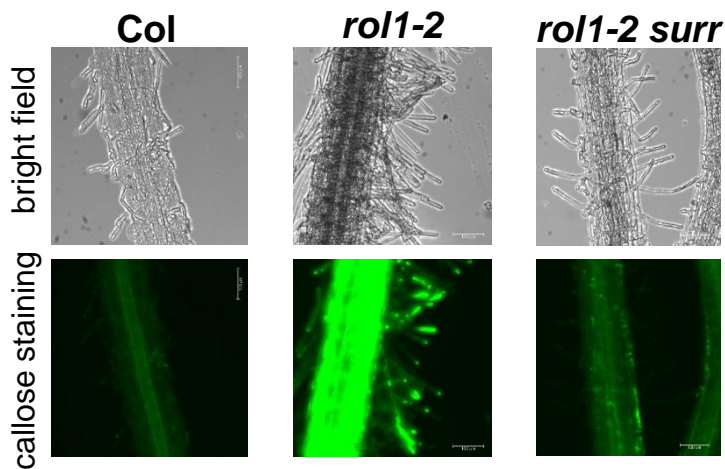


Supplementary Data

Suppl Figure S1



Suppl Figure S1

Ectopic deposition of callose in *rol1-2* roots.

Roots of seedlings were grown for 6 days and callose was stained with aniline blue. In contrast to the wild type, *rol1-2* roots revealed strong staining with aniline blue that was reduced in *rol1-2 surr* roots with only interspersed aniline staining. The overexposure was used to better visualize the remaining aniline staining in the *rol1-2 surr* double mutant. Bright field and fluorescence microscopic picture are shown on top and bottom row, respectively. Bar=100 μ m.

Suppl Fig S2

		surr	rao1-1	
Arab	129	YTVKSLWQLLNGLNYLHSNWIHRDLKPS		158
oryza	133	YTVKSLWQLLNGLNYLHSNWIHRDLKPS		162
vitis	136	YTVKSLWQLLNGLNYLHSNWIHRDLKPS		165
tobacco	129	YTVKSLWQLLNGLNYLHSNWIHRDLKPS		158
chlamy	111	YTVKTVMWEHLLNGLSYMHOHWVHRDLKPS		140
human	126	SMVKSLWQILLDGIHYLHANWVLRDLKPA		155
		::::*:*: *:* :*:***:		

Suppl Figure S2 The *surr* mutation affects a conserved residue in CDK8.

CDK8 protein alignment of different species shows conservation of the Gly141 changed in the *surr* mutant to Glu. The species compared are *Arabidopsis thaliana* (Arab), *Oryza sativa* (Oryza), *Vitis vinifera* (Vitis), *Nicotiana tabacum* (tobacco), *Chlamydomonas reinhardtii* (chlamy), *Homo sapiens* (human).

Asterisks indicate identical and colons highly similar residues in all species. Identical residues are also shown with black background.

Suppl Table S1

primers used for genotyping

Suppl Data Table S1

Primer name	Primer sequence	allele, polymorphism
<i>rol1-2_F</i>	TGAGGCGAACATCAAGTTTGT <u>CGACTGCA</u>	<i>rol1-2</i>
<i>rol1-2_R</i>	TGACTTGGTTTTTCAGATAAAGT	<i>Pst</i> I cuts wild type
<i>cdk8_EMS_F2</i>	GACTGCTATCCGCGAGATCATG	<i>surr</i>
<i>cdk8_EMS_R2</i>	TCCAATTACTGTGAAGATAGTT <u>GAAT</u>	<i>Eco</i> RI cuts mutant
<i>fls15_F</i>	GATTGAGTACATCACTTCAGGTCCA <u>ATT</u>	<i>ndpk2</i>
<i>NDPK2_RT_R</i>	CAATCTCACGCTTGCCGTTTTTCAG	<i>Mfe</i> I cuts mutant
<i>Man2_mut_F</i>	GGTGAGTATATTTCCCTGTCCAG	<i>man2</i>
<i>Man2_mut_R</i>	GAAGTGAATGAGCCAATAGCAG	<i>Nco</i> I cuts wild type
<i>tetra_Mut_F2</i>	CACCACATGTTTCGACCATTTGTC	<i>tpr</i>
<i>tetra_Mut_R</i>	AAGAGAAGCTAGTGTCTCCTGTCC <u>CAG</u>	<i>Bst</i> NI cuts wild type
<i>rao1-1_F</i>	TATCTTCACAGTAATTGGATTAT <u>CTGCA</u>	<i>rao1-1</i>
<i>rao1-1_R</i>	TGCTTCGAACCAAGAAGCAGCTC	<i>Pst</i> I cuts wild type
<i>rao1-2_F2</i>	AAGACTCCGCCTAAAAGACCTA <u>G</u> T	<i>rao1-2</i>
<i>rao1-2_R</i>	ATAGAGATCGTACTCGGCATAATCAAA	<i>Rsa</i> I cuts mutant
<i>ACTIN2F</i>	AATGAGCTTCGTATTGCTCC	
<i>ACTIN2R</i>	GCACAGTGTGAGACACACC	

Primers used for genotyping. Underlined positions are mutated positions to introduce restriction site polymorphism between wild type and mutant.