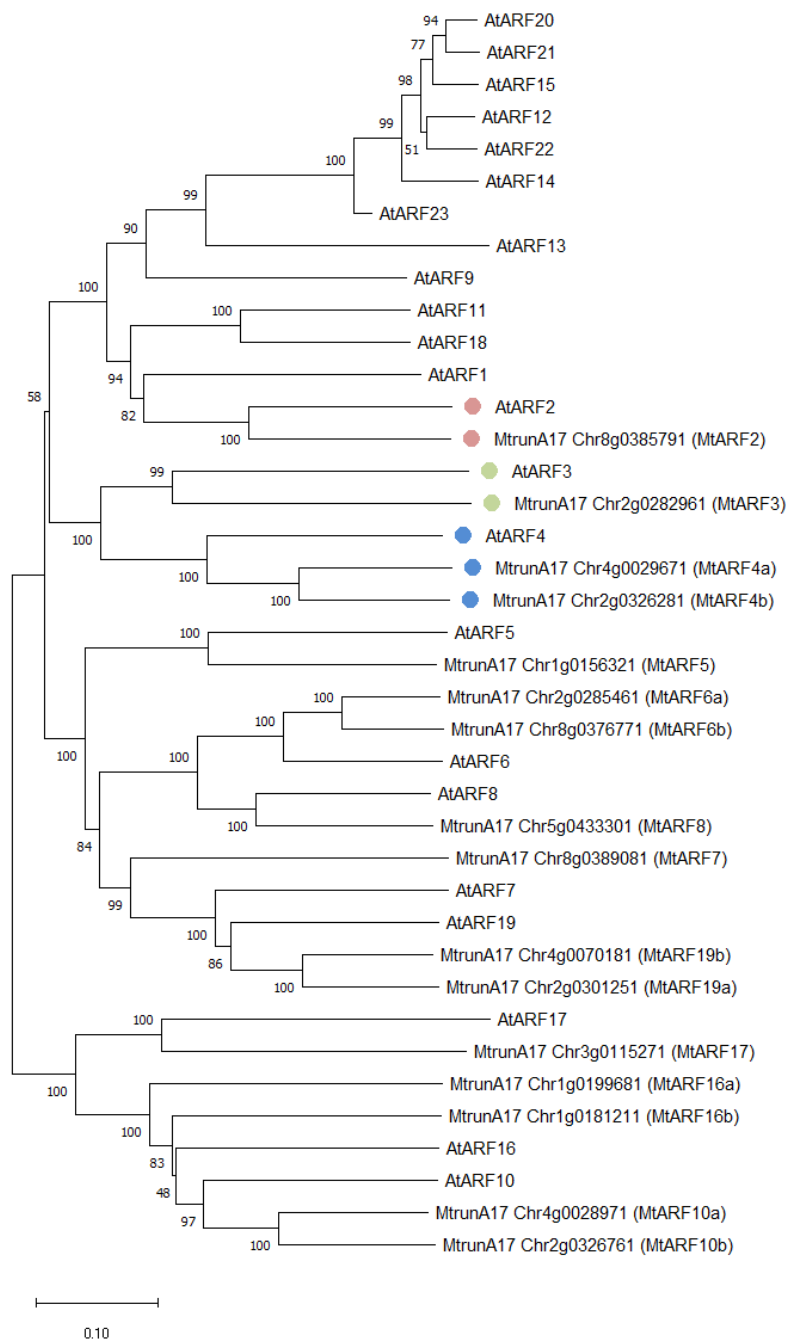


Supplementary Figure 1

MtARF4a	1	MEIDLNNNEVIEVEKNALCHKECEKGF	CFCV--SCLSPSTC	SSSSSTSP	IVSSSYLELWHA
MtARF4b	1	MEIDLNDSITEVKKNVCSNGKCEKSV	CVCTLSSSSSP	TCSSSSSTSA	IVSSSYLELWHA
MtARF4a	59	CAGPLTSLPKKGNVVVYFPOGHLEQ	FASFSPFKOLEIPNYDLQPOIF	CRVNVVQLLANKE	
MtARF4b	61	CAGPLTSLPKKGNVVVYFPOGHLEQ	VASLSLFSSLEIPTYGLQPOIL	CRVNVVQLLANKE	
MtARF4a	119	NDEVYTOVTLLPQAELAGMHMEGKEVIE	ELEGDEEGDGGSP	TKSTPHMFCKTLTV	SDTSTH
MtARF4b	121	NDEVYTOVALLPQAELAGMCLDDKEPE	EGLADDEGNRSP	TKLASHMFCKTLTA	SDTSTH
MtARF4a	179	GGFSVPRRAAEDCFPPI	-----DYKL	QRPSQELVAKDLHGVE	WKFRHIYRGO
MtARF4b	181	GGFSVPRRAAEDCFPPLVQHYEPVWICLF	FEDYKQ	QRPSQELVAKDLHGVE	GWKFRHIYRGO
MtARF4a	226	PRRHLLTTGWSIFVNOKNLVSGDAVL	FLRQG	ENGELRLGIRRAVR	PRPNGLPESIVGNQNCY
MtARF4b	241	PRRHLLTTGWSIFVSQKNLVSGDAVL	FLRGEN	ENGELRLGIRRAAR	PRPNGLPESIIGNQSCS
MtARF4a	286	PNFLSSVANAISSKSMFHV	FYSPRASHAEFVVPYQKYVKS	IKNPMTIGTRFKMRI	EMDES
MtARF4b	301	PSFLSSVANAISSAKSMFHV	FYSPRASHADFVVPYQKYAKS	IRNPVTIGTRFKMK	FEMDES
MtARF4a	346	PERRCSSGMTIGINDLDPYRWP	PKSKWRCLMVRWDD	TETNHQDRVSPWEIDPSS	POPPPLS
MtARF4b	361	PERRCSSGIVTGMSDLDPYKWP	PKSKWRCLMVRWDED	IGANHQDRVSPWEIDPST	SLPPLN
MtARF4a	406	IQSSPRLKKPRTGLLVASPNHLIT	GMNPNGISGMMGF	EESVRS	PKVLQGOENTGFMSLYY
MtARF4b	421	IQSSRRLKKLRTGLHVESPSHFITA	-----GDSG	FMDDESIRSS	SKVLQGOEKTSFMSLYY
MtARF4a	466	GCDKVTNOPGFELSSSSHONLAS	TGIGKV	VTSSSELMSP	HPFSYAGFMESNNFPRVLOGQ
MtARF4b	477	GCDTVTKQKEFDINSLR-HTNLAS	NGAR-KITSSE	FTRTOPSSYADFT	EMNRFPRVLOAQ
MtARF4a	526	EICKLKSLSGKVDENIGAWG	TKP-----SFO	SACFPYGDIDKS	
MtARF4b	535	EIYPLRSLTGKVDLNNNSWG	KTNVSYTKYNLHNATKLN	FHSLGSEVLQNSS	FFPYGDIDHKV
MtARF4a	564	NQA-SMFSSKHTSFMSDNVP	FNTPSIVAGDIRKEVGRSGSN	LIPNEHKLODNVSASASLV	
MtARF4b	595	GQSSMLCSKPTNPFQLGNVS	FNTPSSQIGALRNEVGLSS	FKIRNEOKLONDISAATS-L	
MtARF4a	623	DTNRNAPNDNNVKGKANSCK	LF	GFPLSG--EPSSQNLQNTAKR	SCTKVHKQGS
MtARF4b	653	DANIRISNDENFKEMVNPCK	LF	GFSLSAAAEITTSQNLQNSAKR	SCTKVHKQGS
MtARF4a	681	LSRLSGYNDLLSELEKLF	GM	EGLLRSD	DKGWRILYTDSENDIMVVGDDPWHEFCDVSKI
MtARF4b	713	LSRLSSYNDLVSELERLF	GM	EGLLRDP	DKGWRILYTDSENDIMVVGDDPWHEFCDMVSKI
MtARF4a	741	HIYTKEEVEKMTFGMMTND	DTHSCLDQAPVITEP	SKSSSVGQPDYS	SPTVVRV
MtARF4b	773	HIYTOEEVEKMTIGMMN-DD	NQSCLEQTP	LIMEASKSSSVGQPDS	SSTTVVRI

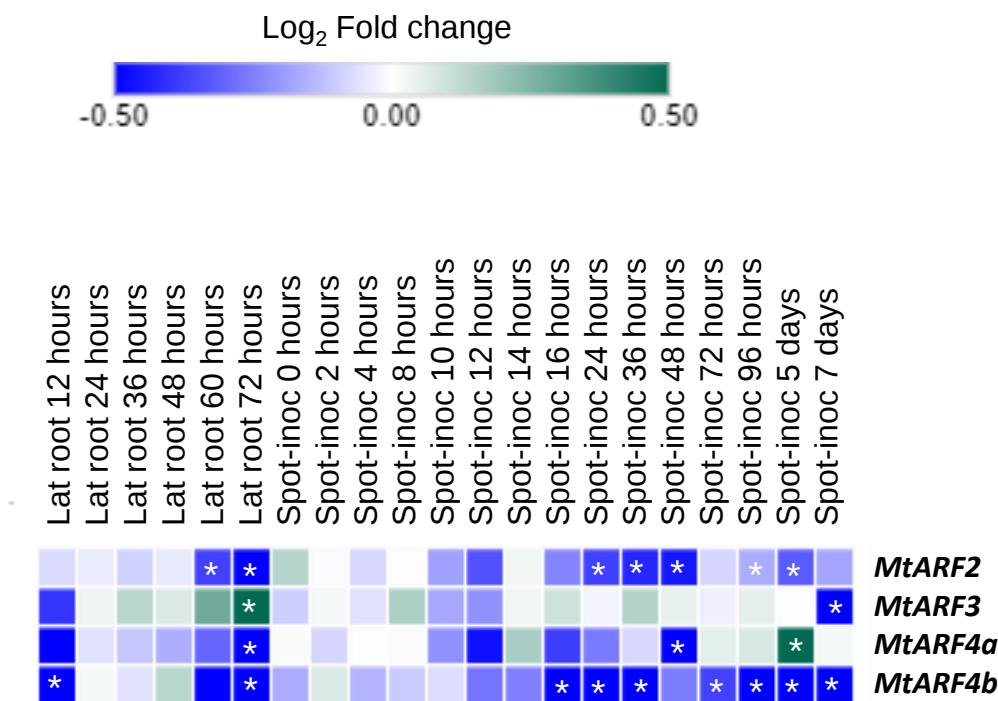
Supplementary Figure 1. Alignment of MtARF4a and MtARF4b amino acid sequences. The multiple alignment was generated using the Clustal Omega algorithm available at EMBL-EBI (<https://www.ebi.ac.uk/Tools/msa/clustalo/>) and decorated with BOXSHADE (<http://sourceforge.net/projects/boxshade/>). Identical amino acids were shaded in black, whereas synonymous substitutions were shaded in gray. Locus IDs are MtrunA17_Ch4g0029671 (Medtr4g060460) and MtrunA17_Ch2g0326281 (Medtr2g093740) for ARF4a and ARF4b, respectively.

Supplementary Figure 2



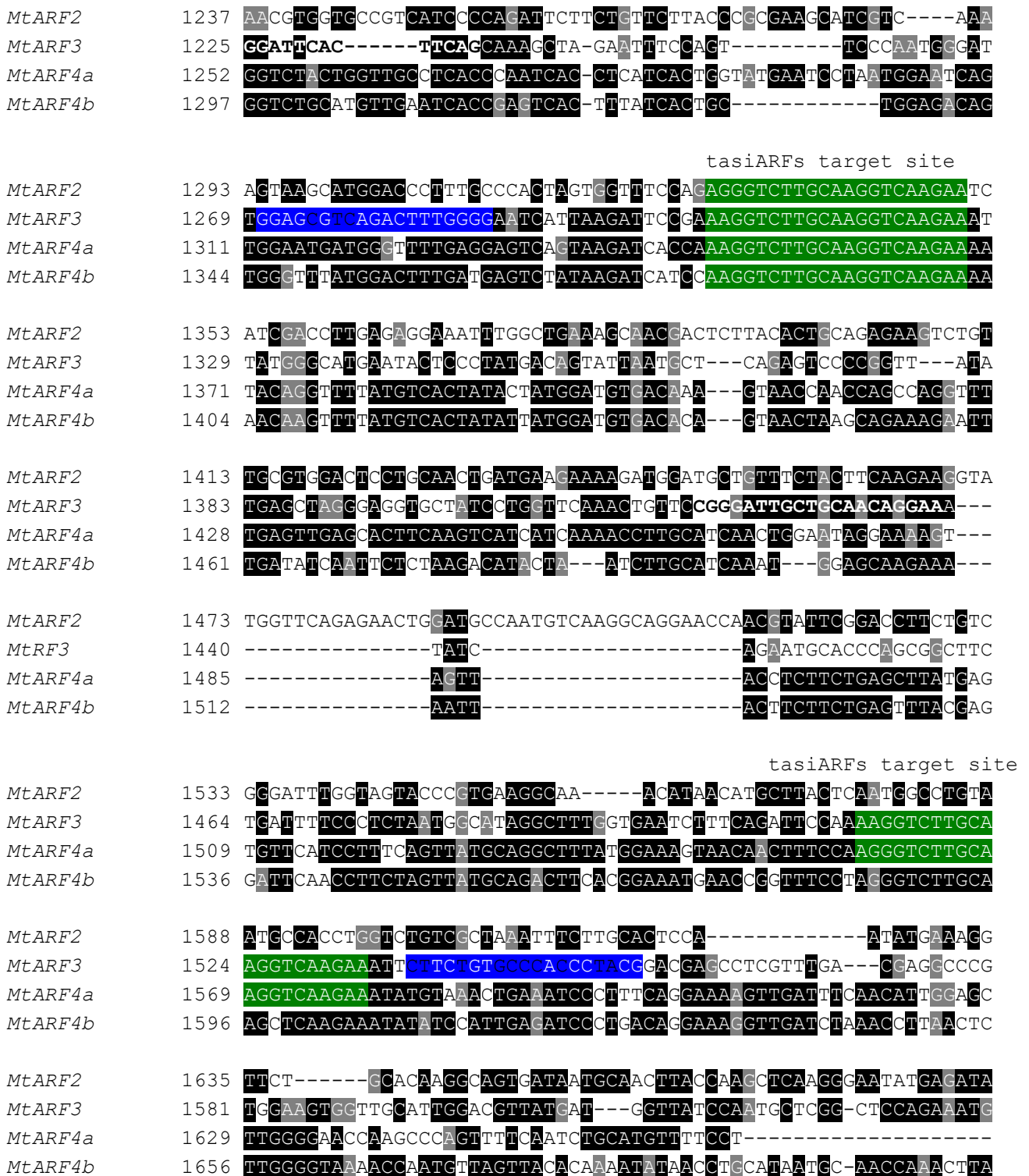
Supplementary Figure 2. Phylogenetic tree of amino acid sequences of Arabidopsis and *M. truncatula* members of the ARF family. All members of the Arabidopsis ARF family were retrieved from the TAIR database (<https://www.arabidopsis.org/>). *M. truncatula* ARF members linked to root development or nodulation were retrieved from the recently released version of the *M. truncatula* genome MtrunA17r5.0-ANR (<https://medicago.toulouse.inra.fr/MtrunA17r5.0-ANR/>, Pecrix et al. 2018). The tree was generated using MEGA X (Kumar et al, 2018) using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10000 replicates) is shown next to the branches (Felsenstein et al, 1985). The evolutionary distances were computed using the p-distance method (Nei and Kumar, 2000). The ARF2, ARF3, and ARF4 clades were labelled with pink, green and blue circles, respectively.

Supplementary Figure 3



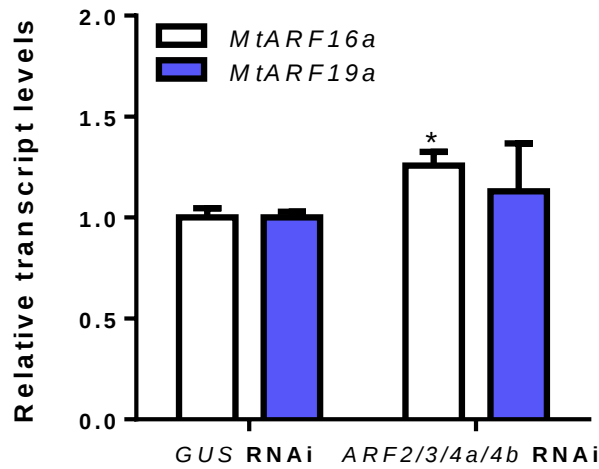
Supplementary Figure 3. Heat map of *MtARF2*, *MtARF3*, *MtARF4a* and *MtARF4b* expression during lateral root and nodule formation. Log₂ Fold change of expression values at indicated time points upon induction of lateral root formation (Lat root) as compared with not induction of lateral roots or upon spot inoculation with droplets of *S. meliloti* suspension (Spot-inoc) as compared with non inoculated roots are presented. Data were retrieved from Schiessl et al. (2019), where genes with Fold changes >1.5 were considered as differentially expressed. The asterisk indicates significant differences at each time point between induced lateral roots not induced roots or between spot inoculated roots and not inoculated roots with an adjusted p value ≤ 0.5.

Supplementary Figure 4



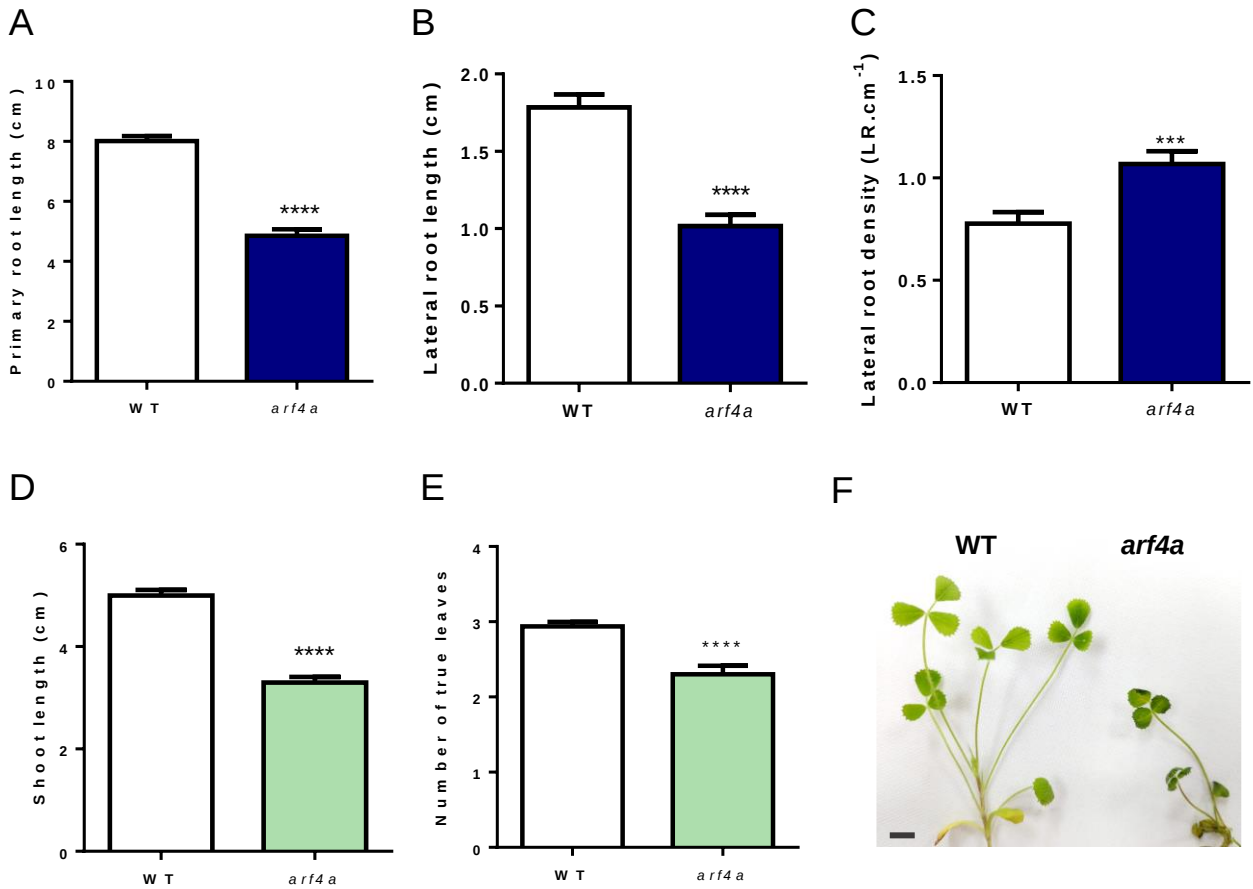
Supplementary Figure 4. Multiple alignment of nucleotide sequences of the region of *MtARF2*, *MtARF3*, *MtARF4a* and *MtARF4b* transcripts used for the design of ARF2/3/4 RNAi primers. The multiple alignment was generated the Clustal Omega algorithm available at EMBL-EBI (<https://www.ebi.ac.uk/Tools/msa/clustalo/>) and shaded with BOXSHADE (<http://sourceforge.net/projects/boxshade/>). Primers used for amplification of ARF2/3/4 RNAi fragments are colored in blue. Targets sites for tasiARFs were colored in green. Locus IDs are MtrunA17_Ch8g0385791 (Medtr8g100050), MtrunA17_Ch2g0282961 (Medtr2g014770), MtrunA17_Ch4g0029671 (Medtr4g060460) and MtrunA17_Ch2g0326281 (Medtr2g093740) *MtARF2*, *MtARF3*, *MtARF4a* and *MtARF4b*, respectively.

Supplementary Figure 5



Supplementary Figure 5. Transcript levels of *MtARF16a* and *MtARF19a* in *GUS* RNAi and *ARF2/3/4a/4b* RNAi roots. Expression values were determined by RT-qPCR, normalized to *MtHIS3L* and expressed relative to the *GUS* RNAi sample, which was set at 1. Each bar represents the mean $\pm$ SE of three biological replicates (whole root tissue from at least three composite plants were collected in each biological replicate) with three technical replicates each. The asterisk indicates statistically significant differences between *GUS* and *ARF2/3/4a/4b* RNAi roots in an unpaired two-tailed Student's *t* test with a *p* value ≤ 0.05 .

Supplementary Figure 6



Supplementary Figure 6. Root and shoot phenotype of *arf4a* mutant plants at 15 days after germination (dag). Primary root length (A), lateral root length (B), lateral root density (C), shoot length (D) and number of true leaves (E) were measured in WT and *arf4a* mutant plants at 15 dag. Error bars represent mean $\pm$ SE of three biological replicates, each with at least 10 plants. Asterisks denote a statistically significant differences between WT and *arf4a* plants in an unpaired two-tailed Student's t test (**: $p \leq 0.01$, ***: $p \leq 0.001$, ****: $p \leq 0.0001$). F. Illustrative pictures of shoots of WT and *arf4a* plants at 15 dag. Scale bar: 0.5 cm