

Figure S1

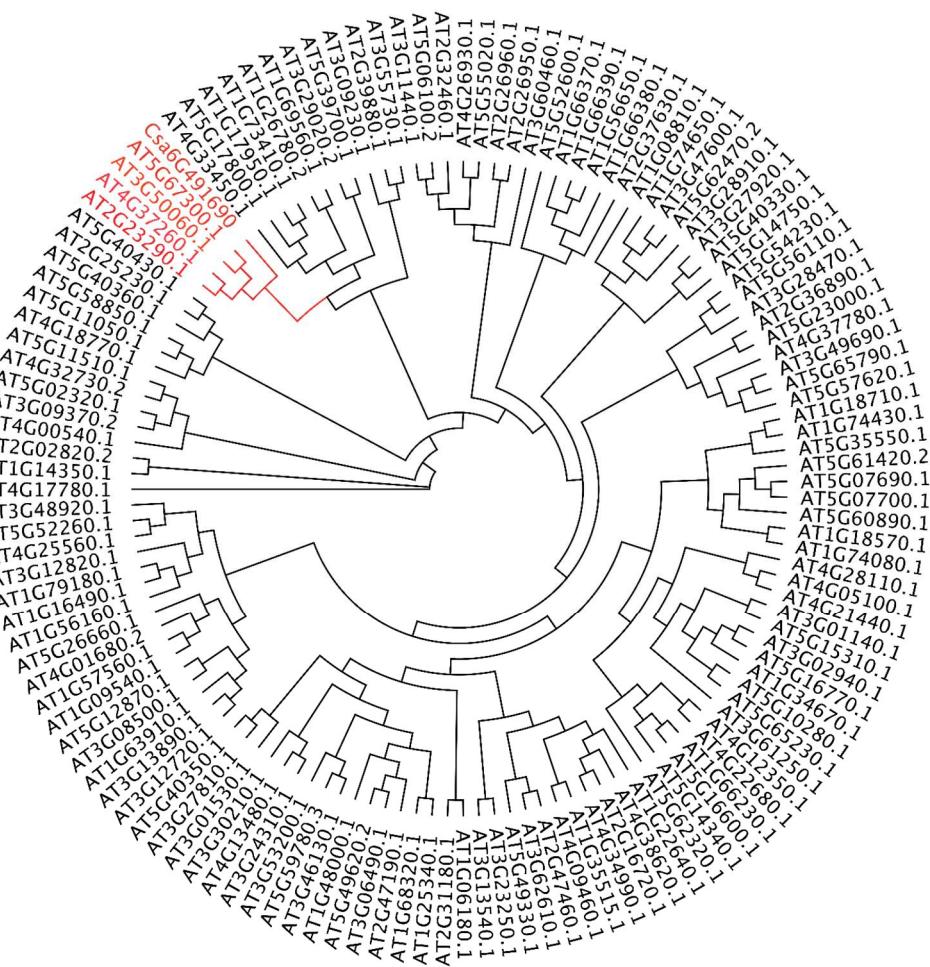


Figure S1. Phylogenetic analysis of the *A. thaliana* MYB family.

Protein sequences of the *Arabidopsis* MYB family, downloaded from The *Arabidopsis* Information Resource (TAIR) database, were aligned by using Clustal Omega

(<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The phylogenetic tree was generated with the neighbor-joining (NJ) method in Geneious software and showed the relationship between the *Arabidopsis* MYB family and the cucumber MYB44, identified as potential phloem mobile mRNA in the previous study [29]. The clade of the MYB family, which showed the closest similarity with the cucumber MYB44, is highlighted in red.

Figure S2

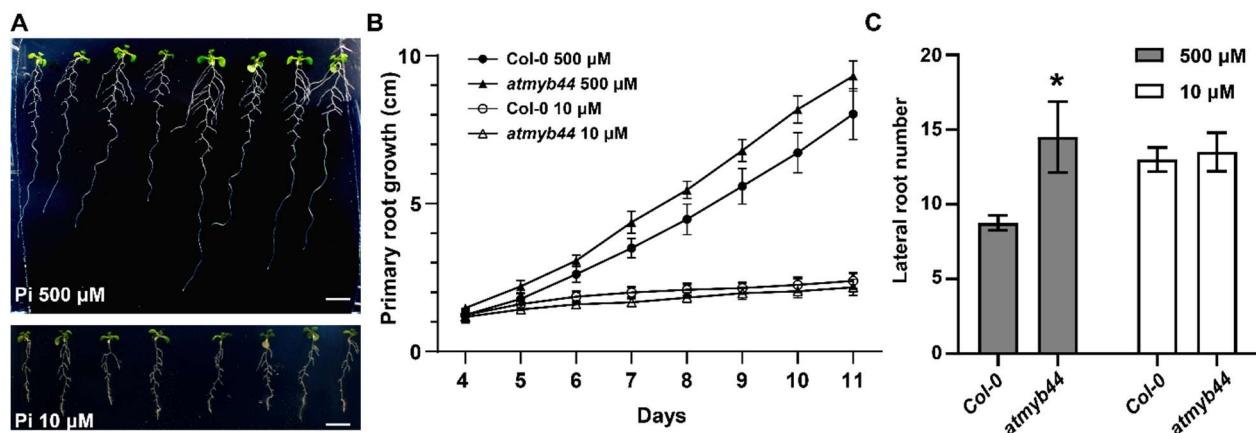


Figure S2. AtMYB44 is involved in primary and lateral root development.

(A) *atmyb44* displays enhanced primary root growth under Pi-sufficient (200 μ M) conditions. WT and *atmyb44* were grown on Pi-sufficient (200 μ M) and -starvation (10 μ M) media for 11 days after germination.

(B) Time course measurement of primary root growth in WT and *atmyb44* seedlings.

(C) *atmyb44* shows enhanced lateral root formation under Pi-sufficient (200 μ M) conditions.

Figure S3

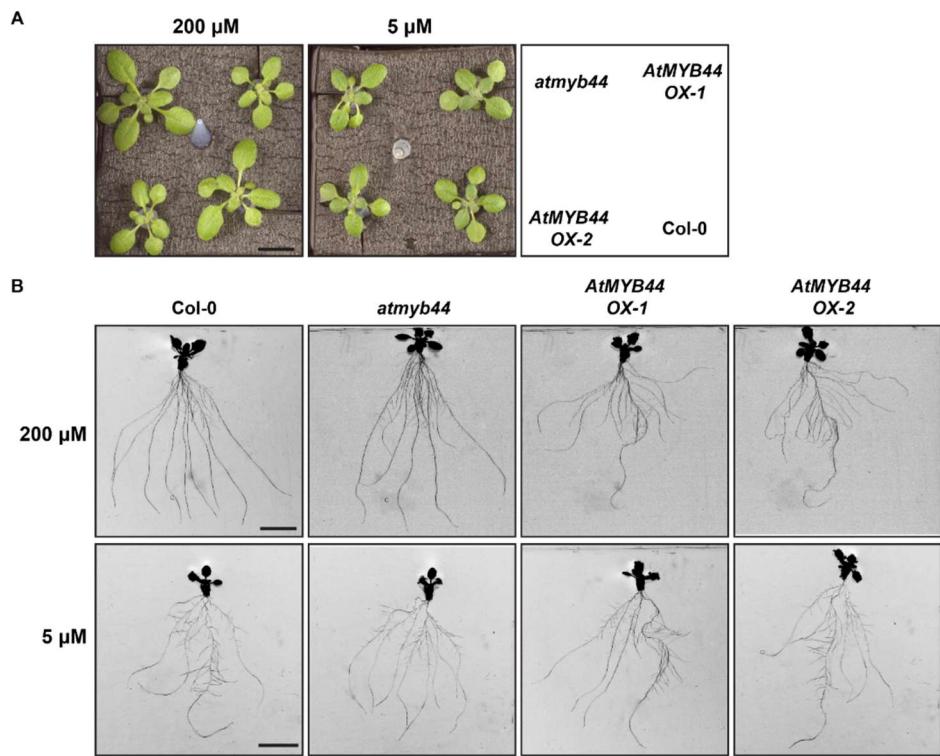


Figure S3. AtMYB44 serves as a potential negative regulator in shoot and root development.
Representative shoot (A) and root (B) images of WT, *atmyb44*, *AtMYB44 OX-1* and *AtMYB44 OX-2* plants grown in a hydroponic culture system with Pi-sufficient (200 μ M, left panel in Figure S3A, upper panel in Figure S3B) and -starvation (5 μ M, middle panel in Figure S3A, lower panel in Figure S3B) treatment. The right panel of Figure S3A indicates the position of WT, *atmyb44*, *AtMYB44 OX-1* and *AtMYB44 OX-2* plants in the hydroponic culture system. Bar = 1 cm.

Figure S4

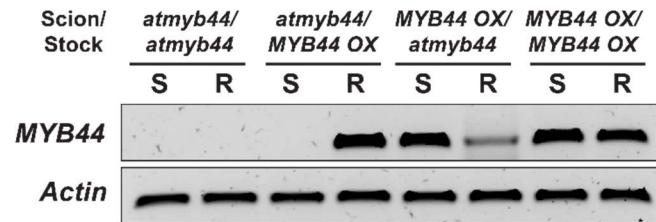


Figure S4. Mobility of *AtMYB44* mRNA.

AtMYB44 is graft-transmissible from the *AtMYB44 OX-1* scion into the *atmyb44* rootstock.

Table S1. List of PCR primers used in this study

Primer Name	Oligonucleotide Sequence 5-3'	Target Gene Name
055F_AtACT2	GAAATCACAGCACTTGCAC	AtActin2
055R_AtACT2	AGCCTTGATCTTGAGAG	AtActin2
F_AtMYB44	TCTCCACCTGTTACTGGCTT	AtMYB44
R_AtMYB44	TTGACTCGTGGCTACGGTTGACT	AtMYB44
060F_AtMYB70	GGCGACGATTGCACGGCTTC	AtMYB70
060R_AtMYB70	CCATCATACCCCTCATTACCACCG	AtMYB70
061F_AtMYB73	GCAGCGTCGAAGGGCAAAGT	AtMYB73
061R_AtMYB73	CCGATGGACTTCCGGGACTCA	AtMYB73
048F_AtMYB77	TGTCTTCGTCTCGGAGGAT	AtMYB77
048R_AtMYB77	CCGCCATGTAACTCCTCACT	AtMYB77
086F_AtPHT1;4	TGACGTGGCCAAGACGCAAT	AtPHT1;4
086R_AtPHT1;4	GGCTTTGTGCGCCTTCCAC	AtPHT1;4
088F_proAtMYB44	CACCAAGATGAAATAGTACTTG	AtMYB44 promoter
088R_proAtMYB44	TGATTGGAATGTTTATCAAA	AtMYB44 promoter
Pht1-2-F	GCAACGAAGCCAAGGGTGT	AtPHT1;2
Pht1-2-R	GAAAGCCCCACGGGTCTTCT	AtPHT1;2