

Supporting Information Fig. S1 and Tables S1–S4

Table S1 List of the 50 eukaryotic complete genome sequences or ESTs used in this study, in addition to the NCBI *nr* database

Species	Lineage
<i>Acanthamoeba castellanii</i>	Amoebozoa
<i>Antonospora locustae</i>	Microsporidians
<i>Aureococcus anophagefferens</i>	Pelagophytes
<i>Batrachochytrium dendrobatidis</i>	Chytrids
<i>Bigelowiella natans</i>	Cercozoans
<i>Blastocystis hominis</i>	Stramenopiles
<i>Brachionus plicatilis</i>	Rotifers
<i>Capitella</i> sp.	Segmented worms
<i>Capsaspora owczarzaki</i>	Opisthokonta
<i>Chlorella</i> sp.	Green algae
<i>Chlorella vulgaris</i>	Green algae
<i>Cyanidioschyzon merolae</i>	Red algae
<i>Cyanophora paradoxa</i>	Glaucocystophyceae
<i>Daphnia pulex</i>	Crustaceans
<i>Dictyostelium purpureum</i>	Cellular slime molds
<i>Emiliana huxleyi</i>	Haptophytes
<i>Euglena gracilis</i>	Euglenoids
<i>Glaucocystis nostochinearum</i>	Glaucocystophyceae
<i>Guillardia theta</i>	Cryptomonads
<i>Hartmannella vermiformis</i>	Amoebozoa
<i>Heterocapsa triquetra</i>	Dinoflagellates
<i>Hyperamoeba</i> sp.	Amoebozoa
<i>Isochrysis galbana</i>	Haptophytes
<i>Karenia brevis</i>	Dinoflagellates
<i>Karlodinium micrum</i>	Dinoflagellates

<i>Lottia gigantea</i>	Gastropods
<i>Malawimonas jakobiformis</i>	Malawimonadidae
<i>Mastigamoeba balamuthi</i>	Amoebozoa
<i>Monosiga ovata</i>	Choanoflagellates
<i>Naegleria gruberi</i>	Heterolobosea
<i>Paracercomonas marina</i>	Cercozoans
<i>Pavlova lutheri</i>	Haptophytes
<i>Physarum polycephalum</i>	Plasmodial slime molds
<i>Phytophthora ramorum</i>	Oomycetes
<i>Phytophthora sojae</i>	Oomycetes
<i>Polysphondylium pallidum</i>	Cellular slime molds
<i>Polytomella parva</i>	Green algae
<i>Porphyra yezoensis</i>	Red algae
<i>Prototheca wickerhamii</i>	Green algae
<i>Reclinomonas americana</i>	Jakobida
<i>Rhizopus oryzae</i>	Fungi
<i>Sawyeria marylandensis</i>	Heterolobosea
<i>Scenedesmus obliquus</i>	Green algae
<i>Seculamonas ecuadoriensis</i>	Jakobida
<i>Sphaeroforma arctica</i>	Opisthokonta
<i>Spironucleus vortens</i>	Diplomonads
<i>Streblomastix strix</i>	Oxymonadida
<i>Thalassiosira pseudonana</i>	Diatoms
<i>Trimastix pyriformis</i>	Unclassified eukaryotes

Table S2 List of *TAL* genes in 17 representative land plant genomes

Lineage	Species	Name	Locus	Length	Intron	Chromosome	Location
	<i>Linum usitatissimum</i>	<i>LuTAL1</i>	Lus10043136	436	6	scaffold25	1384528–1386813
	<i>Linum usitatissimum</i>	<i>LuTAL2</i>	Lus10032613	436	6	scaffold140	1012925–1015257
	<i>Populus trichocarpa</i>	<i>PtTAL1</i>	POPTR_0003s16030	436	6	scaffold_3	15654057–15657021
	<i>Populus trichocarpa</i>	<i>PtTAL2</i>	POPTR_0001s12930	440	6	scaffold_1	10023678–10027179
	<i>Medicago truncatula</i>	<i>MtTAL</i>	Medtr7g006100	443	6	7	845072–850479
Dicots	<i>Arabidopsis thaliana</i>	<i>AtTAL</i>	AT5G13420	438	6	5	4301792–4304312
	<i>Capsella rubella</i>	<i>CrTAL</i>	Carubv10000972m	441	6	scaffold_6	4298572–4301148
	<i>Thellungiella halophila</i>	<i>ThTAL</i>	Thhalv10013572m	439	6	scaffold_2	4380727–4383435
	<i>Citrus sinensis</i>	<i>CsTAL</i>	orange1.1g036665m	440	6	scaffold00081	111594–114983
	<i>Vitis vinifera</i>	<i>VvTAL</i>	GSVIVG01001098001	441	6	1	22628856–22634048
	<i>Mimulus guttatus</i>	<i>MgTAL</i>	mgv1a006041m	460	6	scaffold_39	1460196–1462967
	<i>Sorghum bicolor</i>	<i>SbTAL</i>	Sb03g044500	429	5	chromosome_3	71853994–71856810
	<i>Zea mays</i>	<i>ZmTAL</i>	GRMZM2G134256	429	5	8	160390396–160393378
Monocots	<i>Setaria italica</i>	<i>SiTAL</i>	Si001538m	429	5	scaffold_5	45396389–45399497
	<i>Oryza sativa</i>	<i>OsTAL</i>	LOC_Os01g70170	432	5	1	40610513–40613463
	<i>Brachypodium distachyon</i>	<i>BdTAL</i>	Bradi2g59370	429	5	2	57090545–57093078
Gymnosperm	<i>Picea sitchensis</i>	<i>PsTAL</i>	ABR16241	444			
Fern	<i>Selaginella moellendorffii</i>	<i>SmTAL</i>	74909	423	5	scaffold_0	1351640–1353058
Moss	<i>Physcomitrella patens</i>	<i>PpTAL</i>	Pp1s159_68V6	438	7	scaffold_159	376836–382010

Table S3 The site-specific model parameters

Branch	Model	Log _e <i>L</i>	Parameters	PSS under NEB ^c	PSS under BEB ^d
	M0	-10086.8220	$\omega = 0.0608$	-	-
	M3	-9778.1731**	$p_0 = 0.5461, p_1 = 0.3549, p_2 = 0.0990$ $\omega_0 = 0.0025, \omega_1 = 0.0949, \omega_2 = 0.3612$	NAN	NAN
Land plants ^a	M1a	-9973.4908	$p_0 = 0.9166, p_1 = 0.0834$ $\omega_0 = 0.0438, \omega_1 = 1.0000$	-	-
	M2a	-9973.4908	$p_0 = 0.9166, p_1 = 0.0834, p_2 = 0.0000$ $\omega_0 = 0.0438, \omega_1 = 1.0000, \omega_2 = 9.7249$	NAN	NAN
	M7	-9783.8626	$\beta(0.2728, 3.3243)$	-	-
	M8	-9596.8567	$\beta(0.2728, 3.3247)$ $p_1 = 0.9999, \omega = 1.0000$	NAN	NAN
Actinobacteria ^b	M0	-7869.1297	$\omega = 0.0022$	-	-

M3	-7576.9542 **	$p_0 = 0.2900, p_1 = 0.4343, p_2 = 0.2758$ $\omega_0 = 0.0001, \omega_1 = 0.0023, \omega_2 = 0.0087$	NAN	NAN
M1a	-7732.2492	$p_0 = 0.8041, p_1 = 0.1959$ $\omega_0 = 0.0343, \omega_1 = 1.0000$	-	-
M2a	-7732.2492	$p_0 = 0.8041, p_1 = 0.0086, p_2 = 0.1873$ $\omega_0 = 0.0343, \omega_1 = 1.0000, \omega_2 = 1.0000$	NAN	NAN
M7	-7581.9788	$\beta(0.5597, 99.0000)$	-	-
M8	-7581.9792	$\beta(0.5597, 99.0000)$ $p_1 = 0.0001, \omega = 3.2668$	NAN	NAN

^aAll the *TAL* genes list in Table S2 were used in this analysis. ^bEight Actinobacteria *TAL* genes followed to the same branch of land plants on the phylogeny were used in this analysis. ^cPositively selected sites (PSS) under naive empirical Bayes (NEB) analysis; ^dpositively selected sites (PSS) under Bayes empirical Bayes (BEB) analysis. NAN, not a number.

Table S4 Morphometric analysis of wild-type and *TAL*-RNAi plants

Organ	Wild-type	TAL-Ri
Leaf		
Flag leaf length (cm)	26.1 ± 4.9 (7)	21.0 ± 3.4 (9)*
Flag leaf width (cm)	1.6 ± 0.1 (7)	1.3 ± 0.3 (9)**
Number of large veins of flag leaf	13.6 ± 1.5 (7)	11.9 ± 3.6 (9)*
Number of small veins of flag leaf	49.4 ± 3.6 (7)	34.9 ± 5.9 (9)**
Stem		
Number of large vascular bundles of internode I	14.0 ± 0.8 (7)	10.0 ± 3.8 (9)**
Number of small vascular bundles of internode I	30.0 ± 8.6 (7)	22.0 ± 4.3 (9)*
Number of large vascular bundles of internode II	30.7 ± 1.4 (7)	26.0 ± 4.2 (9)**
Number of small vascular bundles of internode II	30.9 ± 0.9 (7)	25.8 ± 4.3 (9)**

The flag leaf, internode I and internode II morphometric analyses were carried out at heading stage. Results represent means ± SD of populations of the size indicated in parentheses. Asterisks indicate the significance of differences between wild-type and *TAL*-RNAi as determined by Student's *t* test: **, $P = 0.01$ level; *, $P = 0.05$ level.

