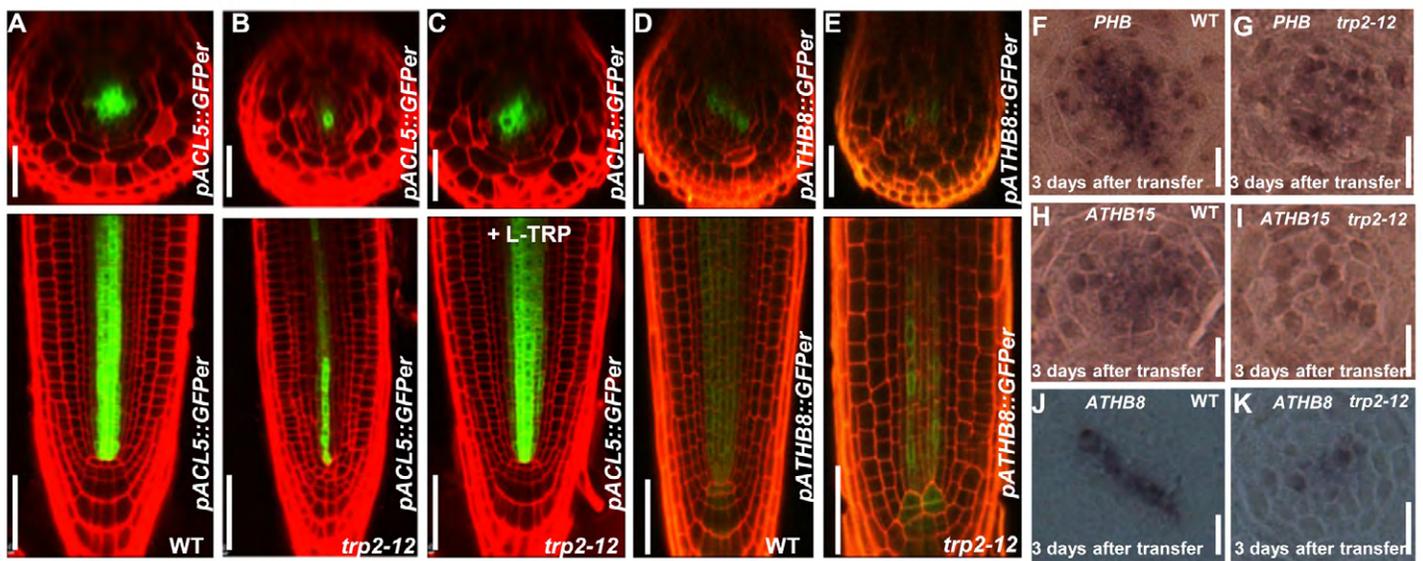
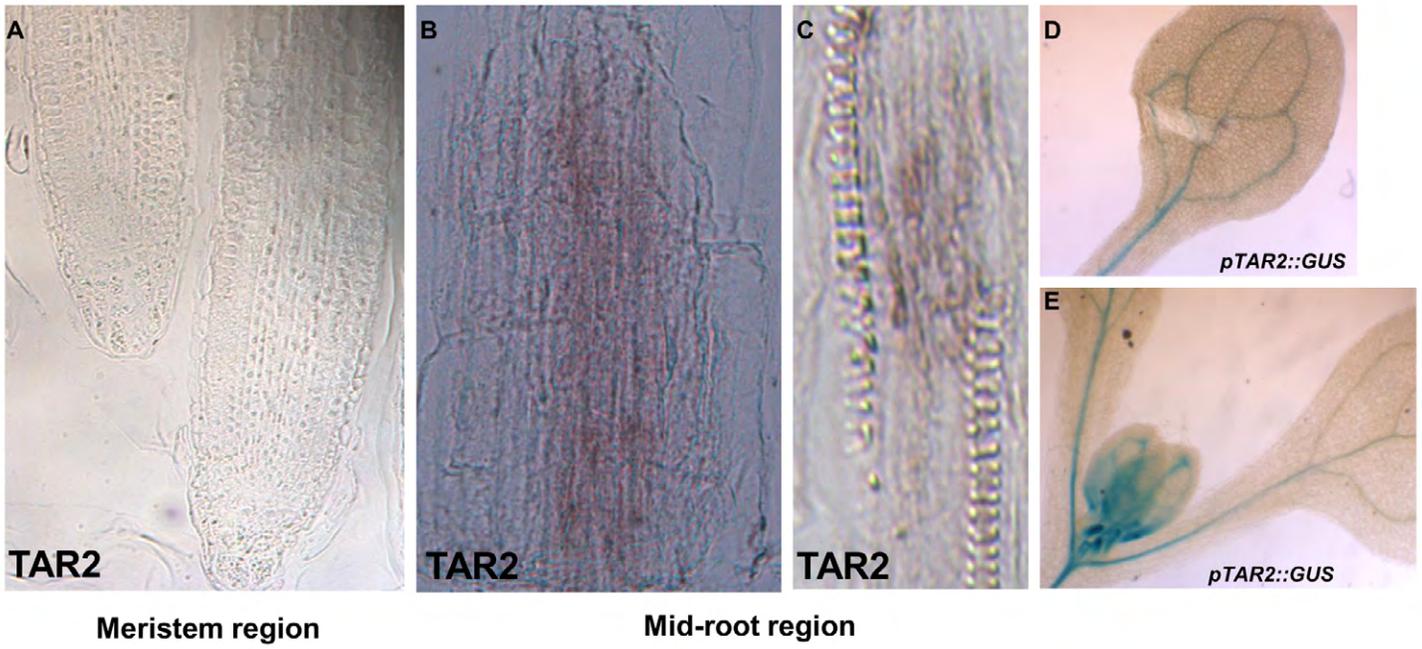


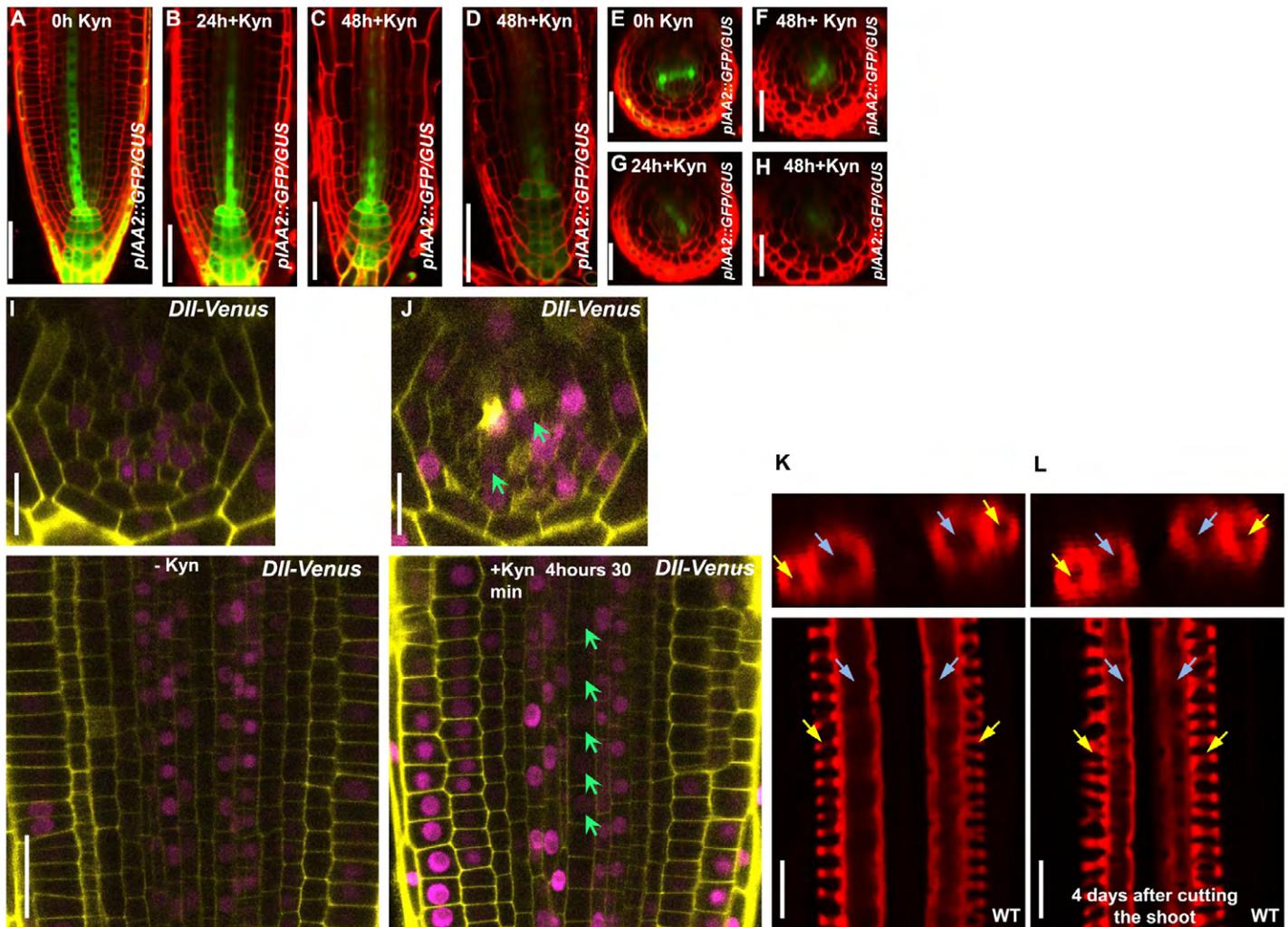
Supplementary Fig. 1. Characterization of *trp2-12* mutant. (A) A schematic representation of the *Arabidopsis* root. (B-D) *pSUC2::GFP* in 5 day-old wild-type (B), *trp2-12* grown without (C) and with L-Trp (D). (Scale bar: 50 μ m.). (E,F) Wild-type and *trp2-12* roots stained with propidium iodide (Scale bars: 25 μ m.). (G,H) Toluidine-blue stained root cross-sections of 5 day-old wild-type and *trp2-12* roots. (Scale bar: 25 μ m.). (I-K) Basic fuchsin-stained xylem of 5-day old wild-type (I), *trp2-12* grown without (J) and with L-Trp (K). (Scale bar: 25 μ m.) Blue arrows indicate metaxylem and yellow arrows indicate protoxylem. (L-N) *pDR5::GFP* in 5-day old wild-type, *trp2-12* and *trp2-13*. (Scale bar: 50 μ m.). (O-Q) Subcellular localization of the TSB1 protein to the plastids in the *Arabidopsis* root epidermis. (Scale bars: 7.5 μ m.).



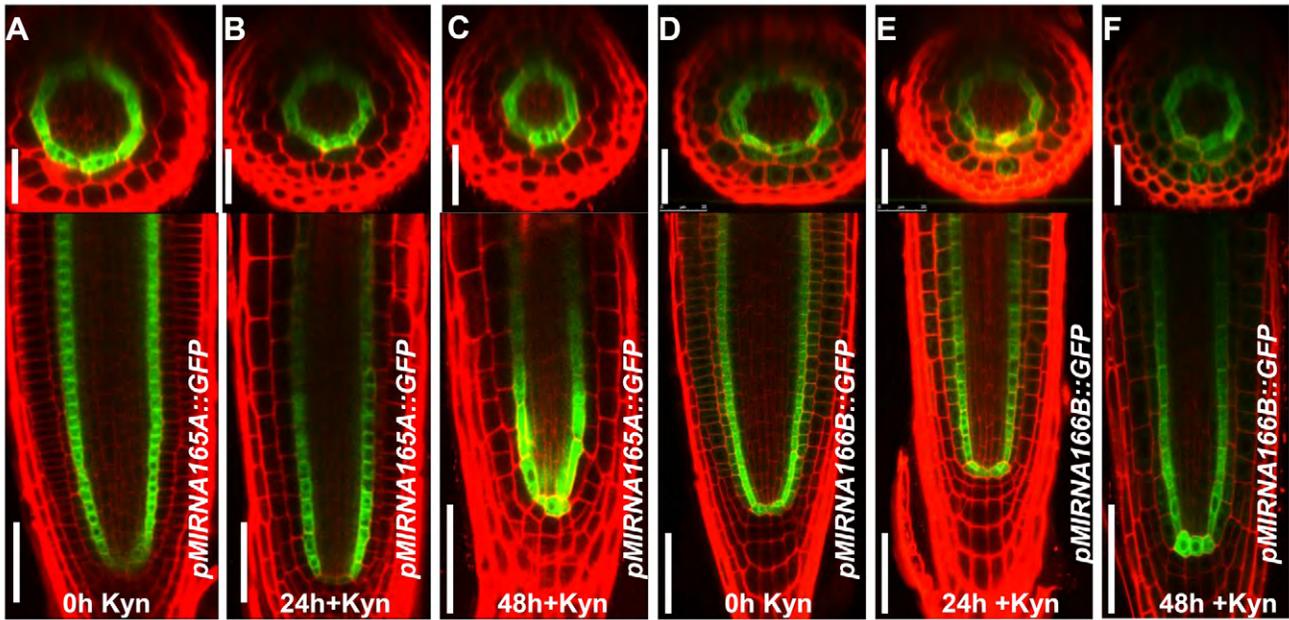
Supplementary Fig. 2. (A-C) *pACL5::GFP* in 5-day old wild-type and *trp2-12* grown with and without L-TRP. (D,E) *pATHB8::GFP* in 5-day old wild-type and *trp2-12* plants (Scale bar: 50 μ m.). (F-K) *In situ* hybridization with *PHB*, *ATHB8* and *ATHB15* mRNA-specific probes on cross sections of the root meristem in the *trp2-12* mutant grown with L-Trp and transferred to a medium without L-Trp. Scale bar: 10 μ m.).



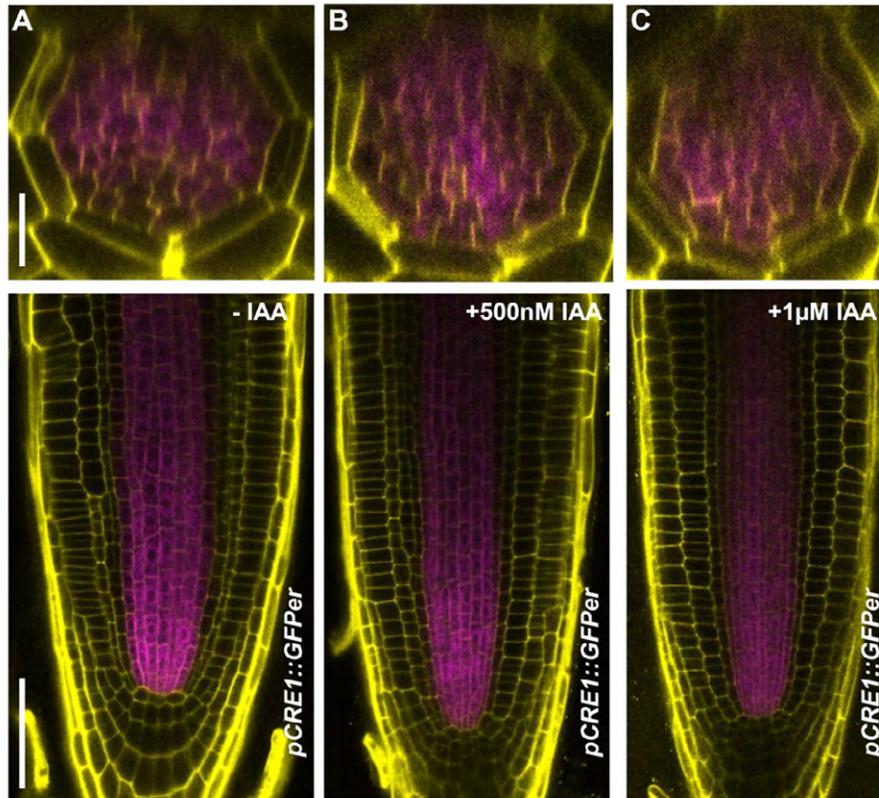
Supplementary Fig. 3. (A-C) TAR2 mRNA-specific probe on longitudinal sections of the root meristem (A) and mid-root region (B,C) of 5 day-old wild-type . (D,E) *pTAR2::GUS* expression in 5-day old leaves.



Supplementary Fig. 4. (A-H) *pIAA2::GFP/GUS* in 5-day old wild type plants (A,E), 3-day old wild-type plants germinated on MS without Kyn and transferred to a medium with Kyn and grown for a further 24h (B,G) and 48h (C,F,H). (I,J) *DII-Venus* expression in wild-type plants grown without Kyn (I) and transferred to a medium with Kyn for 4h 30 minutes (J) (Scale bars: 25 μm for longitudinal and 10 μm for cross-sections). Green arrows indicate *DII-Venus* signal appearing in metaxylem. (K,L) Basic fuchsin-stained xylem of 5 day-old wild-type plants (K) and wild-type plants three days after cutting the shoot off (L) (Scale bar: 25 μm). Blue arrows indicate metaxylem and yellow arrows indicate protoxylem.



Supplementary Fig. 5. (A-C) *pMIR165A::GFP* in 5-day old wild type plants (A), 3-day old wild-type plants germinated on MS without Kyn and transferred to a medium with Kyn and grown for a further 24h (B) and 48h (C). (D-F) *pMIR166B::GFP* in 5-day old wild type plant (D), 3-day old wild-type plants germinated on MS without Kyn and transferred to a medium with Kyn and grown for a further 24h (E) and 48h (F). (Scale bars: 50 μm for longitudinal and 25 μm for cross sections).



Supplementary Fig. 6. (A-C) *pCRE1::GFP* expression in wild-type roots grown on a medium without IAA (A), with 500 nM IAA (B) and 1 μM IAA (C) (Scale bar: 50 μm).

Table S1.**SSLP markers used in *trp2-12* mapping process**

Marker Name	Sequence (5' to 3')
MN1.5 FP	TTATTATCAAGATCAAAGATTGTATGGTT
MN1.5 RP	CTTGTTTTTATATCTGTTTGGTTTAATTGT
CIW12 FP	AGGTTTTATTGCTTTTCACA
CIW12 RP	CTTCAAAGCACATCACA
NGA111 FP	TGTTTTTTAGGACAAATGGCG
NGA111 RP	CTCCAGTTGGAAGCTAAAGGG
NGA1145 FP	GCACATACCACAACCAGAA
NGA1145 RP	CCTTCACATCCAAAACCCAC
NGA361 FP	ACATATCAATATATTAAGTAGC
NGA361 RP	AAAGAGATGAGAATTTGGAC
NGA6 FP	ATGGAGAAGCTTACACTGATC
NGA6 RP	TGGATTTCTCCTCTCTTCAC
NGA172FP	CATCCGAATGCCATTGTTC
NGA172RP	AGCTGCTTCCTTATAGCGTCC
NGA162FP	CTCTGTCACTCTTTTCCTCTGG
NGA162 RP	CATGCAATTTGCATCTGAGG
CIW11 FP	CCCCGAGTTGAGGTATT
CIW11 RP	GAAGAAATTCCTAAAGCATTC
MN4.2 FP	TAAGGTCAGACTATATGTTTACGTTTCATT
MN4.2 RP	GTCATCCTCGTTTAAGTTACGATTG
NGA8 FP	TGGCTTTCGTTTATAAACATCC
NGA8 RP	GAGGGCAAATCTTTATTTTCGG

NGA151 FP	CAGTCTAAAAGCGAGAGTATGATG
NGA151 RP	GTTTTGGGAAGTTTTGCTGG
NGA106 FP	TGCCCCATTTTGTTCCTTCTC
NGA106 RP	GTTATGGAGTTTCTAGGGCACG
NGA139 FP	GGTTTCGTTTCACTATCCAGG
NGA139 RP	AGAGCTACCAGATCCGATGG
NGA76 FP	AGGCATGGGAGACATTTACG
NGA76 RP	GGAGAAAATGTCACTCTCCACC
MBG8 FP	TGTGCCAGATCTTCGTGTTC
MBG8 RP	GGAAGCTGAGATCTGGACAA
MTH12 FP	GTAAAATTTTCTATTGCA
MTH12 RP	ATGTCCTCCTGTTCTGTCCA
SO191 FP	CTCCACCAATCATGCAAATG
SO191 RP	TGATGTTGATGGAGATGGTCA

Table S2.**CAPS markers used in *trp2-12* mapping**

Marker Name	Sequence (5' to 3')	Restriction enzyme
N5-17692527 FP	TCACAGGCAGAGCAAATACG	<i>NdeI</i>
N5-17692527 RP	CCAATAAGGACCACCAAAAA	
N5-18568550 FP	TCAATATGATATGCGAGACTTCAGA	<i>EcoRI</i>
N5-18568550 RP	TCCATGTGCGAATAATAAAAGA	
N5-21038864 FP	GATTCTCATATGCTTCCAGCTGTT	<i>SspI</i>
N5-21038864 RP	AGTTGTCATGAGAGCTGATTTGA	
N5-22116697 FP	CCGGGACGGATGTAGTGAT	<i>HpaI</i>
N5-22116697 RP	ATTTGATCCTGACCGTTGGA	
N5-23412903 FP	CAGTTTCGGTGCCATGAAC	<i>EcoRI</i>
N5-23412903 RP	GAAGGTGCTGGGAGTACAGC	
N5-24832927 FP	TCTTTTTGAGTCATCCATGGTTTT	<i>XmnI</i>
N5-24832927 RP	GTTGTTTAACAGGGCCAGCA	

Table S3.**TSB1 gene sequencing primers**

Primer Name	Sequence (5' to 3')
TRP2seq1	CCAACCGCTTAGCAAGAAGAGCC
TRP2seq2	GGAAACAAGCGTTGGAGAAATGG
TRP2seq3	CCTGCACTGATGGAGTGTGG

Table S4.**Primers Used in Genotyping**

Primer Name	Sequences (5' to 3')
trp2.geno.F	GGAGTCCACTCTGGAACAGC
trp2.geno.R	CGCTTCTTCGTCGGTTATGC
DWLB1	CATACTCATTGCTGATCCATGTAGATTCC
70560-R1	GCTTTTAATGAGCTTCATGTTGG
70560-F8	CATCAGAGAGACGGTGGTGAAC
24670-F1	GCACGCAAGTGAAGCTCCAAGC
JMLB1	GGCAATCAGCTGTTGCCCGTCTCACTGGTG
iaah.F	ATGGTGGCCATTACCTCGTTAG
iaah.R	CTAATTGGGTAAACCGG
YUC3.F	CTGTCTATGTTATAATCGTCGC
YUC3.R	CTCTCTTGGTAAAACATGAAC
YUC8.F	GAACTGACGCTTCGTCGGGTA
YUC8.R	CATCCTCTCCACGTGGCTTCC
YUC5.F	GGAGATTTCAAACACTAGATTTG
T-DNA	ACCCGACCGGATCGTATCGGT
YUC5.R	CGGACTCTAATCAAAGTCCC
YUC7.F	CATGGAGTGGGCTTATCTCTTTGA
YUC7.R	ACGAAAACAGAGCACCCCTGA
YUC9.F	GAAGGAAATGCCCAATGAGAC
YUC9.R	GCTCGGTAAGCAAACAAAACACTG
SAII-LB1	GCC TTTTCAGAAATGGATAAATAGCCTTGCTTCC
T-DNA SPM32	TACGAATAAGAGCG CCATTTTAGAGTGA