Table S1: Primer list.

qRT-GL2 F	ATGAAGCTCGTCGGCATGAGTGGG	Morohashi et al., 2007
qRT-GL2 R	TGGATTGCCACTGAGTTGCCTCTG	Morohashi et al., 2007
qRT-TTG1 F	GTCTTCTTCGCAGCCTGATT	Kleindt et al., 2010
qRT-TTG1 R	AAACCAGCATGAAGTTTCCAA	Kleindt et al., 2010
qRT-WER F	CTAATGTGAAAAGAGGCAATTTCA	This study
qRT-WER R	CCCGGCACTCTTTTAGCA	This study
qRT-TRY F	GTGAGCAGTATCGAATGGGAGT	Morohashi et al., 2007
qRT-TRY R	CACCGACAAGTCTGTACATTCG	Morohashi et al., 2007
qRT-RSL4-F	GTGCCAAACGGGACAAAAGT	Yi et al., 2010
qRT-RSL4R	TTGTGATGGAACCCCATGTC	Yi et al., 2010
qRT-WRKY75 F	CGTCAAGAACAACAAGTTCCCTA	This study
qRT-WRKY75 R	CTTTGCACTTGCTTCTTCACAT	This study
qRT-EF1α F	TGAGCACGCTCTTCTTGCTTTCA	Yi et al., 2010
qRT-EF1α R	GGTGGTGGCATCCATCTTGTTACA	Yi et al., 2010
AtTSP(Spm32)	TACGAATAAGAGCGTCCATTTTAGAGTGA	Encinas-Villarejo et al., 2009
AtWRKY-F	TTATAATTTGGATTCGGGAACA	Encinas-Villarejo et al., 2009
WRKY75 RNAi PF	GGACTAGTCCATGGCCAGAGCTGCATCAAGG	Devaiah et al., 2007
WRKY75 RNAi PR	CGGGATCCGGCGCGCCATCCTCCATATGTACC	Devaiah et al., 2007
AtWRKY-R	GACGGTGCTGAAGAACAATG	Encinas-Villarejo et al., 2009
WRKY75-for-attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTA ATGGAGGGATATGATAATGGG	This study
WRKY75-rev-Stop/ost-attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTAC WAGAAAGAAGAGTAGATTTGC	This study
80bp CPC-Promotor-Trimer	AGAATTCAAAGGATCCGATCTCGGTGACGGG	This study
80bp CPC-Promotor-Trimer	AGGTACCATAGAGAAAGAAGAACGACAGAT ACAACC	This study
80bp CPC-Promotor-	AGGTACAAAGGATCCGATCT CGGTG ACGGG	This study

Trimer		
80bp CPC-Promotor-Trimer	AGGATCCATAGAGAAAGAAGAACGA CAGAT ACAACC	This study
80bp CPC-Promotor-Trimer	AGGATCCAAAGGATCCGATCTCGGTG ACGGG	This study
80bp CPC-Promotor-Trimer	ATCTAGAGATAGAGAAAGAAGAACG ACA GATACAACC	This study
Pr185-mutWRKY EcoRI-KpnI for	aattcAACGAGGAATTTTTACAACCGCAAcccggA GGATTTAAAATAAGTAGTTATGGTTGTATCTG TCGTTCTTCTTTCTCTATggtac	This study
Pr185-mutWRKY EcoRI-KpnI rev	cATAGAGAAAGAAGAACGACAGATACAACC ATAACTACTTATTTTAAATCCTccgggTTGCGG TTGTAAAAATTCCTCGTTg	This study
Pr185-mutWRKY KpnI-BamHI for	cAACGAGGAATTTTTACAACCGCAAcccggAG GATTTAAAATAAGTAGTTATGGTTGTATCTG TCGTTCTTCTTTCTCTATg	This study
Pr185-mutWRKY KpnI-BamHI rev	gatccATAGAGAAAGAAGAACGACAGATACAA CCATAACTACTTATTTTAAATCCTccgggTTGC GGTTGTAAAAATTCCTCGTTggtac	This study
Pr185-mutWRKY BamHI-XbaI for	gatccAACGAGGAATTTTTACAACCGCAAcccgg AGGATTTAAAATAAGTAGTTATGGTTGTATC TGTCGTTCTTCTTTCTCTATt	This study
Pr185-mutWRKY BamHI-XbaI rev	ctagaATAGAGAAAGAAGAACGACAGATACAA CCATAACTACTTATTTTAAATCCTccgggTTGC GGTTGTAAAAATTCCTCGTTg	This study
AtTSP(Spm32)	TACGAATAAGAGCGTCCATTTTAGAGTGA	Encinas-Villarejo et al., 2009
GW-WRKY75-CDS F	GGGGACAAGTTTGTACAAAAAAGCAGGCTT CATGGAGGGATATGATAATGGG	This study
GW-WRKY75-CDS R	GGGGACCACTTTGTACAAGAAAGCTGGGTC CTTCCTAGAAAGAAGATAGATTT	This study
EFα F	ATGCCCCAGGACATCGTGATTTCAT	(Kirik et al., 2007)
EFα R	TTGGCGGCACCCTTAGCTGGATCA	(Kirik et al., 2007)
Asc1-pWRKY75 F	GGCGCGCCATTAGTAATAGTTACGTTGTAAC TGC	This study
Xho1-pWRKY75 R	CTCGAGATTCCTAATTATTTGTGGAATC	This study
Asc1-pSCR F	GGCGCGCCAGATTGTGATCCTCTGCAAC	This study
Xho1-pSCR R	CTCGAGGGAGATTGAAGGGTTGTTGG	This study

3'WRKY75 F	CTCGAGTTAATTCTCTCAAAATCTTTTATACC	This study
3'WRKY75 R	GGATCCAAAGATTTCAGGCTCAATTAC	This study

Table S2: Real time PCR results

Gene	Line	Average ± Standard deviation	p-value
GL2	*wrky75-25*	0.54 ± 0.20	4.6E-05
	WRKY75 RNAi	0.51 ± 0.19	1.5E-05
	p35S:WRKY75	1.35 ± 0.30	3.2E-03
TTG1	*wrky75-25*	1.73 ± 1.21	1.1E-01
	WRKY75 RNAi	0.93 ± 0.44	6.1E-01
	p35S:WRKY75	1.83 ± 1.10	5.3E-02
WER	*wrky75-25*	0.93 ± 0.42	7.3E-01
	WRKY75 RNAi	0.79 ± 0.32	2.2E-01
	p35S:WRKY75	1.06 ± 0.35	7.3E-01
CPC	*wrky75-25*	2.70 ± 0.27	2.2E-10
	WRKY75 RNAi	1.34 ± 0.18	7.2E-05
	p35S:WRKY75	0.70 ± 0.17	1.2E-04
TRY	*wrky75-25*	1.72 ± 0.33	3.0E-03
	WRKY75 RNAi	1.31 ± 0.17	6.7E-03
	p35S:WRKY75	0.44 ± 0.06	2.4E-06
RSL4	*wrky75-25*	2.19 ± 0.72	2.6E-04
	WRKY75 RNAi	1.36 ± 0.15	3.6E-05
	p35S:WRKY75	0.62 ± 0.27	4.8E-04

Table S3: Summary of root hair phenotype of *wrky75-25* T1 plants transformed with p*WRKY75*:*YFP-WRKY75* 3'-*WRKY75*

Root hair phenotype	Number of plants
no ectopic root hairs	4
few ectopic root hairs	6
wrky75-25 phenotype	2
total	12

Table S4. Root hair numbers in the patterning zone of the primary roots. Seven-day old *A. thaliana* plants were analysed for each treatment

	T1 *pWRKY75:YFP-WRKY75:-WRKY75* in *Col-0* background		T2 *pWRKY75:YFP-WRKY75:3'-WRKY75* in *wrky75-26* background	
Analyzed seedling	**Root hairs in root hair position (%)**	**Root hairs in non-root hair position (%)**	**Root hairs in root hair position (%)**	**Root hairs in non-root hair position (%)**
Seedling 1	100	0	100	0
Seedling 2	100	0	100	0
Seedling 3	100	0	100	0
Seedling 4	100	0	100	20
Seedling 5	100	0	100	0
Seedling 6	100	0	100	0
Seedling 7	80	0	100	0
Seedling 8	90	0	100	0
Seedling 9	100	0	100	10
Seedling 10	90	0	100	20
Seedling 11	100	0	NA	NA
Average	96.3	0	10	5
Standard deviation	6.74	0	0	8.49

Table S5: Summary of root hair phenotype of *wrky75-25* T1 plants transformed with p*SCR*:*YFP-WRKY75*

Root hair phenotype	**Number of plants**
no ectopic root hairs	9
few ectopic root hairs	5
wrky75-25 phenotype	3
total	17

Fig. S1

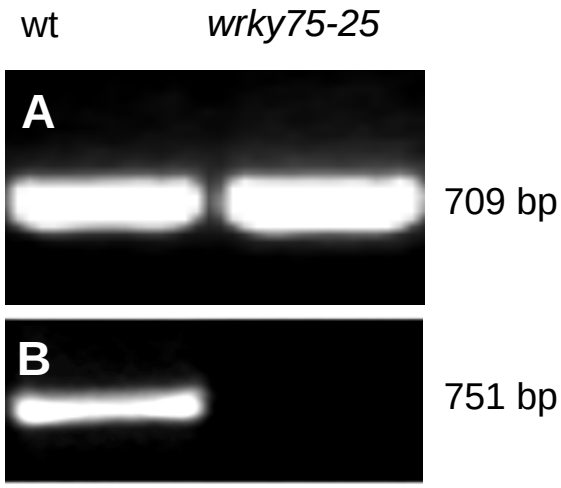

Figure S1: Agrose gel electrophoresis showing RT-PCR for the *wrky75-25* mutant. RNA was extracted from plants growing on MS media. (a) PCR product of the *GTP BINDING ELONGATION FACTOR* (EFα1) cDNA. (b) PCR product of the *WRKY75* cDNA. Primers used to amplify the fragments were GW-WRKY75-CDS F and GW-WRKY75-CDS R for WRKY75 cDNA, EFα F and EFα R for *EFα1.*

Fig. S2

Figure S2: Nucleotide sequence showing the position of *T-DNA* inserion in *wrky75-25* mutant. The *T-DNA* is inserted 143bp downstream of the stop codon. Dots indicate that the sequence of the *spm* element is not fully sequenced. The primers used: AtTSP(Spm32) and 3’WRKY75 R. Exon=black, intron: pink, STOP codon: blue, green SPM element, “…..” not sequenced SPM, red 3’UTR.

Fig. S3

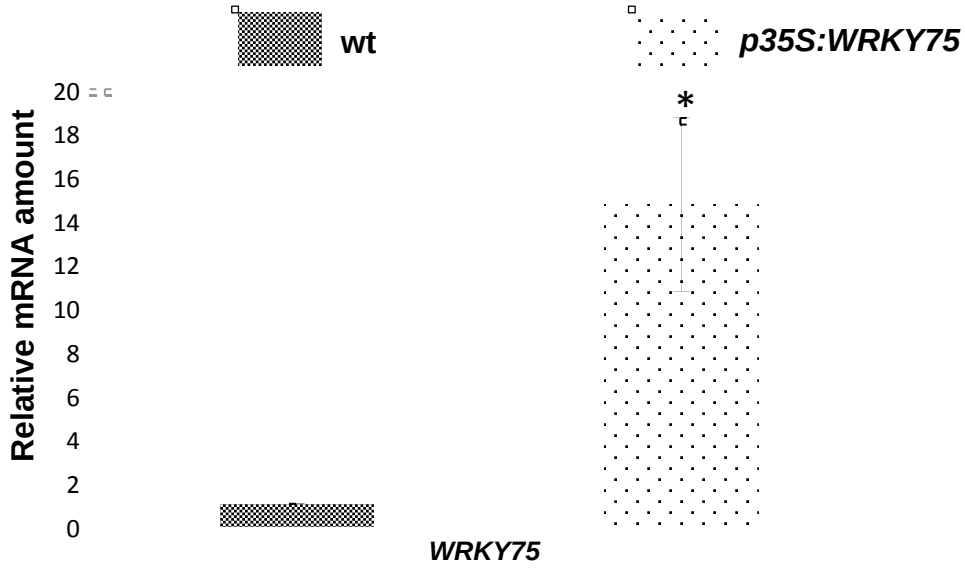

Figure S3: qRT-PCR of mRNA obtained from root hair-patterning zone of 7-day old seedlings grown on MS media. The expression levels of genes of wt plants was set to one and subsequently used to calculate the relative changes of *WRKY75* expression of P_{35S}:*WRKY75* plants. Error bars indicate the standard deviation of three different biological replicates. * indicates statistical significance: P value <0.005 (T-test).

Fig. S4

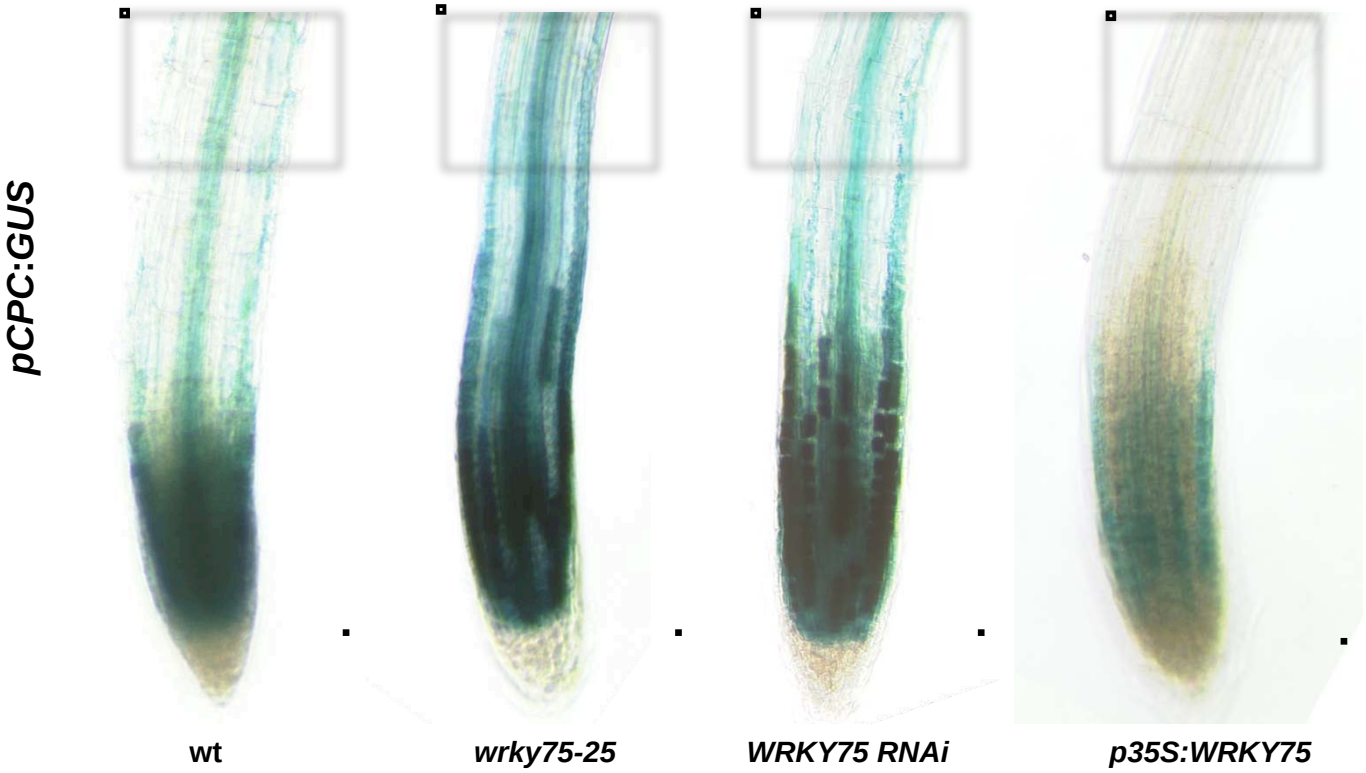

Fig. supp.4: Expression analysis of CPC in the stele.
Expression of CPC is monitored in pCPC:GUS transgenic plants as indicated. Squares mark the analyzed region. Seedlings were stained for 8 hours. Scale bar= 50 µm.

Fig. S5

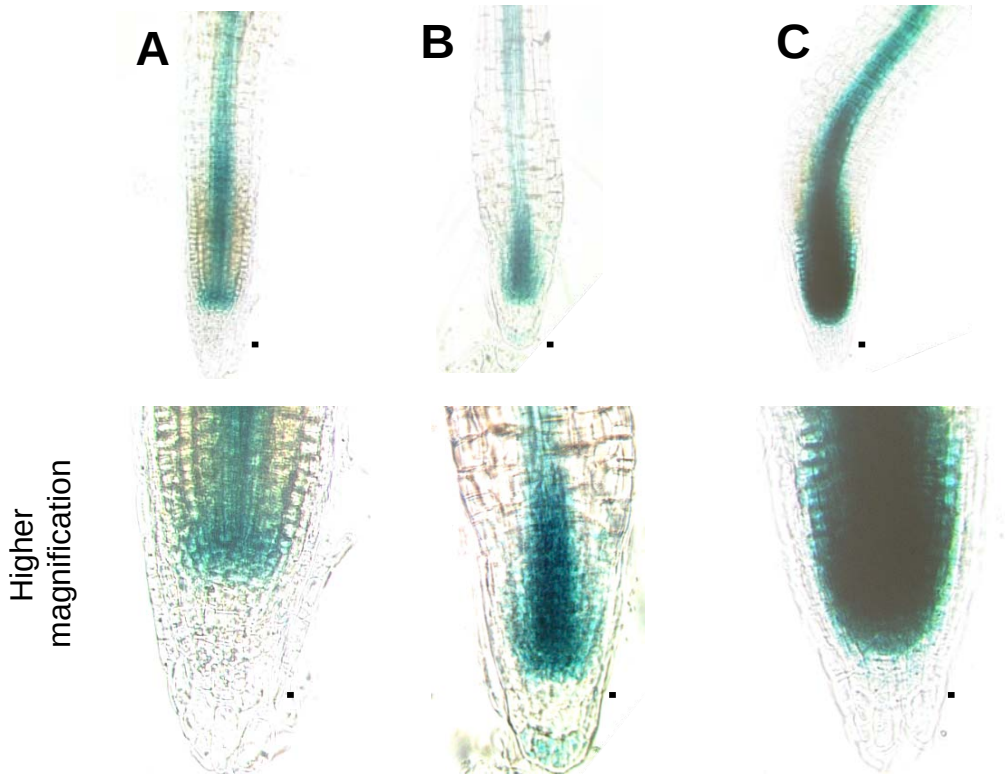

Figure S5: Time series for *pWRKY75:GUS:3'WRKY75* GUS staining. The seedlings were GUS-stained for 9, 12 and 24 hours labled as (A), (B) and (C) respectively. Scale bar= 50 µm

Fig. S6

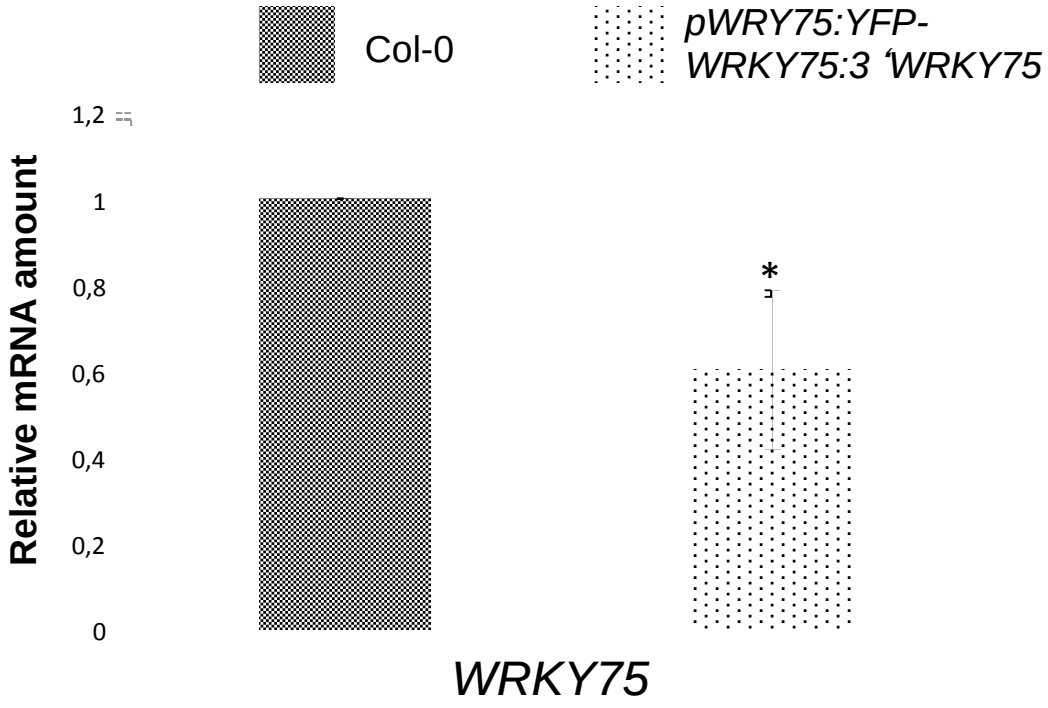

Figure S6: qRT-PCR of mRNA obtained from root hair-patterning zone of 7-day old seedlings grown on MS media The expression levels of genes of wt plants was set to one and subsequently used to calculate the relative changes of *WRKY75* expression of pWRKY75:YFP-WRKY75:3'WRKY75 plants. Error bars indicate the standard deviation of three different biological replicates. * indicates statistical significance: P value <0.005 (T-test).

Fig. S7

Fig. S7: 3D reconstruction of *pWRKY75:YFP-GUS:3'WRKY75*.
YFP signal shows that *WRKY75* is expressed in the stele and vascular tissue of the primary root. Scale bar= 40 µm.

Fig. S8

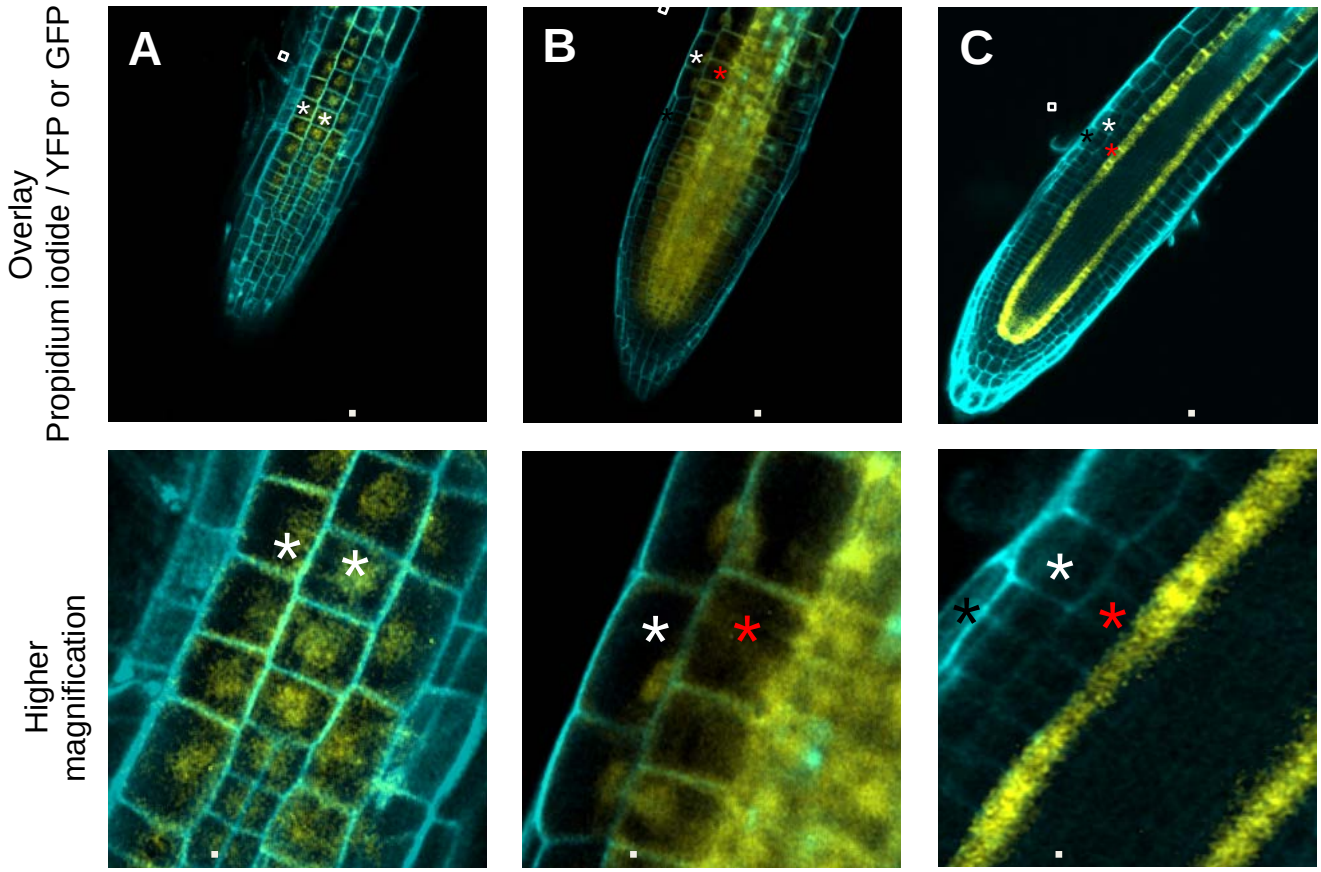

Fig. S8: Movement of WRKY75 when expressed under the *SCR* promoter. A) Epidermal section of *pSCR:YFP-WRKY75* B) Median section of *pSCR:YFP-WRKY75* . C) Median section of *pSCR:GFPer.* Squares mark the region shown at a higher magnification in the figure below.Black stars point at lateral root cap cells, white stars point at epidermal cells, red stars point at cortical cells. Scale bar=50 µm.