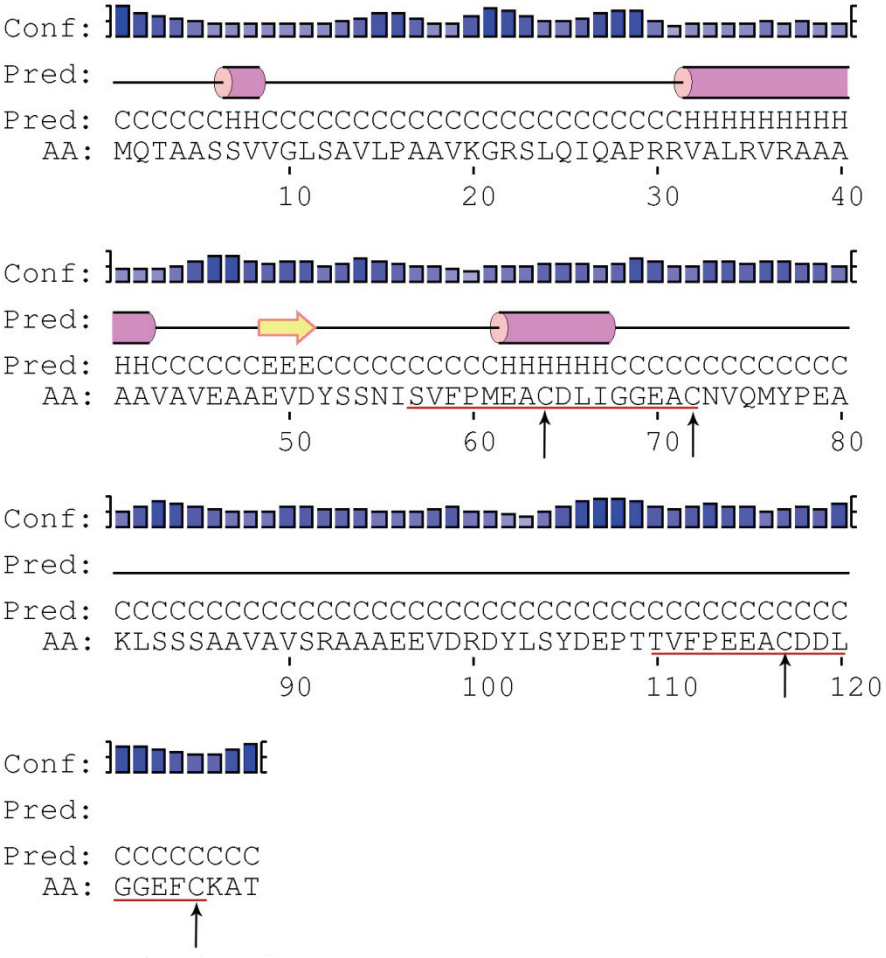
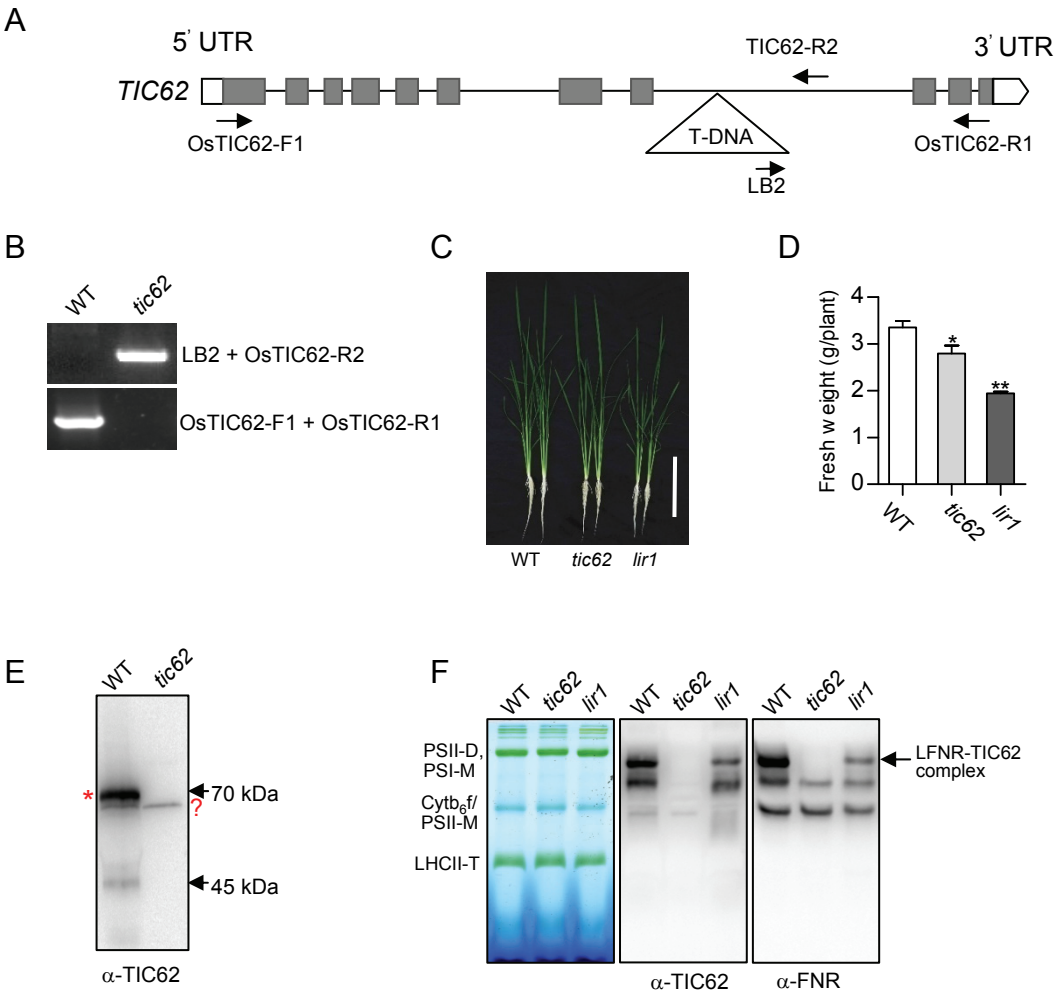
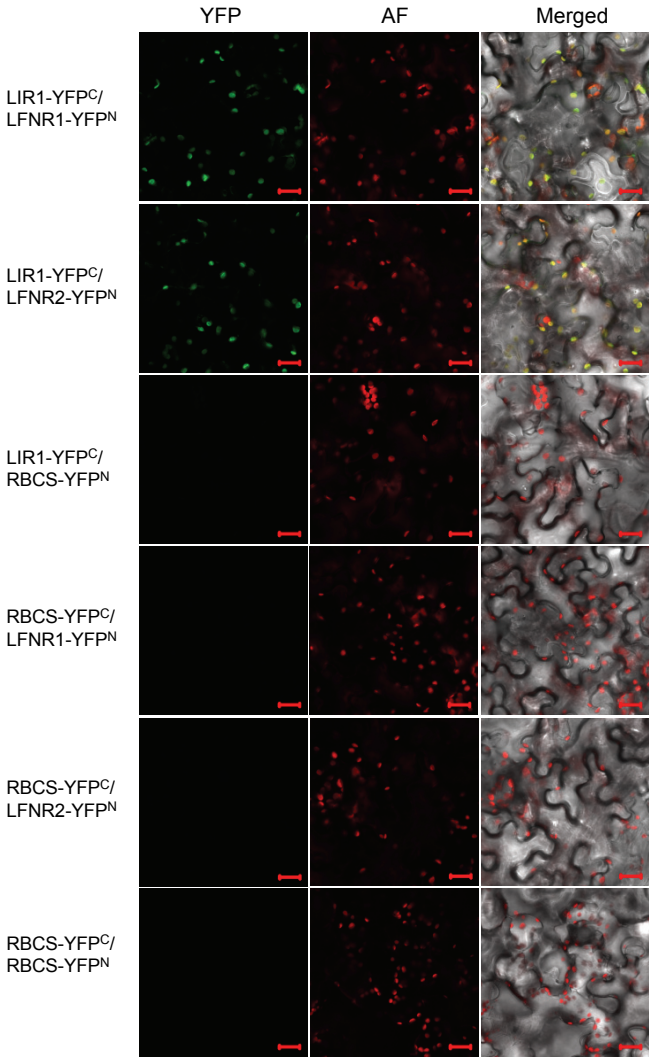


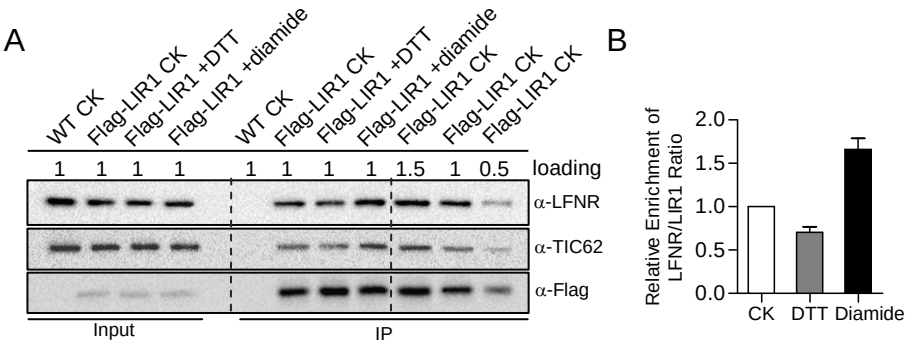
Supplemental Figure 1. Amino Acid Sequence and Structural Predictions of Rice LIR1.
The conserved LIR1 motifs are underlined (red) and the conserved Cys residues are indicated by black arrows. The secondary structure prediction was performed by PSIPRED (http://bioinf.cs.ucl.ac.uk/psipred). H stands for helix, C for coil, and E for strand. The height of the blue bars for each amino acid represents the level of confidence of each prediction.



Supplemental Figure 2. Characteristics of Rice *tic62* Plants.
(A) Genomic structure of *TIC62*. Gray boxes denote exons, black lines introns, and white boxes 5'- and 3'-untranslated regions. The T-DNA insertion site is indicated by a triangle. Binding sites of *TIC62* gene-specific primers (OsTIC62-F1, OsTIC62-R1, OsTIC62-R2) and T-DNA-specific left border primer (LB2) used for screening of *tic62* homozygous plants are depicted.
(B) PCR analysis of WT and *tic62* using genomic DNA (upper panel) and cDNA (lower panel) as PCR templates, respectively, with the primers indicated in (A).
(C) Phenotypes of WT, *tic62*, and *lir1* plants grown in hydroponic culture for 35 d. Bar = 10 cm.
(D) Fresh weights of 35 d-old WT, *tic62*, and *lir1* plants grown in hydroponic culture.
(E) Immunoblot of SDS-PAGE of WT and *tic62* total leaf extracts; 10 μg protein was loaded onto the gel and immunodetected with anti-TIC62 antibody. The 70 kDa major TIC62 band is indicated by a red star and the putative TROL band by a question mark.
(F) BN PAGE analysis of WT, *tic62*, and *lir1* plants after 4 h in the dark. The left panel shows the thylakoid protein complexes, and the middle and right panels show immunoblots using anti-TIC62 and LFNR antisera, respectively; 5 μg chlorophyll was loaded onto the gel. PSII-D/M, PSII dimers/monomers; PSI-M, PSI monomers; LHCII-T, LHCII trimers.



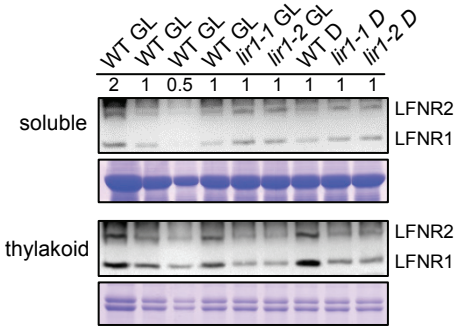
Supplemental Figure 3. Bimolecular Fluorescence Complementation (BiFC) Analysis of Protein Interactions in *Nicotiana tabacum*.
Bimolecular fluorescence complementation (BiFC) analysis for interaction between rice LIR1 and LFNRs. C- and N-terminal fragments of yellow fluorescence protein (YFP^{C} and YFP^{N}) were fused to LIR1 and LFNR1 or LFNR2, respectively. Combinations of plasmids (indicated on the left panel) were transiently transformed into leaves of *Nicotiana tabacum*. RBCS (ribulose bisphosphate carboxylase small chain, LOC_Os12g19470) serves as a chloroplast localized negative control. Presence of YFP signal (green) indicates reconstitution of YFP through protein interaction of the tested pairs. Positions of the chloroplasts are indicated by red auto-fluorescence (red). The scale bar represents 20 μm.



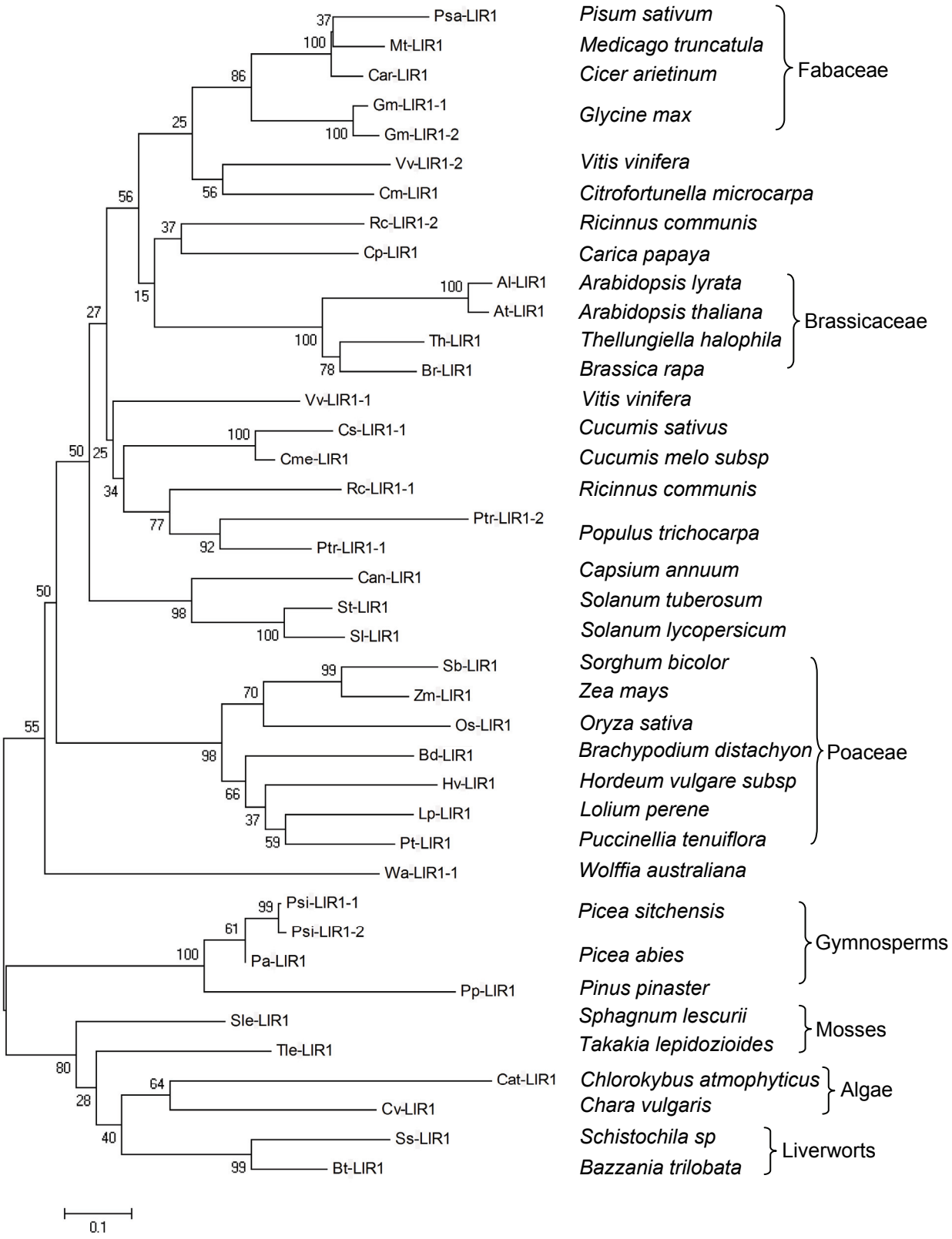
Supplemental Figure 4. Effect of DTT and Diamide on the Interaction Between Rice LIR1 and LFNR.

(**A)** Coimmunoprecipitation assay between Flag-LIR1, LFNR and TIC62 in CK (IP buffer as control check, pH 6.8), DTT (IP buffer supplement with 20 mM DTT) and diamide (IP buffer supplement with 5 mM diamide) buffers. Total proteins extracted from 30 d-old WT or *35S:Flag-LIR1* rice seedlings were incubated with anti-Flag M2 magnetic beads. The immuoprecipitation (IP) and total extracts (Input) were subjected to immunoblot analysis with Flag, LFNR, and TIC62 antibodies. For each well, 0.05% of total protein extracts (10 ÕL from 20 mL total protein extract) and 8.3% eluted proteins (10 ÕL from 120 ÕL eluted proteins) were loaded as x1 input and x1 IP, respectively. The loaded dilution series (0.5x to 1.5x) were used to avoid possible saturation of the immunodetection.

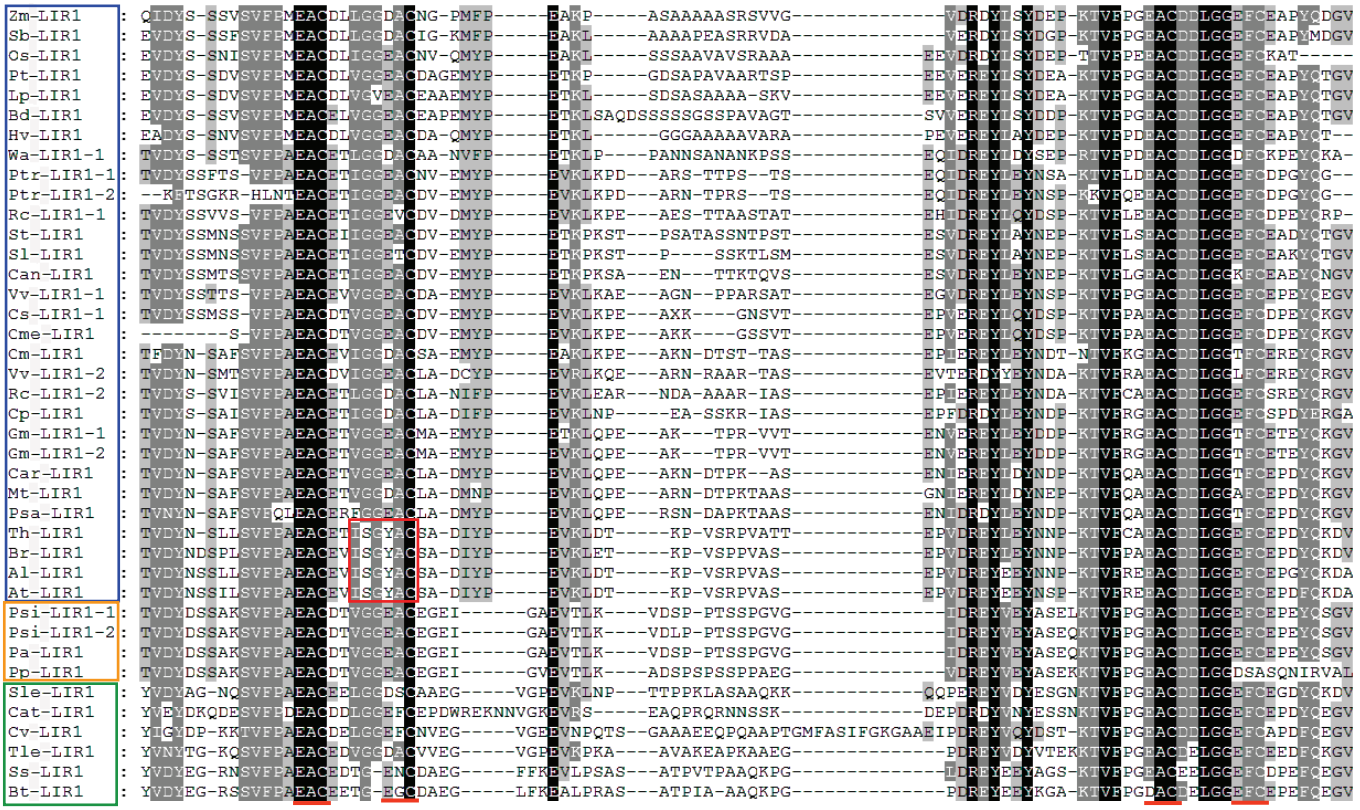
(B) The relative enrichment ratio of LFNR/LIR1 of coimmunoprecipitation analysis in (A). The relative enrichment ratio of LFNR/LIR1 is defined as (IP of LFNR/ input of LFNR)/(IP of LIR1/ input of LIR1). The enrichment of LFNR and LIR1 (Flag-LIR1) was calculated by the ratio of IP signal to their respective input signal on the same gel. 3 independent experiments were performed. The enrichment ratio under CK condition was normalized as 1. Data are means ¤ s.d. (n = 3).



Supplemental Figure 5. Comparison of the Two Rice LFNR Isoforms Between WT and *lir1* Plants. Representative native-PAGE gels of soluble leaf extract and thylakoid membranes isolated from plants treated for 4 h in the dark (D) or under standard growth light (GL; 1000 µmol photons m-2 s-1). Proteins were immunodetected with LFNR antibodies. The dilution series (0.5x to 2x) was made with the corresponding control (WT GL) in each gel to avoid possible saturation of the immunodetection. 1x loading = 10 µg protein

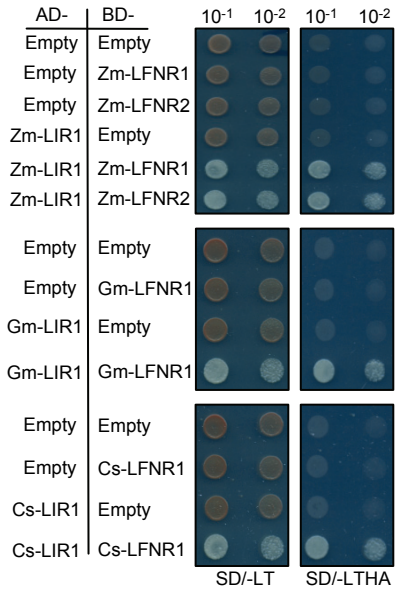


Supplemental Figure 6. Phylogenetic Analysis of LIR1.
The aligned LIR1 amino acid sequences from a variety of plant species were exported into MEGA 4. The phylogenetic tree was constructed using the minimal evolution method with 1000 bootstrap tests. The numbers at the nodes refer to bootstrap support percentage.

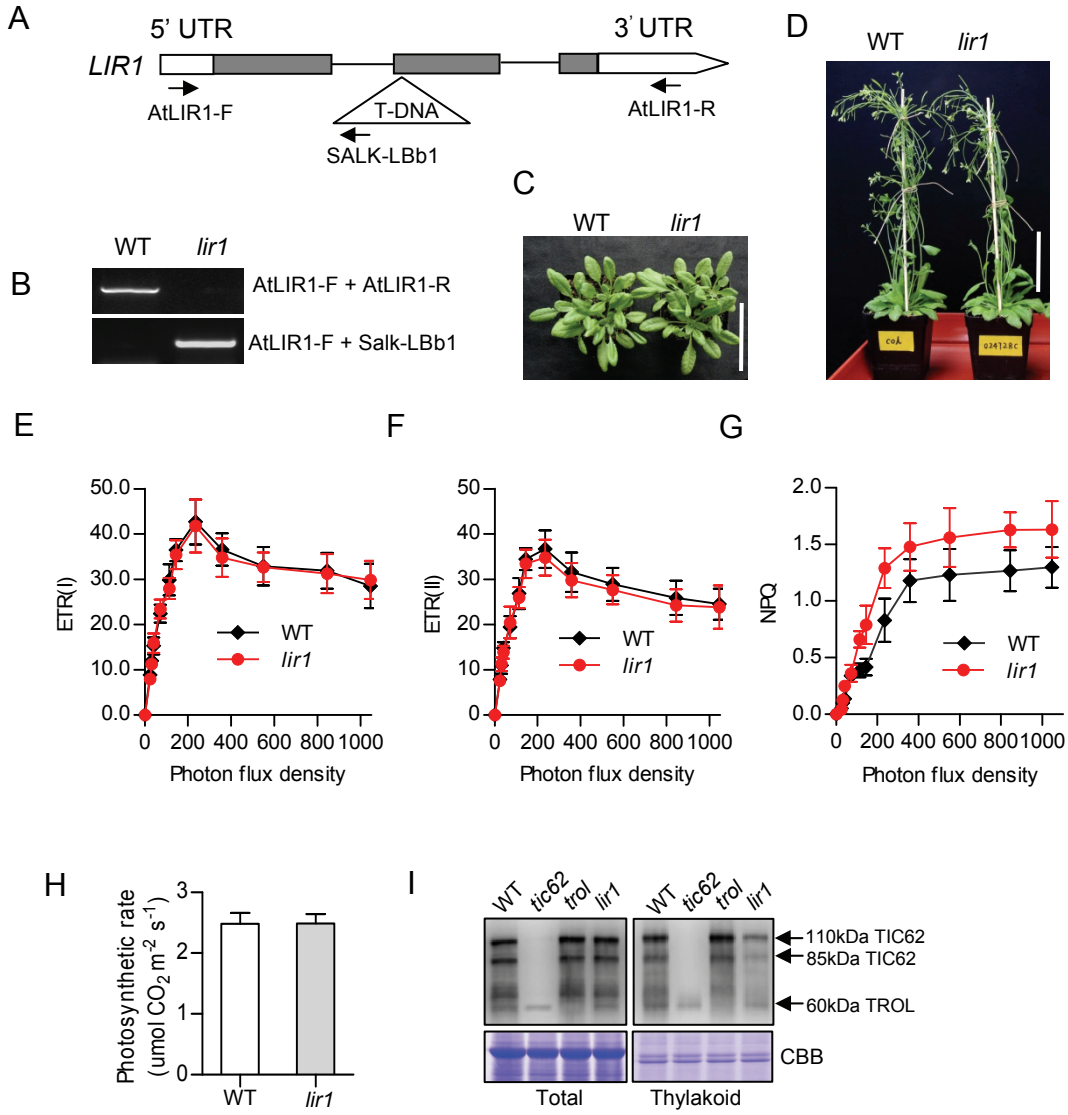


Supplemental Figure 7. Alignment of LIR1 Amino Acid Sequences.
Alignment of LIR1 domain amino acid sequences from the plant species shown in Supplemental Figure 6. Blue frames indicate angiosperms, orange frames gymnosperms (two isoforms of *Picea sitchensis*, *Picea abies*, *Pinus pinaster)* and green frames lower plants (moss, liverwort and green algae). The four EAC motifs are underlined in red. The red frames depict the sequences of *Brassicaceae* (*Arabidopsis thaliana*, *Arabidopsis lyrata*, *Thellungiella halophila*, *Brassica rapa*), which differ from the conserved motif. Zm denotes *Zea mays*, Sb *Sorghum bicolor*, Os *Oryza sativa*, Pt *Puccinellia tenuiflora*, Lp *Lolium perene*, Bd *Brachypodium distachyon*, Hv *Hordeum vulgare subsp*, Wa *Wolffia australiana*, Ptr *Populus trichocarpa*, Rc *Ricinnus communis,* St *Solanum tuberosum*, Sl *Solanum lycopersicum*, Can *Capsium* annuum, Vv *Vitis vinifera*, Cs *Cucumis sativus*, Cme *Cucumis melo subsp*, Cm *Citrofortunella microcarpa*, Cp *Carica papaya*, Gm *Glycine max*, Car *Cicer arietinum*, Mt *Medicago truncatula*, Psa *Pisum sativum*, Th *Thellungiella halophila*, Br *Brassica rapa*, Al *Arabidopsis lyrata*, At *Arabidopsis thaliana*, Psi *Picea sitchensis*, Pa *Picea abies*, Pp *Pinus pinaster*, Sle *Sphagnum lescurii*, Cat *Chlorokybus atmophyticus*, Cv *Chara vulgaris*, Tle *Takakia lepidozioides*, Ss *Schistochila sp*, and Bt *Bazzania trilobata*.

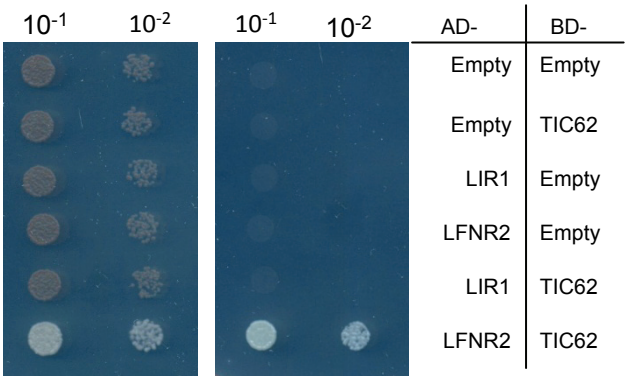
A



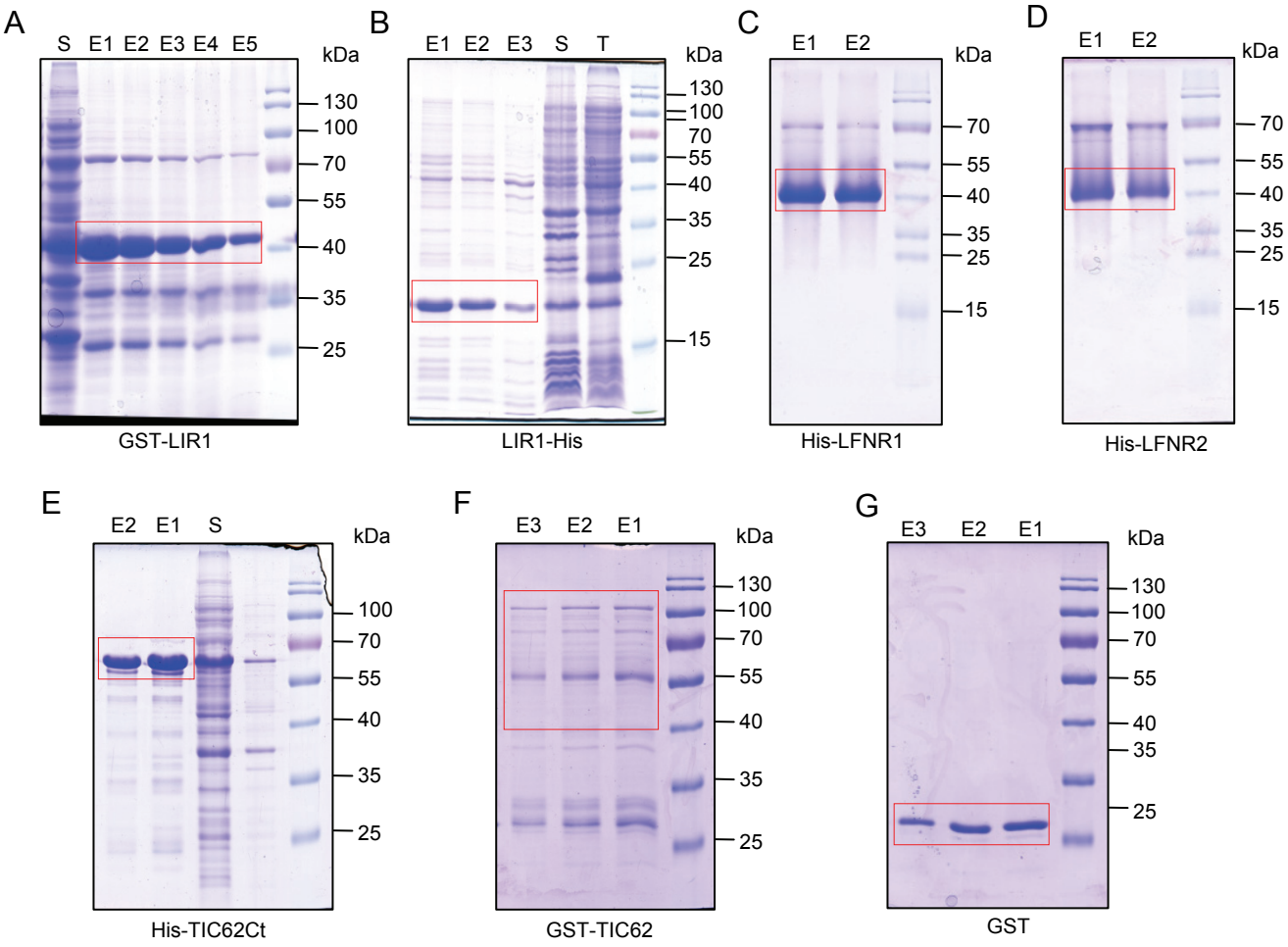
Supplemental Figure 8. Interaction between LIR1 and LFNR from Maize, Soybean, and Cucumber. Yeast two-hybrid analysis of interactions between LIR1 and LFNR proteins from *Zea mays*, *Glycine max*, and *Cucumis sativus*. Yeast lines harboring either the empty control plasmids (AD; activation domain, BD; bait domain) or plasmids containing the fusion constructs (AD-)Zm-/Gm-/Cs-LIR1 or (BD-)Zm-/Gm-/Cs-LFNR1/2 were grown on synthetic medium supplied with dextrose (SD) in the absence of Trp and Leu (SD/-LT, left panels) and on SD medium in the absence of Trp, Leu, His, and Ade (SD/-LTHA, right panels). Yeast cells were incubated until OD600=1, diluted 10 and 100-fold, and grown on culture medium for 3 d.



Supplemental Figure 9. Characteristics of Arabidopsis *lir1* Plants.
(A) Genomic structure of Arabidopsis *LIR1*. Gray boxes denote exons, black lines introns, and white boxes 5'- and 3'-untranslated regions. The insertion site of SALK_024728c (*lir1*) is indicated by a triangle. The binding sites for *LIR1* gene-specific primers (AtLIR1-F, AtLIR1-R) and T-DNA-specific left border (Salk-LBb1) used to screen *lir1* homozygous plants are depicted.
(B) PCR analysis of WT and *lir1* using genomic DNA as PCR template with the primers indicated in (A).
(C) and **(D)** Phenotypes of WT and *lir1* plants in the vegetative growth (C) and reproductive growth (D) stages. Bars = 10 cm.
(E) and (**F)** Electron transfer rate (ETR) of PSI (D) and PSII (E) of WT and *lir1* plants under different actinic light intensities. Bars represent means ± s.d.
(G) Nonphotochemical quenching (NPQ) of WT and *lir1* plants under different actinic light intensities. Bars represent means ± s.d.
(H) Photosynthetic rates of WT and *lir1* plants at 150 µmol photons m^{-2} s^{-1}.
(I) Immunoblot analysis of WT, *tic62*, *trol*, and *lir1* plants; 10 µg total leaf extract or thylakoid proteins was loaded onto the SDS gel and immunolabeled with TIC62 antibody. Coomassie Brilliant Blue (CBB) staining was used to verify equal loading of the gel.



Supplemental Figure 10. Interaction Test between Rice LIR1 and TIC62 by Yeast Two-Hybrid Assay. Yeast lines harboring either the empty control plasmids (AD; activation domain, BD; bait domain) or plasmids containing the fusion proteins (AD-LIR1, AD-LFNR2 or BD-TIC62) were grown on synthetic medium supplemented with dextrose (SD) in the absence of Trp and Leu (SD/-LT, left panels) and on SD medium in the absence of Trp, Leu, His, and Ade (SD/-LTHA, right panels). Yeast cells were incubated until OD_{600} = 1, diluted 10 and 100-fold, and grown on culture medium for 3 d. The interaction test between LFNR2 and TIC62 was used as a positive control.



Supplemental Figure 11. The CBB-Stained Gels of All Purified Proteins from *Escherichia coli* Used in this Research.

(A) to **(G)** CBB staining of purified GST-LIR1 (A), LIR1-His (B), His-LFNR1 (C), His-LFNR2 (D), His-TIC62Ct (E), GST-TIC62 (F) and GST (G) from *E.coli*. The red rectangle indicates the relevant purified proteins. After elution, 3 μL purified proteins were loaded in each well. S denotes the supernatant after ultrasonication of bacteria, T denotes the total proteins of bacteria, and E1 to E5 denote proteins of the first, second, third, fourth or fifth elution, respectively.

Supplemental Table 1. List of LC-MS identified unique peptide fragments in the 35 kDa band from coimmunoprecipitation.

Protein	UPC	Cover %	Peptide Sequence	MH+	XC	ΔCn	Ions
LFNR2	14	45.58	K.DGIDWADYK.K	1083.132	2.7849	0.3096	14|16
Os06g01850		%	K.DGIDWADYKK.Q	1211.305	2.489	0.3468	15|18
			K.DNTYVYMCGLK.G	1364.543	2.8134	0.2746	17|20
			K.DPNANIIMLATGTGIAPFR.S	1973.286	4.5745	0.5426	24|36
			K.EMLMPK.D	748.9782	2.0418	0.1154	8|10
			K.GIDDIMVSLAAK.D	1233.46	3.8084	0.4442	18|22
			K.GVCSNFLCDLKPGSDVK.I	1897.106	2.4579	0.3749	15|32
			K.HDEGVVTNK.Y	999.0601	2.5856	0.5069	13|16
			K.ITADDAPGETWHMVFSTEGEIPYR.E	2723.955	3.8867	0.5037	30|92
			K.KHDEGVVTNK.Y	1127.233	2.557	0.2475	13|18
			K.RLVYTNDQGEIVK.G	1535.727	2.9613	0.2067	16|24
			R.EGQSIGVIADGVDK.N	1388.506	3.1348	0.4238	18|26
			R.LVYTNDQGEIVK.G	1379.584	2.9499	0.1002	15|22
			R.MAEYKEELWELLK.K	1682.962	3.3502	0.3737	18|24
LFNR1	15	50.00	K.DGIDWLDYKK.Q	1253.385	2.4642	0.4864	14|18
Os02g01340		%	K.DNTYVYMCGLK.G	1364.543	2.8134	0.2746	17|20
			K.DPNATIIMLGTGTGIAPFR.S	1946.26	4.4318	0.3195	22|36
			K.EMLMPK.D	748.9782	2.0418	0.1154	8|10
			K.GIDDIMIDLAAK.D	1275.497	3.6524	0.3802	18|22
			K.GVCSNFLCDLKPGSDVK.I	1897.106	2.4579	0.3749	15|32
			K.KQVDGVVTNK.Y	1088.24	2.5345	0.3719	13|18
			K.RLVYTNDQGEIVK.G	1535.727	2.9613	0.2067	16|24
			R.EGQSIGVIPDGIDK.N	1428.57	2.7549	0.137	16|26
			R.FRLDFAVSR.E	1111.278	3.0978	0.2028	13|16
			R.ITGDDAPGETWHMVFSTDGEIPYR.E	2695.901	3.1482	0.2326	22|46
			R.LVYTNDQGEIVK.G	1379.584	2.9499	0.1002	15|22
			R.LYSIASSAIGDFADSK.T	1645.792	3.1821	0.5452	19|30
			R.MAEYKDELWELLKK.D	1797.108	4.1151	0.3621	29|52
			R.MKEIAPER.F	974.1603	2.459	0.2446	13|14

Supplemental Table 2. List of LC-MS identified unique peptide fragments in the 25 kDa band from coimmunoprecipitation.

Protein	UPC	Cover %	Peptide Sequence	MH+	XC	∆Cn	Ions
LIR1	5	41.41	K.LSSSAAVAVSR.A	1048.176	1.9954	0.3605	10|20
Os01g01340		%	R.AAAEEVDR.D	860.8923	1.9482	0.2318	8|14
			R.AAAEEVDRDYLSYDEPTTVFPEEAC	3901.05	4.2106	0.5681	33|132
			R.DYLSYDEPTTVFPEEACDDLGGEFC	3059.18	3.0163	0.4019	19|50
			R.SLQIQAPR.R	913.0567	2.0658	0.2043	11|14

UPC: (Unique peptide count) the count of unique peptide sequences associated with specific protein. Cover %: protein's sequence coverage. The fields enumerated for each unique peptide include sequence, MH+ (the molecular weight of the peptides), XC (Xcorr, the cross-correlation value), ∆Cn (the change in cross-correlation), Ions (the ion value = dividing the number of matched ions by the total number of ions).

Supplemental Table 3. Primers used in this research.

Purpose	Primer name	Primer sequence
Os-LIR1 CRISPR	OsLIR1-CRISPR-F	GTGTGGGGCGCAGCCTGCAGATTC
	OsLIR1-CRISPR-R	AAACGAATCTGCAGGCTGCGCCCC
P *Os-LIR1*:Os-LIR1-GFP	pOsLIR1-EcoR I-F	CGGAATTCTCAGCATGGAGCCCAACCTCCCGTC
	pOsLIR1-Kpn I-R	GGGGTACCCTTCTTCTTCTTCTTTCTTCTTCTT
	OsLIR1-Kpn I-F	GGGGTACCATGCAGACCGCTGCTAGCAGTG
	OsLIR1-Xba I-R	GCTCTAGAGGTGGCCTTGCAGAACTCT
qRT-PCR	OsACTIN-qRT-F	CAACACCCCTGCTATGTACG
	OsACTIN-qRT-R	CATCACCAGAGTCCAACACAA
qRT-PCR	OsLIR1-qRT-F	CTGCGGAGGTGGACTACAG
	OsLIR1-qRT-R	AGAGCTTGGCCTCTGGGTA
qRT-PCR	GFP-qRT-F	TATATCATGGCCGACAAGCA
	GFP-qRT-R	GATGTTGTGGCGGATCTTG
qRT-PCR	Flag-qRT-F	AGCTTATCGATACCGTCGAG
GST-Os-LIR1	OsLIR1-EcoR I-F	CGGAATTCATGCAGACCGCTGCTAGCAGTG
	OsLIR1-Xho I-R	CCGCTCGAGTCAGGTGGCCTTGCAGAACTCT
35S:Flag-Os-LIR1	OsLIR1-Kpn I-F	GGGGTACCATGCAGACCGCTGCTAGCAGTG
	OsLIR1-Sac I-R	AAAGAGCTCTCAGGTGGCCTTGCAGAACTCT
35S:Os-LFNR1-MYC	OsLFNR1-Kpn I-F	GAAGGTACCATGGCCGCCGTCACGGCTGCGGCCGTC
	OsLFNR1-MYC-BamH I-R	CGCGGATCCCGTAGACTTCCACATTCCATTGC
35S:Os-LFNR2-MYC	OsLFNR2-Kpn I-F	GAAGGTACCATGGCCGCCGTGAACACAGTGTCG
	OsLFNR2-MYC-BamH I-R	CGCGGATCCCGTAGACTTCCACGTTCCATTGC
Os-*tic62* T-DNA test	LB2	CGCTCATGTGTTGAGCATAT
	OsTIC62-F1	ATGGAGCAAGCAGCGAAGGCCA
	OsTIC62-R1	CTATAGTTTGGGGGTAGATGGG
	OsTIC62-R2	GACTAAATTACTTCTTATACAT
His-Os-TIC62Ct	OsTIC62-EcoR Ⅰ-F	CCGGAATTCCCTCCGCCCGAACCTGAGGTAGTT
	OsTIC62-Not Ⅰ-R	ATAAGAATGCGGCCGCCTATAGTTTGGGGGTAGATGGG
GST-Os-TIC62	OsTIC62-EcoR Ⅰ-F	CCGGAATTCATGGAGCAAGCAGCGAAGGCCA
	OsTIC62-Not Ⅰ-R	ATAAGAATGCGGCCGCCTATAGTTTGGGGGTAGATGGG
Os-LIR1-His	OsLIR1-Nde1-F	GGAATTCCATATGCAGACCGCTGCTAGCAGTG
	OsLIR1-Xho1-R noTGA	CCGCTCGAGGGTGGCCTTGCAGAACTCTCCG
His-Os-LFNR1	OsLFNR1-Nde1-F	GGAATTCCATATGATGGCCGCCGTGAACACAGTGT
	OsLFNR1-Xho1-R	CCGCTCGAGTCAGTAGACTTCCACATTCCAT
His-Os-LFNR2	OsLFNR2-Nde1-F	GGAATTCCATATGATGGCCGCCGTCACGGCTGCGG
	OsLFNR2-Xho1-R	CCGCTCGAGTTAGTAGACTTCCACGTTCCAT
Os-LIR1 pGADT7	OsLIR1-EcoR I-F	CGGAATTCATGCAGACCGCTGCTAGCAGTG
	OsLIR1-Xho I-R	CCGCTCGAGTCAGGTGGCCTTGCAGAACTCT
Os-LFNR1 pGBKT7	OsLFNR1-EcoR I-F	CGGAATTCATGGCCGCCGTCACGGCTGCGGCCGTC
	OsLFNR1-BamH I-R	CGCGGATCCTCAGTAGACTTCCACATTCCATTGC
Os-LFNR2 pGBKT7	OsLFNR2-Kpn I-F	GAAGGTACCATGGCCGCCGTGAACACAGTGTCG

	OsLFNR2-MYC-BamH I-R	CGCGGATCCTTAGTAGACTTCCACGTTCCATTGC
Os-TIC62 pGBKT7	OsTIC62-Sfi I-F	GCAGGCCATGGAGGCCATGGAGCAAGCAGCGAAGGCCA
	OsTIC62-Sfi I-R	GCAGGCCTCCATGGCCCTATAGTTTGGGGGTAGATGGG
Zm-LIR1 pGADT7	ZmLIR1-EcoR I-F	CCGGAATTCATGCAGGCTGCCGCTACTGCCGC
	ZmLIR1-Xho I-R	CCGCTCGAGTCAGGCGTGCGCCAGCTCCTTGGAG
Zm-LFNR1 pGBKT7	ZmLFNR1-EcoR I-F	CCGGAATTCATGGCTGCCGTGACCGCGGCGG
	ZmLFNR1-BamH I-R	CGCGGATCCTCAGTAGACTTCGACGTTCCATTGC
Zm-LFNR2 pGBKT7	ZmLFNR2-EcoR I-F	CCGGAATTCATGGCCACCGTCATGGCCGCG
	ZmLFNR2-BamH I-R	CGCGGATCCTTAGTAGACCTCCACATTCCATTGA
Gm-LIR1 pGADT7	GmLIR1-EcoR I-F	CCGGAATTCATGCAAACATCCTTAACCTTTGCTG
	GmLIR1-Xho I-R	CCGCTCGAGCTAGTAGACACCCTTCTGATACTCG
Gm-LFNR1-pGBKT7	GmLFNR1-EcoR I-F	CCGGAATTCATGGCTGCTGCGGTTAGTGCTGC
	GmLFNR1-BamH I-R	CGCGGATCCTTAATAGACTTCGACATTCCATTGC
Gm-LFNR2 pGBKT7	GmLFNR2-EcoR I-F	CCGGAATTCATGGCTGCTGCGGTTAGTGCTG
	GmLFNR2-BamH I-R	CGCGGATCCTTAATAGACTTCGACATTCCATTGC
Cs-LIR1 pGADT7	CsLIR1-BamH I-F	CGGGATCCATGCAGTTCCAGGCAGCTCTTTCCA
	CsLIR1-Xho I-R	CCGCTCGAGCTAGTAAACTCCTTTTTGATACTCT
Cs-LFNR1 pGBKT7	CsLFNR1-EcoR I-F	CGGAATTCATGGCCGCCGCCGTAACCGCCGCCG
	CsLFNR1-Bam H I-R	CGGGATCCTCAATAAACTTCCACATTCCATTGC
Os-*lir1-1* test	OsLIR1-dCAPS-F	GGCCGTGTTGCCCGCTGCTGTGAAGGGGCGCAGCCTGCG AATT
	OsLIR1-dCAPS-R	TGTTAGAGCTGTAGTCCACCTCCGCAGCCTCC
At-*lir1* T-DNA test	AtLIR1-F	TCACTAAACCTATCTTCTTAACCA
	AtLIR1-R	CTTAATTCTTGTGTAAAACCCA
	Salk-LBb1	GCGTGGACCGCTTGCTGCAACT
BiFC for Os-LIR1	OsLIR1-Pac I-F	CCCTTAATTAATATGCAGACCGCTGCTAGCAGTG
	OsLIR1-Asc I-R	TTGGCGCGCCCGGTGGCCTTGCAGAACTCTCCG
BiFC for Os-LFNR1	OsLFNR1-Pac I-F	CCCTTAATTAACATGGCCGCCGTCACGGCTGCGG
	OsLFNR1-Asc I-R	TTGGCGCGCCCGTAGACTTCCACGTTCCATTGCTCG
BiFC for Os-LFNR2	OsLFNR2-Pac I-F	CCCTTAATTAACATGGCCGCCGTGAACACAGTGT
	OsLFNR2-Asc I-R	TTGGCGCGCCCGTAGACTTCCACATTCCATTGCTCC
BiFC for Os-RBCs	OsRBCs-Pac I-F	CCCTTAATTAACATGGCTCCCTCGGTGATGGCTTCGT
	OsRBCs-Asc I-R	AAAGGCGCGCCCTTAGTTGCCGCCTGACTCCTCGCAA

Supplemental Methods. Phylogenetic Analysis.

The protein sequences of LIR1 from 37 plant species were aligned with MUSCLE tools (Edgar, 2004) from EBI webserver (http://www.ebi.ac.uk/Tools/msa/muscle/). The resulting alignment was used for phylogenetic analysis. The topology was inferred using minimal evolution (ME) as implemented in MEGA version 4 (Tamura et al., 2007) using a Jones-Taylor-Thornton (JTT) substitution model with 1000 bootstrap replicates, uniform rates among sites and gaps with pairwise deletion. The initial tree was obtained by Neighbor joining (NJ) method and we used close-neighbor-interchange search to examine the neighborhood of the NJ tree to find the potential ME tree. The numbers at the nodes refer to bootstrap support percentage.

Supplemental References.

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