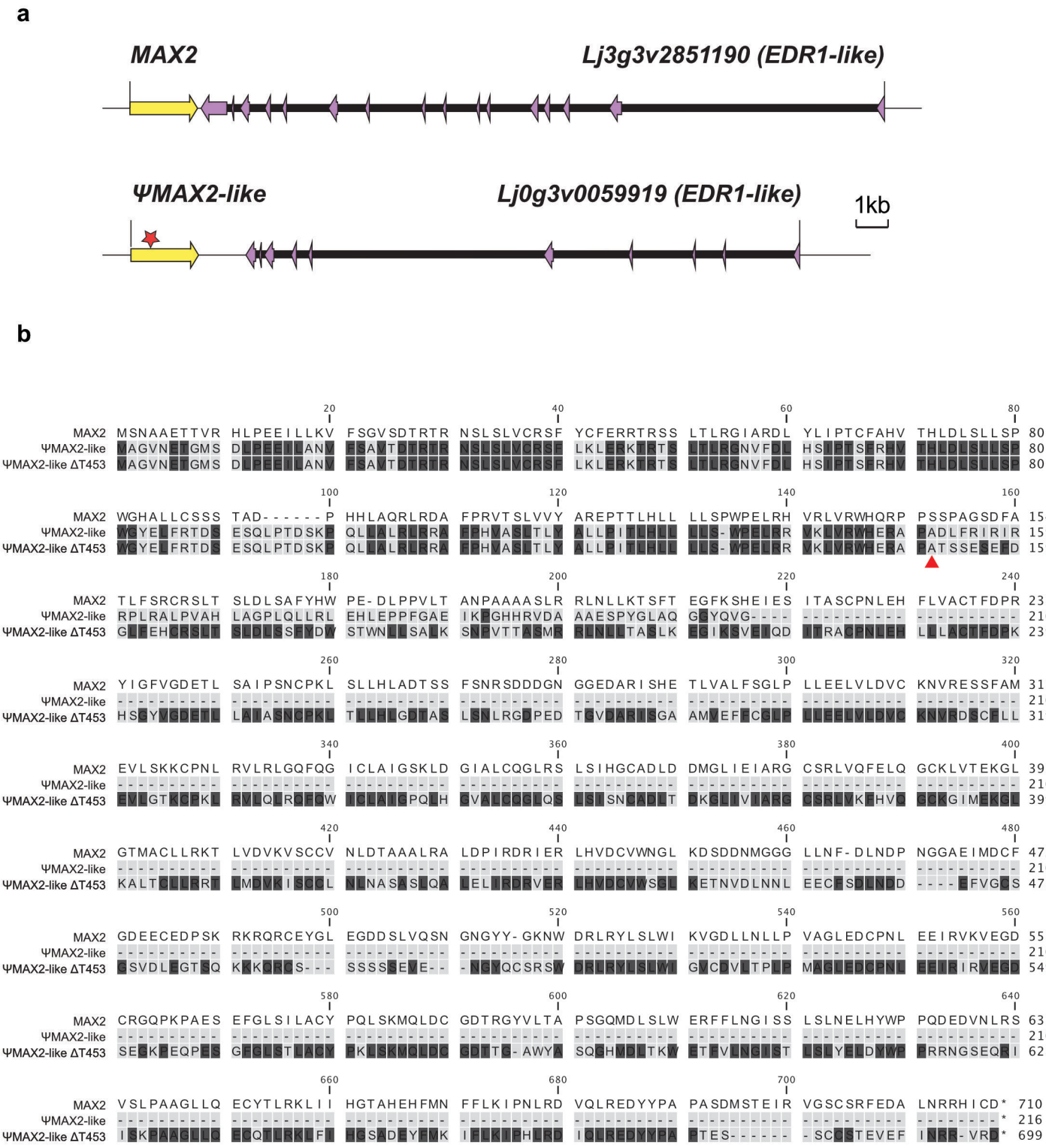
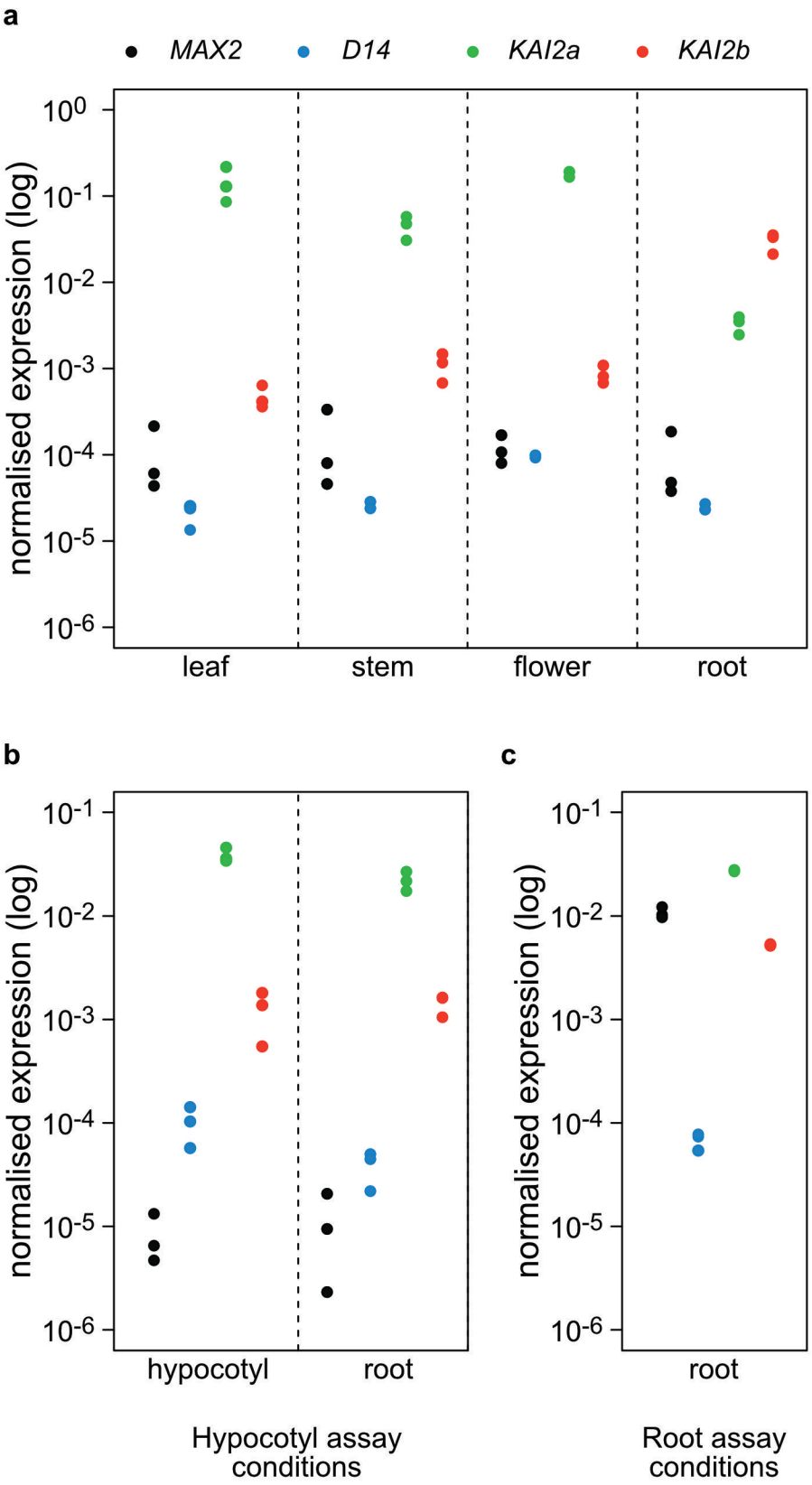


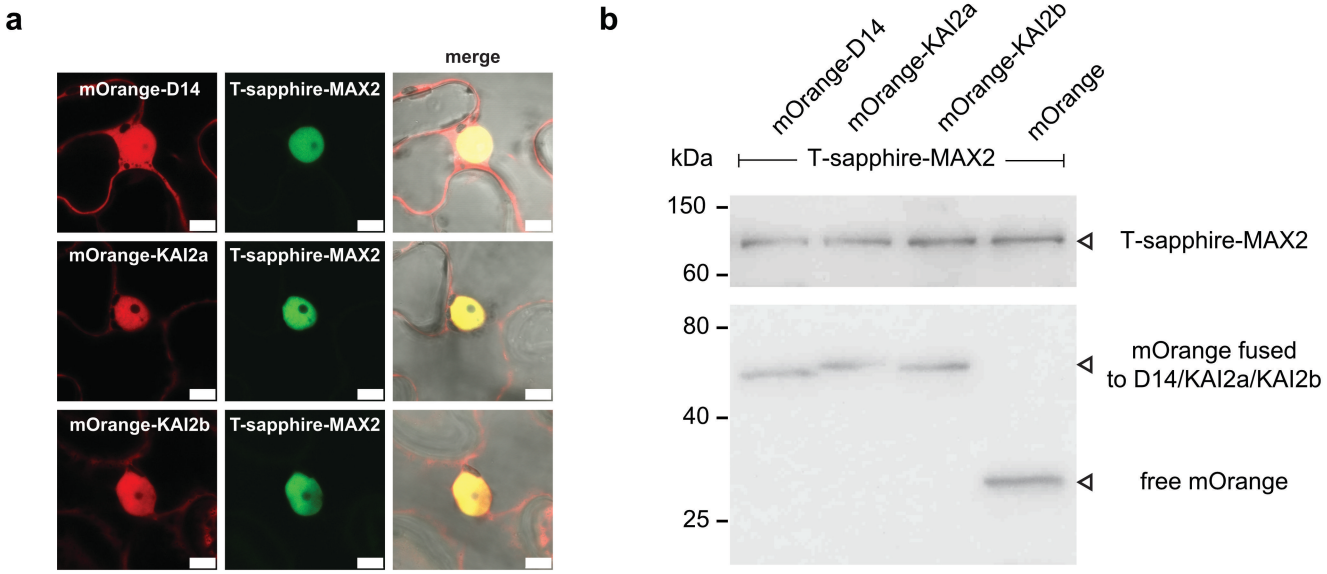
Supplementary Figure 1 | MAX2-like underwent pseudogenization.

(**a**) Schematic representation of the synthenic regions containing the *MAX2* and *MAX2-like* loci in *L. japonicus*. Coloured arrows and black lines show exons and introns respectively. (**b**) Protein alignment of LjMAX2, LjMAX2-like and an artificial LjMAX2-like with a deletion of the thymine at the position 453 in the coding sequence (LjMAX2-like ΔT453). Position of the nucleotide deletion is indicated in the translated sequence by a red triangle. Amino-acid conservation between MAX2 and MAX2-like is indicated by a dark background.



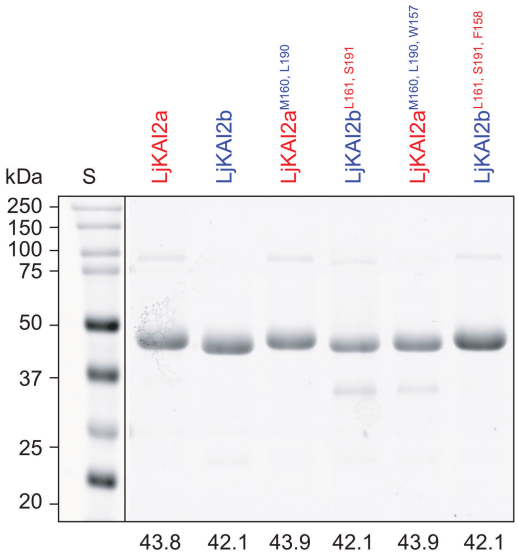
Supplementary Figure 2 | Organ-specific accumulation of *D14*, *KAI2a*, *KAI2b* and *MAX2* transcripts.

(**a-c**) Transcript accumulation in wild-type of *D14*, *KAI2a*, *KAI2b* and *MAX2*, in (**a**) leaf, stem, flower and root of plants grown in pots, and in (**b**) hypocotyl and roots of 1 wpg plants grown on Petri dishes in 8h light / 16h dark cycles, and in (**c**) roots of 2 wpg plants grown on Petri dishes in 16h light / 8h dark cycles (n = 3).



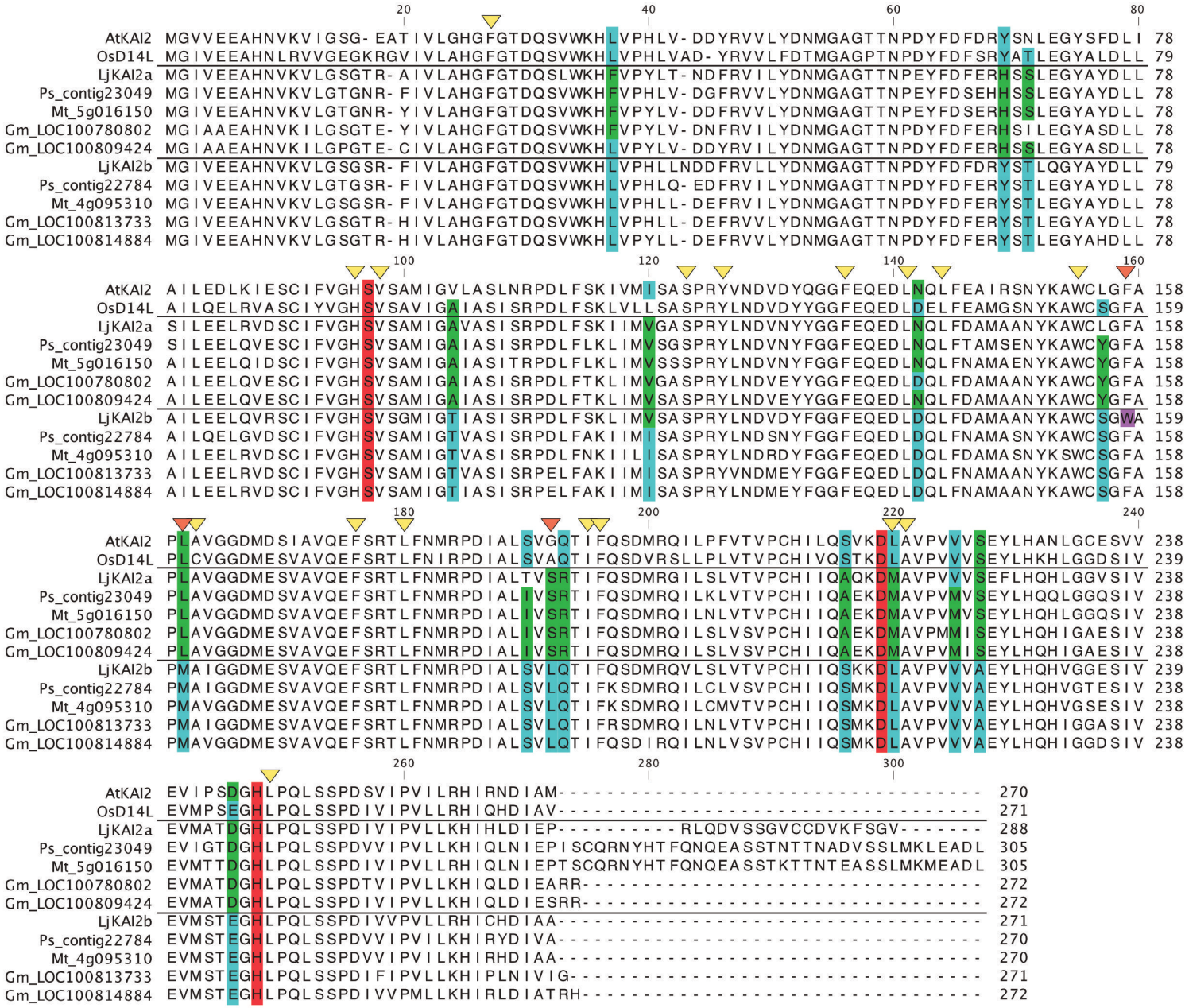
Supplementary Figure 3 | Subcellular localisation of LjD14, LjKAI2a, LjKAI2b and LjMAX2 in *Nicotiana benthamiana* leaves.

(**a**) Subcellular localization of LjD14, LjKAI2a, LjKAI2b and LjMAX2 in *N. benthamiana* leaf epidermal cells. LjD14, LjKAI2a and LjKAI2b are N-terminally fused with mOrange. LjMAX2 is N-terminally fused with T-Sapphire. Scale bars: 25 μm. (**b**) Western blot of protein extracts from *N. benthamiana*, showing that the mOrange tag fused with LjD14, LjKAI2a and LjKAI2b was not cleaved at detectable amounts.



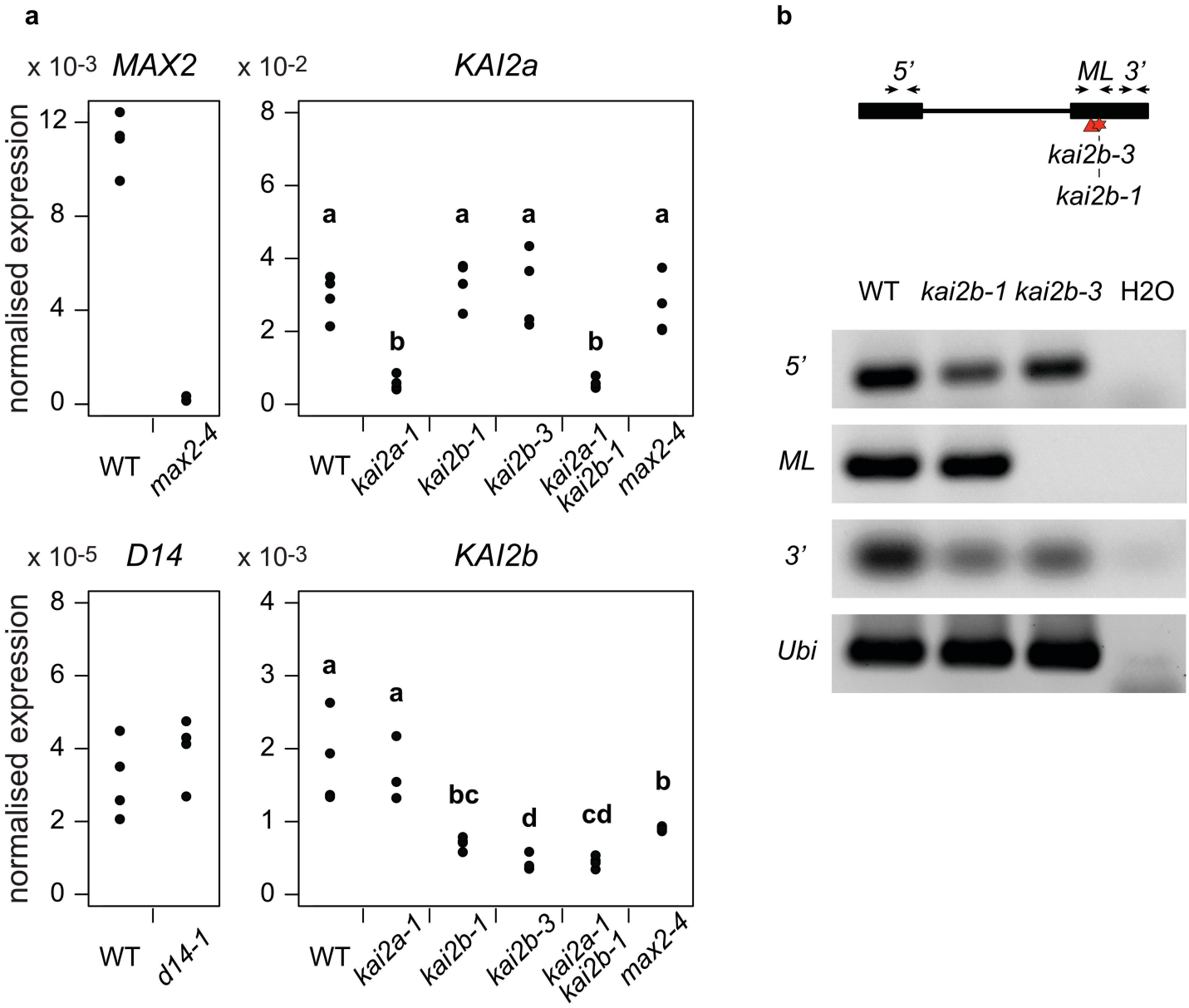
Supplementary Figure 4 | SDS-PAGE of purified SUMO fusion proteins.

200 pmol (approx. 8 µg) of purified proteins were separated by 12% SDS-PAGE containing 2,2,2 trichlorethanol as a vizualization agent. Below each lane is the calculated protein size in kiloDaltons. S, protein size standards (Precision Plus Dual Color Standards, Bio-Rad #1610394) with corresponding sized in kDa shown on the left. Optimal exposures of recombinant proteins and size standards were taken separately under UV transillumination and red epi-illumination, respectively. The two images were merged in post-processing, and the junction between them is indicated by a vertical line.



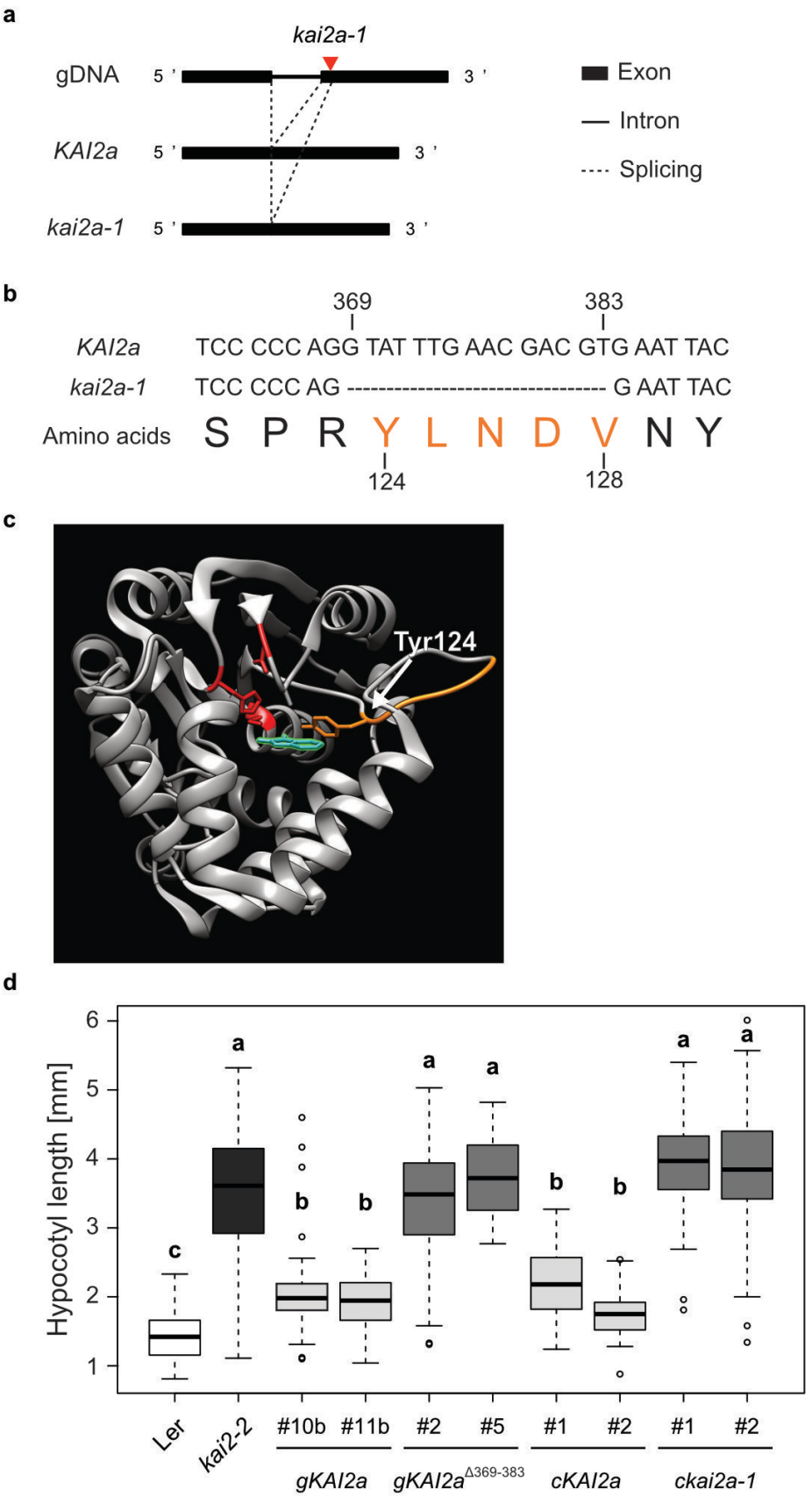
Supplementary Figure 5 | Amino acid differences between the legume KAI2a and KAI2b clades.

Protein sequence alignment of KAI2a and KAI2b homologs from the legumes *Lotus japonicus, Pisum sativum, Medicago truncatula* and *Glycine max*, in comparison with Arabidopsis KAI2 and rice D14L. Residues conserved within the KAI2a and KAI2b clades but different between these clades are coloured in green and blue. Residues of the catalytic triad are coloured in red. A non-conserved tryptophan in LjKAI2b located in the protein cavity is coloured in violet. Yellow and orange triangles indicate amino acid residues located in the ligand-binding cavity of the proteins. Orange triangles indicate the three amino acids responsible for differences in GR24$^{ent\text{-}5DS}$-binding between LjKAI2a and LjKAI2b.



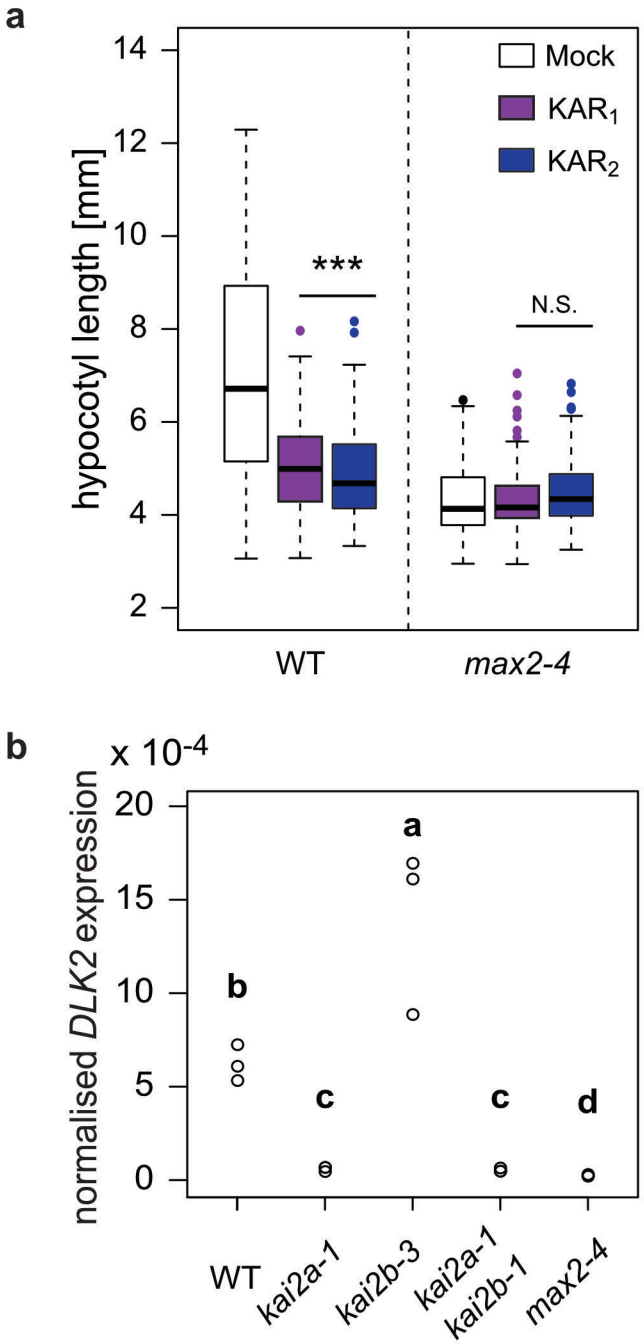
Supplementary Figure 6 | Transcript accumulation in the *L. japonicus* KAR and SL receptor mutants.

(**a**) qRT-PCR based transcript accumulation of *LjKAI2a* and *LjKAI2b*, in roots of wild type and *kai2a-1*, *kai2b-1*, *kai2b-3*, *kai2a-1 kai2b-1* and *max2-4* as well as *LjMAX2* and *LjD14* in *max2-4* and *d14-1*, respectively (n=4). (**b**) *LjKAI2*b transcript accumulation in wild-type, *kai2b-1* (stop codon) and *kai2b-3* (LORE1 insertion) mutants by semi-quantitative RT-PCR using primer pairs located 5' and 3' of the mutations, as well as flanking (ML) the mutations. Transcript accumulation of the housekeeping gene Ubiquitin is also shown.



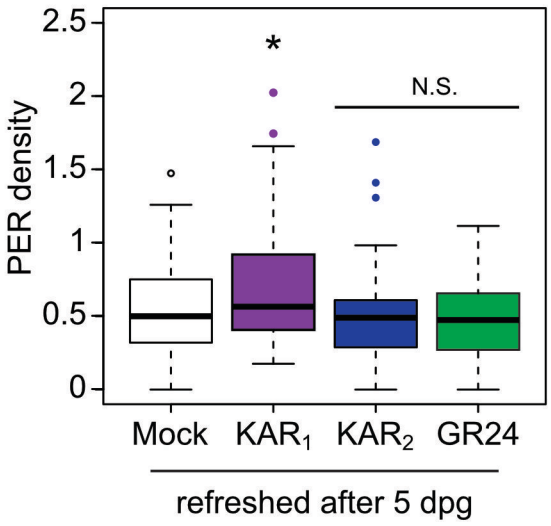
Supplementary Figure 7 | Characterisation of the *kai2a-1* allele.

(**a**) Schematic representation of mis-splicing caused by the LORE1 insertion in the *kai2a-1* mutant. (**b**) cDNA alignment showing the absence of nucleotides 369 to 383 in the *kai2a-1* transcript, causing a deletion of amino acids 124 to 128 (orange). (**c**) Protein model of LjKAI2a based on the AtKAI2-KAR_1 complex 4JYM [5] showing KAR_1 in green, residues of the catalytic triad in red and the amino acids missing in a hypothetical LjKAI2a-1 protein in orange. (**d**) Hypocotyl elongation at 6 dpg in Arabidopsis *kai2-2* mutants transgenically complemented with genomic and the cDNA of wild-type *LjKAI2a* and *Ljkai2a-1* driven by the *AtKAI2* promoter (n = 75-106). Plants were grown in 8h light / 16h dark cycles. Letters indicate different statistical groups (ANOVA, post-hoc Tukey test).



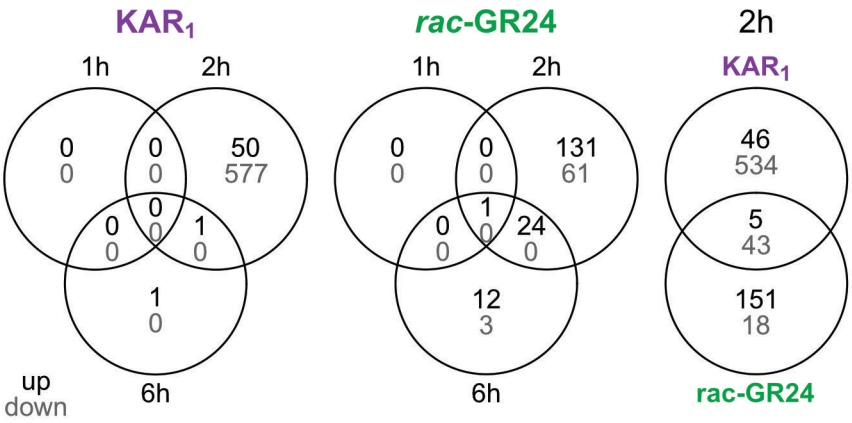
Supplementary Figure 8 | Suppression of *L. japonicus* hypocotyl growth by KAR treatment depends on *MAX2*.

(**a**) Hypocotyl length of wild-type and *max2-4* seedlings one-week post germination after treatment with solvent (Mock), 1 µM KAR_1, 1 µM KAR_2 (n = 66-96). Asterisks indicate significant differences of the compounds versus mock treatment (ANOVA, post-hoc Dunnett test, N.S.>0.05, *≤0.05, **≤0.01, ***≤0.001). (**b**) Comparison of *DLK2* transcript accumulation in hypocotyls of mock treated wild-type, *kai2a-1, kai2b-3, kai2a-1 kai2b-1* and *max2-4* displayed in Fig 7C (n=3). Letters indicate different statistical groups (ANOVA, post-hoc Tukey test).



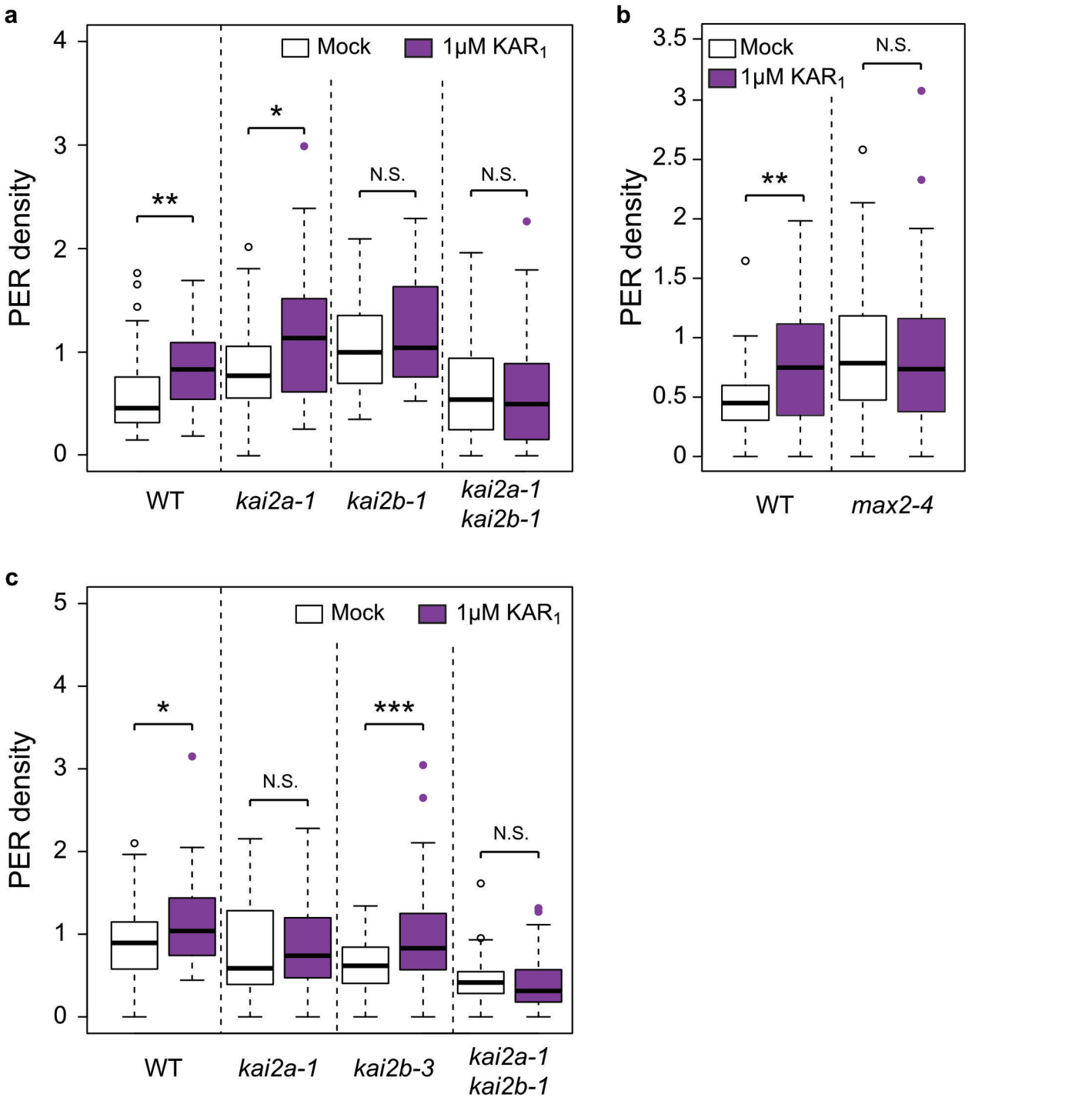
Supplementary Figure 9 | Refreshing *rac*-GR24 in the medium does not influence root architecture.

PER density of wild-type plants at 2 wpg and treated with solvent (Mock) 1 µM KAR_1, 1 µM KAR_2, or 1 µM *rac*-GR24 (n = 43-51). Plants were transferred onto fresh hormone-containing medium after 5 days. Asterisks indicate significant differences (ANOVA, Dunnett test, N.S.>0.05, *≤0.05).



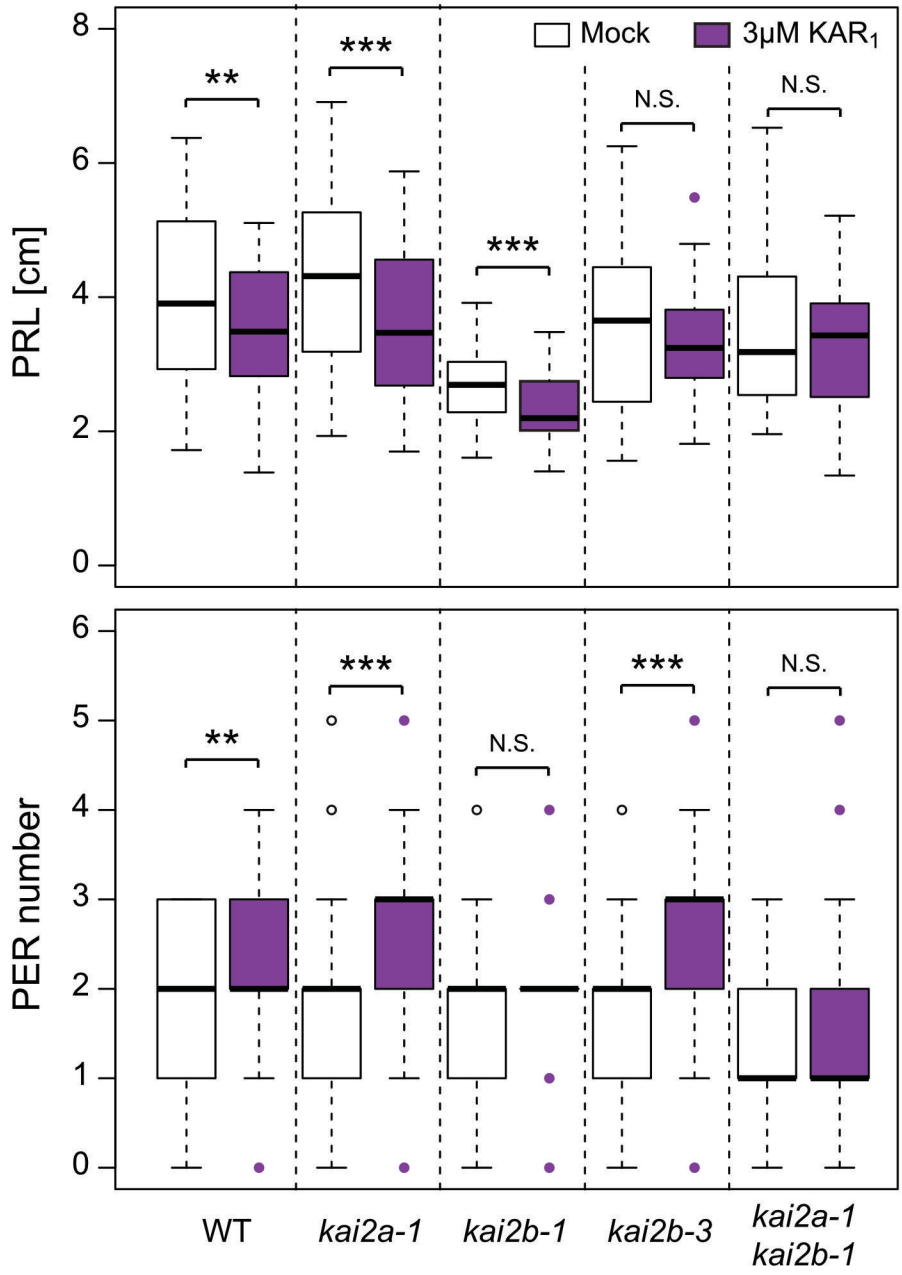
Supplementary Figure 10 | Small overlap between transcriptional responses of *Lotus japonicus* roots to KAR_1 and *rac*-GR24.

Number of differentially expressed genes (DEGs, adjusted p-value < 0.01) as assessed by microarray analysis. Left panel: DEGs responding to 1 µM KAR_1 after 1h, 2h and 6h incubation. Middle panel: DE genes responding to 1 µM *rac*-GR24 1h, 2, 6h incubation. Right panel: comparison of DE genes responding to 2 h treatment with KAR_1 and *rac*-GR24.



Supplementary Figure 11 | KAR perception mutants are less responsive to KAR$_1$ treatment.

(**a-c**) Post-embryonic-root (PER) density of *L. japonicus* plants, 2 wpg after treatment with solvent (Mock) or 1 μM KAR$_1$, of wild-type, (**a**) *kai2a-1*, *kai2b-1* and *kai2a-1 kai2b-1* (n= 32-50); (**b**) *max2-4* (n= 34-43); (**c**) *kai2a-1*, *kai2b-3* and *kai2a-1 kai2b-1* (n= 37-72). (**a-c**) Asterisks indicate significant differences versus mock treatment (Welch t.test, *≤0.05, **≤0.01, ***≤0.001).



Supplementary Figure 12 | KAR_1 response in roots requires *LjKAI2a* or *LjKAI2b* and *LjMAX2*.

Primary-root length (PRL) and post-embryonic-root (PER) number of *L. japonicus* plants, 2 wpg after treatment with solvent (Mock) or 3 μM KAR_1 (n=34-72) displayed in Fig 9A. Asterisks indicate significant differences versus mock treatment (Welch t.test, *≤0.05, **≤0.01, ***≤0.001).

Supplemental Table 1 | *L. japonicus* mutants used in this study and information on seed production.

allele	type	reference	position from ATG	comments
Ljd14-1	EMS	SL4580	C685T (Q > stop)	hardly produce flowers
Ljkai2a-1	LORE1 insertion	30008990	387	-
Ljkai2b-1	EMS	SL1281	C640T (Q > stop)	-
Ljkai2b-2	EMS	SL2723	G462A (W > stop)	produced no seeds
Ljkai2b-3	LORE1 insertion	30034333	535	-
Ljmax2-1	LORE1 insertion	30031159	83	hardly produce flowers
Ljmax2-2	LORE1 insertion	P0860_3	504	hardly produce flowers
Ljmax2-3	LORE1 insertion	30019601	1132	produce few flowers
Ljmax2-4	LORE1 insertion	30049531	1230	produce few flowers

Supplemental Table 3 | Primers.

Primers used for LORE1 insertion mutant genotyping. Forward primer was used to amplify specifically LORE1 insertion with a specific P2 primer (CCATGGCGGTTCCGTGAATCTTAGG).

mutant	Forward		Reverse	
Ljkai2a-1	Sc403	TATGGTCTCTCACGCTGTTTCCGCC ATGATCG	Sc283	TCCACAATAGACACGCCACC
Ljkai2b-3	Sc285	CCTCCGTTGACATGACCTCC	Sc17	TTGAAGACTACCCCTTAAACA AGGGGTTTGAG
Ljmax2-1	Sc130	ATGAAGACTTTACGGGTCTCACACC ATGAGTAACGCTGCTGAAAC	CG416	CAGTAGAAGCTCCGGCAAAC
Ljmax2-2	CG383	TTGGGGAGGGGTTTAATAGG	CG424	CGATTTCGTGAGACTTGAAGC
Ljmax2-3	Sc163	TCACCTCGCTGGATCTCTC	Sc131	TTGAAGACTACCACCTCCCAT GTTGTCATC
Ljmax2-4	Sc131	TTGAAGACTACCACCTCCCATGTTG TCATC	Sc163	TCACCTCGCTGGATCTCTC

Primers used for EMS mutant genotyping. dCAPS strategy was used to genotype EMS mutants.

mutant	Forward		Reverse		Site
Ljd14-1	Sc429	GCCGGCGGCGGCCGCGAGGT ACCTG	Sc242	TTTCGTCTCACCTTGTGTGCCC CCGCCAGTGC	PstI (Cut WT)
Ljkai2b-1	Sc431	GGTAACTGTGCCATGTCACAG TATA	Sc285	CCTCCGTTGACATGACCTCC	AccI (Cut WT)

Primers used for cloning.

Use	Primers	
cloning promoter *AtD14* in LI	Sc224	TTTCGTCTCAGCGGGTCTACACATTCATCAATCTCGC
	Sc225	TTTCGTCTCACAGATTTTTTATGTGTTTGGGTTTGAG
cloning promoter *AtKAI2* fragment 1 in LI	Sc232	TTTCGTCTCAGCGGGGCGATTCAGTGCCATGATT
	Sc233	TTTCGTCTCACGATTCGTTCAGATTCTCGCT
cloning promoter *AtKAI2* fragment 2 in LI	Sc234	TTTCGTCTCAATCGACTCGAATTTGATGGATCTTTC
	Sc235	TTTCGTCTCACAGACTCTCTAAAGAAGATTCTTC
cloning genomic *AtD14* in LI	Sc236	TTTCGTCTCACACCATGAGTCAACACAACATCTTAGAAG
	Sc237	TTTCGTCTCACCTTTCACCGAGGAAGAGCTCGCC
cloning genomic *AtKAI2* in LI	Sc238	TTTCGTCTCACACCATGGGTGTGGTAGAAGAAG
	Sc239	TTTCGTCTCACCTTTCACATAGCAATGTCATTACGAATG
cloning genomic *LjD14* in LI	Sc240	TTTCGTCTCACACCATGGCCACTTCAATCCTCGACG
	Sc241	TTTCGTCTCACCTTTCAGTGTGCCCCCGCCAGTG
cloning genomic *LjKAI2a* and cDNA *Ljkai2a-1* in LI	Sc243	TTTCGTCTCACACCATGGGGATAGTGGAGGAAGCTCAC
	Sc244	TTTCGTCTCACCTTTTACACCCCACTAAATTTTACATCAC

cloning genomic *LjKAI2b* in LI	Sc246	TTTCGTCTCACACCATGGGGATAGTGGAAGAAGCTC
	Sc247	TTTCGTCTCACCTTTCAAGCTGCAATATCATGGCAAATG
cloning genomic *Ljkai2a-1* in LI	Sc243	TTTCGTCTCACACCATGGGGATAGTGGAGGAAGCTCAC
	ST97	CAAATCCTTCCATAGTAATTTGCGGAAGAAAATCATC
	ST96	TTGAAGACTATCTTCAGATATCTCATATAC
	Sc244	TTTCGTCTCACCTTTTACACCCCACTAAATTTTACATCAC
cloning cDNA *LjKAI2a* (3b) fragment 1 in L0	Sc505	ATGAAGACTTCCATCGGAGCCCACCCTAAAC
	ST161	ATGAAGACTTTACGTCGTCTCACACCATGGG
cloning cDNA *LjKAI2a* (3b) fragment 2 in L0	ST163	ATGAAGACTTATGGCGGTGGGTGGAGACATG
	ST164	ATGAAGACTTCGCAAAACGGTTAGAGCAATATC
cloning cDNA *LjKAI2a* (3b) fragment 3 in L0	ST165	ATGAAGACTTTGCGGACCATTTTTCAGAGC
	Sc498	ATGAAGACTACAGACGTCTCACCTTTTACACCCCACTAA ATTTTAC
cloning cDNA *LjKAI2b* (3a) fragment 1 in L0	Sc506	ATGAAGACTTCCAGCGGGGCAAAGCCTGAAC
	ST169	ATGAAGACTTTACGTCGTCTCACACCATGGG
cloning cDNA *LjKAI2b* (3a) fragment 2 in L0	ST171	ATGAAGACTTCTGGCTATCGGAGGAGACATG
	ST172	ATGAAGACTTTGCGATACGCTTAAGGCTATG
cloning cDNA *LjKAI2b* (3a) fragment 3 in L0	ST173	ATGAAGACTTCGCAGACAATTTTTCAAAGTG
	Sc503	ATGAAGACTACAGACGTCTCACCTTTCAAGCTGCAATATC
cloning pSUMO *LjKAI2a* (2b)	Sc604	CGTGGTGTTTAGGGTTTGCTCCGATGGCGGTG
	Sc605	CACCGCCATCGGAGCAAACCCTAAACACCACG
cloning pSUMO *LjKAI2b* (2a)	Sc606	CATGGTGTTCAGGCTGGGCCCCGCTGGCTATC
	Sc607	GATAGCCAGCGGGGCCCAGCCTGAACACCATG

Primers used for gene amplification by RT-qPCR.

Use	**Primers**	
qPCR *Ubiquitin*	Ubi F	ATGCAGATCTTCGTCAAGACCTTG
	Ubi R	ACCTCCCCTCAGACGAAG
qPCR *LjMAX2*	Sc302	GAATGTTACACCCTGAGGAAGC
	Sc303	TCAGGTTTGGGATCTTGAGG
qPCR *LjKAI2a*	Sc282	CGGTGCAGGAGTTTAGCAGA
	Sc283	TCCACAATAGACACGCCACC
qPCR *LjKAI2b*	Sc284	AAGAAAGACCTGGCGGTTCC
	Sc285	CCTCCGTTGACATGACCTCC
qPCR *LjDLK2*	MG027	CTCCTTGGTGCTTCTCCCAG
	MG028	AAAGCCGAAGCCAGTTTTCA
qPCR *LjD14*	D14_qPCR_F	ACAGCGTCCGAGAAAACTC
	D14_qPCR_R	AGCAATGGAGGCCAACTAC

Supplemental Table 4 | Plasmids.

Name	Description
Golden Gate Level 0	
L0 c*LjKAI2a*$^{M160,\ L190,W157}$ A	PCR amplification of *L. japonicus* Gifu cDNA with primers Sc505 +ST161. Assembly by StuI cut ligation into L0-Amp (BB01)
L0 c*LjKAI2a*$^{M160,\ L190,W157}$ B	PCR amplification of *L. japonicus* Gifu cDNA with primers ST163 +ST164. Assembly by StuI cut ligation into L0-Amp (BB01)
L0 c*LjKAI2a*$^{M160,\ L190,W157}$ C	PCR amplification of *L. japonicus* Gifu cDNA with primers ST165 +Sc498. Assembly by StuI cut ligation into L0-Amp (BB01)
L0 c*LjKAI2b*^{L161,S191,F158} A	PCR amplification of *L. japonicus* Gifu cDNA with primers Sc506 +ST169. Assembly by StuI cut ligation into L0-Amp (BB01)
L0 c*LjKAI2b*^{L161,S191,F158} B	PCR amplification of *L. japonicus* Gifu cDNA with primers ST171 +ST172. Assembly by StuI cut ligation into L0-Amp (BB01)
L0 c*LjKAI2b*^{L161,S191,F158} C	PCR amplification of *L. japonicus* Gifu cDNA with primers ST173 +Sc503. Assembly by StuI cut ligation into L0-Amp (BB01)
Golden Gate Level I	
LI Esp3I p*AtKAI2* A	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc232 + Sc233. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I p*AtKAI2 B*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc234 + Sc235. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I p*AtD14*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc224 + Sc225. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *gAtKAI2*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc238 + Sc239. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *gAtD14*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc237 + Sc238. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *gLjKAI2a*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc243 + Sc244. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *gLjKAI2b*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc246 + Sc247. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *gLjD14*	PCR amplification of *L. japonicus* Gifu genomic DNA with primers Sc240 + Sc241. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *gLjkai2a-1*	PCR amplification of *L. japonicus kai2a-1* genomic DNA with primers Sc243 + ST97 and ST96 +Sc244. Assembly by BpiI and StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *cLjkai2a-1*	PCR amplification of *L. japonicus kai2a-1* coding DNA with primers Sc243 + Sc244. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I *cLjKAI2a*	PCR amplification of *L. japonicus* Gifu coding DNA with primers Sc243 + Sc244. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I c*LjKAI2b*	PCR amplification of *L. japonicus* Gifu cDNA with primers Sc246 + Sc248. Assembly by StuI cut ligation into LI-pUC57 (BB02)
LI Esp3I c*LjKAI2a*$^{M160,\ L190,W157}$	Assembled by BpiI cut ligation from: L0 c*LjKAI2a*$^{M160,\ L190,W157}$ A + L0 c*LjKAI2a*$^{M160,\ L190,W157}$ B + L0 c*LjKAI2a*$^{M160,\ L190,W157}$ C + LI-BpiI (BB03)
LI Esp3I c*LjKAI2b*^{L161,S191,F158}	Assembled by BpiI cut ligation from: L0 c*LjKAI2b*^{L161,S191,F158} A + L0 c*LjKAI2b*^{L161,S191,F158} B + L0 c*LjKAI2b*^{L161,S191,F158} C + LI-BpiI (BB03)
Golden Gate Level II	

LIIc F 1-2 POI:GOI:*HygroR*	Assembled by BsaI cut ligation from: LI A-B POI (G082) + LI B-C dy (BB06) + LI C-D GOI + LI D-E dy (BB08) + LI E-F nos-T (G006) + LI F-G HygroR (G095) + LIIc F 1-2 (BB30)
LIIc R 3-4 p*35S:mCherry*	Assembled by BsaI cut ligation from: LI A-B p*35S* (G005) + LI B-C dy (BB06) + LI C-D *mCherry* (G023) + LI D-E dy (BB08) + LI E-F 35S-T (G059) + LI F-G dy (BB09) + LIIc R 3-4 (BB34)
Golden Gate Level III	
LIIIβ POI:GOI:*HygroR*	Assembled by BpiI cut ligation from: LIIc F 1-2 POI:GOI:HygroR + LII 2-3 ins (BB43) + LIIc R 3-4 p35S:*mCherry* + LII 4-6 dy (BB41) + LIIIβ F A-B (BB53)
LIIIβ p*AtKAI2:gAtKAI2*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *gAtKAI2*
LIIIβ p*AtKAI2:gAtD14*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *gAtD14*
LIIIβ p*AtKAI2:gLjKAI2a*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *gLjKAI2a*
LIIIβ p*AtKAI2:gLjKAI2b*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *gLjKAI2b*
LIIIβ p*AtKAI2: gLjkai2a-1*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *gLjkai2a-1*
LIIIβ p*AtKAI2: cLjkai2a-1*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *cLjkai2a-1*
LIIIβ p*AtKAI2:gLjD14*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKAI2* A + LI Esp3I *pAtKAI2* A + LI Esp3I *gLjD14*
LIIIβ p*AtD14:gAtD14*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKD14* + LI Esp3I *gAtD14*
LIIIβ p*AtD14:gAtKAI2*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKD14* + LI Esp3I *gAtKAI2*
LIIIβ p*AtD14:gLjD14*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKD14* + LI Esp3I *gLjD14*
LIIIβ p*AtD14:gLjKAI2a*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKD14* + LI Esp3I *gLjKAI2a*
LIIIβ p*AtD14:gLjKAI2b*	Assembled by Esp3I cut ligation from: LIIIβ F A-B POI:GOI:HygroR + LI Esp3I *pAtKD14* + LI Esp3I *gLjKAI2b*
Protein induction	
pSUMO c*LjKAI2a*	PCR amplification from LI Esp3I *cLjKAI2a* with primers MW1002 + MW1003. Assembly by Gibson cloning
pSUMO c*LjKAI2b*	PCR amplification from LI Esp3I *cLjKAI2b* with primers MW1002 + MW1004. Assembly by Gibson cloning
pSUMO c*LjKAI2a*$^{M160,\ L190,W157}$	PCR amplification from LI Esp3I *cLjKAI2a (3b)* with primers MW1002 + MW1003. Assembly by Gibson cloning
pSUMO c*LjKAI2b*^{L161,S191,F158}	PCR amplification from LI Esp3I *cLjKAI2b (3a)* with primers MW1002 + MW1004. Assembly by Gibson cloning
pSUMO c*LjKAI2a*$^{M160,\ L190}$	Rolling circle PCR amplification from pSUMO *LjKAI2a (3b)* with primers Sc604 + Sc605.
pSUMO c*LjKAI2b*^{L161,S191,F158}	Rolling circle PCR amplification from pSUMO *LjKAI2b (3a)* with primers Sc606 + Sc607.

Supplemental Table 5 | Statistical results of ANOVA for multiple comparisons.

Figure	genotype/treatment/gene	*post hoc* test	p-value	F-value
Fig. 2a	-	Tukey	≤ 0.001	$F_{14/1438}$ = 125.3
Fig. 2c	-	Tukey	≤ 0.001	$F_{11/132}$ = 45.6
Fig. 3a	WT (Ler)	Tukey	≤ 0.001	$F_{2/311}$ = 244
	kai2-2		= 0.18	$F_{2/300}$ = 1.71
	AtKAI2 #1		≤ 0.001	$F_{2/122}$ = 31.9
	AtKAI2 #3		≤ 0.001	$F_{2/303}$ = 116.4
	LjKAI2a #10b		≤ 0.001	$F_{2/316}$ = 65.7
	LjKAI2a #11b		≤ 0.001	$F_{2/313}$ = 42
	LjKAI2b #1b		≤ 0.001	$F_{2/296}$ = 33.4
	LjKAI2b #5b		≤ 0.001	$F_{2/288}$ = 87.4
Fig. 3b	WT (Col)	Tukey	≤ 0.001	$F_{2/311}$ = 158.3
	K02821		≤ 0.001	$F_{2/353}$ = 100.3
	WT (Ler)		≤ 0.001	$F_{2/384}$ = 499.6
	htl-2		≤ 0.05	$F_{2/391}$ = 3.2
	#18		≤ 0.001	$F_{2/383}$ = 104.8
	#23		≤ 0.001	$F_{2/253}$ = 127
Fig. 3c	WT (Col)	Tukey	≤ 0.001	$F_{2/415}$ = 1008
	d14-1 kai2-2		= 0.22	$F_{2/353}$ = 1.54
	LjKAI2a #32		≤ 0.001	$F_{2/287}$ = 50
	LjKAI2a #46		≤ 0.001	$F_{2/184}$ = 85
	LjKAI2b #29		≤ 0.001	$F_{2/283}$ = 9.4
	LjKAI2b #31		≤ 0.05	$F_{2/244}$ = 3.9
Fig. 4b	LjKAI2a	Dunnett	≤ 0.0001	$F_{5/12}$ = 96.1
	LjKAI2a^{M160,L190}		≤ 0.001	$F_{5/12}$ = 9.5
	LjKAI2a$^{M160,L190, W157}$		= 0.227	$F_{5/12}$ = 1.63
	LjKAI2b		= 0.632	$F_{5/12}$ = 0.70
	LjKAI2b^{L161,M191}		= 0.001	$F_{5/12}$ = 8.9
	LjKAI2b ^{L161,M191,F158}		≤ 0.0001	$F_{5/12}$ = 56.9
Fig. 6c	-	Tukey	≤ 0.001	$F_{6/103}$ = 35
Fig. 6d	-	Tukey	≤ 0.001	$F_{6/605}$ = 26.5
Fig. 7a	KAR1	Tukey	≤ 0.001	$F_{3/396}$ = 33.1
	KAR2		≤ 0.001	$F_{3/390}$ = 16.5
	rac-Gr24		≤ 0.001	$F_{3/392}$ = 35
Fig. 7b	WT	Dunnett	≤ 0.001	$F_{2/313}$ = 30
	kai2a-1		= 0.08	$F_{2/234}$ = 2.51
	kai2b-1		≤ 0.001	$F_{2/302}$ = 29.3
	kai2b-3		≤ 0.001	$F_{2/308}$ = 14.2
	kai2a-1 kai2b-1		= 0.99	$F_{2/272}$ = 0.01
Fig. 7c	WT	Dunnett	≤ 0.001	$F_{3/8}$ = 28.4

	kai2a-1		≤ 0.001	$F_{3/8} = 53$
	kai2b-3		≤ 0.001	$F_{3/8} = 26$
	kai2a-1 kai2b-1		≤ 0.001	$F_{3/8} = 105.8$
	max2-4		= 0.99	$F_{3/8} = 0.04$
Fig. 8a	KAR1 PRL	Tukey	≤ 0.001	$F_{3/209} = 7.40$
	KAR1 PER		≤ 0.001	$F_{3/209} = 11.1$
	KAR1 PER density		≤ 0.01	$F_{3/209} = 5.51$
	KAR2 PRL		= 0.51	$F_{3/217} = 0.77$
	KAR2 PER		= 0.18	$F_{3/217} = 1.64$
	KAR2 PER density		= 0.72	$F_{3/217} = 0.44$
	rac-GR24 PRL		= 0.74	$F_{3/203} = 0.42$
	rac-GR24 PER		= 0.07	$F_{3/203} = 2.45$
	rac-GR24 PER density		= 0.43	$F_{3/203} = 0.92$
Fig. 8b	WT	Tukey	≤ 0.001	$F_{2/9} = 30.7$
	max2-4		= 0.20	$F_{2/9} = 1.97$
Supp. Fig. 6a	*KAI2a*	Tukey	≤ 0.001	$F_{5/18} = 39.5$
	KAI2b		≤ 0.001	$F_{5/18} = 33.7$
Supp. Fig. 7d	-	Tukey	≤ 0.001	$F_{9/714} = 178.8$
Supp. Fig. 8a	WT	Dunnett	≤ 0.001	$F_{2/246} = 51$
	d14-1		≤ 0.001	$F_{2/260} = 74.3$
	max2-4		= 0.25	$F_{2/204} = 1.38$
Supp. Fig. 8b	-	Tukey	≤ 0.001	$F_{4/10} = 148$
Supp. Fig. 9	-	Dunnett	≤ 0.01	$F_{3/188} = 4.1$