

Supplementary material

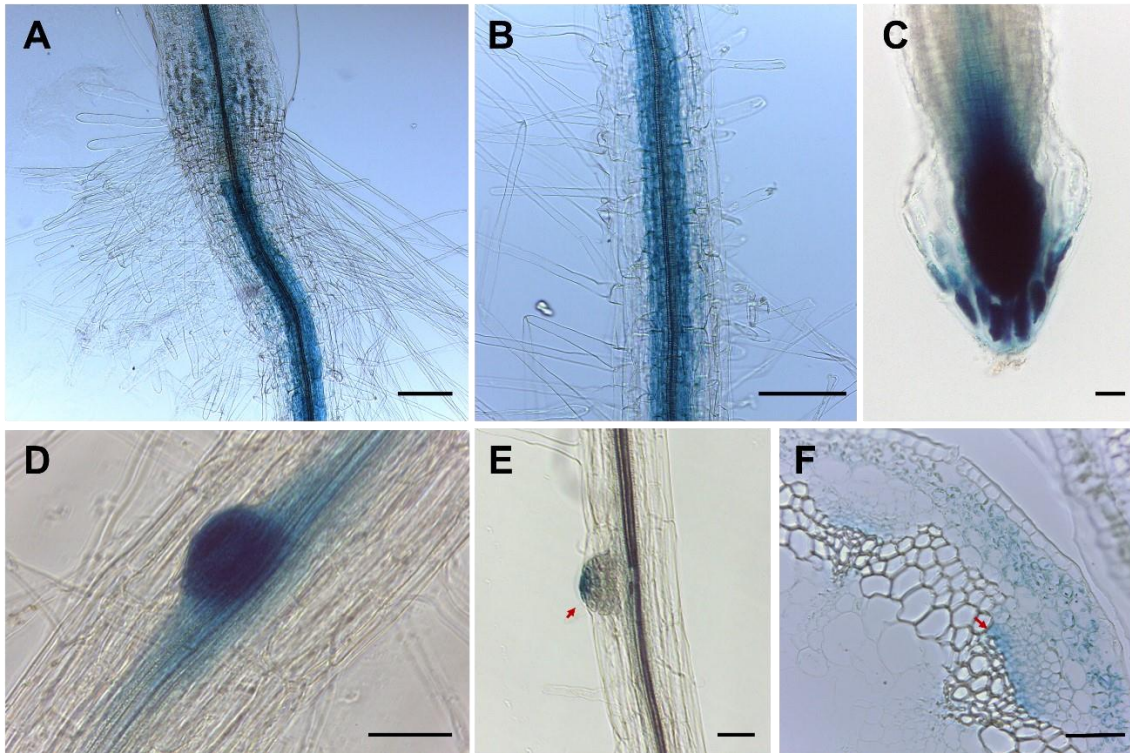


Figure S1. *pWIP::GUS* expression in roots and stem. A) *pWIP2::GUS* expression in the vasculature of the hypocotyl, root and the region between them at 9 dag. B) *pWIP2::GUS* expression in the vasculature of the mature root (9 dag). C) *pWIP2::GUS* expression in the root apical meristem and surrounding tissues. D) *pWIP2::GUS* expression in an emergent lateral root. E) *pWIP4::GUS* expression in the incipient root apical meristem (red arrow) of an emergent lateral root. F) Stem transversal section showing *pWIP2::GUS* expression in vascular bundle (red arrow). Scale bars represent 50 μm .

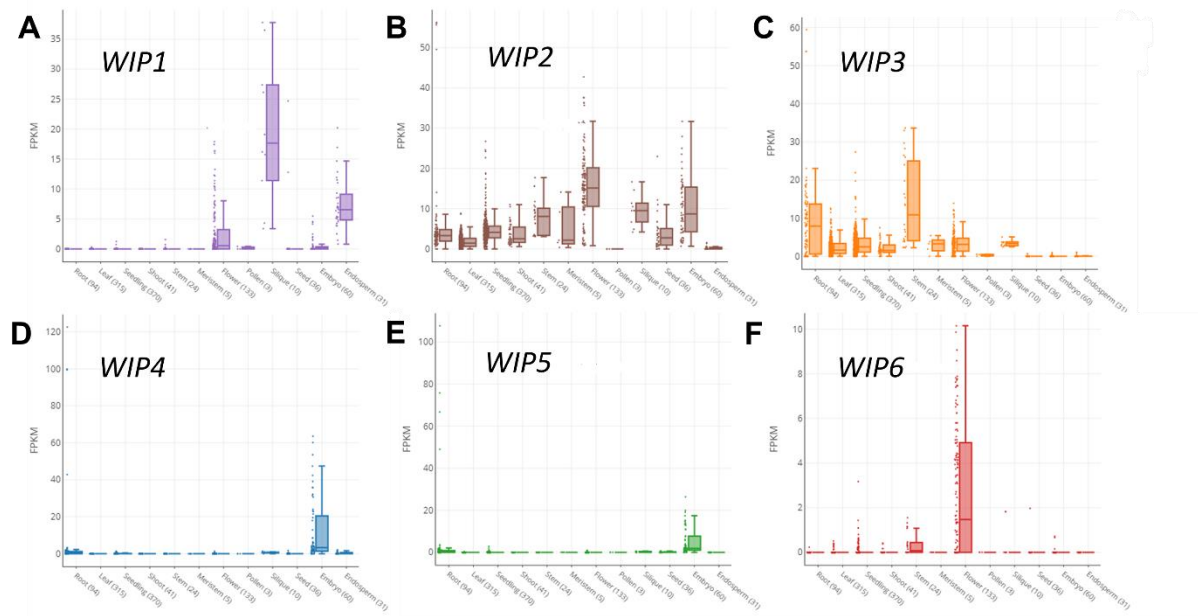


Figure S2. RNA expression levels of *WIP* genes in different tissues. A) AT1G34790 (*WIP1*), B) AT3G57670 (*WIP2*), C) AT1G08290 (*WIP3*), D) AT3G20880 (*WIP4*), E) AT1G51220 (*WIP5*), F) AT1G13290 (*WIP6*). Data obtained from the ARS database [21]

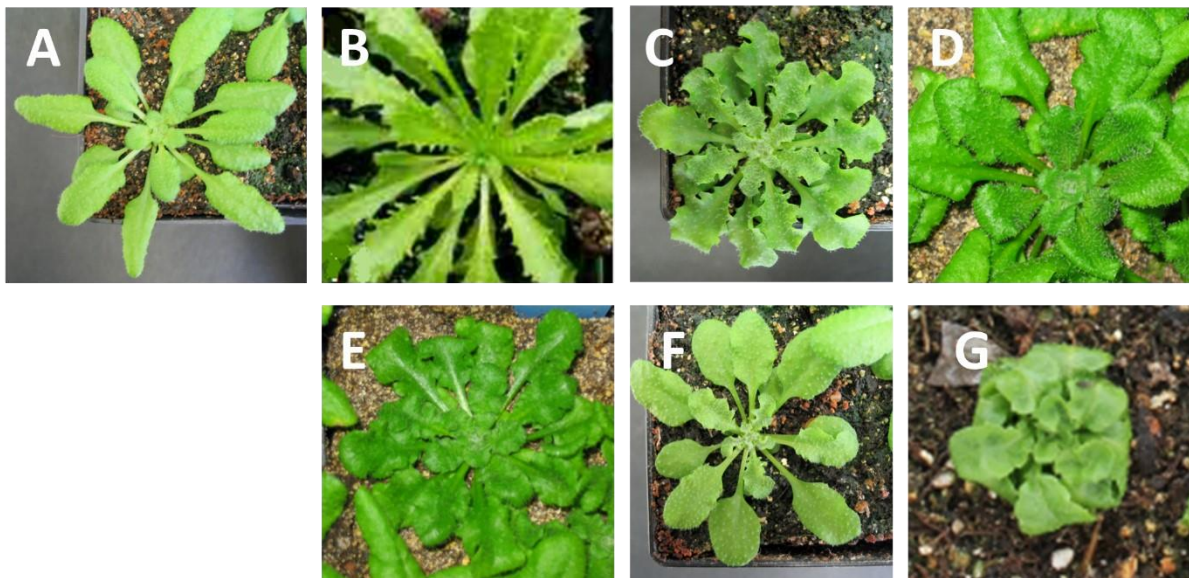


Figure S3. Leaf edge phenotypes of *WIP* overexpressors. A) Col-0, B) 35S::*WIP1*, C) 35S::*WIP2*, D) 35S::*WIP3*, E) 35S::*WIP4*, F) 35S::*WIP5*, G) 35S::*WIP6*. Images are presented at different magnifications, to better observe leaf edge alterations, and are not comparable in size.

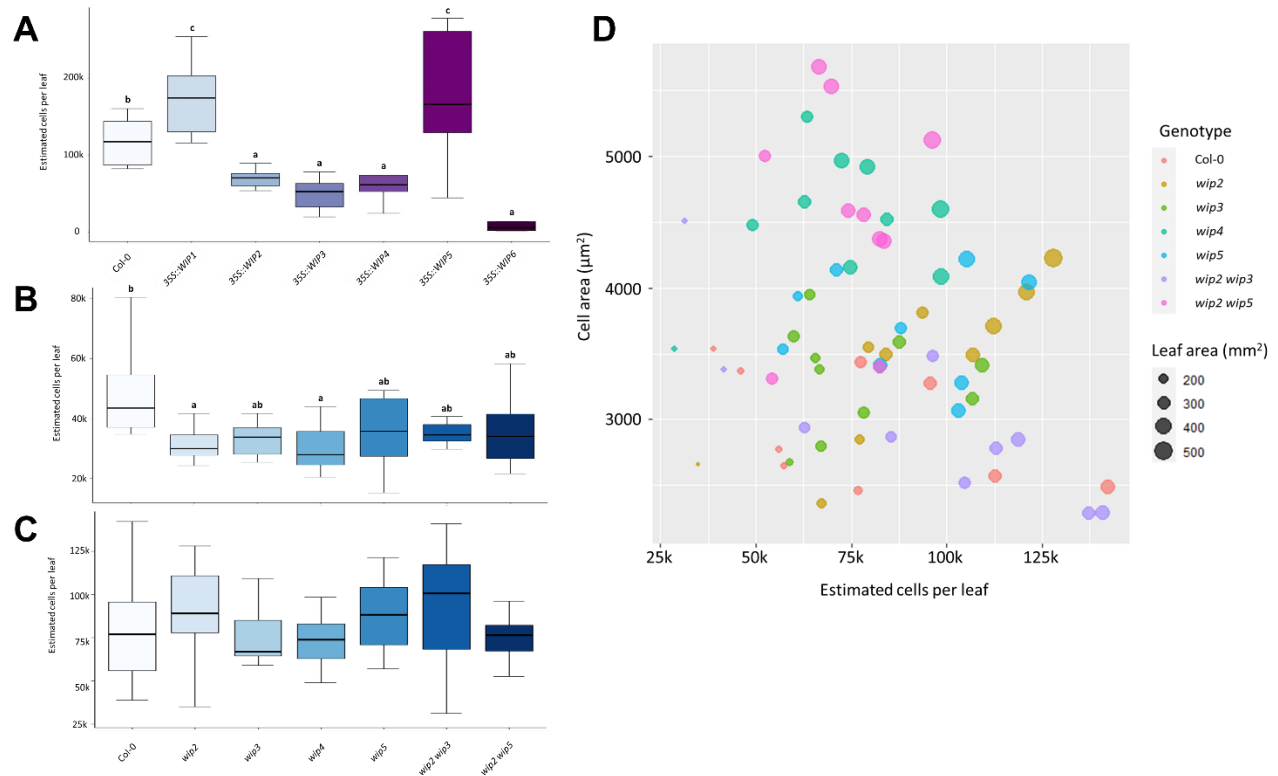


Figure S4. Estimated cell number in *wip* mutants. A) Estimated cell number per leaf at 35 dag in wild type plants and *WIP* overexpressors. B) Estimated cell number per leaf at 30 dag in wild type plants and *wip* mutants. Letters represent different statistic groups. C) Estimated cell number per leaf at 60 dag in wild type plants and *wip* mutants. D) Bubble plot representing the integration of leaf area, leaf cell area and estimated cell number data per leaf, of wild type and *wip* mutant plants at 60 dag.

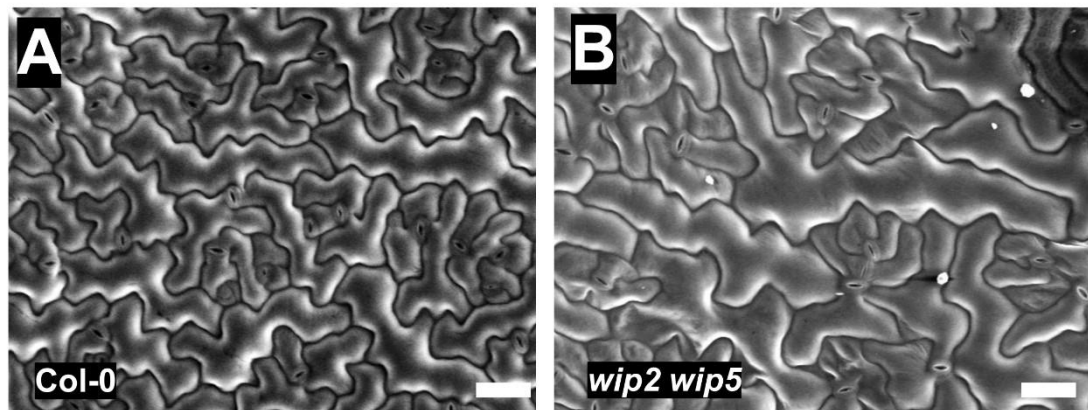


Figure S5. Representative SEM micrographs of leaf pavement cells in wild type (A) and in *wip2 wip5* (B) leaves. Scale bars represent 40 μm.

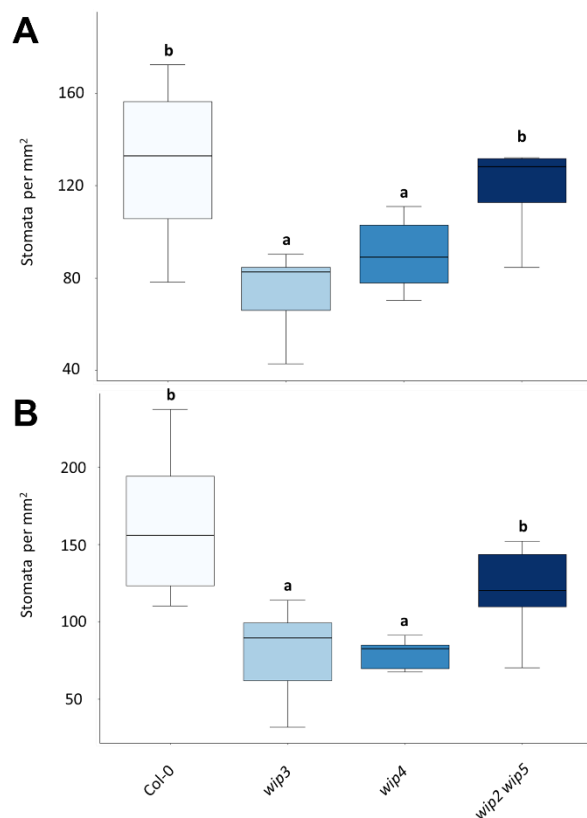


Figure S6. Stomatal density in *wip3*, *wip4* and *wip2 wip5* mutants. A) Stomatal density of *wip* mutants at 30 dag. B) Stomatal density of *wip* mutants at 60 dag. K.W. test p-value < 0.001 Letter represent different statistical groups. (Dunn's test).

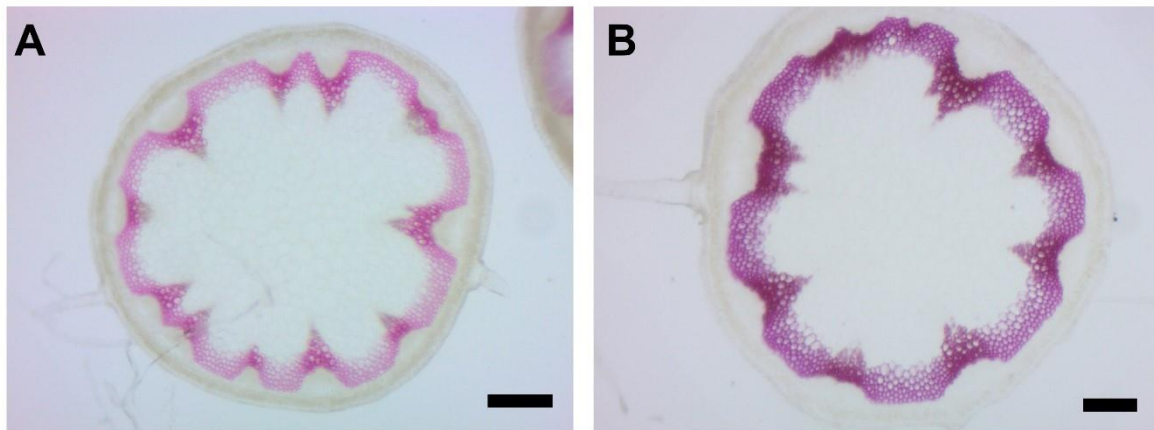


Figure S7. Representative image of stem transverse sections, stained with phloroglucinol, where vascular bundles can be observed. Col-0 (A), and *wip2 wip5* (B) stems. Scale bars represent 200 μm.

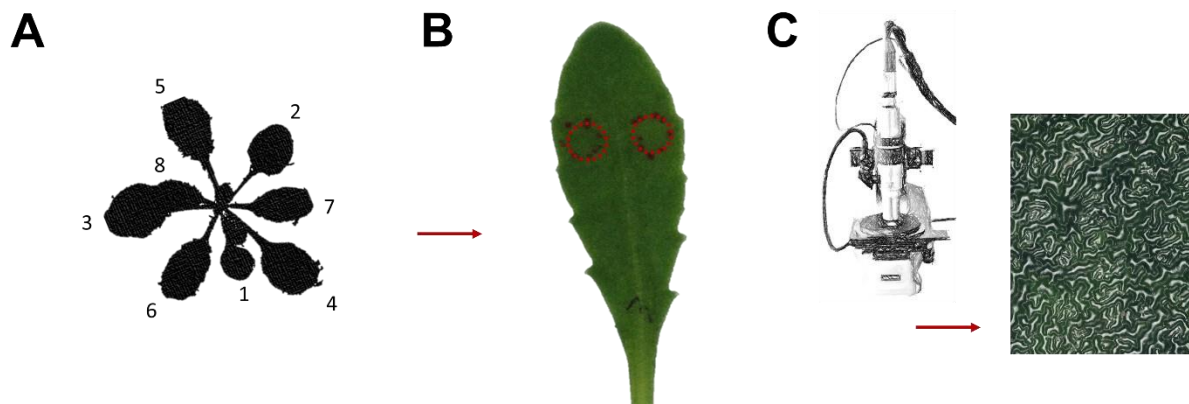


Figure S8. Leaf imaging experiments workflow. A) Leaves were numbered as depicted from older to younger, the 8th leaf was collected at 30 dag and the 10th at 60 dag. B) the same region was micrographed in every leaf, two regions per leaf, in each side of the central vein C) micrographs were taken with a Keyence digital microscope, and images analyzed.

Table S1. *pWIP::GUS* expression.

Line	SAM	RAM	Siliqua base	Root vasc.	Cotyledon vasc.	Leaves vasc.	Hypocotyl vasc.	Inflorescence stem vasc.
<i>pWIP1::GUS</i>			✓		✓			✓
<i>pWIP2::GUS</i>	✓	✓	✓	✓	✓	✓	✓	✓
<i>pWIP3::GUS</i>	✓		✓	✓	✓	✓	✓	✓
<i>pWIP4::GUS</i>	✓	✓	✓					✓
<i>pWIP5::GUS</i>		✓	✓					✓
<i>pWIP6::GUS</i>			✓					✓

Table S2. Primers used for GUS and OE constructs and mutant analyses.

Gene Alias	Gene ID	Experiment	Primer Name (site introduced)	Sequence	Fragment length (bp)	
WIP3	AT1G08290	promoter	S287 (EcoRI)	TTTGAATTCTAGTACTATTGTATTGG	1528	
		GUS line	S288 (NcoI)	TCTCCATGGCTCGCTTTCTCTCCTCTCTTTCAC		
WIP4	AT3G20880	promoter	S311 (EcoRI)	AGTGAATTCATCATGGTAAGCACCTATTAAGG	1280	
		GUS line	S312 (XhoI)	TTACTCGAGAAGATAGTGAGAAAAAAGAAGAAGAAG		
WIP5	AT1G51220	promoter	S307 (ClaI)	AGAATCGATACGAGACCACCAAAGCAAGTGC	1172	
		GUS line	S308 (NcoI)	AGACCATGGCTCTGAGGAGAAGACAAAGAAG		
WIP6	AT1G13290	promoter	S319 (EcoRI)	ATAGAATTCTAATAATATCATCATCACTGAGACTATCAC	1013	
		GUS line	S310 (NcoI)	TCTCCATGGAGTAGAGAGAAAGAGAGATGA		
WIP5	AT1G51220	CDS cloning	S245 (NcoI)	AGACCATGGCTTCTAATCCAGCTTGTTCTGAATCTC	1014	
			S267 (SacI)	TATGAGCTCATTGCTCGATATCAGAAGCAGCATC		
WIP2	Primer name				Allele	
	AT3G57670	Genotyping gene	Sdf222	TCTCTTCACCATGACTGATCC	ntt-2	
			Sdf223	GCTATTTAGACTGCATTGACTC		
		Genotyping insertion	IC77	CTTACCTTTTTTCTGTAGTG		ntt-3
			Sdf277	CATCGTCATCTTCTCCTCTCC		
			IC51	ATTTTGCCGATTCGGAAC		
			Sdf223	GCTATTTAGACTGCATTGACTC		
		AT1G08290	Genotyping gene	IC13	AGGATGATGTGGTTACCCTCC	
				IC14	TATTGCGAATGATACACCAACCG	
	Genotyping insertion		IC13	AGGATGATGTGGTTACCCTCC		
			IC51	ATTTTGCCGATTCGGAAC		
	AT3G20880	Genotyping gene	IC60	GAACTGCGCAAAAATCAAGAG		
			IC61	TCCCTCTCACGCATCTACAAC		
		Genotyping insertion	IC60	GAACTGCGCAAAAATCAAGAG		
			IC62	ATAATAACGCTGCGGACATCTACATTTT		
	AT1G51220	Genotyping gene	Sdf299	CCTCAGAGTCATGTCTAATCCAG		
			Sdf300	TCTTATTGCTCGATATCAGAAGC		
		Genotyping insertion	IC51	ATTTTGCCGATTCGGAAC		
			Sdf300	TCTTATTGCTCGATATCAGAAGC		
	WIP1	AT1G34790	transcript	S152	ATGGAGTCACCACCACTATAC	
WIP2	AT3G57670	transcript	GH01	AAAAAACAAAGTCTCGGAGAC		
			GH45	ATTTAGACTGCATTGACTCATG		
WIP3	AT1G08290	transcript	S183	ATTCTTATGAGACGAAAGGC		
			GH46	ACTCTGTGGTGACGCATTC		
WIP4	AT3G20880	transcript	S243	CTATTTTCCACTGTTTTGTCACATCG		
			GH47	ATTCTTGCTGCTCGACATCAG		
WIP5	AT1G51220	transcript	S245	TCTAATCCAGCTTGTTCTGAATCTC		
			GH48	ATTGCTCGATATCAGAAGCAG		
WIP6	AT1G13290	transcript	S247	TATAATAATAACCAATATAGCTTCTCC		
			GH49	AGTAATTGTCATCAGAAATCTGAC		

Table S3. Mutant *wip* lines used in this study.

<i>wip</i> mutants	Line	Gene ID
<i>wip2 (ntt)</i>	[▮] SM_3_16705	AT3G57670
<i>wip3</i>	*SALK_072471	AT1G08290
<i>wip4</i>	^ϕ gabi_176E02	AT3G20880
<i>wip5</i>	*SALK_114838	AT1G51220
<i>wip2wip3</i>	*SALK_007406C, *SALK_072471	AT3G57670, AT1G08290
<i>wip2wip5</i>	[▮] SM_3_16705, *SALK_114838	AT3G57670, AT1G51220

[▮] [22], *[23], ^ϕ[24].