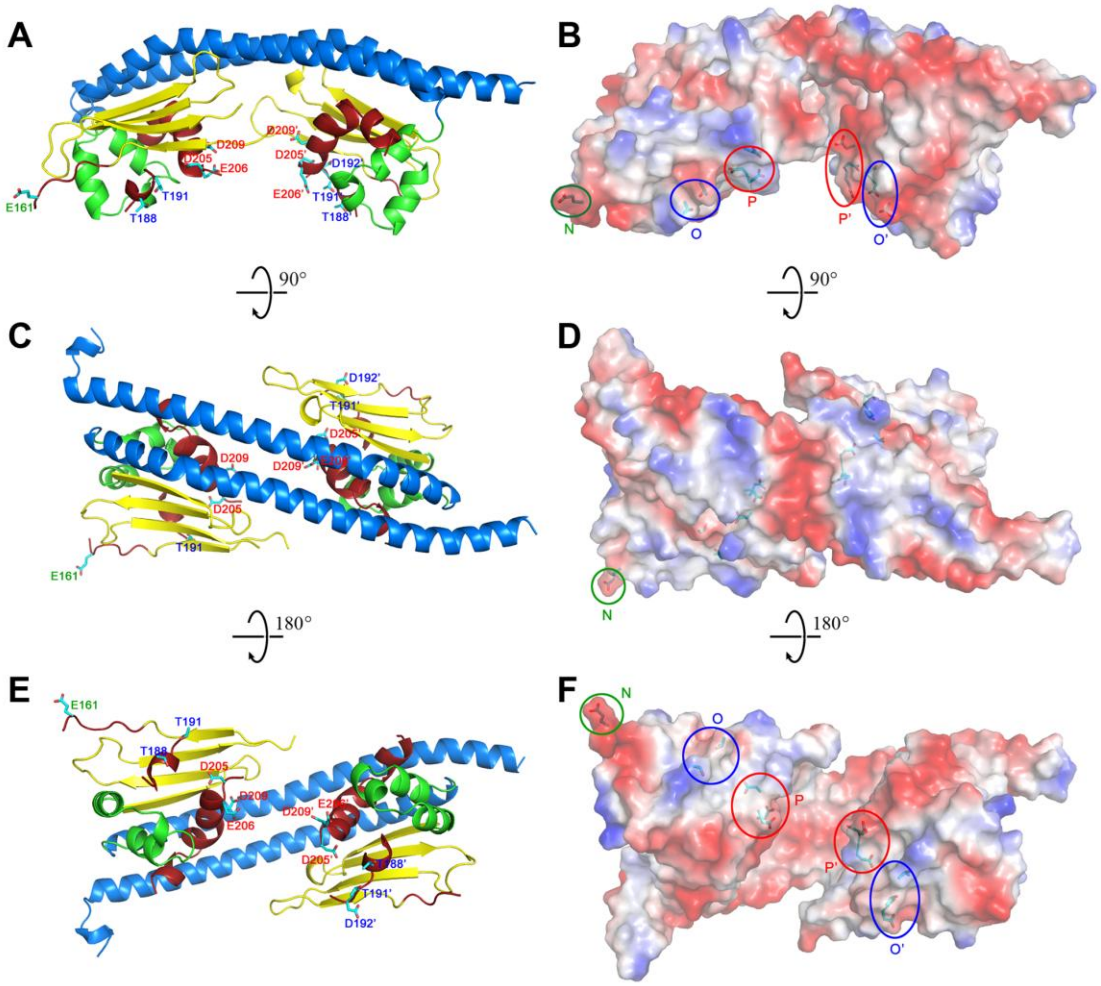


Supplemental Figure 8. Structural Comparison of AtNRP1 with ScNAP1, ScVps75, and HsTAF-Iβ.

(**Supports Figure 5.**)

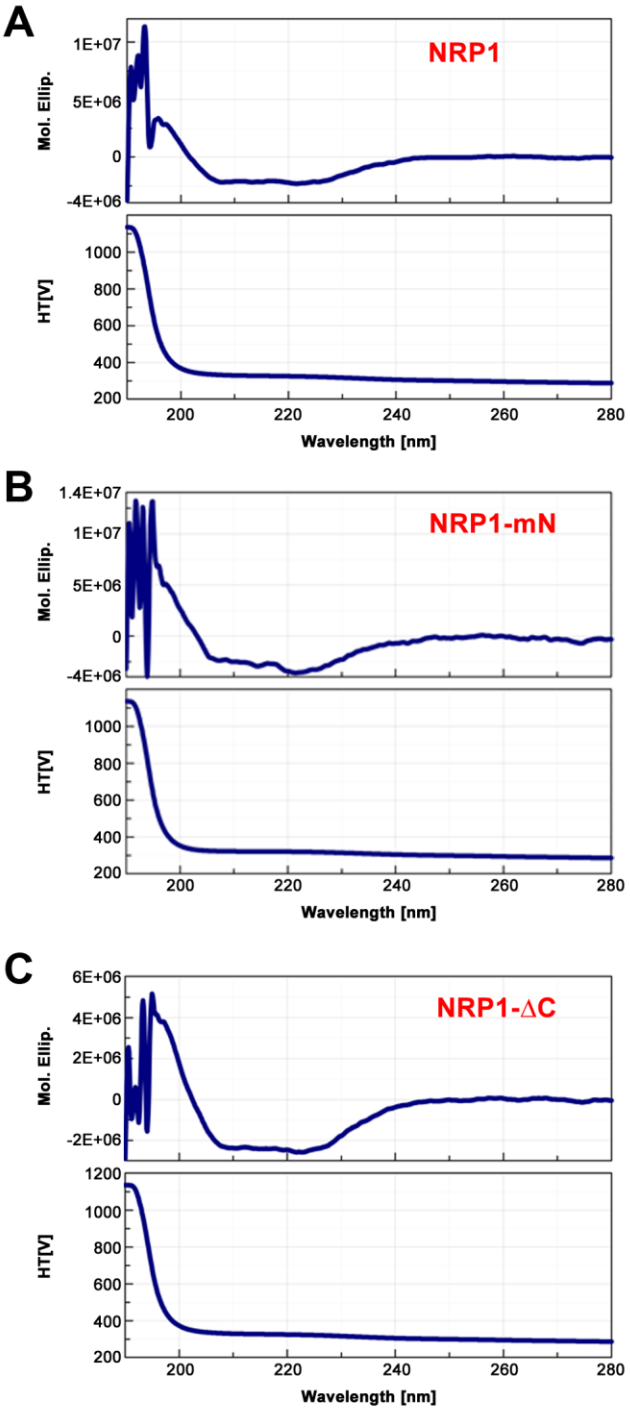
(A,B,C) AtNRP1 (19–225 amino acids, aa, magenta) superimposed with ScNAP1 (green), ScVps75 (10–223 aa, cyan), and HsTAF-Iβ (1-222 aa, blue). Regions of ScNAP1 or ScVPS75 (10–223 aa) that are not found in AtNRP1 (19–225 aa) are shown in yellow.

(D) Superimposed N-terminal dimerization domains of four NAP1-family proteins.



Supplemental Figure 9. Charge Distribution of NRP1 (19–225 aa) Dimer. (**Supports Figure 5.**)

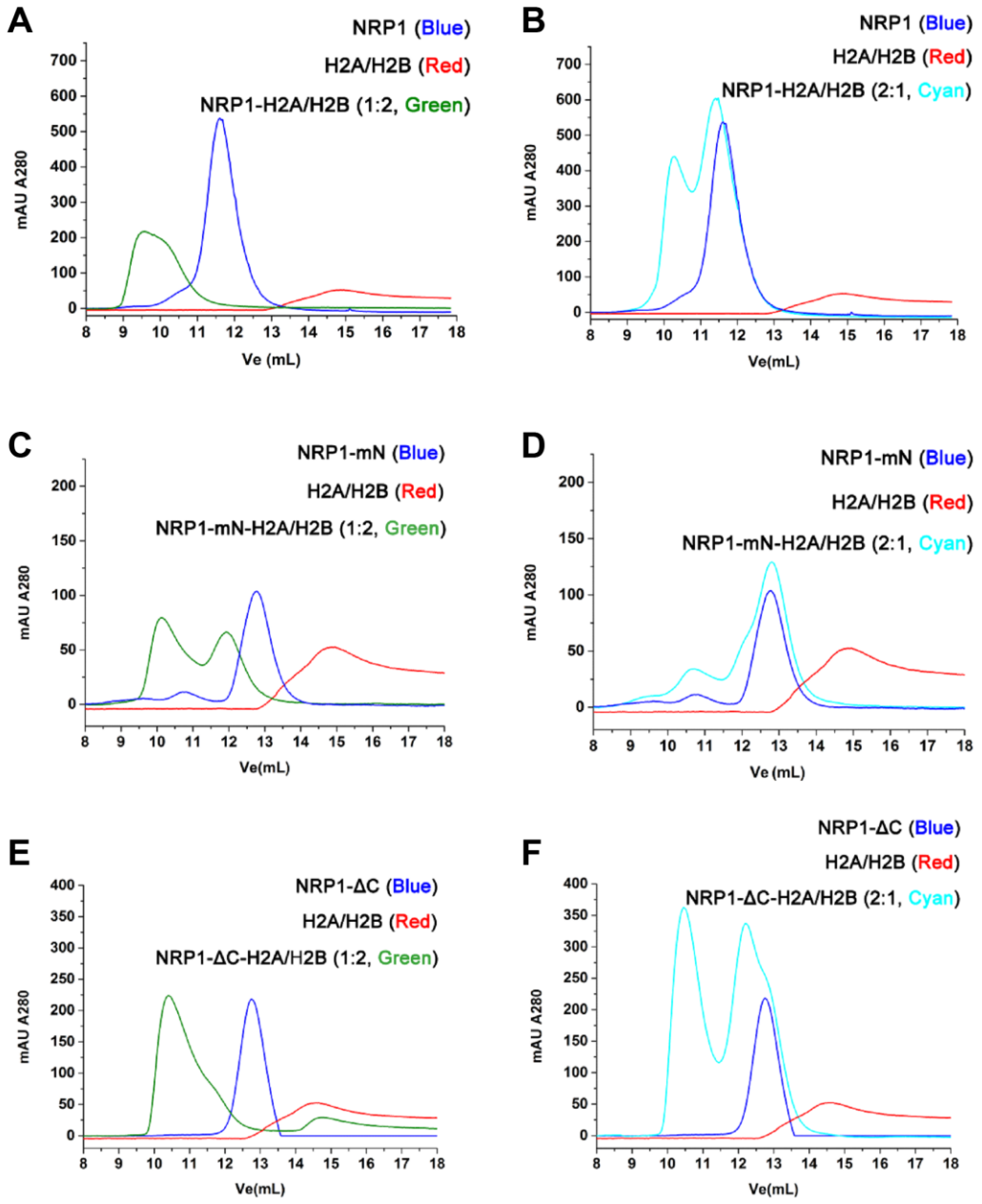
(A, C, E) Overall structure of NRP1 (19–225 aa) shown in three different directions. (B, D, F) Relative charge distribution on surface of NRP1 (19–225 aa) corresponding to A, C, E, respectively. Seven amino acids E161, T188, T191, D192, D205, E206 and D209 on the NRP1 surface correspond respectively to S162, T191, T194, D195, D202, E203 and E206 in HsTAF-Iβ. The amino acids within N (E161), O (T188/T191/D192) and P (D205/E206/D209) of NRP1 are marked in green, blue and red circles, respectively.



Supplemental Figure 10. Circular Dichroism Spectroscopy of NRP1, NRP1-mN, and NRP1-ΔC.

(**Supports Figure 6.**)

The wavelength range of the circular dichroism spectrum is 190-280 nm.



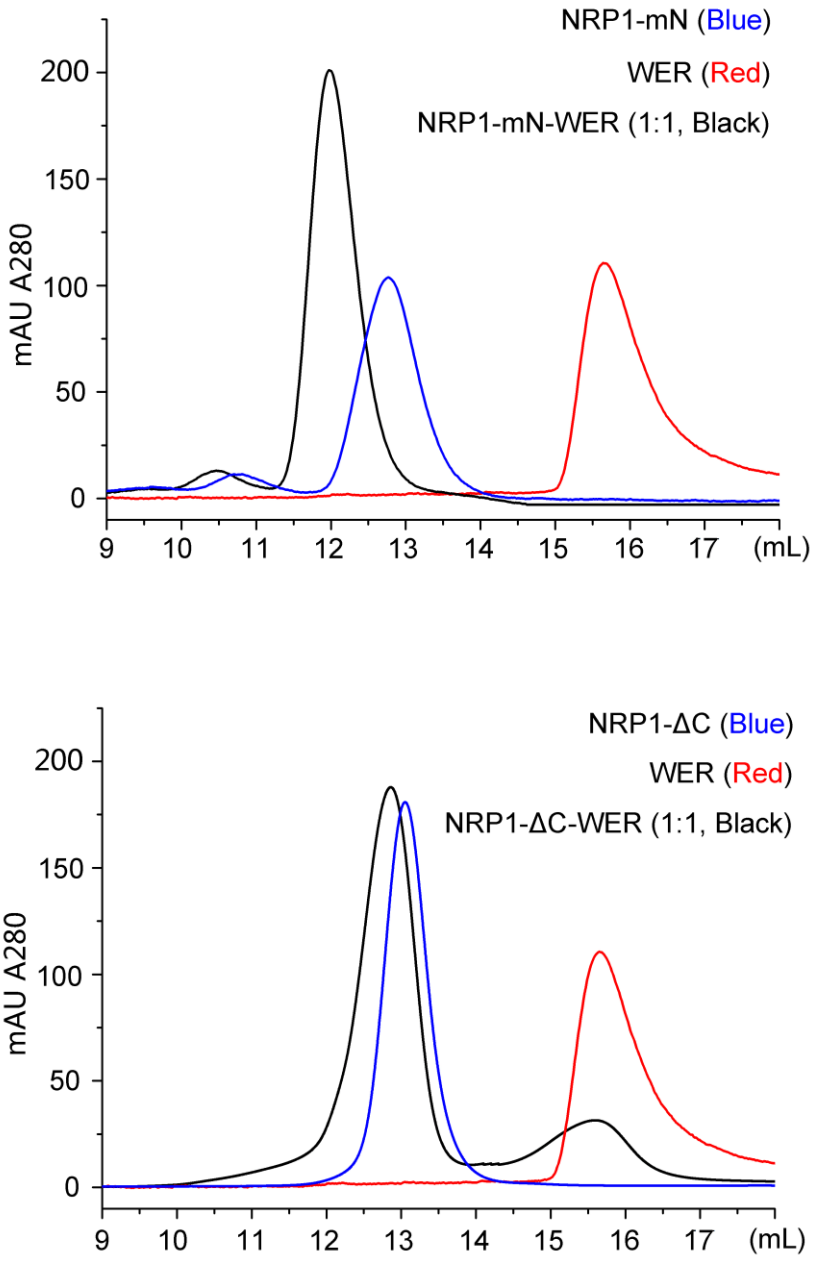
Supplemental Figure 11. Size exclusion chromatography of the H2A/H2B dimer with NRP1, NRP1-mN, or NRP1-ΔC.

(**Supports Figure 6.**)

(A,B) Size exclusion chromatography profiles (Superdex 200 10/300 GL) of H2A/H2B dimer (red) and NRP1 (blue), as well as their mixtures in buffer with 150 mM NaCl (A, molar ratio of 1:2 in green; B, molar ratio of 2:1 in cyan).

(C,D) Size exclusion chromatography profiles for NRP1-mN

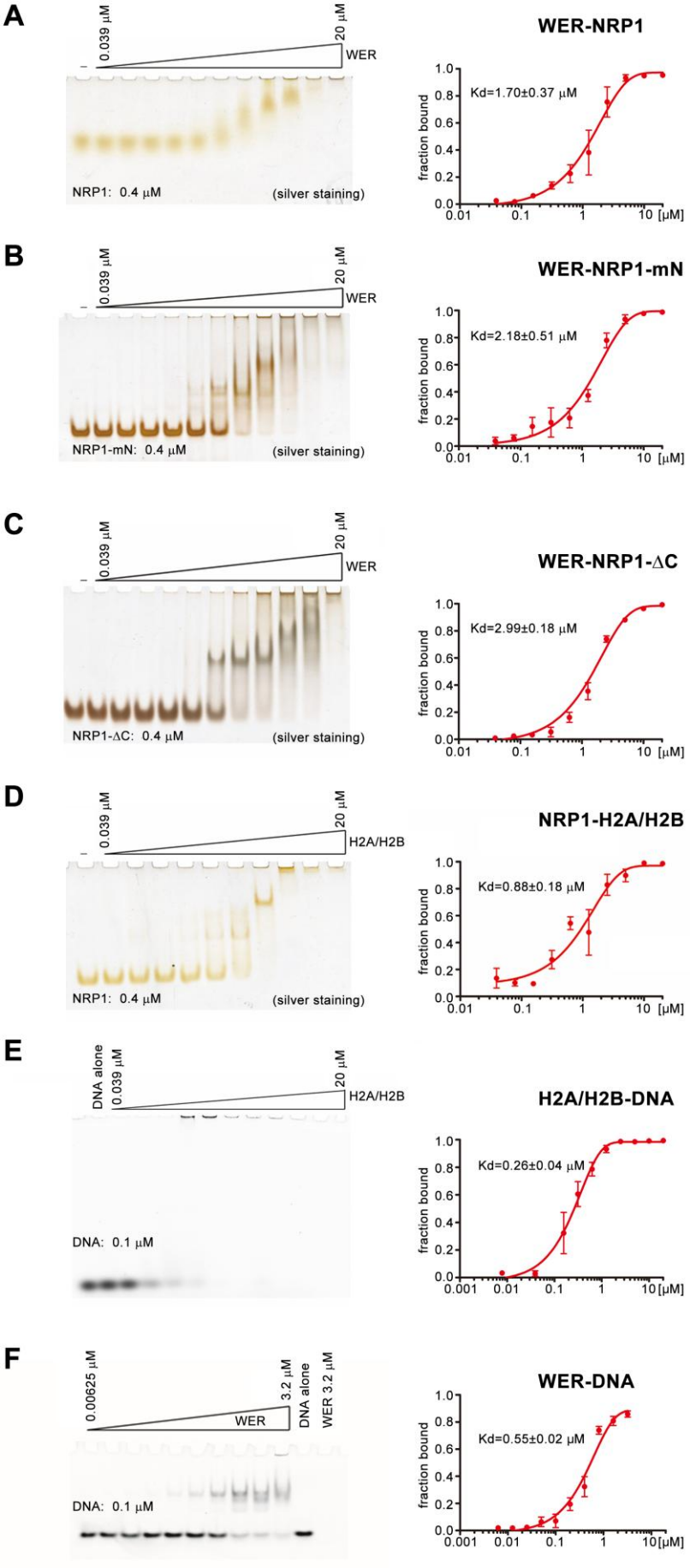
(E,F) Size exclusion chromatography profiles for NRP1-ΔC



Supplemental Figure 12. Size exclusion chromatography of WER-NRP1-mN and WER-NRP1-ΔC.

(**Supports Figure 6.**)

Size exclusion chromatography profiles (Superdex 200 10/300 GL) of WER (red) and NRP1-mN/NRP1-ΔC (blue), as well as their mixture at a molar ratio of 1:1 (black).


A
0.039 μM
20 μM
WER
NRP1: 0.4 μM
(silver staining)
WER-NRP1
Kd=1.70±0.37 μM
fraction bound
[μM]
B
0.039 μM
20 μM
WER
NRP1-mN: 0.4 μM
(silver staining)
WER-NRP1-mN
Kd=2.18±0.51 μM
fraction bound
[μM]
C
0.039 μM
20 μM
WER
NRP1-ΔC: 0.4 μM
(silver staining)
WER-NRP1-ΔC
Kd=2.99±0.18 μM
fraction bound
[μM]
D
0.039 μM
20 μM
H2A/H2B
NRP1: 0.4 μM
(silver staining)
NRP1-H2A/H2B
Kd=0.88±0.18 μM
fraction bound
[μM]
E
DNA alone
0.039 μM
20 μM
H2A/H2B
DNA: 0.1 μM
H2A/H2B-DNA
Kd=0.26±0.04 μM
fraction bound
[μM]
F
0.00625 μM
3.2 μM
DNA alone
WER 3.2 μM
WER
DNA: 0.1 μM
WER-DNA
Kd=0.55±0.02 μM
fraction bound
[μM]

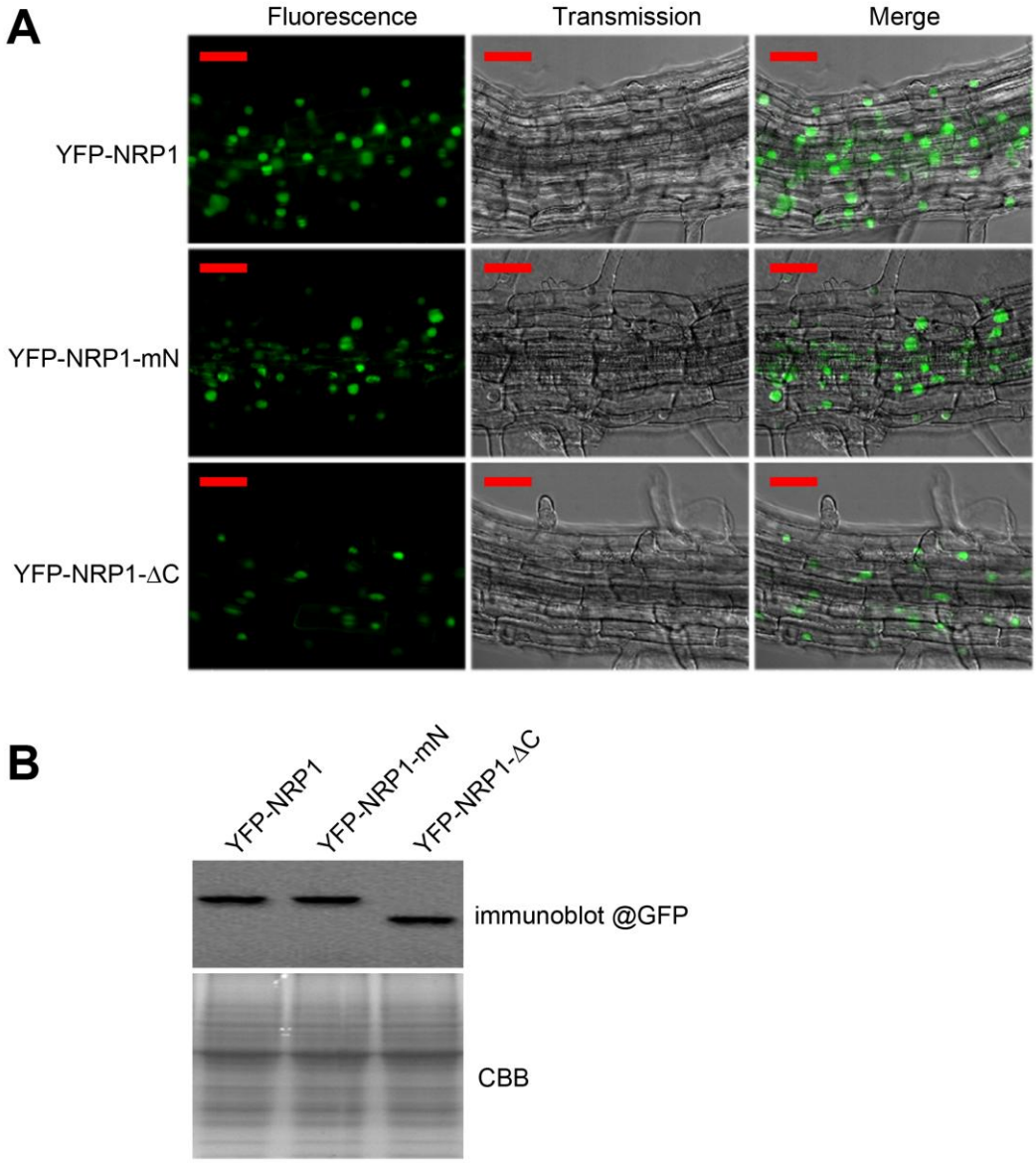
Supplemental Figure 13. Binding Affinity by Electrophoretic Mobility Shift Assay.

(**Supports Figure 6.**)

(A, B, C) 0.4 μM NRP1 (A), NRP1-mN (B) or NRP1-ΔC (B) was mixed with WER increased from 0.039 μM to 20 μM. The native PAGE gel was visualized by silver staining. The decreased intensity of NRP1, NRP1-mN or NRP1-ΔC was calculated by ImageJ and the curve was fitted using GraphPad Prism5.

(D) 0.4 μM NRP1 was mixed with H2A/H2B from 0.039 μM to 20 μM.

(E, F) 0.1 μM DNA labeled by FAM at 5' end was mixed with H2A/H2B (E) from 0.039 μM to 20 μM or WER (F) from 0.00625 μM to 3.2 μM. The native PAGE gel was visualized by Typhoon FLA 9000. The decreased intensity of DNA was calculated by ImageJ and the curve was fitted using GraphPad Prism5.

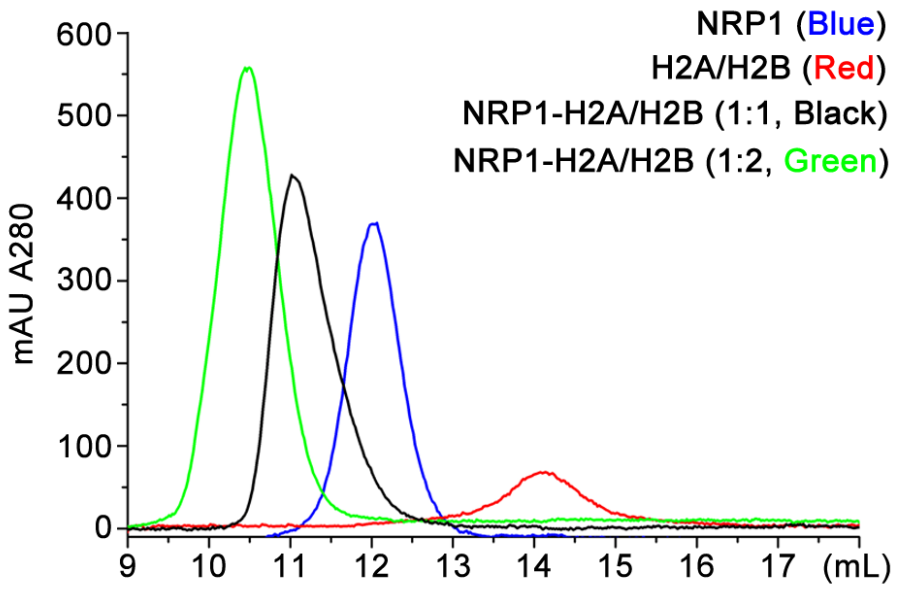


Supplemental Figure 14. Both YFP-NRP1-mN and YFP-NRP1-ΔC Localize in the Nucleus, Like YFP-NRP1.

(**Supports Figure 6.**)

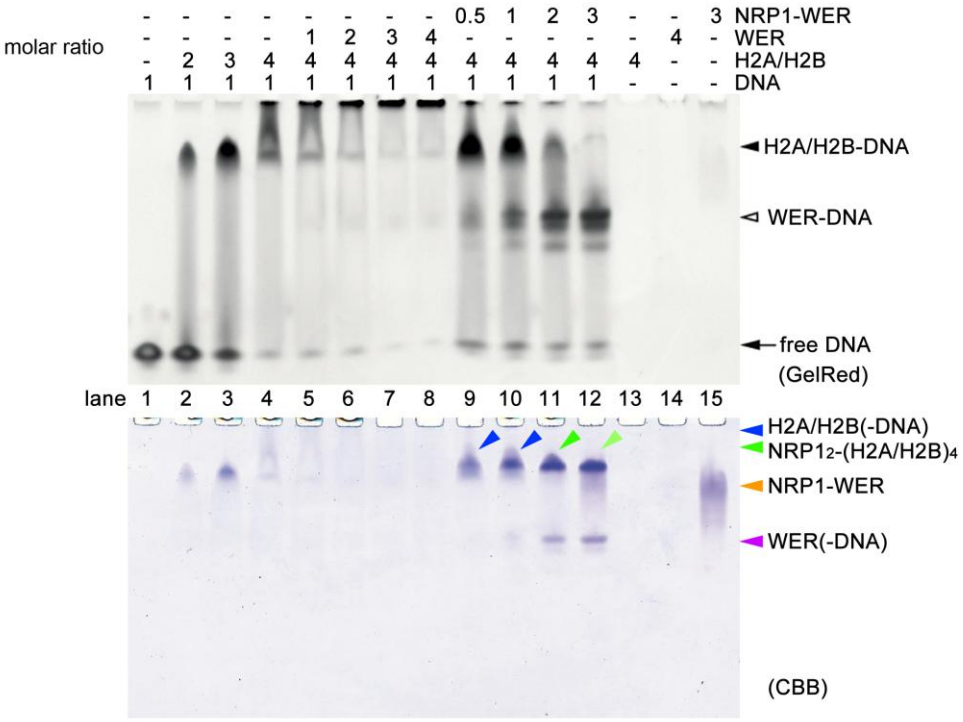
(A) Similar to YFP-NRP1, YFP-NRP1-mN and YFP-NRP1-ΔC localize in the nucleus in roots of transgenic plants harboring *ES:YFP-NRP1*, *ES:YFP-NRP1-mN*, and *ES:YFP-NRP1-ΔC*. Plants were grown vertically in culture medium supplemented with 4 µM estradiol. Figure shows YFP fluorescence (in green) and differential interference contrast images. Bar = 20 µm.

(B) Protein extracts of transgenic plants were examined by Western blot using anti-GFP antibody and also stained with Coomassie Brilliant Blue (CBB) as loading control, indicating the similar expression levels of YFP-NRP1, YFP-NRP1-mN and YFP-NRP1-ΔC *in planta*.



Supplemental Figure 15. Size exclusion chromatography of NRP1-H2A/H2B. (**Supports Figure 9.**)

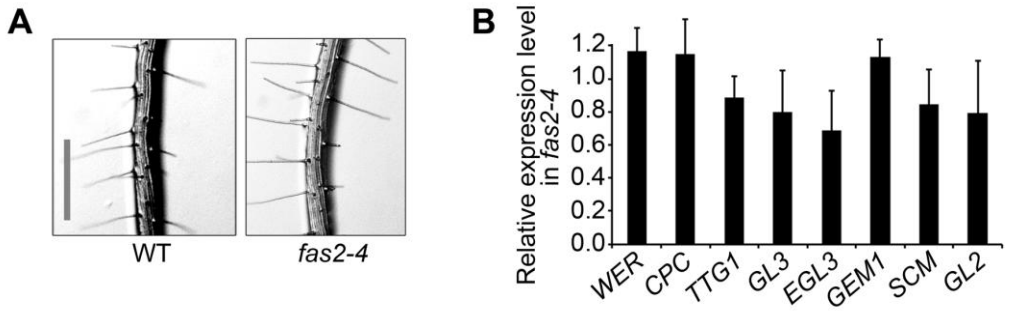
Size exclusion chromatography profiles (Superdex 200 10/300 GL) of H2A/H2B dimer (red) and NRP1 (blue), as well as their mixtures in buffer with 200 mM NaCl.



Supplemental Figure 16. The WER-NRP1 Complex More Efficiently Binds to H2A/H2B-Coated DNA Than WER Alone.

(**Supports Figure 9.**)

Lane 1-12, 2 μM DNA (black arrow, set as relative molar ratio at 1), Lanes 2-4, H2A/H2B titrated against DNA at molar ratios of 2:1, 3:1, and 4:1 to form histone-coated DNA. Lane 5-13, amount of H2A/H2B was held at 4:1 molar ratio. Lanes 5-8, WER titrated against DNA at molar ratios of 1:1, 2:1, 3:1, and 4:1. Lanes 9-12, NRP1-WER complex titrated against DNA at molar ratios of 0.5:1, 1:1, 2:1, and 3:1. Lanes 13, 8 μM H2A/H2B. Lane 14, 8 μM WER. Lane 15, 6 μM NPR1-WER complex. All samples were separated on 6% native PAGE gel, stained with GelRed, and visualized by UV (upper panel). The GelRed-stained gel shows bands of DNA bound to H2A/H2B (black arrowhead) and DNA bound to WER (open arrowhead). Gel was further stained by CBB to show bands of H2A/H2B bound to DNA (blue arrowheads), $NRP1_2$-$(H2A/H2B)_4$ complex (green arrowheads), NRP1-WER complex (orange arrowhead) and WER bound to DNA (purple arrowhead) (lower panel). Note that the bands of H2A/H2B-DNA and $NRP1_2$-$(H2A/H2B)_4$ showed similar electrophoretic mobility in the native PAGE gel.



Supplemental Figure 17. Normal Root Hair Phenotype of *fas2-4* Mutant in Col Background.

(A) Root hair of wild type (WT) and *fas2-4* (Col ecotype). Plants were grown vertically in culture medium and images were taken at 12 days after germination (DAG). Bar = 0.5 mm.

(B) Relative expression levels of root hair-related genes in *fas2-4*. Roots of WT and *fas2-4* were collected at 12 DAG for RNA isolation and quantitative RT-PCR. Values are normalized to *ACTIN2*. Error bars show standard deviation from three biological replicates. Mean values of the relative gene expression levels in *fas2-4* compared with that in WT (set to 1) are shown with error bars.

Supplemental Table 1. Crystallographic Statistics

Data collection	Native NRP1(19–225)	Se-Met NRP1(19–225)
Space group	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions		
a, b, c (Å)	60.537, 60.808, 135.250	59.197, 61.945, 134.059
α, β, γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 90.0
Resolution (Å)	50.00-2.41 (2.41-2.33)	30-2.59 (2.59-2.50)
R_{sym}	0.055 (0.270)	0.106 (0.543)
I/σI	43.7 (5.81)	8.49 (1.38)
Completeness (%)	98.2(91.6)	90.1 (82.3)
Redundancy	6.0 (5.0)	2.5 (1.9)
Refinement		
Resolution (Å)	2.33	
No. reflections	21784	
R_{work}/R_{free}	0.230/0.269	
No. atoms		
protein	2841	
ligand/ion	3	
water	101	
B factors	61.6	
R.M.S. Deviations		
Bond lengths (Å)	0.007	
Bond angles (°)	0.833	

Ramachandran plot	
Favored	96.07%
Allowed	3.93%

Supplemental Table 2. Primers Used in This Study.

For RT-PCR analyses	
WER-qF1	GTGAAAAGAGGCAATTTCACCGAGC
WER-qR1	TATCCGTTCGACCCGGCACTC
CPC-qF1	CGAATGGGAAGCTGTGAAGATGTCA
CPC-qR1	ACGCCGTGTTTCATAAGCCAATATC
TTG1-qF1	CGCCGACTATGCCTGTTGCTGA
TTG1-qR1	ACAGCTCTGAGGCGCCCAAG
GL3-qF1	GATCGGTTCGTTTGGTAATGAGGTG
GL3-qR1	TCGCTATTTTTGACCCCTTGTGC
EGL3-qF1	AACCGCCGATAGCAAAGTCTTCA
EGL3-qR1	ATATGTTCGGTCGTGCCAATCTCAA
MYB23-rF1	CTCGGCAACAGATGGTCGTT
MYB23-rR1	CCGAGACCAAGTTTCTTGCTG
GEM1-qF1	TCCAGCTGAGACTTCAGATGCTTCG
GEM1-qR1	GCAAAACTCGGAGCAGTTCTCAGG
SCM-qF1	GTCAGAGCGACGTATTTAGCCTTGG
SCM-qR1	CGCTCCGTGTAATGACGGATCAAC
GL2-qF1	CGCCGCACACAGATCAAGGCTA
GL2-qR1	ATCATCGGGGCCTCCTCCGC
NRP1-qF1	TGCATTGCCAGAGGAGAGTT
NRP1-qR1	CAGCAACCTGCTCATCATGAATC
ACT2-qF1	AGTGTTAGCTGCTGCCGCTGT
ACT2-qR1	ACCAGCAAAACCAGCCTTCACCA
For ChIP and MNase analyses	
GL2-P7-F	CGACGACTAACAAAGAAA
GL2-P7-R	ACGTAAATGGACGAAGAC
GL2-P6-F	ATGCGTATAGTGAATAGGAAAG

GL2-P6-R	AGGTCAGCGAGAGGCATTG
GL2-P5-F	TCGACGTCTCTTTCCGCTGCTG
GL2-P5-R	ACGGTAAAGGCAGGAAAGAAGAGTTTGT
GL2-P4-F	TTCCATGTAGCGCTGCAATATACTGTT
GL2-P4-R	GGAAACTGGGACTCTGGGAGAAGC
GL2-P3-F	AGTTGAGTCCATCTCAGTATC
GL2-P3-R	AGACGAACTTCTCTGTCTCTTC
GL2-P2-F	TCATGCAATTGTAACCCTTCCT
GL2-P2-R	AGCCATATTGAAACATGAGCAA
GL2-P1-F	TGAAGTCGATCGATGGCTG
GL2-P1-R	CTTCCATTTCTCTACTGCTC
GL2-T1-F	TGCGAGGAGAAGAGGGAAGAGA
GL2-T1-R	AGAGAGAGGGCTGGAGAGGAGA
GL2-T2-F	ATGCATCCTCCGGCAGCACC
GL2-T2-R	TGGGTCCTGAGTTCTCGCTGC
GL2-T3-F	TCATCGTCACACCACCGATCAGA
GL2-T3-R	AGCCCTAATGAATCGGAATCCCCT
FLC-F	AGAAGTCGGAAGAGTTCAAACCAGT
FLC-R	TCTTTCCTCCCCTACGATACGGAT
ACT2-F	GATGAGGCAGGTCCAGGAATC
ACT2-R	AACCCCAGCTTTTTAAGCCTTT