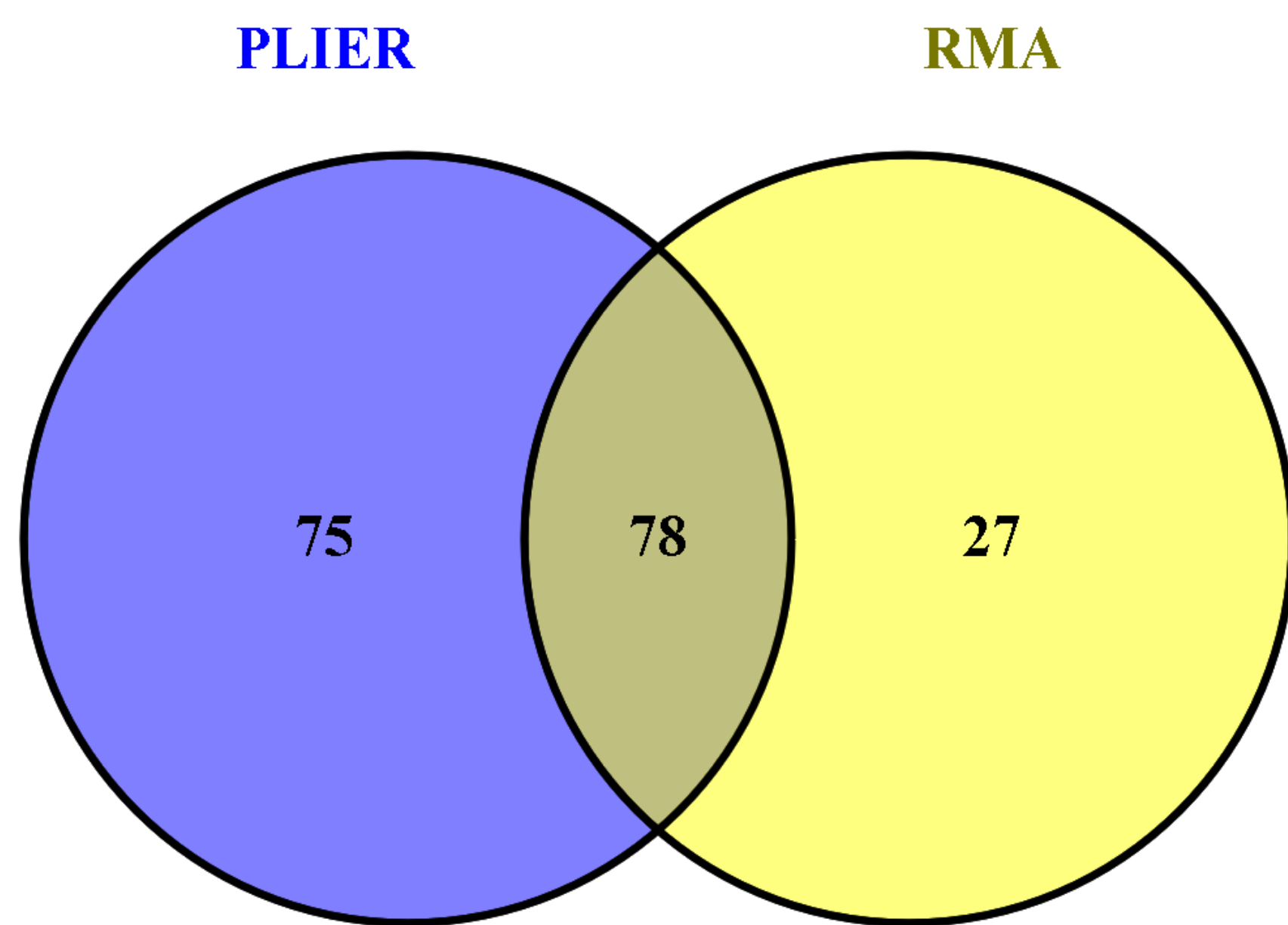
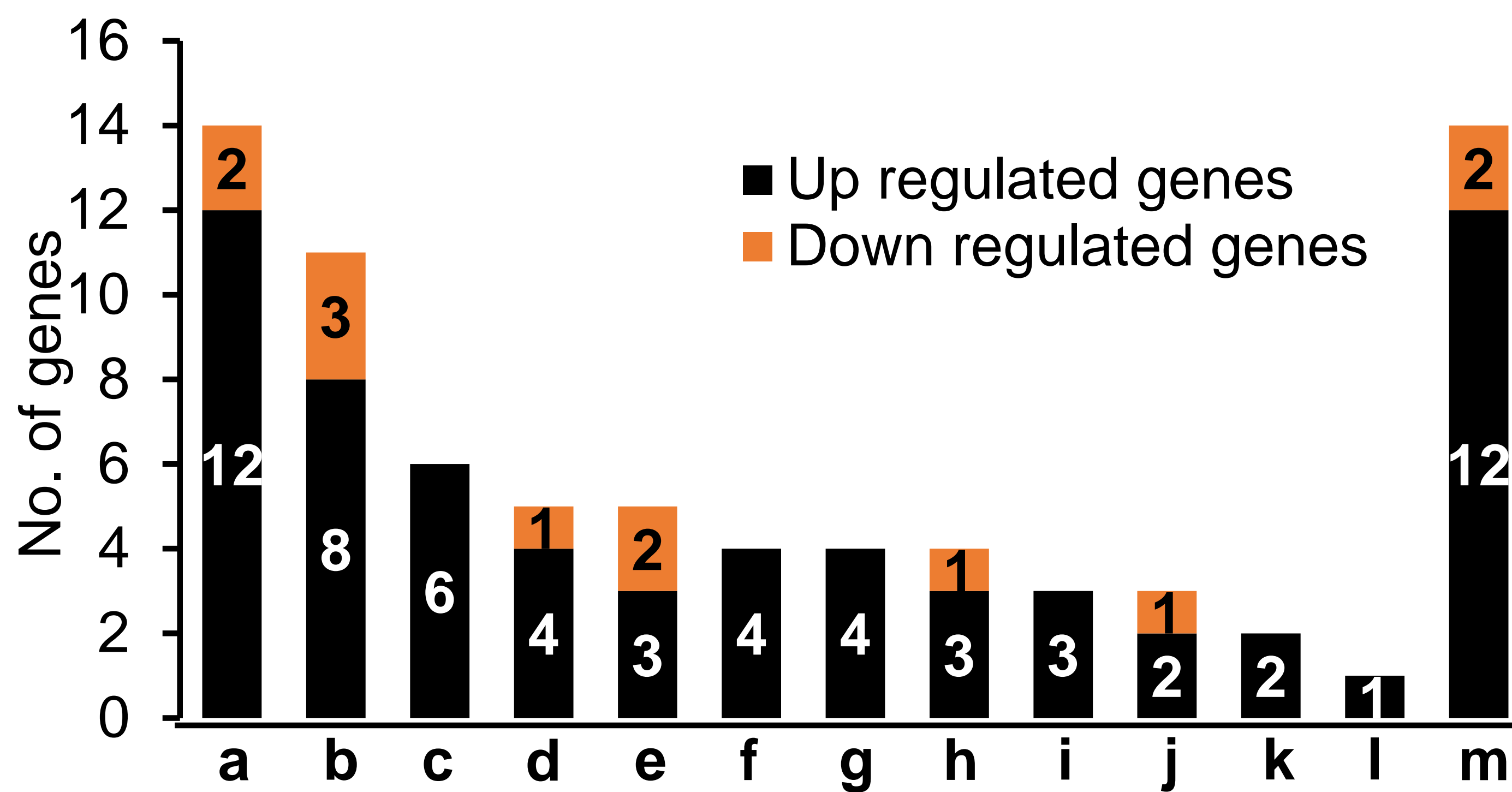


Supplemental Figure 1

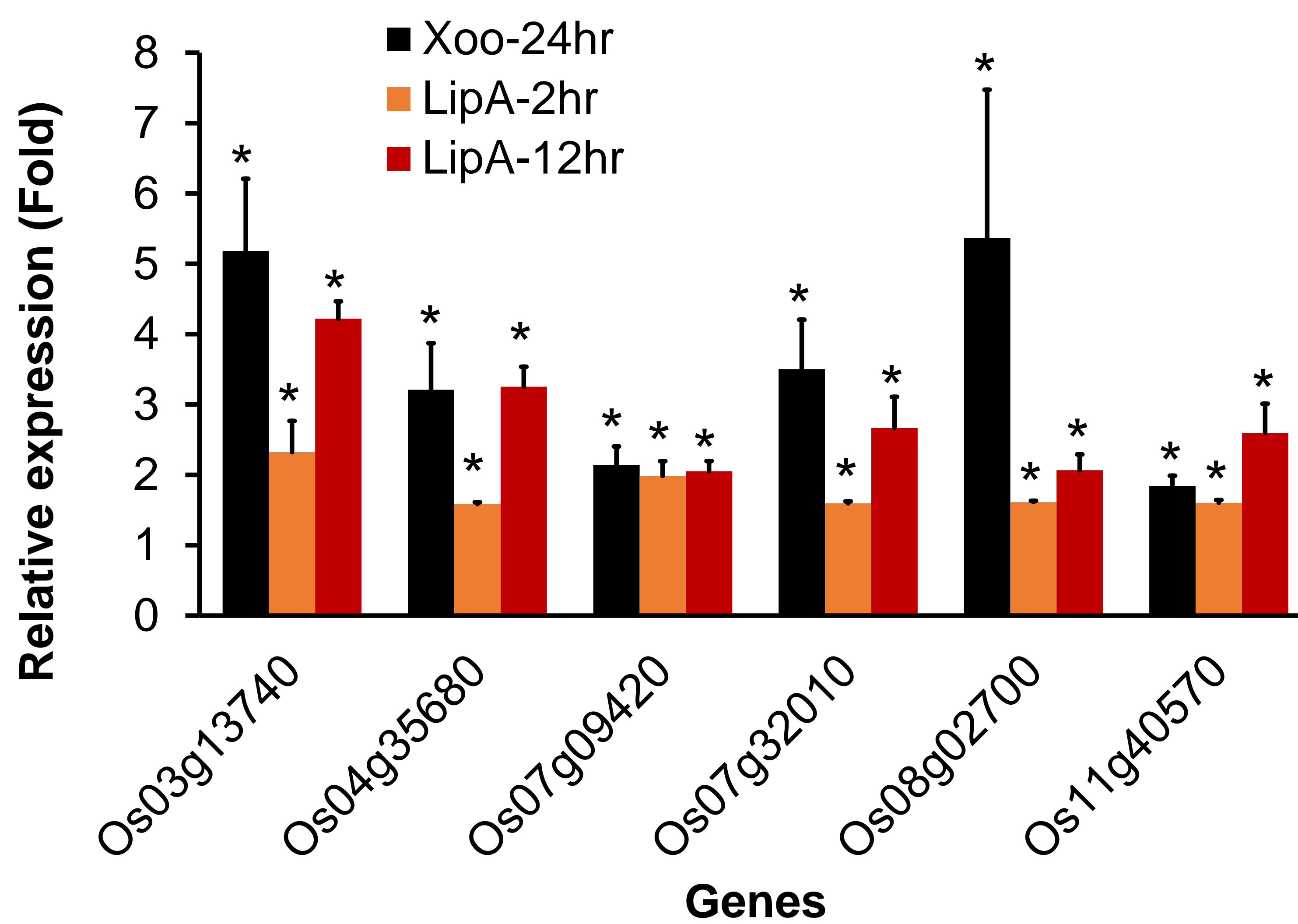
A



B



C

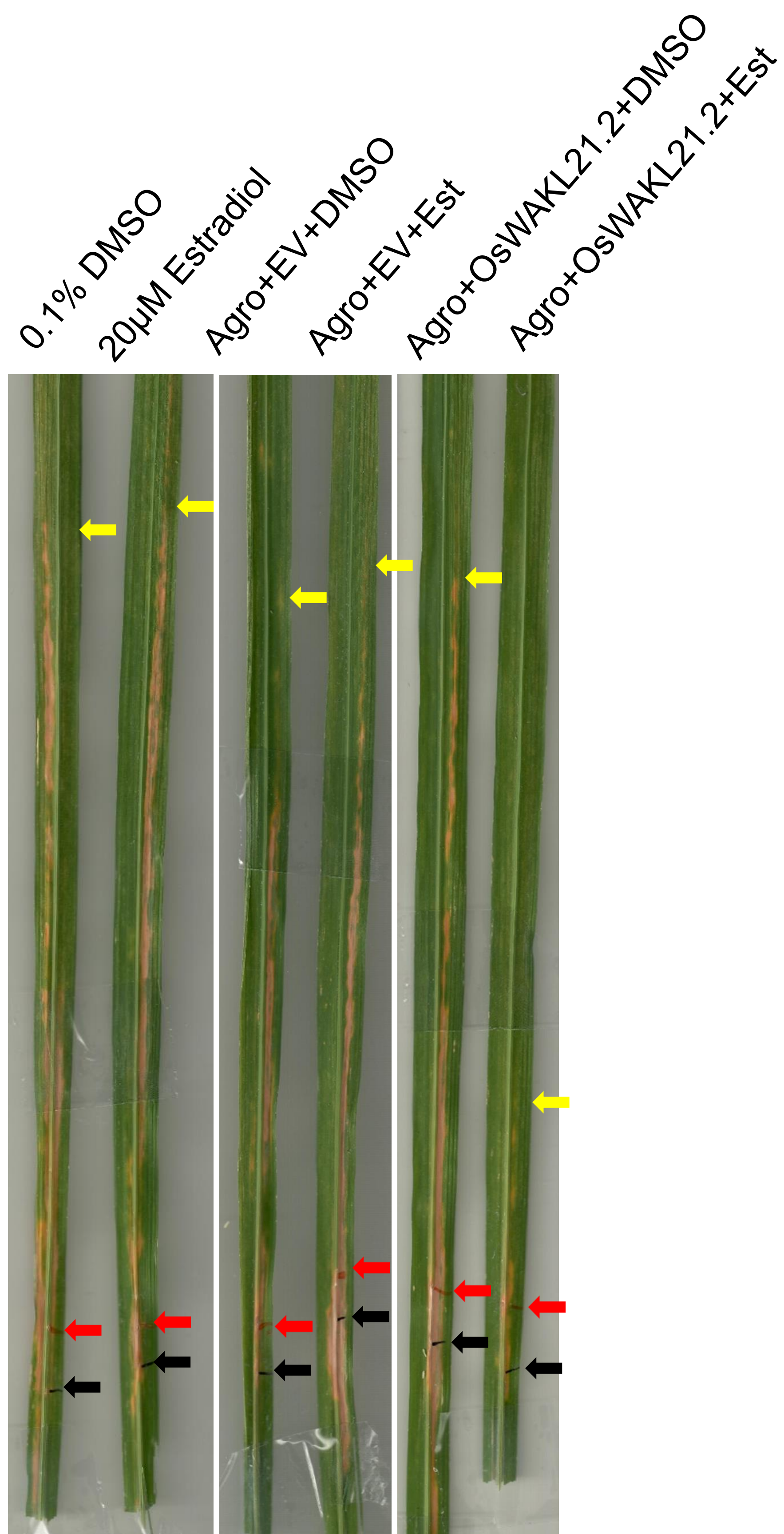


Supplemental Figure 1: Transcriptome profiling of rice leaves after treatment with LipA.

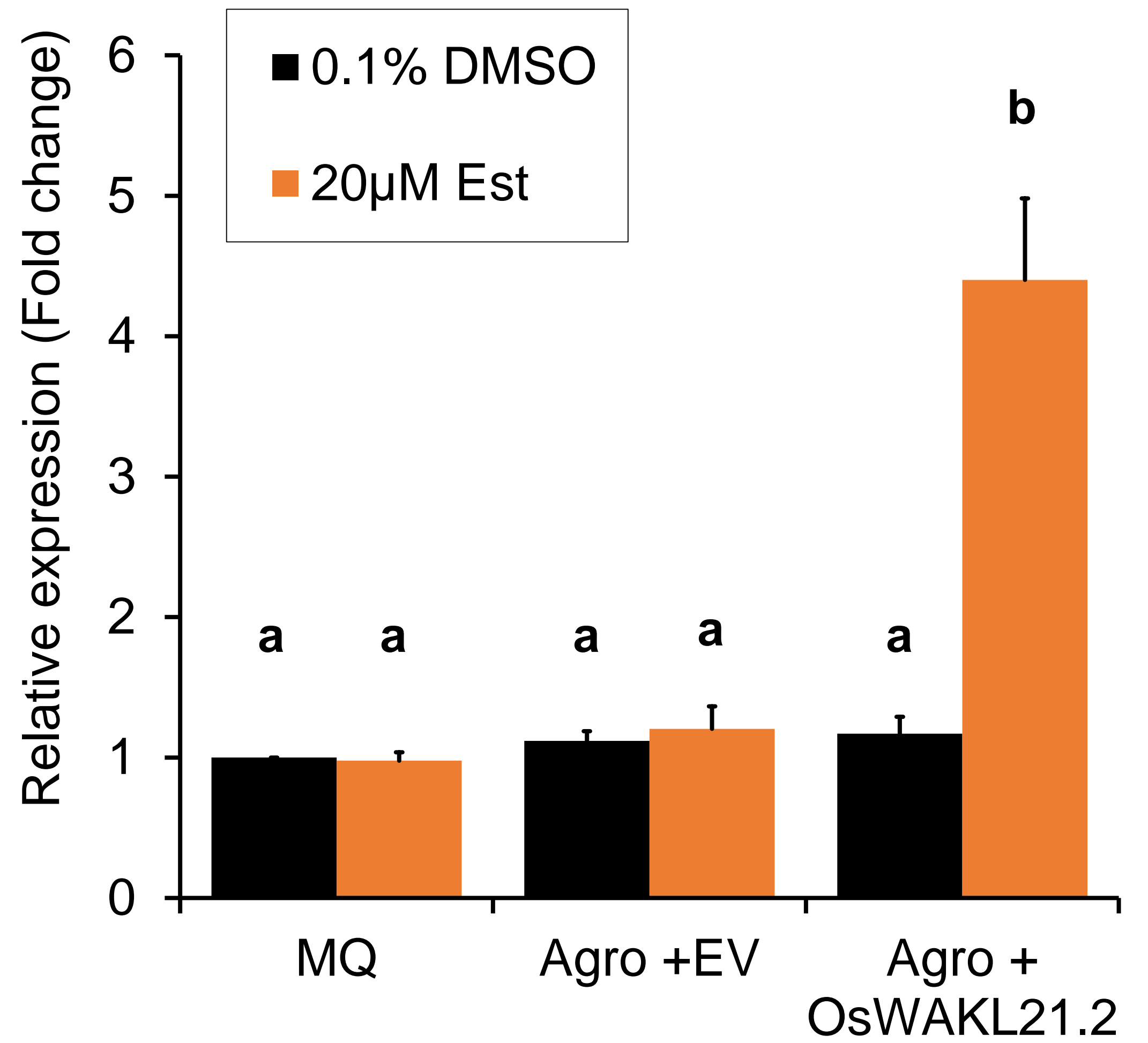
- (A) Venn diagram indicating number of unique and common genes differentially expressed after 2hr of LipA treatment using RMA and PLIER16 analysis.
- (B) Functional categorization using MapMan tool showing number of upregulated and downregulated genes in various functional categories. a: Signal transduction, b: Transcription/transcription factors, c: Defense, d: Hormone metabolism, e: Transport, f: Stress, g: Protein synthesis/turnover, h: Metabolism, i: Secondary metabolites, j: Redox, k: Cell wall structure/synthesis, l: Transposons, m: Others.
- (C) qRT-PCR validation of six differentially expressed genes after 2hr and 12hr of LipA treatment and also after 24hr of *Xoo* treatment. 12-14 days old rice leaves were infiltrated either with LipA (0.5mg/ml) or *Xoo* (O.D. 1.0). Each bar represents average value and error bar denotes standard error (SE) of at least three different experiments. Relative expression was calculated in leaves treated with LipA or *Xoo* with respect to leaves treated with buffer. Asterisk (*) represents significant difference in fold change with $p < 0.05$. *OsActin1* was used as internal control for qRT-PCR. The relative fold change was calculated by using $2^{-\Delta\Delta Ct}$ method.

Supplemental Figure 2

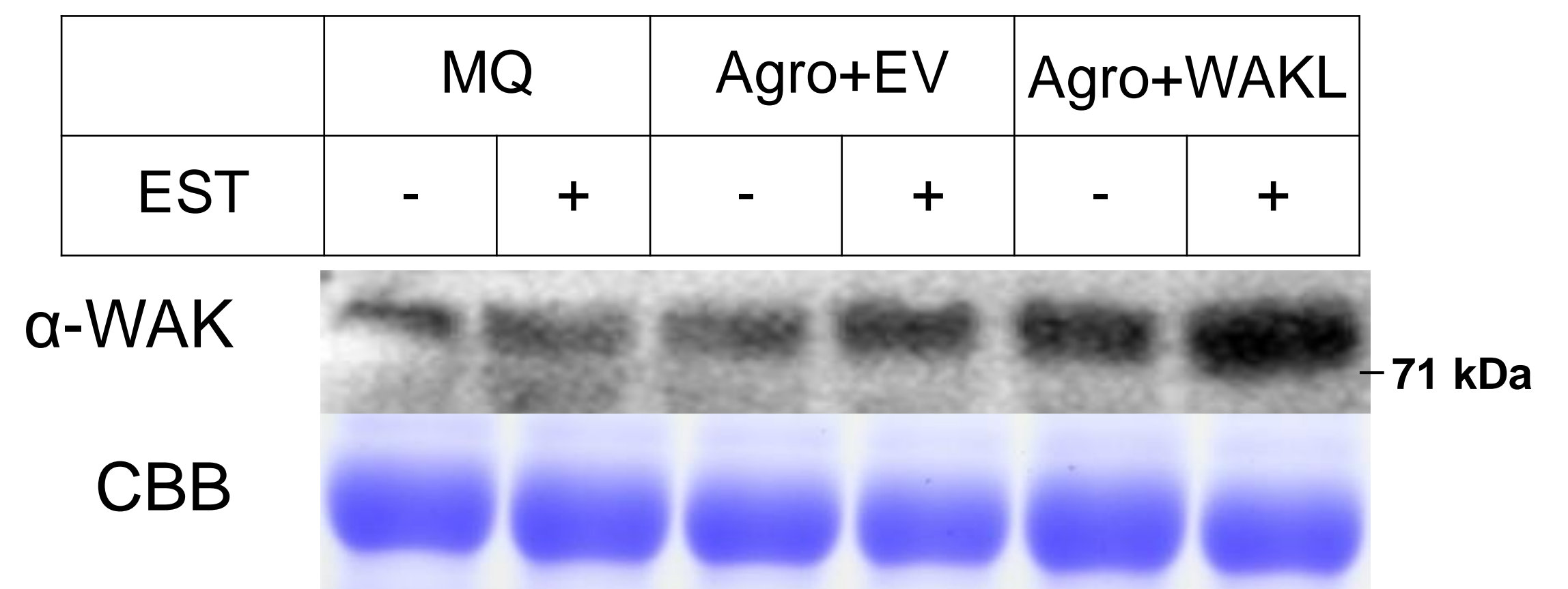
A



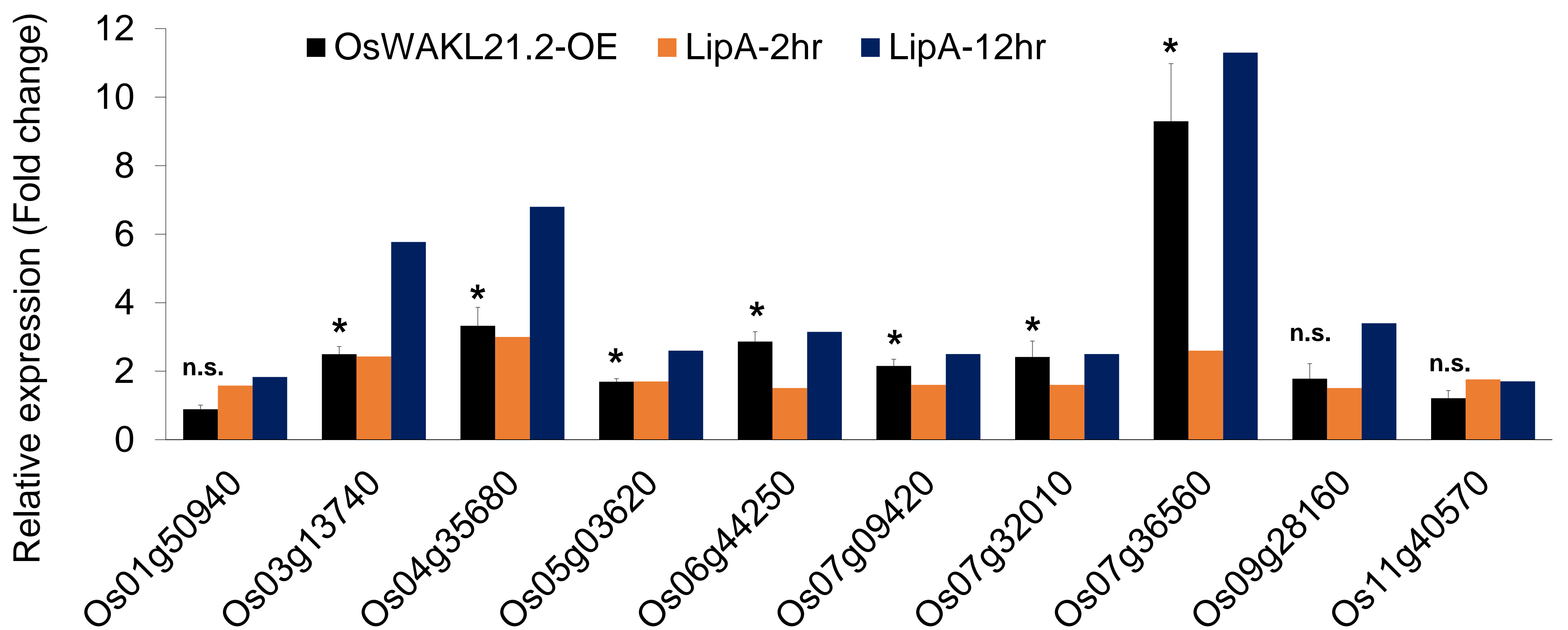
B



C



D

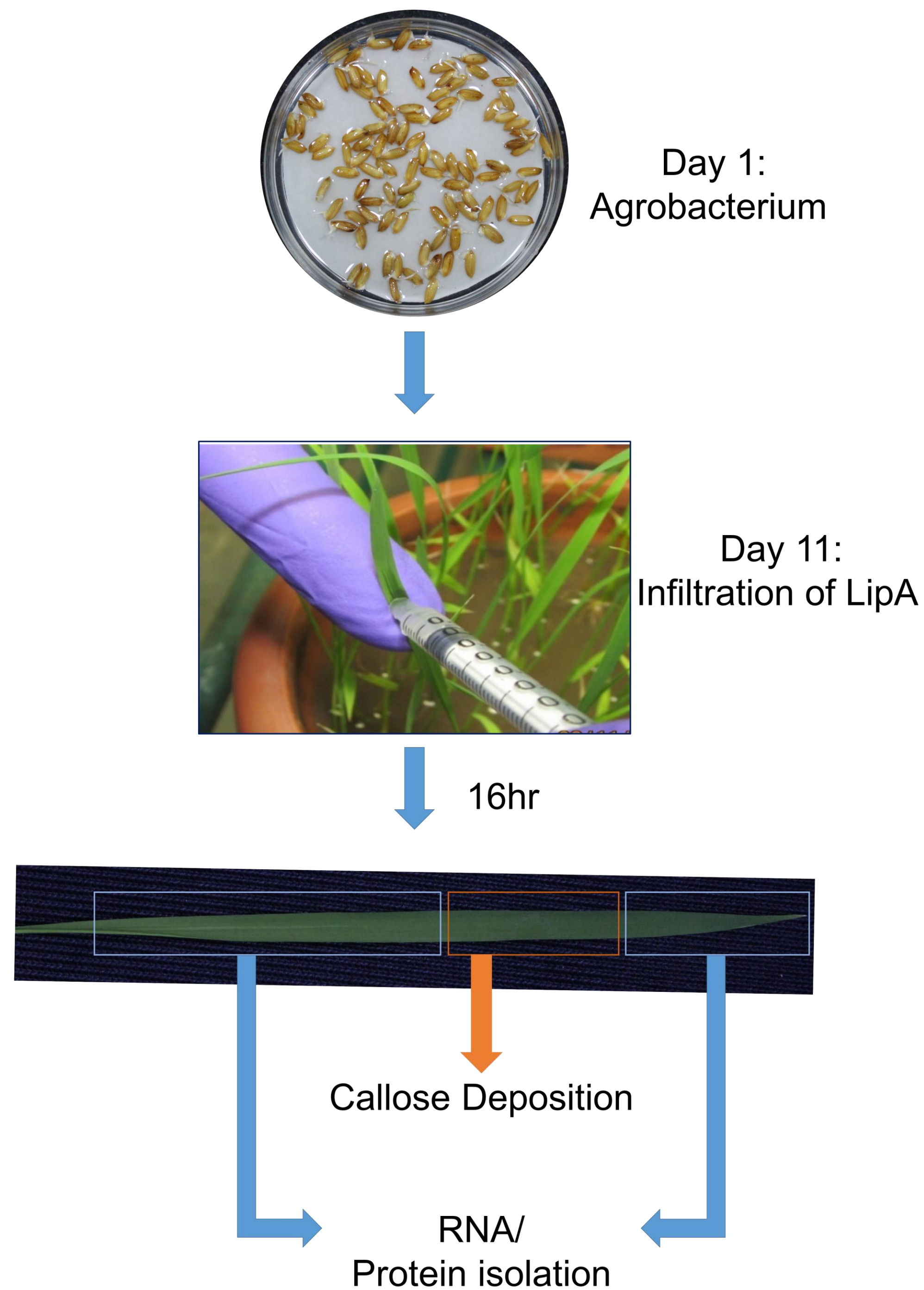


Supplemental Figure 2: Overexpression of *OsWAKL21.2* induces rice immune responses:

- (A) Representative image of lesion length caused by *Xoo*. The rice leaf samples mentioned in Supplemental figure 1A were pin prick inoculated with *Xoo*. The black mark indicate point of *Agrobacterium* injection while red mark indicate point of pin prick inoculation of *Xoo*. The yellow mark indicate the last point of disease progression. The quantification of lesion length in an experiment is mentioned in Figure 3C.
- (B) qRT-PCR indicating relative expression of *OsWAKL21.2* in rice leaves after 24hr of injection with either MQ (Mock), *Agrobacterium* containing empty vector or *Agrobacterium* containing wild type *OsWAKL21.2* under uninduced (0.1% DMSO) and induced (20 μ M estradiol) condition. Expression level in leaves treated with mock (0.1% DMSO) was considered as 1 and relative expression was calculated with respect to it. small letters (a, b and c) above the bars indicates significant difference with $p < 0.05$.
- (C) Western blot performed from protein isolated from rice mid-veins samples as mentioned in the Supplemental figure 1A. Anti *OsWAKL21.2*₃₇₆₋₇₂₅ antibody (α -WAK) was used for Western blotting. CBB indicate Coomassie brilliant blue staining of gel ran parallelly for loading control.
- (D) Relative expression of ten LipA responsive genes either after *OsWAKL21.2* overexpression or 2hr and 12hr post LipA treatment. These genes are LOC_Os03g13740 (a ubiquitin ligase, *OsPUB41*), LOC_Os04g35680 (a ubiquitin ligase, *OsPUB38*), LOC_Os05g03620 (a Crinkly4 subfamily protein, *OsCRR3*), LOC_Os06g44250 (a haemolysin-III), LOC_Os07g09420 (An AAA-type ATPase), LOC_Os07g32010 (a UDP-glucuronosyl and UDP-glucosyl transferase domain-containing protein), LOC_Os07g36560 (a transferase family protein), LOC_Os01g50940 (a Myc-type, basic helix-loop-helix (bHLH) domain-containing protein), LOC_Os09g28160 (a mitochondrial phosphate carrier protein) and LOC_Os11g40570 (a plant viral response family protein). Expression change after *OsWAKL21.2* overexpression was analyzed by qRT-PCR while 2hr and 12hr post LipA treatment data represent the microarray data. For each gene, transcript level of uninduced condition (treatment with *Agrobacterium* carrying *OsWAKL21.2* with 0.1% DMSO) was considered as 1 and was compared to induced condition (treatment with *Agrobacterium* carrying *OsWAKL21.2* with 20 μ M estradiol). Asterisk (*) represents significant difference with $p < 0.05$. n.s. indicate not significant difference in relative expression.

In **B** and **D**, each bar represents average value and error bar denotes standard error (SE) of at least three different experiments. *OsActin1* was used as internal control for qRT-PCR. The relative fold change was calculated by using $2^{-\Delta\Delta C_t}$ method.

Supplemental Figure 3

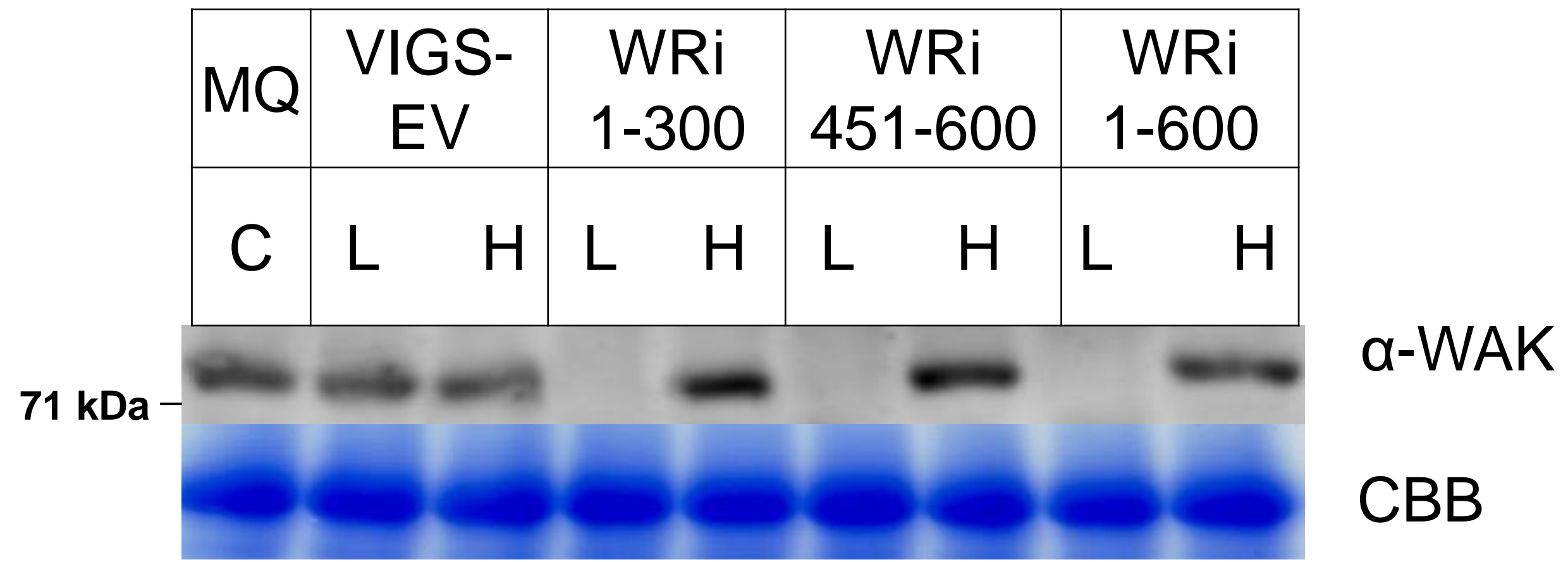


Supplemental Figure 3: Methodology for downregulation of *OsWAKL21.2* in rice seedlings using Virus Induced Gene Silencing (VIGS).

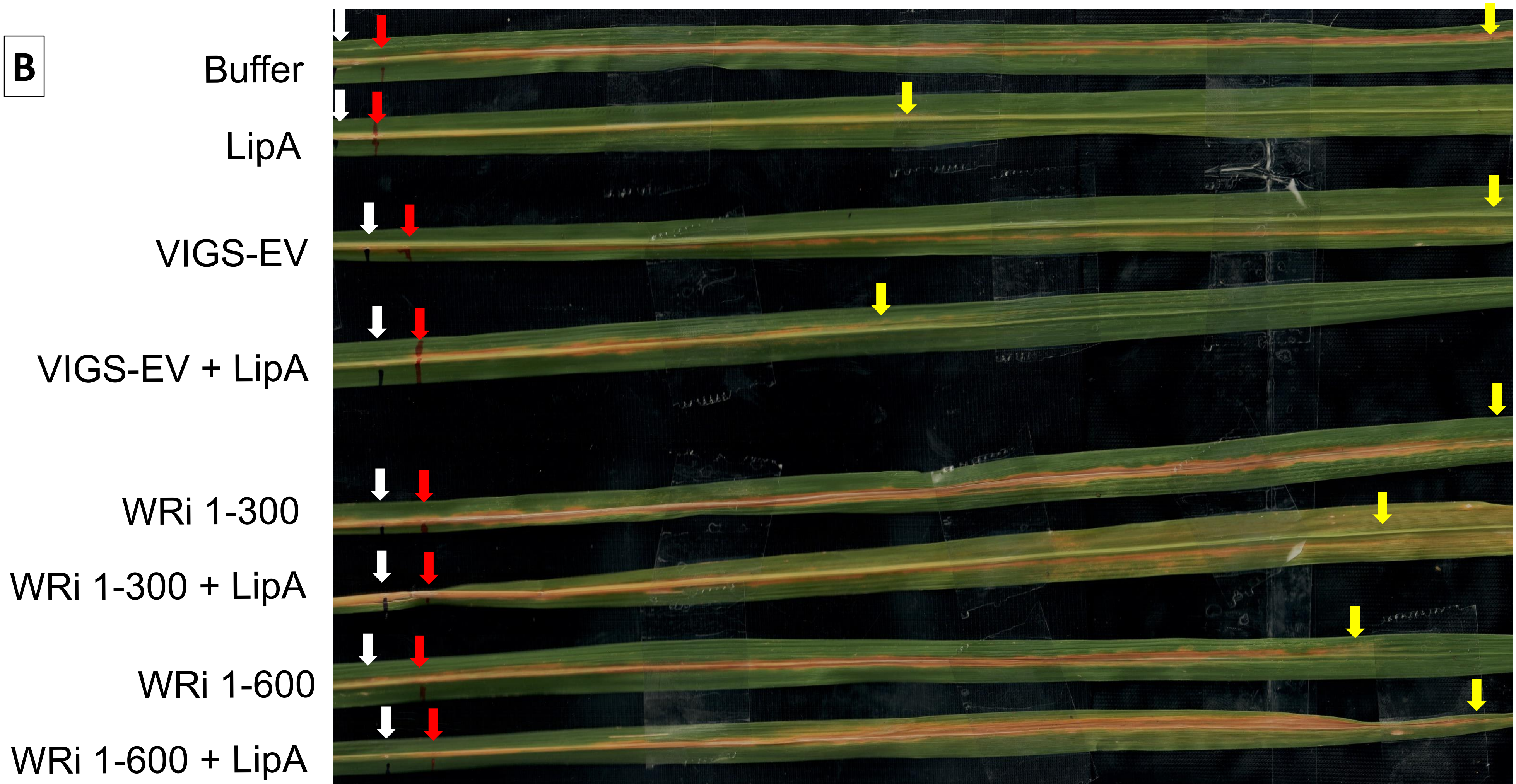
One day old seedlings were submerged in *Agrobacterium* suspension carrying VIGS vector for 24hr and washed subsequently. Seedlings were grown on water and third leaf was infiltrated with LipA (0.5mg/ml) on day 11. After 16hr, infiltrated zone (in orange box) was collected for visualization of callose deposition while the rest of the leaf (in blue box) was collected for Western blot or qRT-PCR analysis.

Supplemental Figure 4

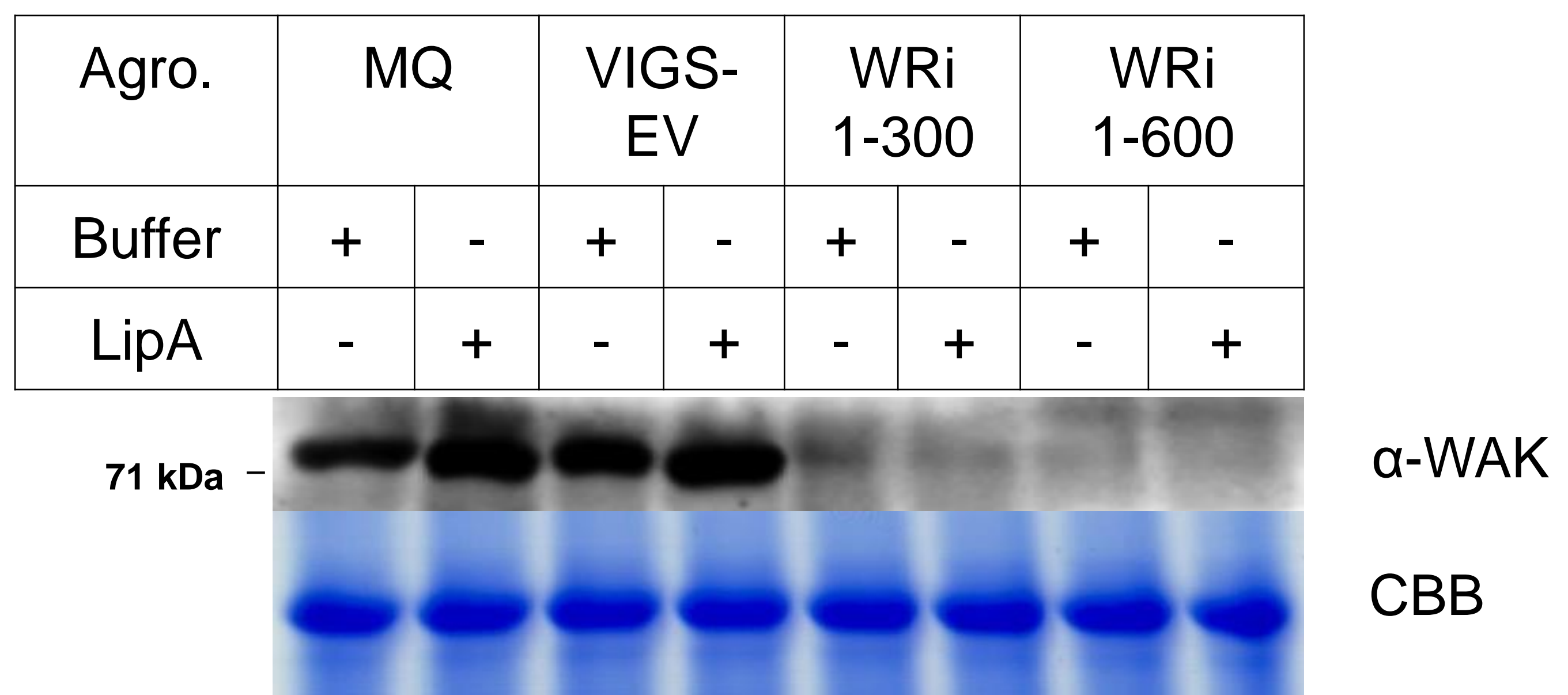
A



B



C

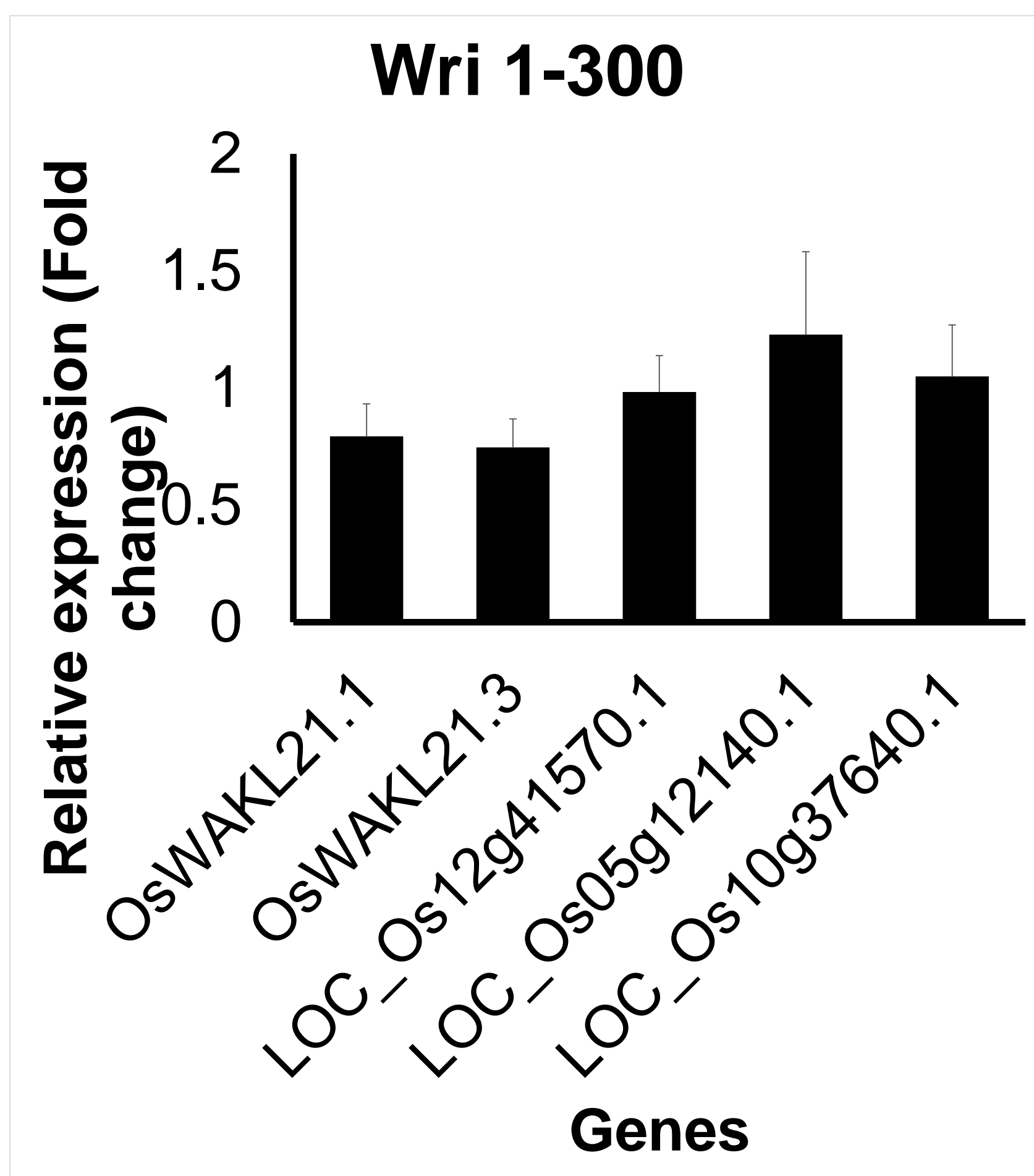
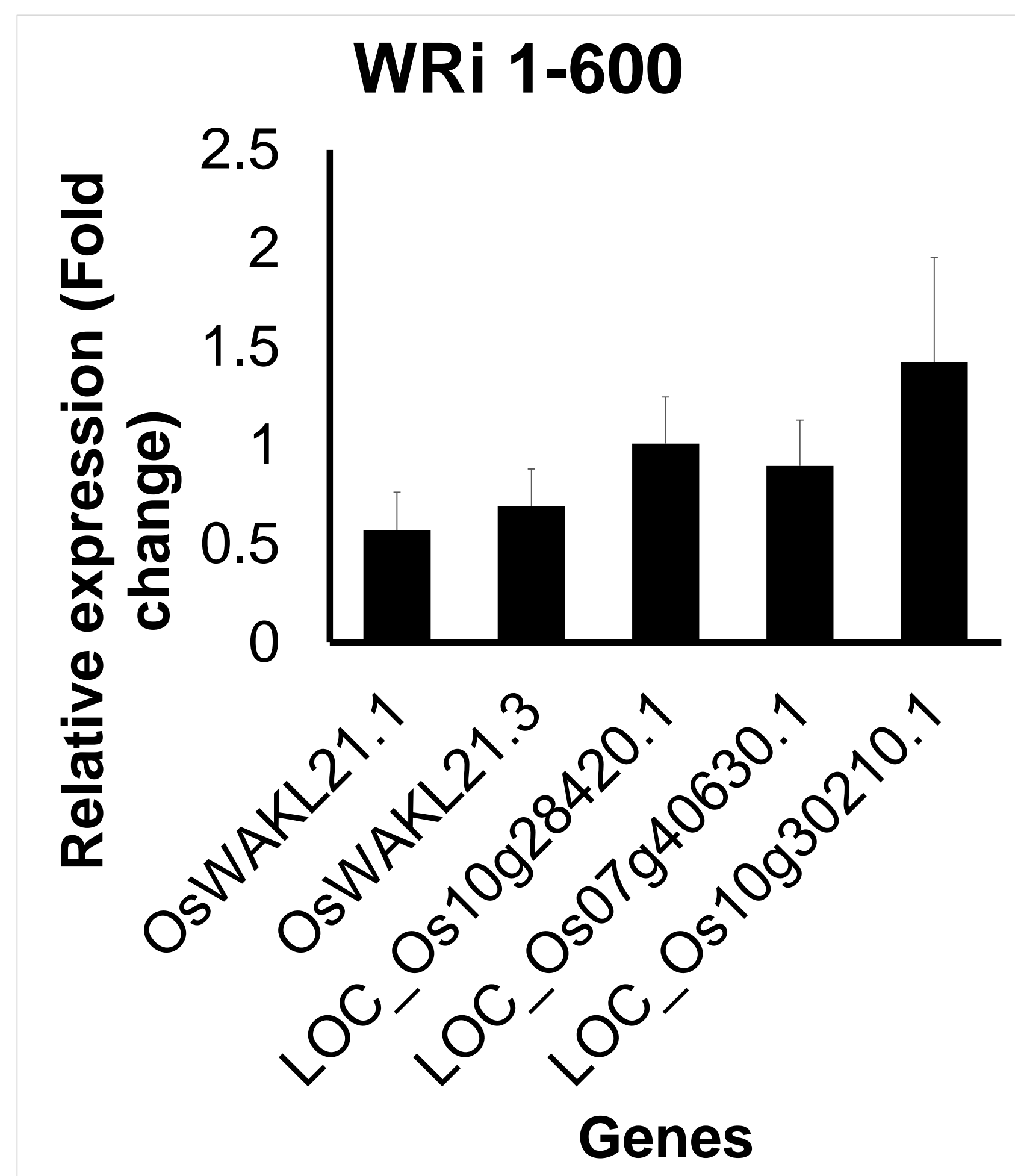
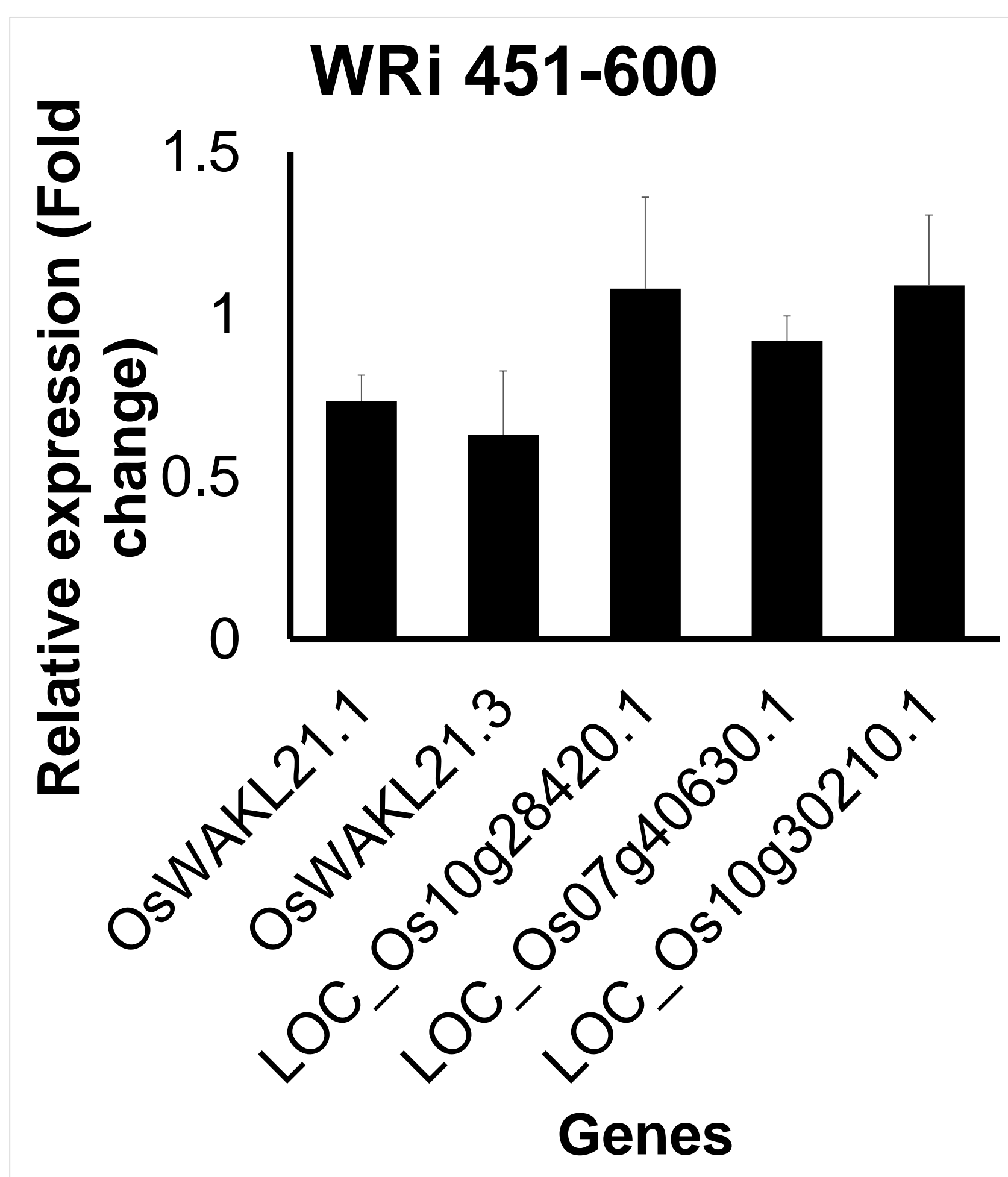


Supplemental Figure 4: Downregulation of OsWAKL21.2

- (A) Western blot indicating protein level in representative leaves whose transcript level was shown in Figure 3D. 'L' indicates protein isolated from leaves showing low callose deposition while 'H' indicates protein isolated from leaves showing high callose deposition.
- (B) Lesion length caused by *Xoo* after 10 days of pin prick inoculation on rice leaves when leaves were pre-injected with respective treatments (Buffer, LipA, or Agrobacterium along with buffer/LipA). The white mark indicate point of Agrobacterium injection while red mark indicate point of pin prick inoculation of *Xoo*. The yellow mark indicate the last point of disease progression. The quantification of lesion length is shown in Figure 4F.
- (C) Western blot indicating protein level in representative leaves whose transcript level was shown in Figure 3F. Protein was isolated from 10-12 leaves after 12hr of respective treatment.

In A and C anti OsWAKL21.2₃₇₆₋₇₂₅ antibody (α -WAK) was used for Western blotting. CBB indicate Coomassie brilliant blue staining of gel ran parallelly for loading control.

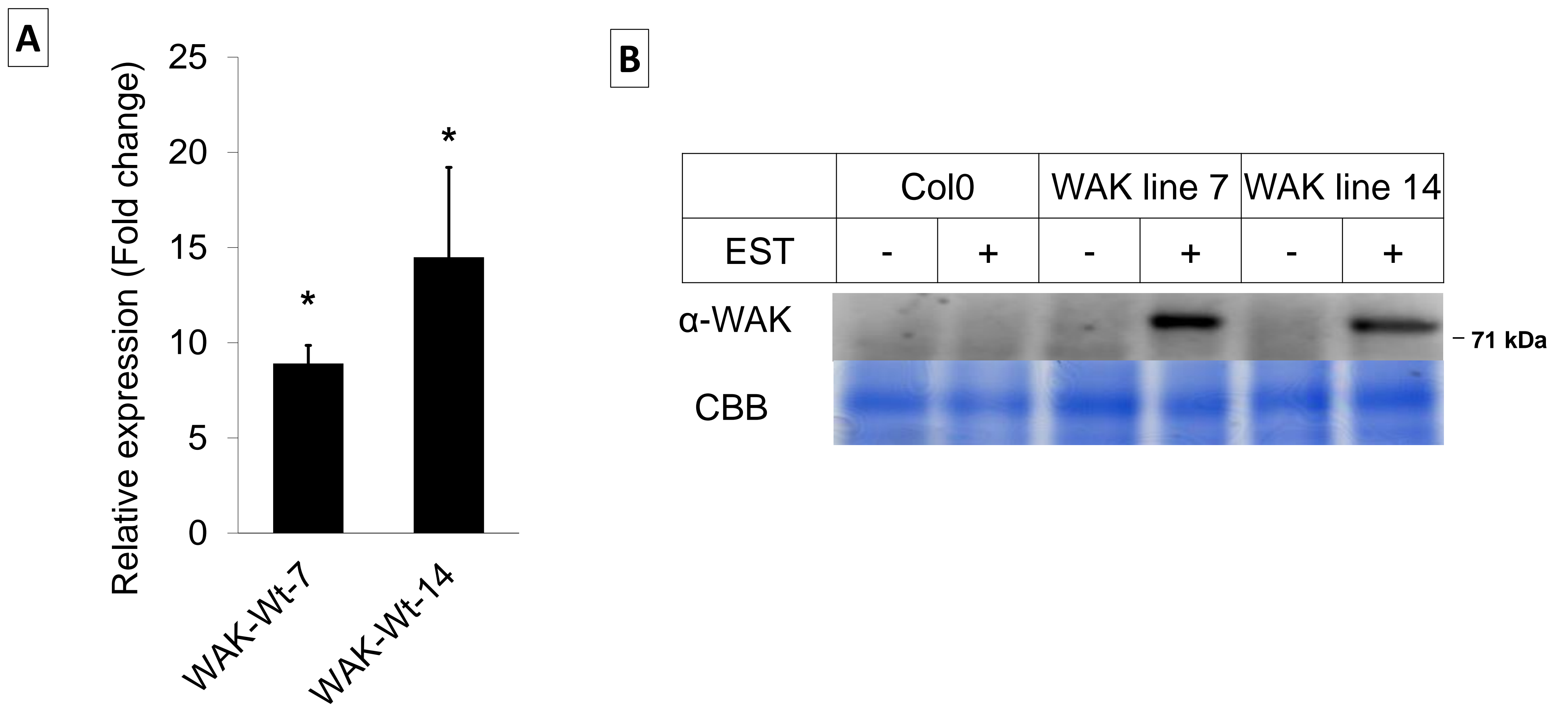
Supplemental Figure 5

A**B****C**

Supplemental Figure 5: VIGS mediated transient downregulation of *OsWAKL21.2* does not have significant effect on expression of predicted off-targets genes

Expression of genes showing highest identity with respective *OsWAKL21.2* sequence used for VIGS was also tested following treatment with *OsWAKL21.2*-RNAi constructs. RNA that was used to test expression of *OsWAKL21.2* in Fig. 3 F was used for qRT-PCR. Each bar represents average of three independent experiments, $n > 10$ in each experiment. Transcript level of buffer injected leaves was considered as 1 and fold change in *Agrobacterium* containing respective RNAi vector treated leaves was calculated with respect to it.

Supplemental Figure 6



Supplemental Figure 6: qRT-PCR and Western blot validation for ectopically expressing *OsWAKL21.2* transgenic *Arabidopsis* plants.

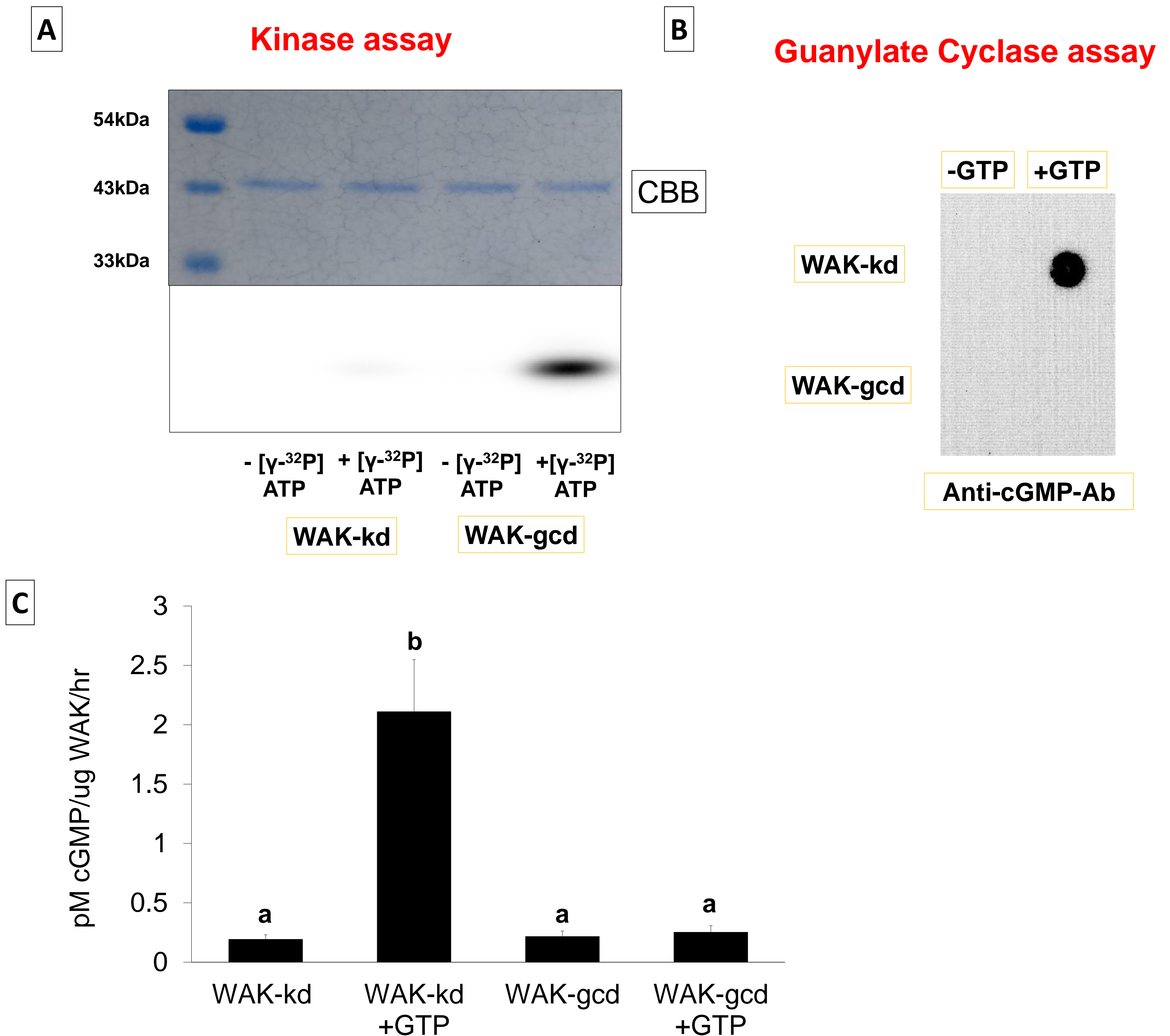
- (A) qRT-PCR indicate induction of expression of *OsWAKL21.2* in transgenic *Arabidopsis* lines (Line 7 and line 14). Expression in 0.1% DMSO treated leaves was considered as 1 and relative expression in 20 μ M estradiol treated leaves was calculated with respect to it. Each bar represents the average of three independent experiments for each line. *AtActin2* was used as internal control for qRT-PCR. The relative fold change was calculated by using $2^{-\Delta\Delta C_t}$ method.
- (B) Estradiol treatment induces protein level of *OsWAKL21.2* in *Arabidopsis* transgenic lines expressing *OsWAKL21.2* under estradiol inducible promoters. Est+ indicate infiltration with 20 μ M estradiol while Est- indicate control that is infiltrated with 0.1% DMSO. Anti *OsWAKL21.2*₃₇₆₋₇₂₅ antibody (α -WAK) was used for Western blotting. CBB indicate Coomassie brilliant blue staining of gel ran parallelly for loading control. Asterisk (*) represents significant difference in expression with $p < 0.05$.

In an experiment, for each treatment, RNA/protein was isolated from 3 leaves. Leaves were collected after 12hr of infiltration with DMSO/Est.

Supplemental Figure 7: Biochemical characterization of OsWAKL21.2

- (A) Alignment of kinase domain of OsWAKL21.2 with other known plant moonlighting receptor kinases that have GC activity. The residues highlighted in red box indicate key residues for kinase activity. The residues highlighted in green box indicate GC motif. Black star above the residues indicate residues substituted with Alanine (A) in kinase deficient mutant.
- (B) Score obtained after submission of amino acid sequence of OsWAKL21.2 for prediction of GC motif using Gcpred tool (<http://gcpred.com/>). The second predicted GC motif (569-685) have high probability of having GC activity as score in all the parameters is above required cut-off score (so indicated by green color by tool).
- (C) Alignment of OsWAKL21.2 GC motif with GC motif of other representative plant species (*Arabidopsis* and *Hippeastrum hybridum*). The residues highlighted in red boxes indicate conserved key residues. The red star above the residues indicate residues mutated in GC deficient mutant. S569 and F571 were substituted with Alanine while K582 was substituted with Glutamine as previously done by Ma et al. 2012.
- (D) Dot blot performed using anti cGMP antibody after GC assay. 50µg of purified protein (WAK) was incubated with/without GTP for 12hr and subsequently used for dot blot. GTP alone and GC buffer + GTP were used as controls. The blot was probed using anti cGMP antibody.

Supplemental Figure 8

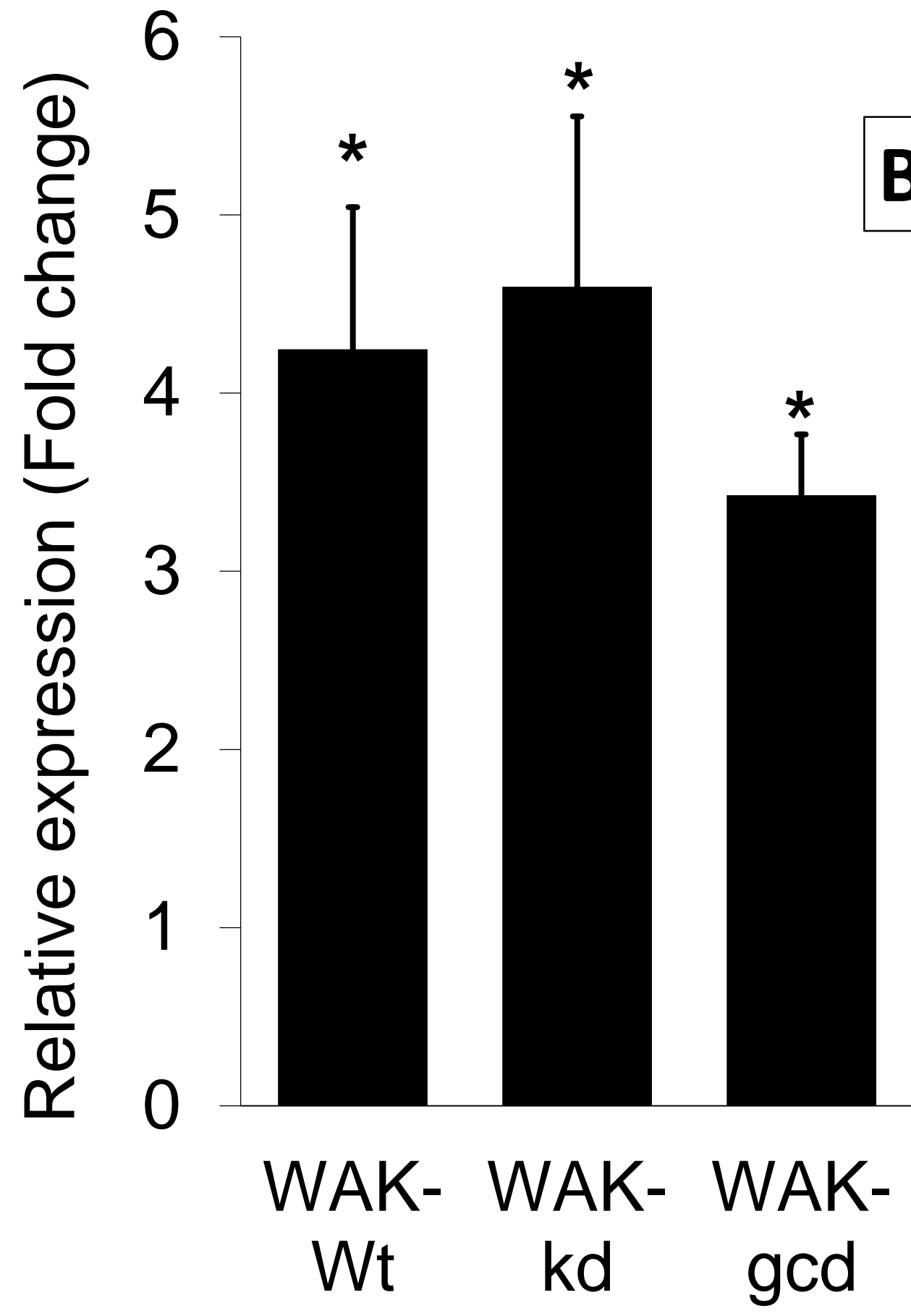


Supplemental Figure 8: Biochemical activities of purified kinase domain of mutant versions of OsWAKL21.2

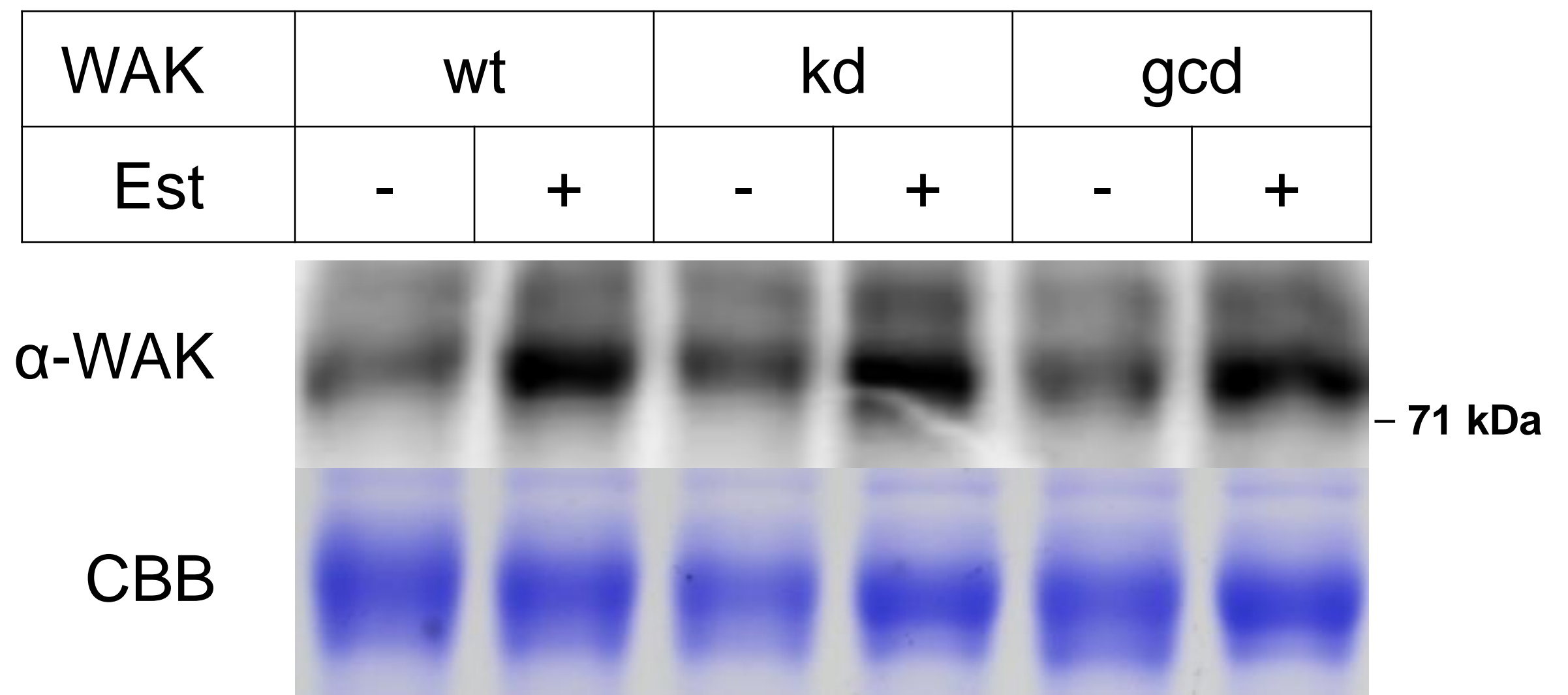
- (A) Kinase assay using kinase deficient (WAK-kd) or guanylate cyclase deficient (WAK-gcd) versions of OsWAKL21.2 kinase domain. 50 μ g of purified protein was incubated with radiolabeled ATP (γ -³²P] ATP) for 1hr and used for autoradiography. CBB indicate Coomassie brilliant blue staining of gel ran parallelly for loading control.
- (B) Qualitative GC assay performed using WAK-kd or WAK-gcd mutants of OsWAKL21.2 kinase domain. 50 μ g of purified protein was incubated with/without GTP for 12hr and subsequently used for dot blot. The blot was probed using anti cGMP antibody.
- (C) Quantification of cGMP produced by kinase domain of WAK-kd or WAK-gcd after 1hr of incubation with cGMP. Each bar represents average and error bar indicate standard error of three individual experiments. Small letters (a and b) above the bars indicate significant difference with $p < 0.05$. All experiments were repeated three times and similar results were obtained.

Supplemental Figure 9

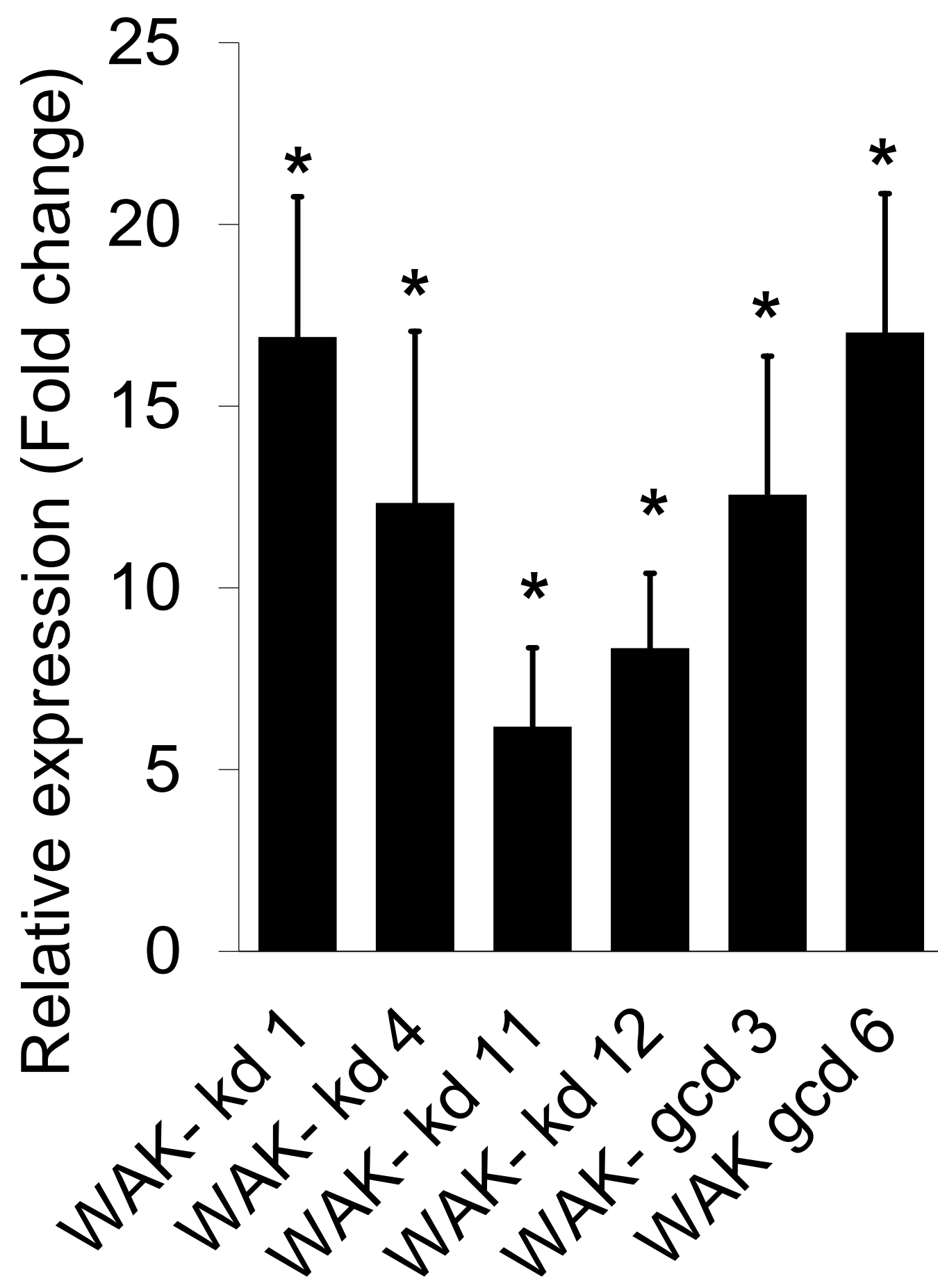
A



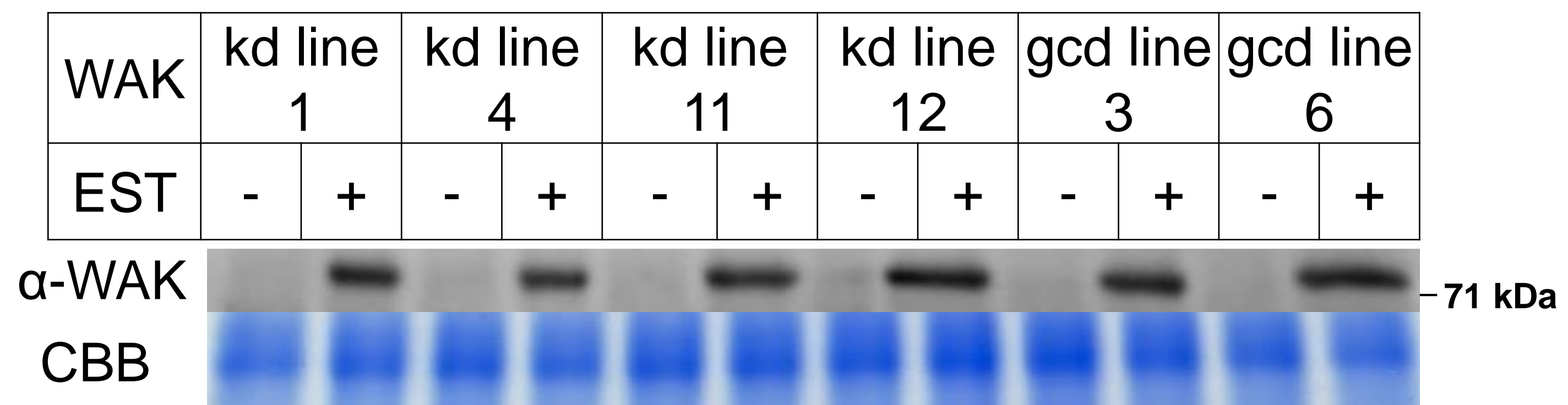
B



C



D

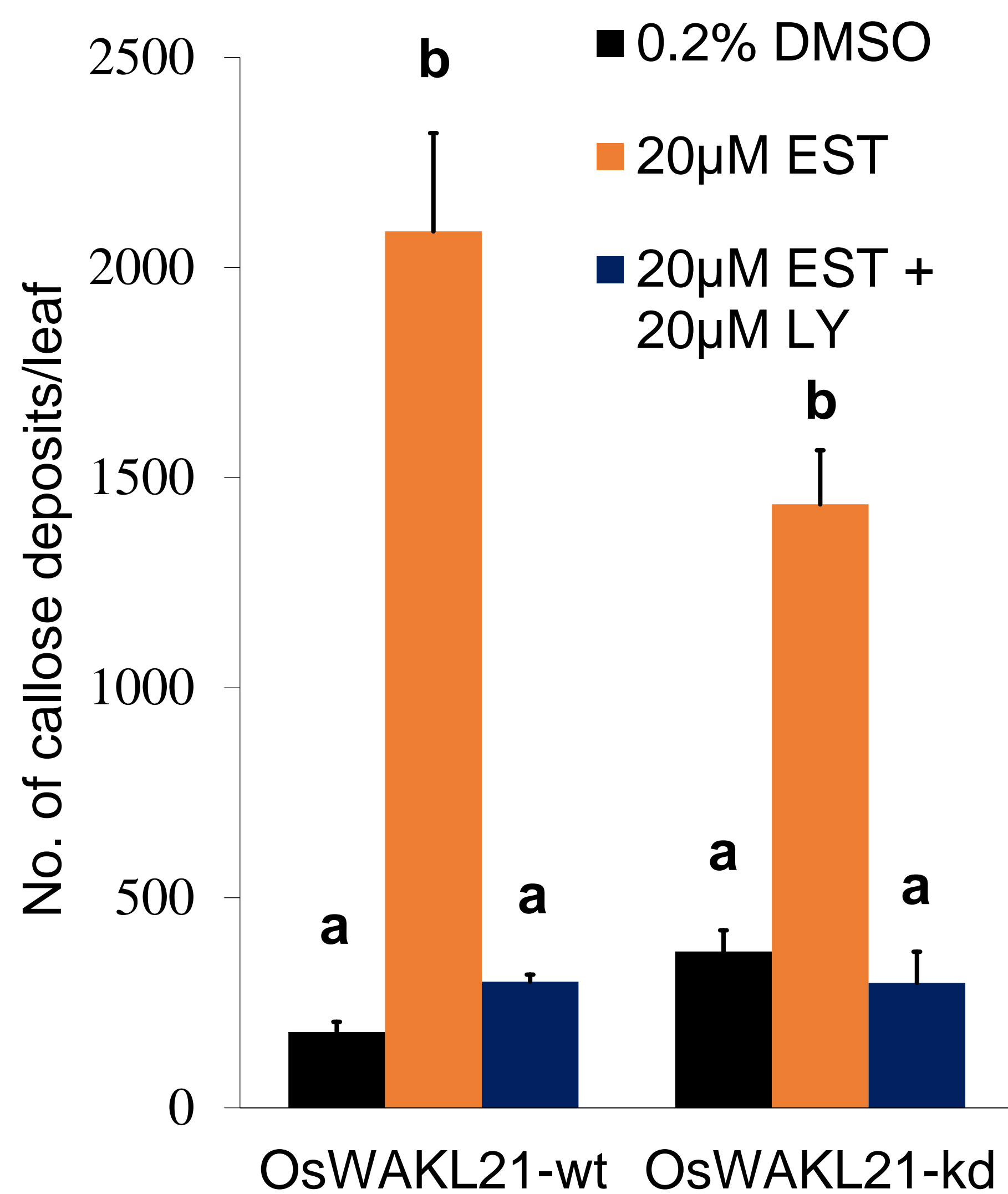


Supplemental Figure 9: qRT-PCR and Western blot validation of expression of mutant versions of OsWAKL21.2 by transient transformation in rice and ectopic expression in Arabidopsis transgenic lines.

- (A) qRT-PCR indicate overexpression of OsWAKL21.2 and mutants (WAK-kd and WAK-gcd) in rice following Agrobacterium mediated transient transformation. OsActin1 was used as the internal control.
- (B) Western blot indicating protein level of OsWAKL21.2 or its mutants after Agrobacterium mediated transient transformation in rice leaves.
- (C) qRT-PCR indicating induced expression of ectopically expressing OsWAKL21.2 mutants [OsWAKL21.2-kd (WAK-kd) or OsWAKL21.2-gcd (WAK-gcd)] in respective transgenic Arabidopsis lines. Four different lines (line 1, 4, 11 and 12) were used for WAK-kd while two different lines (line 3 and 6) were used for WAK-gcd. AtActin2 was used as the internal control.
- (D) Western blot indicating induced expression of ectopically expressing OsWAKL21.2 mutants [OsWAKL21.2-kd (WAK-kd) or OsWAKL21.2-gcd (WAK-gcd)] in respective transgenic Arabidopsis lines. Four different lines were used for WAK-kd while two different lines were used for WAK-gcd as mentioned in Supplemental Figure 8C.

In B and D Est+ indicate infiltration with 20 μ M estradiol while Est- indicate control that is infiltrated with 0.1% DMSO. In A and C Expression level in leaves treated with control (0.1% DMSO) was considered as 1 and expression level in leaves treated with 20 μ M estradiol was calculated with respect to it. Asterisk (*) represents significant difference in expression with $p < 0.05$. In A and B, Samples were collected after 18hr of treatment with Agrobacterium constructs. In C and D, samples were collected after 12hr of infiltration of DMSO/Est. In B and D anti-OsWAKL21.2₃₇₆₋₇₂₅ antibody (α -WAK) was used for Western blotting. CBB indicate Coomassie brilliant blue staining of gel ran parallelly for loading control.

Supplemental Figure 10

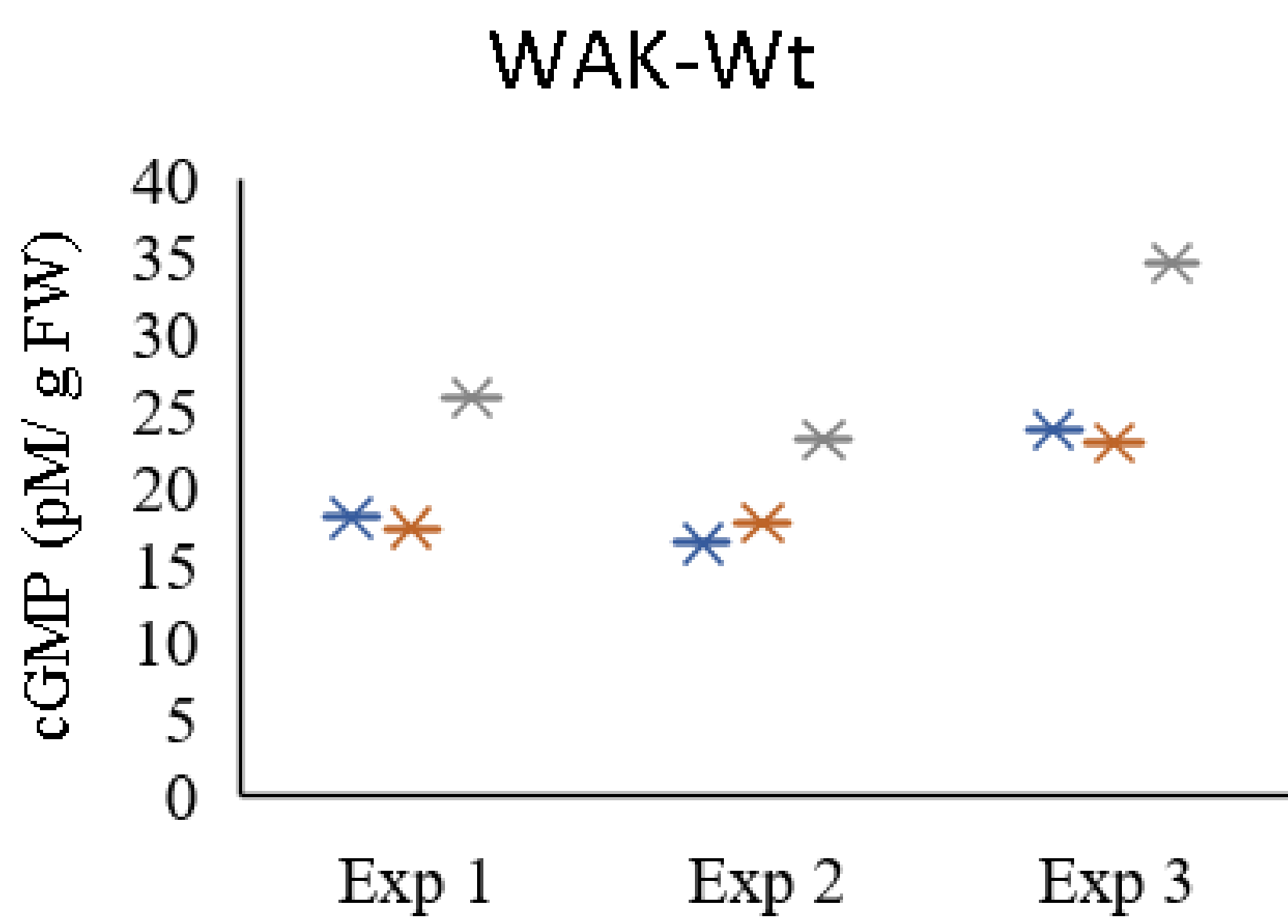


Supplemental Figure 10: Treatment with GC inhibitor attenuates *OsWAKL21.2* induced callose deposition in transgenic *Arabidopsis* leaves.

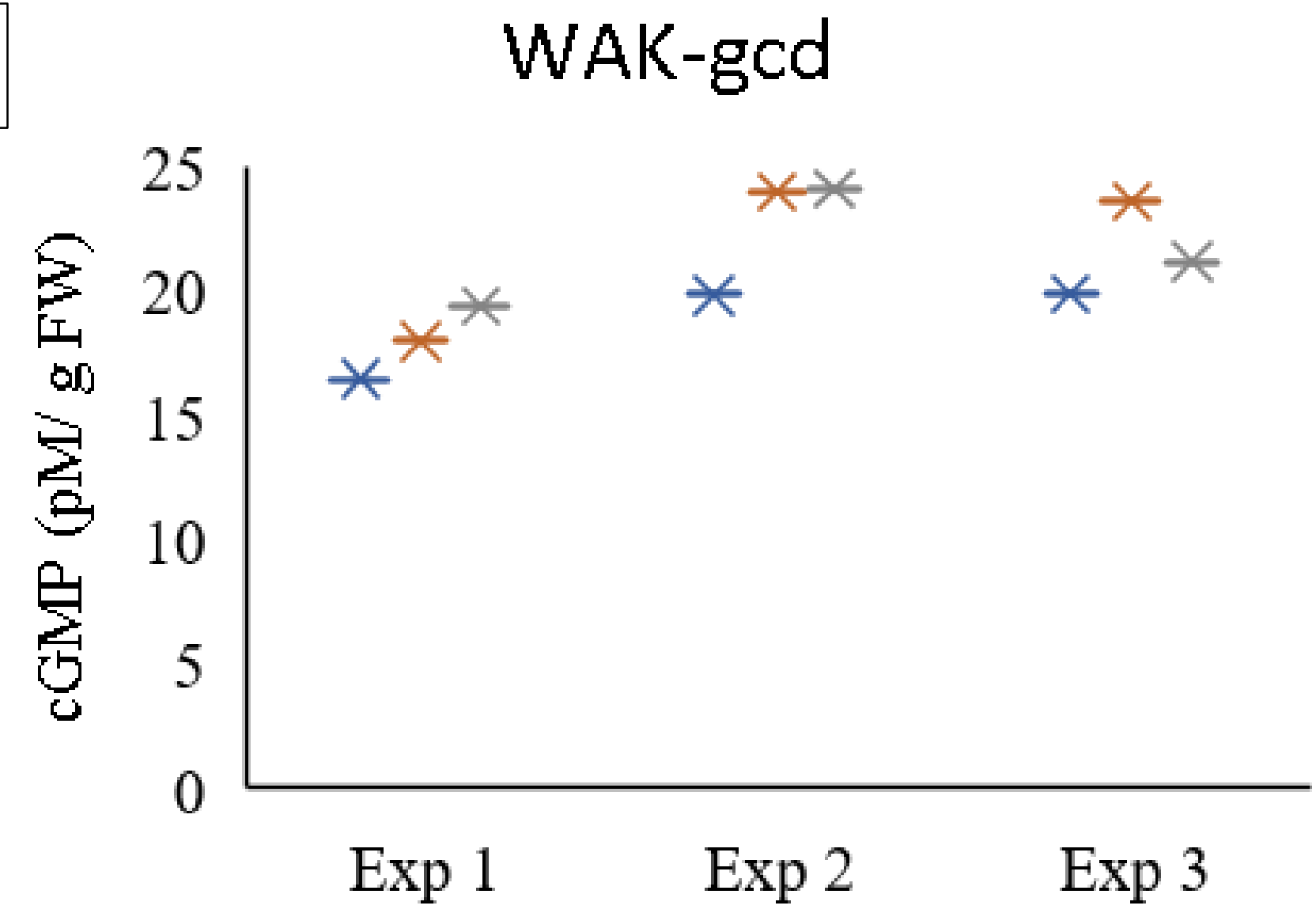
Leaves of *OsWAKL21.2* or *OsWAKL21.2*-kd transgenic plants were treated with either 0.2%DMSO, 20µM estradiol or 20µM estradiol + 20µM GC inhibitor (LY83583 or LY). Each bar represents the average and error bar represents SE of three different leaves for each treatment in an experiment. Small letters (a and b) above the bars indicate significant difference with $p < 0.05$. The experiment was repeated three times and similar results were obtained.

Supplemental Figure 11

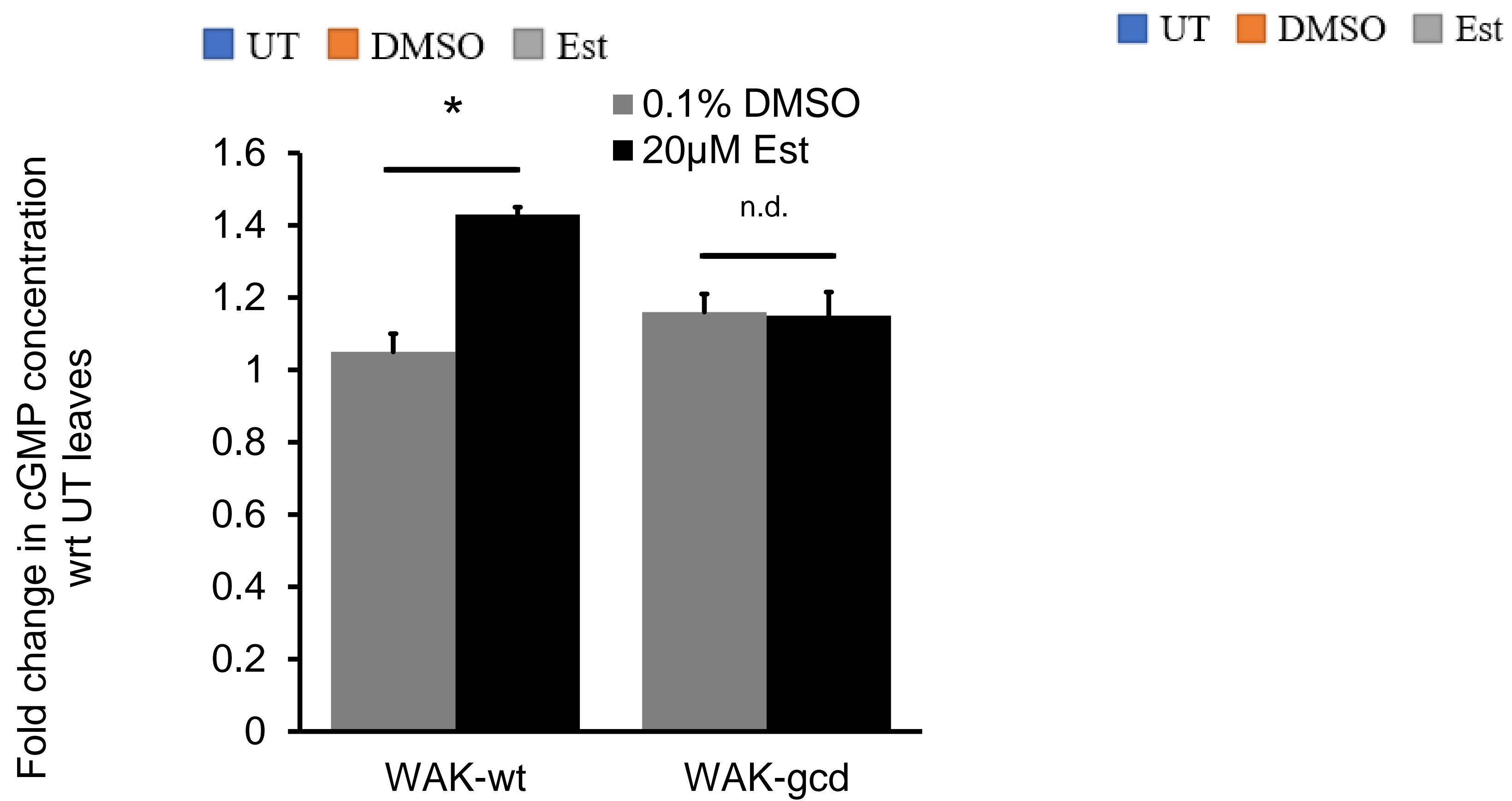
A



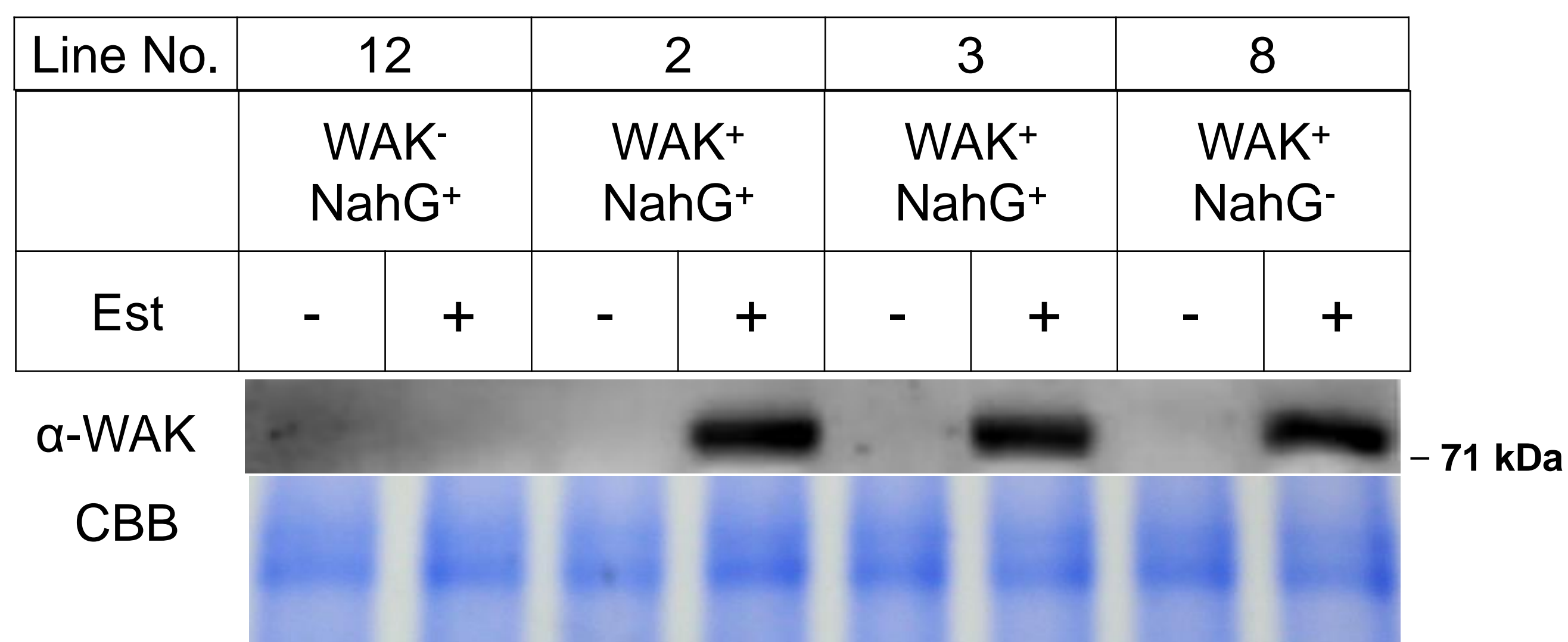
B



C



D



Supplemental Figure 11: Ectopic expression of OsWAKL21.2 in Arabidopsis enhances *in planta* cGMP level by its GC activity.

- (A) Concentration of cGMP in transgenic Arabidopsis plants ectopically expressing OsWAKL21.2 after 3hr of treatment of 0.1% DMSO, 20 μ M estradiol or untreated (UT) control plants in three different experiments.
- (B) Concentration of cGMP in transgenic Arabidopsis plants ectopically expressing OsWAKL21.2-gcd 3hr post treatment of 0.1% DMSO, 20 μ M estradiol or untreated (UT) control plants in three different experiments.
- (C) Fold change in the *in planta* cGMP concentration 3hr post treatment of respective transgenic plants with either DMSO or estradiol with respect to untreated plants. In each experiment, cGMP concentration in untreated samples was considered 1 and fold change after 3hr of treatment with either 0.1% DMSO or 20 μ M estradiol was calculated with respect to it.
- (D) Western blot from Arabidopsis leaves from sister lines carrying either OsWAKL21.2, *NahG* or both. Est+ indicate infiltration with 20 μ M estradiol while Est- indicate control that is infiltrated with 0.1% DMSO. Anti OsWAKL21.2₃₇₆₋₇₂₅ antibody (α -WAK) was used for Western blotting. CBB indicate Coomassie brilliant blue staining of gel ran parallelly for loading control.

Supplemental Table 1: Differentially expressed genes after two hour of LipA treatment

Affymetrix Probe ID	MSU ID ^a	RAP ID ^b	FC ^c	MSU name ^d
Os.50533.1.S1_at	LOC_Os04g35680.1	Os04g0437300	3.00	U-box domain containing protein, expressed
OsAffx.31223.1.S1_at	LOC_Os11g30290.1	Os11g0495400	2.83	PHF5-like protein domain containing protein, expressed
Os.30000.1.S1_at	LOC_Os07g36560.1	Os07g0550600	2.63	transferase family protein, putative, expressed
Os.22312.3.A1_a_at	LOC_Os05g28740.1	Os05g0355400	2.45	universal stress protein domain containing protein, putative, expressed
Os.6244.1.S1_x_at	LOC_Os03g13740.1	Os03g0240600	2.43	immediate-early fungal elicitor protein CMPG1, putative, expressed
	LOC_Os01g57735.1	Os01g0787300	2.43	expressed protein
Os.54936.1.S1_at	LOC_Os03g57640.1	Os03g0790500	2.36	gibberellin receptor GID1L2, putative, expressed
Os.6288.1.S1_at	LOC_Os08g31850.1	Os08g0412700	2.31	expressed protein
Os.6244.1.S1_at	LOC_Os03g13740.1	Os03g0240600	2.29	immediate-early fungal elicitor protein CMPG1, putative, expressed
Os.27507.1.S1_at	LOC_Os06g35700.1	Os06g0549900	2.18	reticuline oxidase-like protein precursor, putative, expressed
Os.29859.1.S1_at	LOC_Os07g14080.1	Os07g0244200	2.14	transferase family protein, putative, expressed
Os.38447.1.S1_s_at	LOC_Os06g07030.1	Os06g0166400	2.10	AP2 domain containing protein, expressed
Os.26626.1.S1_at	LOC_Os05g33400.1	Os05g0402900	2.01	basic 7S globulin precursor, putative, expressed
Os.1043.1.S1_at	LOC_Os01g42860.1	Os01g0615100	1.99	inhibitor I family protein, putative, expressed
Os.36283.1.S1_at	LOC_Os12g25090.1	Os12g0437800	1.97	expressed protein
	LOC_Os12g25090.2		1.97	expressed protein
Os.10579.1.S1_at	LOC_Os08g02700.1	Os08g0120600	1.97	fructose-bisphosphate aldolase isozyme, putative, expressed
Os.4804.1.S1_at	LOC_Os06g07030.1	Os06g0166400	1.94	AP2 domain containing protein, expressed
Os.53936.1.S1_at	LOC_Os03g15270.1	Os03g0258200	1.91	gibberellin receptor GID1L2, putative, expressed
Os.19861.1.S1_at	LOC_Os07g03730.1	Os07g0129300	1.89	SCP-like extracellular protein, expressed
Os.53744.2.S1_x_at	LOC_Os12g40419.1	Os12g0595800	1.88	WAKL21 wall associated kinase like receptor kinase
	LOC_Os12g40419.2		1.88	
	LOC_Os12g40419.3		1.88	

Os.9206.1.S1_at	LOC_Os10g35630.1	Os10g0499400	1.85	cystathionin beta synthase protein, putative, expressed
	LOC_Os10g35630.2		1.85	
Os.38299.1.S1_at	LOC_Os07g02330.1	Os07g0114000	1.85	protein phosphatase 2C, putative, expressed
Os.27043.1.A1_at	LOC_Os05g03920.1	Os05g0130100	1.81	TKL_IRAK_DUF26-lf.3 - DUF26 kinases have homology to DUF26 containing loci, expressed
Os.34962.1.S1_at	LOC_Os01g38110.1	Os01g0561600	1.80	cytochrome P450, putative, expressed
OsAffx.30533.1.S1_s_at	LOC_Os10g25830.1	Os10g0397800	1.78	mitochondrial carrier protein, putative, expressed
Os.40428.1.S1_at	LOC_Os01g73770.1	Os01g0968800	1.78	dehydration-responsive element-binding protein, putative, expressed
Os.1665.2.S1_x_at	LOC_Os01g07300.1	Os01g0167400	1.77	uncharacterized 50.6 kDa protein in the 5region of gyrA and gyrB, putative, expressed
	LOC_Os01g07300.2		1.77	
Os.24003.2.S1_x_at	LOC_Os11g40570.1	Os11g0621000	1.76	plant viral response family protein, putative, expressed
	LOC_Os11g40570.2		1.76	
	LOC_Os11g40570.3		1.76	
Os.1665.1.S1_a_at	LOC_Os01g07300.1	Os01g0167400	1.75	uncharacterized 50.6 kDa protein in the 5region of gyrA and gyrB, putative, expressed
	LOC_Os01g07300.2		1.75	
Os.6321.1.S1_at	LOC_Os01g63690.1	Os01g0855600	1.74	hs1, putative, expressed
Os.50013.1.S1_at	LOC_Os10g28210.1	Os10g0417800	1.73	plant-specific domain TIGR01615 family protein, expressed
Os.31344.1.S1_at	LOC_Os01g63970.1	Os01g0858900	1.73	sialyltransferase family domain containing protein, expressed
Os.54944.1.S1_at	LOC_Os02g52670.1	Os02g0764700	1.73	AP2 domain containing protein, expressed
	LOC_Os01g54340.1	Os01g0747300	1.73	plant-specific domain TIGR01615 family protein, expressed
OsAffx.19579.1.S1_at	LOC_Os12g09640.1	Os12g0198200	1.72	protein phosphatase 2C, putative, expressed
OsAffx.26677.1.S1_x_at	LOC_Os05g01444.1	Os05g0104700	1.70	polygalacturonase inhibitor 2 precursor, putative, expressed
	LOC_Os05g01430.1	Os05g0104600	1.70	polygalacturonase inhibitor 2 precursor, putative, expressed
Os.55944.1.S1_at	LOC_Os11g06150.1	Os11g0160400	1.70	basic proline-rich protein precursor, putative, expressed

Os.57041.1.S1_at	LOC_Os12g18560.1	Os12g0283400	1.69	invertase/pectin methylesterase inhibitor family protein, putative, expressed
OsAffx.23706.1.S1_at	LOC_Os01g48120.1		1.69	expressed protein
OsAffx.26845.1.S1_at	LOC_Os05g12090.1	Os05g0211700	1.69	VQ domain containing protein, putative
Os.17036.1.S1_x_at	LOC_Os05g03620.1	Os05g0127300	1.68	TKL_IRAK_CR4L.4 - The CR4L subfamily has homology with Crinkly4, expressed
Os.18229.1.S1_at	LOC_Os01g72610.1	Os01g0956200	1.66	glycosyltransferase, putative, expressed
Os.52414.1.S1_at	LOC_Os02g19650.1	Os02g0299300	1.66	hydrolase, alpha/beta fold family domain containing protein, expressed
	LOC_Os02g19650.3		1.66	
Os.27395.1.S1_a_at	LOC_Os04g57760.1	Os04g0674000	1.65	expressed protein
OsAffx.14458.1.S1_x_at	LOC_Os04g57760.1	Os04g0674000	1.64	expressed protein
Os.52004.1.S1_at	LOC_Os09g31940.1		1.64	retrotransposon protein, putative, unclassified
Os.30376.1.S1_at	LOC_Os01g02130.1	Os01g0111700	1.62	expressed protein
Os.48131.1.S1_s_at	LOC_Os04g58890.1	Os04g0685700	1.61	expressed protein
Os.18717.2.S1_at	LOC_Os09g28180.1	Os09g0454900	1.60	D-mannose binding lectin family protein, expressed
Os.12030.1.S1_at	LOC_Os01g67480.1	Os01g0900800	1.60	helix-loop-helix DNA-binding domain containing protein, expressed
Os.17181.1.S1_at	LOC_Os07g32010.1	Os07g0503300	1.60	UDP-glucuronosyl and UDP-glucosyl transferase domain containing protein, expressed
Os.3581.1.A1_at	LOC_Os06g05070.1	Os06g0142650	1.60	protein kinase domain containing protein, expressed
Os.10872.1.S1_at	LOC_Os07g09420.1	Os07g0192000	1.59	ATPase, putative, expressed
Os.46956.1.S1_at	LOC_Os01g50940.1	Os01g0705700	1.58	helix-loop-helix DNA-binding domain containing protein, expressed
Os.37865.1.S1_at	LOC_Os02g40700.1	Os02g0620400	1.58	enzyme of the cupin superfamily protein, putative, expressed
Os.27138.1.S1_at	LOC_Os10g21590.1	Os10g0360100	1.57	transporter family protein, putative, expressed
	LOC_Os10g21590.2		1.57	

Os.10709.1.S1_at	LOC_Os03g22720.1	Os03g0349600	1.57	expressed protein
	LOC_Os03g22720.2		1.57	
	LOC_Os03g22720.3		1.57	
Os.50310.1.S1_at	LOC_Os01g66544.1	Os01g0888900	1.57	expressed protein
OsAffx.7301.1.S1_at	LOC_Os11g35410.1	Os11g0558400	1.56	expressed protein
Os.12921.1.S1_at	LOC_Os04g57770.1	Os04g0674050	1.55	expressed protein
Os.49855.1.S1_at	LOC_Os02g57560.1	Os02g0821400	1.54	tyrosine protein kinase domain containing protein, putative, expressed
Os.55582.1.S1_at	LOC_Os09g28650.1	Os09g0460700	1.54	gibberellin receptor, putative, expressed
Os.32022.1.S1_x_at	LOC_Os07g37620.1	Os07g0563400	1.52	fiber expressed protein, putative, expressed
OsAffx.4103.1.S1_s_at	LOC_Os04g45940.1	Os04g0543500	1.52	transcription factor like protein, putative, expressed
Os.14823.1.S1_s_at	LOC_Os03g20090.1	Os03g0315400	1.52	MYB family transcription factor, putative, expressed
Os.55671.1.S1_at	LOC_Os06g44250.1	Os06g0652200	1.51	haemolysin-III, putative, expressed
Os.6671.2.S1_x_at	LOC_Os05g39930.1	Os05g0476700	1.51	spotted leaf 11, putative, expressed
Os.19326.1.S1_at	LOC_Os07g34940.1	Os07g0533800	1.51	aspartic proteinase nepenthesin-1 precursor, putative, expressed
OsAffx.17942.1.S1_at	LOC_Os09g28160.1	Os09g0454600	1.51	phosphate carrier protein, mitochondrial precursor, putative, expressed
Os.49607.1.S1_at	LOC_Os03g09880.1	Os03g0194600	1.50	AIR12, putative, expressed
Os.50292.1.S1_at	LOC_Os02g13560.1	Os02g0229400	-1.52	transporter family protein, putative, expressed
	LOC_Os02g13560.2		-1.52	
	LOC_Os02g13560.3		-1.52	
	LOC_Os02g13560.4		-1.52	
Os.46223.1.S1_s_at	LOC_Os09g33690.1	Os09g0511700	-1.55	Os9bglu32 - beta-glucosidase homologue, similar to G. max hydroxyisourate hydrolase, expressed
	LOC_Os09g33690.2		-1.55	
	LOC_Os09g33690.3		-1.55	
	LOC_Os09g33690.4		-1.55	
Os.27705.1.S1_a_at	N.A	N.A	-1.60	N.A

Os.49564.1.S1_at	LOC_Os04g33610.1	Os04g0412100	-1.64	expressed protein
Os.5318.1.S1_a_at	LOC_Os10g42610.1	Os10g0576600	-1.68	expressed protein
	LOC_Os10g42610.2		-1.68	
Os.7370.1.S1_at	LOC_Os03g40540.1	Os03g0602300	-1.68	cytochrome P450, putative, expressed
Os.338.1.S1_x_at	LOC_Os03g17980.2	Os03g0289100	-1.68	CAMK_KIN1/SNF1/Nim1_like_AMPKh.2 - CAMK includes calcium/calmodulin deperdent protein kinases, expressed
	LOC_Os03g17980.1		-1.68	
	LOC_Os08g37800.1	Os08g0484600	-1.68	CAMK_KIN1/SNF1/Nim1_like_AMPKh.4 - CAMK includes calcium/calmodulin deperdent protein kinases, expressed
Os.27967.1.A1_at	LOC_Os01g63620.1	Os01g0855200	-1.69	expressed protein
Os.54940.1.S1_at	LOC_Os04g44150.1	Os04g0522500	-1.71	gibberellin 2-beta-dioxygenase 7, putative, expressed
Os.3386.1.S1_x_at	LOC_Os06g10350.1	Os06g0205100	-2.08	MYB family transcription factor, putative, expressed

^a: Gene ID on Michigan State University database

^b: Gene ID on Rice Annotation Project Database

^c: FC: Fold change

^d: Name assigned in MSU database

N.A.: Not annotated

Supplemental Table 2: List of differentially expressed genes after 2hr and 12hr of LipA treatment

Common probes IDs	MSU ID^a	RAP ID^b	FC-2hr	FC-12hr	MSU name^c
Os.50533.1.S1_at	LOC_Os04g35680.1	Os04g0437300	3	6.75	U-box domain containing protein, expressed
OsAffx.31223.1.S1_at	LOC_Os11g30290.1	Os11g0495400	2.83	2.35	PHF5-like protein domain containing protein, expressed
Os.30000.1.S1_at	LOC_Os07g36560.1	Os07g0550600	2.63	11.25	transferase family protein, putative, expressed
Os.6244.1.S1_x_at	LOC_Os03g13740.1	Os03g0240600	2.43	5.77	immediate-early fungal elicitor protein CMPG1, putative, expressed
Os.54936.1.S1_at	LOC_Os03g57640.1	Os03g0790500	2.36	3.16	gibberellin receptor GID1L2, putative, expressed
Os.6288.1.S1_at	LOC_Os08g31850.1	Os08g0412700	2.31	2.69	expressed protein
Os.6244.1.S1_at	LOC_Os03g13740.1	Os03g0240600	2.29	5.94	immediate-early fungal elicitor protein CMPG1, putative, expressed
Os.27507.1.S1_at	LOC_Os06g35700.1	Os06g0549900	2.18	4.00	reticuline oxidase-like protein precursor, putative, expressed
Os.29859.1.S1_at	LOC_Os07g14080.1	Os07g0244200	2.14	1.72	transferase family protein, putative, expressed
Os.26626.1.S1_at	LOC_Os05g33400.1	Os05g0402900	2.01	2.60	basic 7S globulin precursor, putative, expressed
Os.1043.1.S1_at	LOC_Os01g42860.1	Os01g0615100	1.99	2.61	inhibitor I family protein, putative, expressed
Os.10579.1.S1_at	LOC_Os08g02700.1	Os08g0120600	1.97	1.92	fructose-bisphosphate aldolase isozyme, putative, expressed
Os.53744.2.S1_x_at	LOC_Os12g40419	Os12g0595800	1.88	2.43	WAKL21 wall associated kinase like receptor kinase
Os.9206.1.S1_at	LOC_Os10g35630	Os10g0499400	1.85	1.77	cystathionin beta synthase protein, putative, expressed
Os.38299.1.S1_at	LOC_Os07g02330.1	Os07g0114000	1.85	2.24	protein phosphatase 2C, putative, expressed
Os.27043.1.A1_at	LOC_Os05g03920.1	Os05g0130100	1.81	1.78	TKL_IRAK_DUF26-lf.3 - DUF26 kinases have homology to DUF26 containing loci, expressed
Os.34962.1.S1_at	LOC_Os01g38110.1	Os01g0561600	1.8	3.13	cytochrome P450, putative, expressed
Os.24003.2.S1_x_at	LOC_Os11g40570	Os11g0621000	1.76	1.70	plant viral response family protein, putative, expressed
Os.6321.1.S1_at	LOC_Os01g63690.1	Os01g0855600	1.74	2.85	hs1, putative, expressed

Os.31344.1.S1_at	LOC_Os01g63970.1	Os01g0858900	1.73	1.85	sialyltransferase family domain containing protein, expressed
OsAffx.26677.1.S1_x_at	LOC_Os05g01444.1	Os05g0104700	1.7	1.59	polygalacturonase inhibitor 2 precursor, putative, expressed
Os.55944.1.S1_at	LOC_Os11g06150.1	Os11g0160400	1.7	1.84	basic proline-rich protein precursor, putative, expressed
Os.57041.1.S1_at	LOC_Os12g18560.1	Os12g0283400	1.69	2.23	invertase/pectin methylesterase inhibitor family protein, putative, expressed
OsAffx.26845.1.S1_at	LOC_Os05g12090.1	Os05g0211700	1.69	1.89	VQ domain containing protein, putative
Os.17036.1.S1_x_at	LOC_Os05g03620.1	Os05g0127300	1.68	2.56	TKL_IRAK_CR4L.4 - The CR4L subfamily has homology with Crinkly4, expressed
Os.30376.1.S1_at	LOC_Os01g02130.1	Os01g0111700	1.62	4.22	expressed protein
Os.17181.1.S1_at	LOC_Os07g32010.1	Os07g0503300	1.6	2.52	UDP-glucuronosyl and UDP-glucosyl transferase domain containing protein, expressed
Os.10872.1.S1_at	LOC_Os07g09420.1	Os07g0192000	1.59	2.48	ATPase, putative, expressed
Os.46956.1.S1_at	LOC_Os01g50940.1	Os01g0705700	1.58	1.83	helix-loop-helix DNA-binding domain containing protein, expressed
Os.37865.1.S1_at	LOC_Os02g40700.1	Os02g0620400	1.58	2.21	enzyme of the cupin superfamily protein, putative, expressed
Os.27138.1.S1_at	LOC_Os10g21590.1	Os10g0360100	1.57	2.20	transporter family protein, putative, expressed
Os.12921.1.S1_at	LOC_Os04g57770.1	Os04g0674050	1.55	1.60	expressed protein
Os.14823.1.S1_s_at	LOC_Os03g20090.1	Os03g0315400	1.52	1.96	MYB family transcription factor, putative, expressed
Os.55671.1.S1_at	LOC_Os06g44250.1	Os06g0652200	1.51	3.16	haemolysin-III, putative, expressed
Os.6671.2.S1_x_at	LOC_Os05g39930.1	Os05g0476700	1.51	2.54	spotted leaf 11, putative, expressed
Os.19326.1.S1_at	LOC_Os07g34940.1	Os07g0533800	1.51	1.87	aspartic proteinase nepenthesin-1 precursor, putative, expressed
OsAffx.17942.1.S1_at	LOC_Os09g28160.1	Os09g0454600	1.51	3.40	phosphate carrier protein, mitochondrial precursor, putative, expressed
Os.27705.1.S1_a_at	N.A	N.A	-1.6	-1.68	N.A

^a: Gene ID in Michigan State University database

^b: Gene ID in Rice Annotation Project database

^c: Name assigned in MSU database

FC: Fold change

N.A.: Not annotated

Supplemental Table 3: Frequency of differentially expressed genes after LipA treatment in the microarray data performed after 24hr of *Xanthomonas oryzae* treatment in GEO submission GSE36272

Affy. Probe ID	MSU ID ^a	RAP ID ^b	MSU annotation ^c	Data points ^d	Ave FC	SD	Min FC	Max FC	Lip A 2hr FC	LipA 12hr FC
Os.50533.1.S1_at	LOC_Os04g35680.1	Os04g0437300	U-box domain containing protein, expressed	16	3.52	1.73	1.65	8.91	3.00	6.75
Os.10579.1.S1_at	LOC_Os08g02700.1	Os08g0120600	fructose-bisphosphate aldolase isozyme, putative, expressed	16	4.62	2.30	1.63	9.66	1.97	1.92
Os.53744.2.S1_x_at	LOC_Os12g40419.1	Os12g0595800	WAKL21 wall associated kinase like receptor kinase	16	3.91	2.08	1.56	8.77	1.88	2.43
Os.30000.1.S1_at	LOC_Os07g36560.1	Os07g0550600	transferase family protein, putative, expressed	15	53.28	71.96	1.94	248.34	2.63	11.25
Os.17181.1.S1_at	LOC_Os07g32010.1	Os07g0503300	UDP-glucuronosyl and UDP-glucosyl transferase domain containing protein, expressed	15	2.08	0.43	1.57	2.92	1.60	2.52
Os.55671.1.S1_at	LOC_Os06g44250.1	Os06g0652200	haemolysin-III, putative, expressed	15	10.37	11.76	2.12	38.59	1.51	3.16
Os.46956.1.S1_at	LOC_Os01g50940.1	Os01g0705700	helix-loop-helix DNA-binding domain containing protein, expressed	14	6.70	4.50	2.48	18.17	1.58	1.83
OsAffx.17942.1.S1_at	LOC_Os09g28160.1	Os09g0454600	phosphate carrier protein, mitochondrial precursor, putative, expressed	14	4.54	2.04	1.82	8.13	1.51	3.40
Os.27043.1.A1_at	LOC_Os05g03920.1	Os05g0130100	TKL_IRAK_DUF26-lf.3 - DUF26 kinases, expressed	13	2.99	0.97	1.56	4.46	1.81	1.78
Os.24003.2.S1_x_at	LOC_Os11g40570.1	Os11g0621000	plant viral response family protein, putative, expressed	12	2.31	0.68	1.51	3.44	1.76	1.70
Os.6321.1.S1_at	LOC_Os01g63690.1	Os01g0855600	hs1, putative, expressed	12	1.51	3.14	-3.89	5.68	1.74	2.85

Os.17036.1.S1_x_at	LOC_Os05g03620.1	Os05g0127300	TKL_IRAK_CR4L.4 - The CR4L subfamily has homology with Crinkly4, expressed	12	2.70	0.49	1.91	3.32	1.68	2.56
Os.10872.1.S1_at	LOC_Os07g09420.1	Os07g0192000	ATPase, putative, expressed	12	2.74	0.58	1.66	3.73	1.59	2.48
Os.6244.1.S1_x_at	LOC_Os03g13740.1	Os03g0240600	immediate-early fungal elicitor protein CMPG1, putative, expressed	11	7.34	5.49	2.02	18.92	2.43	5.77
Os.37865.1.S1_at	LOC_Os02g40700.1	Os02g0620400	enzyme of the cupin superfamily protein, putative, expressed	10	2.59	0.52	1.81	3.21	1.58	2.21
Os.6244.1.S1_at	LOC_Os03g13740.1	Os03g0240600	immediate-early fungal elicitor protein CMPG1, putative, expressed	9	9.86	6.66	3.43	21.33	2.29	5.94
Os.31344.1.S1_at	LOC_Os01g63970.1	Os01g0858900	sialyltransferase family domain containing protein, expressed	9	1.78	0.20	1.56	2.19	1.73	1.85
Os.55944.1.S1_at	LOC_Os11g06150.1	Os11g0160400	basic proline-rich protein precursor, putative, expressed	9	3.17	2.28	1.51	8.92	1.70	1.84
Os.19326.1.S1_at	LOC_Os07g34940.1	Os07g0533800	aspartic proteinase nepenthesin-1 precursor, putative, expressed	9	3.26	1.07	1.91	5.55	1.51	1.87
Os.30376.1.S1_at	LOC_Os01g02130.1	Os01g0111700	expressed protein	8	2.65	2.95	-4.45	5.64	1.62	4.22
Os.57041.1.S1_at	LOC_Os12g18560.1	Os12g0283400	invertase/pectin methylesterase inhibitor family protein, putative, expressed	6	-13.94	7.99	-31.27	-6.42	1.69	2.23
Os.6671.2.S1_x_at	LOC_Os05g39930.1	Os05g0476700	spotted leaf 11, putative, expressed	6	2.38	0.74	1.7	3.79	1.51	2.54
Os.54936.1.S1_at	LOC_Os03g57640.1	Os03g0790500	gibberellin receptor GID1L2, putative, expressed	5	5.42	0.32	5.07	5.86	2.36	3.16
Os.29859.1.S1_at	LOC_Os07g14080.1	Os07g0244200	transferase family protein, putative, expressed	5	2.15	0.37	1.74	2.77	2.14	1.72
Os.27138.1.S1_at	LOC_Os10g21590.1	Os10g0360100	transporter family protein, putative, expressed	4	-0.58	2.13	-1.89	3.11	1.57	2.20
Os.27705.1.S1_a_at	N.A.	N.A.	N.A.	4	1.97	0.30	1.52	2.35	-1.60	-1.68
OsAffx.31223.1.S1_at	LOC_Os11g30290.1	Os11g0495400	PHF5-like protein domain containing protein, expressed	3	4.65	1.45	2.81	6.34	2.83	2.35
Os.26626.1.S1_at	LOC_Os05g33400.1	Os05g0402900	basic 7S globulin precursor, putative, expressed	3	3.67	0.62	2.82	4.28	2.01	2.60
Os.9206.1.S1_at	LOC_Os10g35630.1	Os10g0499400	cystathionin beta synthase protein, putative, expressed	3	-2.36	0.18	-2.52	-2.11	1.85	1.77

OsAffx.26845.1.S1_at	LOC_Os05g12090.1	Os05g0211700	VQ domain containing protein, putative	3	2.04	0.19	1.77	2.19	1.69	1.89
Os.14823.1.S1_s_at	LOC_Os03g20090.1	Os03g0315400	MYB family transcription factor, putative, expressed	2	-0.21	1.78	-1.99	1.57	1.52	1.96
Os.38299.1.S1_at	LOC_Os07g02330.1	Os07g0114000	protein phosphatase 2C, putative, expressed	1	1.52	0	1.52	1.52	1.85	2.24
Os.34962.1.S1_at	LOC_Os01g38110.1	Os01g0561600	cytochrome P450, putative, expressed	1	3.03	0	3.03	3.03	1.80	3.13
Os.6288.1.S1_at	LOC_Os08g31850.1	Os08g0412700	expressed protein	0					2.31	2.69
Os.27507.1.S1_at	LOC_Os06g35700.1	Os06g0549900	reticuline oxidase-like protein precursor, putative, expressed	0					2.18	4.00
Os.1043.1.S1_at	LOC_Os01g42860.1	Os01g0615100	inhibitor I family protein, putative, expressed	0					1.99	2.61
OsAffx.26677.1.S1_x_at	LOC_Os05g01444.1	Os05g0104700	polygalacturonase inhibitor 2 precursor, putative, expressed	0					1.70	1.59
Os.12921.1.S1_at	LOC_Os04g57770.1	Os04g0674050	expressed protein	0					1.55	1.60

^a: Gene ID in Michigan State University database

^b: Gene ID in Rice Annotation Project database

^c: Name assigned in MSU database

^d: Number of times gene was differentially expressed out of 18 data points

Ave FC: Average fold change

SD: Standard deviation

N.A.: Not annotated

FC: Fold change

Min FC: Minimum fold change

Max FC: Maximum fold change

Supplemental Table 4: Primers used in this study

Primers used for cloning	
Primer	Sequence (5'-3')
OsWAKL21.2 F	CACCATGCACCTCGCCGGCGGCC
OsWAKL21 R	CTAAGCAAATCGCGGCATGGAGCC
OsWAKL21-Ter R	AGCAAATCGCGGCATGGAGCC
OsWAKL21 ₃₇₆ -F	CACCTCCTTCTCCCACACGCACCG
M13 F	GTAAAACGACGGCCAGT
M13 R	GGAAACAGCTATGACCATG
pMDC7 F	CAGCAGTCGAGGTAAGAT
pMDC7 R	GGTGTGTGGGCAATGAAA
pH7FWG2 F	CCGCACTAGTGATATCACAAGTTT
pH7FWG2 R	TTACTTGTACAGCTCGTCCATG
T7 F	TAATACGACTCACTATAGGG
T7 R	GCTAGTTATTGCTCAGCGG
PACI+WAK 1-20 F	TTAATTAATGCACCTCGCCGGCGGCCG
PACI+WAK 451-470 F	TTAATTAATGCAGCGTCCCCGCCGAAGC
MLUI+WAK 300-282 R	ACGCGTTTGAACGACTTGCCGACGA
MLUI+WAK 600-582 R	ACGCGTAACAGGCCACACCCCTTCG
pRTBV F	GGATCCGGGCCCTTAATTA
pRTBV R	AGGCTGGAGGCATAAACGC
Primers used for site directed mutagenesis	
Primer Name	Sequence (5'-3')
OsWAKL21.2 D504A F	GCCCATCCTCCACCGCGCGGTCAAGTCCAGCAACAT
OsWAKL21.2 D504A R	ATGTTGCTGGACTTGACCGCGCGGTGGAGGATGGGC
OsWAKL21.2 K407A F	CGCTGGTGGCGATCGCGCGGATGCGGCCGGC
OsWAKL21.2 K407A R	GCCGCCGCATCCGCGCGATCGCCACCAGCG
OsWAKL21.2 T542AT547A F	TGTCGCACGTCTCGGCGGCGCCGCAGGGCGC GCCGGGGTACCTC
OsWAKL21.2 T542AT547A R	GAGGTACCCCGGCGCGCCCTGCGGCGCCGC CGAGACGTGCGACA
WAKL21.2-S569A, G571A F	AAGAGCGACGTCTACGCTTTCGCTGTCTCCTCCTCG
WAKL21.2-S569A, G571A R	CGAGGAGGACGACAGCGAAAGCGTAGACGTCGCTCTT
WAKL21.2 K582Q F	TCACCGCCATGCAAGTCGTCGACTT
WAKL21.2 K582Q R	AAGTCGACGACTTGCATGGCAGGTGA
Primers used for qRT-PCR in rice	
Primer name	Sequence (5'-3')
OsActin1 F	TGGATTGGAGGATCCATCTTGGC
OsActin1 R	CCTTGGAATCCACATCTGCTG
OsGAPDH F	ACGGGAATGTCCTTCCGTGTTC
OsGAPDH R	AGCTTTCCTCTGATGCAGACTTG
OsWAKL21.1 F	CCTTGGAATCCACATCTGCTG

OsWAKL21.1 R	AACTCGGCAAGCGAGCCTAATG
OsWAKL21.2 F	GCCACTTTCCCGCTAAGAAGAG
OsWAKL21.2 R	CGCCAAGACACCTCCAACCTATG
OsWAKL21.3 F	GGATGCAACCTTTCCGCTAAGAAG
OsWAKL21.3 R	CGCCAAGACACCTCCAACCTATG
OsPR1a F	AGCTGTACTGTCAGCCGTATTTGC
OsPR1a R	ACCATGCATGTAACCACGAAGGAC
OsPR10a/PBZ1 F	ACGCCGCAAGTCATGTCCTAAAG
OsPR10a/PBZ1 R	TCGAGTGTGACTTGAGCTTCCC
OsPR10/PBZ14 F	ATGAAGCTCAACCCTGCTGTGG
OsPR10/PBZ14 R	TAATGTGAGCTGCGTTGTCACG
OsSERK2 F	ACTCTGGTCAATCCGTGCACTTG
OsSERK2 R	AGTGCAGCATTCCCAAGATCAAC
OsPAL3 F	TCATGTCCTCCACGTTCTTGCTC
OsPAL3 R	GCTCTTGACGTTCTCCTCGATTTG
LOC_Os01g50940 F	TGCGTACGGTATAGCTGCCAAC
LOC_Os01g50940 R	TGCTTGAAGTCACAAGGAGTTGC
LOC_Os02g43790 F	TGGTGAGCTAAGTGGCGATGTG
LOC_Os02g43790 R	AGCAGCAATCGATCACGCACAG
LOC_Os03g08310 F	CGGTTCGAGTTGGAAGATGGTTC
LOC_Os03g08310 R	TCAGGCTCGGCGAAATCAACTC
LOC_Os03g08330 F	AACTCACCAAGCAAAGCACCAG
LOC_Os03g08330 R	AACGCGGCTTCTCTTCACCTTC
LOC_Os03g13740 F	GCTCAACAAGCACAAAGGGTTGG
LOC_Os03g13740 R	TTGAGCCCTCTGAAATCCACAGC
LOC_Os03g55800 F	TCGACGAATTGACACCATCTGCAC
LOC_Os03g55800 R	AGCTCCAAGTCAAGTCCACAG
LOC_Os04g23550 F	TGGCGCGAACAAGAACATCCTC
LOC_Os04g23550 R	GACGCCTTGTCCATCTTGGTGATG
LOC_Os04g35680 F	TGAGGAGCTCTTGATTTCGATTCGG
LOC_Os04g35680 R	AGGTGCGGAATGCTCATCTCTTC
LOC_Os05g03620 F	ACAACAGCTCGTGCAAATGCG
LOC_Os05g03620 R	TCACAGAACCTTCTGCAGATGACG
LOC_Os06g44250 F	TGTGTATGTATGTGCGTGCCATTG
LOC_Os06g44250 R	CCAAAGAATCACCTGTGCTACGTC
LOC_Os06g51050 F	AGCTATGGCGATAACCTGGATTGC
LOC_Os06g51050 R	TATCAACTAGGAAGGCGGGTAGGG
LOC_Os07g09420 F	TTGGTCAAGGAGCTCGAGAAGG
LOC_Os07g09420 R	AGTCTACTCCTCGTCGTCATCG
LOC_Os07g32010 F	TCCCGAAGAACTGAGCATACTGTG
LOC_Os07g32010 R	ACAAGCGGCATCATCTCTTGTTAC
LOC_Os07g36560 F	GCTCCTCTTCATTCAGGTGACG

LOC_Os07g36560 R	GTCGGCGATGTTGTGGCATATC
LOC_Os08g02700 F	TTCCCGCCATCTCTGCATCTTC
LOC_Os08g02700 R	GCGTTCCTGATCAACTCATCCTTG
LOC_Os08g36920 F	ACTCACATGACCAACCGGATCTC
LOC_Os08g36920 R	GCCGTCGAATCGGATCATGTACTC
LOC_Os08g39840 F	GATCGACATCAGGGATCTCATCGG
LOC_Os08g39840 R	GTTGCTTTCTCCTTCCCGGTCTTC
LOC_Os08g39850 F	AAGGGCTTCTCAACAGCCTGAG
LOC_Os08g39850 R	CTTCTTCTTCCCTGTCTTCGCTTC
LOC_Os09g28160 F	CAGGAACGAAAGCTATGCAGGTC
LOC_Os09g28160 R	AGATGCTTGTATGCCATCTCCAC
LOC_Os10g25230 F	AAGGACCGGTGATCATCTTGGC
LOC_Os10g25230 R	GACGGACGGTCAAACATTGGATAC
LOC_Os11g40570 F	TTAGCGAGAGAGGTTGGGCAGTAG
LOC_Os11g40570 R	GCGTTGACGTGAGTGATGAGATTC
Primers used for qRT-PCR in Arabidopsis	
Primer name	Sequence (5'-3')
AtActin2 F	TCTTCCGCTCTTTCTTTCCAAGC
AtActin2 R	ACCATTGTCACACACGATTGGTTG
AtUBQ5 F	AAGAAGACTTACACCAAGCCGAAG
AtUBQ5 R	ACAGCGAGCTTAACCTTCTTATGC
AtPR2 F	TCTTGAACCCACTTGTCCGC
AtPR2 R	GGCTCTGACATCGAGCTCATC
AtPR5 F	TCCTTGACCGGCGAGAGTT
AtPR5 R	AGGAACAATTGCCCTACCACC
AtGSL5 F	CCACCACGAGTACATTCAGGTC
AtGSL5 R	GTACACATCTCGGCTGAGAACC
AtPDF1.2 F	CTTGTTCTCTTTGCTGCTTTCGAC
AtPDF1.2 R	TTGGCTCCTTCAAGGTTAATGCAC
AtWRKY33 F	CTTCCACTTGTTTCAGTCCCTCTC
AtWRKY33 R	CTGTGGTTGGAGAAGCTAGAACG
AtSARD1 F	AGAATCCCTCAACCAGCCCTAC
AtSARD1 R	GTGGCTCGCAGCATATTGTTGG
AtCBP60G F	CGATAGGACCTTTGTGGGTCATCC
AtCBP60G R	ACTTCCTTGAAAGTCGATGTGCTG
AtNPR3 F	TCAGCGGCGGCTTTGTAACCTTG
AtNPR3 R	CCTCGCCACTCTCTCAATACTG
AtWRKY38 F	ACTGCGAAGCAAGAAAGCATGAAC
AtWRKY38 R	TGGTGGCCAAAGTAAGTGGTTCG
AtSH3 F	TATCGGCGACCAAATGCAGGTC
AtSH3 R	ACTACGGCTCTATGGAGCACAC
AtSID2 F	GCTTGGCTAGCACAGTTACAGC

AtSID2 R

CACTGCAGACACCTAATTGAGTCC

Supplemental Table 5: Accession numbers of genes used in this study

Rice			
Gene name	MSU ID^a	RAP ID^b	Gene Family
WAKL21	LOC_Os12g40419	Os12g0595800	Wall associated kinase
PR10/PBZ14	LOC_Os12g36830	Os12g0555000	Pathogenesis related
PAL3	LOC_Os02g41670	Os02g0626600	Phenylalanine ammonia lyase
SERK2	LOC_Os04g38480	Os04g0457800	LRR-Receptor like kinase
PR1a	LOC_Os07g03710	Os07g0129200	Pathogenesis related
PR10a/PBZ1	LOC_Os12g36880	Os12g0555500	Pathogenesis related
Actin1	LOC_Os03g50885	Os03g0718100	Actin
GAPDH	LOC_Os04g40950	Os04g0486600	Glyceraldehyde 3-phosphate dehydrogenase
bHLH116	LOC_Os01g50940	Os01g0705700	Basic helix-loop-helix transcription factor
N.D.	LOC_Os02g43790	Os02g0654700	ethylene-responsive transcription factor
N.D.	LOC_Os03g08310	Os03g0180800	ZIM domain-containing protein
N.D.	LOC_Os03g08330	Os03g0181100	ZIM domain-containing protein
PUB41	LOC_Os03g13740	Os03g0240600	ubiquitin ligase
N.D.	LOC_Os03g55800	Os03g0767000	Allene oxide synthase
OsRERJ1	LOC_Os04g23550	Os04g0301500	Basic helix loop helix transcription factor
PUB38	LOC_Os04g35680	Os04g0437300	ubiquitin ligase
CRR3	LOC_Os05g03620	Os05g0127300	Crinkly4 subfamily protein
N.D.	LOC_Os05g12140	Os05g0212200	LRR-Receptor like kinase
N.D.	LOC_Os06g44250	Os06g0652200	haemolysin-III
CHIT7/PR3	LOC_Os06g51050	Os06g0726100	Chitinase
N.D.	LOC_Os07g09420	Os07g0192000	AAA-type ATPase
N.D.	LOC_Os07g32010	Os07g0503300	UDP-glucuronosyl domain containing
N.D.	LOC_Os07g36560	Os07g0550600	transferase
N.D.	LOC_Os07g40630	Os07g0597200	BRI-1 precursor, putative, expressed
N.D.	LOC_Os08g02700	Os08g0120600	fructose-bisphosphate aldolase
N.D.	LOC_Os08g36920	Os08g0474000	AP2 transcription factor
N.D.	LOC_Os08g39840	Os08g0508800	Lipoxygenase
N.D.	LOC_Os08g39850	Os08g0509100	Lipoxygenase
N.D.	LOC_Os09g28160	Os09g0454600	Mitochondrial phosphate carrier
N.D.	LOC_Os10g25230	Os10g0391400	ZIM domain-containing protein
N.D.	LOC_Os10g28420	Os10g0420200	IQ calmodulin-binding motif family protein
N.D.	LOC_Os10g30210	Os10g0438300	-
N.D.	LOC_Os10g37640	Os10g0520700	HIT zinc finger domain containing protein
N.D.	LOC_Os11g40570	Os11g0621000	viral response family protein

N.D.	LOC_Os12g41570	-	-
Arabidopsis			
Gene name	TAIR ID^c		
Actin2	AT3G18780		
PR2	AT3G57260		
PR5	AT1G75040		
GSL5	AT4G03550		
WRKY33	AT2G38470		
PDF1.2a	AT5G44420		
CBP60G	AT5G26920.1		
SH3	AT4G10500		
NPR3	AT5G45110.1		
WRKY38	AT5G22570		
SARD1	AT1G73805		
SID2	AT1G74710		
UBQ5	AT3G62250		
BRI1	AT4G39400		
PSKR1	AT2G02220		
WAKL10	AT1G79680		
PEPR1	AT1G73080		
PEPR2	AT1G17750		

^a: Gene ID in Michigan State University database

^b: Gene ID in Rice Annotation Project database

^c: Gene ID in The Arabidopsis Information Resource database

N.D.: Name not defined