Supplementary Materials and methods

Construction of vector

For the construction of *DsRed*-fused *OsNAC4* expression vector, *OsNAC4* coding sequence was PCR-amplified from rice cDNA and amplified fragments were cloned into a pGEM-T plasmid vector (Promega, Madison, WI). The *DsRed* coding sequence was amplified by PCR, and the amplified fragments were digested with *SpeI* and *BamHI* and cloned in-frame into the *SpeI* and *BamHI* sites of the pGEM-T vector contained with *OsNAC4* gene. The plasmid was further digested with *BamHI* and cloned into the *BamHI* site of the expression vector *pAHC17*.

To obtain *NES*-fused *OsNAC4* expression vector, *NES* sequence (Leu-54 to Gln-69) in *OsNAP1* (AJ438611) was synthesized by DNA synthesizer (Applied Biosystems, Foster City, CA), (5'-CTCTCCCCCAATGTCAGGAAGCGTGTCGAATATTTGAGGGAGATCCAG-3') and PCR-amplified using one set of specific primers, (5'-ATGCTCTCCCCCAATGTCAGGAA-3', 5'-CTGGATCTCCCTCAAATATT). Amplified fragment was cloned in-frame into *OsNAC4-DsRed* vector.

For cell death detection in protoplasts using Evans blue dye, protoplasts were transformed with appropriate expression vectors using PEG-mediated transformation method. After cultivation for 12 or 24 h at 30°C, all protoplasts were incubated for 15 min with 0.05% Evans blue containing KMC solution (117 mM KCl, 82 mM $MgCl_2$, and 85 mM $CaCl_2$) then washed extensively to remove the excess dye. The number of dead protoplasts and survived protoplasts were determined by counting under light microscopy within fifty individual fields (Takai et al., 2006).

Transmission electron microscopy (TEM)

Cultured cells were fixed with 2.5% glutaraldehyde containing 0.05 M sodium cacodylate (pH 7.0) for 2 h at 4°C and then washed with 0.05 M sodium cacodylate (pH 7.0). The cells were post-fixed with 1% OsO4 for 2 h on ice. After washing with water, the cells were dehydrated in a graded acetone series. The dehydrated cells were embedded in Spurr's resin (TAAB Lab., Aldermaston, UK) and sectioned. Ultra-thin sections were stained with lead (Reynolds 1963) and observed under a transmission electron microscope (H-7100, Hitachi, Tokyo, Japan) at an accelerating voltage of 75 kV.

Immunogold electron microscopy

To examine OsNAC4 distribution by immunogold electron microscopy, we fixed cultured rice cells with 0.6% glutaraldehyde and 4% paraformaldehyde in a 0.05 M sodium cacodylate buffer (pH 7.4) for 5 min at 4°C under a vacuum. After storage at 4°C for 1 h, tissues were rinsed with a 0.05 M sodium cacodylate buffer (pH 7.4) for 2 h at 4°C. Fixed materials were dehydrated with an ethanol series at 4°C, embedded in LR White resin (The London Resin Co., London, UK), and polymerized using UV irradiation at room temperature. Ultrathin sections were cut with a diamond knife and mounted on uncoated nickel grids. Prior to incubation in primary antibody, sections were blocked with 1% BSA and 1% goat serum in PBS for 30 min at room temperature. We diluted a rabbit antibody specific for OsNAC4 in PBS supplemented with 1% goat serum. Samples were incubated with primary antibody overnight at 4°C, followed by washing in 0.05% Tween 20 in PBS (PBST, pH 7.4). Sections were then incubated in secondary antibody, a goat anti-rabbit IgG conjugated to 15 nm gold particles (Biocell Research Laboratories, Cardiff, UK) and diluted in PBST, for 90 min at room temperature. Sections were then washed sequentially in PBST and distilled water, followed by staining with uranyl acetate for 20 min. Sections were observed using a transmission electron microscope (H-7100; Hitachi, Tokyo, Japan) at an accelerating voltage of 75 kV.

Protoplast preparation and gene transformation

Rice protoplasts were isolated from cultured Oc rice cells. After four days of culture, cells were harvested, and protoplasts were isolated as described previously (Takai et al., 2006). Cultured rice cells was digested in an enzyme solution containing 1.0% (w/v) cellulase "Onozuka" RS (Yakult, Tokyo, Japan), 0.5% (w/v) macerozyme R10 (Yakult), 0.1% (w/v) pectolyase Y23 (Kyowa Chemical Products, Osaka, Japan), 0.6 M mannitol, 5 mM MES-KOH (pH 5.7), 10 mM $CaCl_2$, and 0.1% (w/v) BSA (bovine serum albumin) at 30°C for 2-3 h without shaking. Protoplasts were separated from undigested cell clumps by filtration using a 100 μm cell strainer and collected by centrifugation at 80*g* for 3 min at room temperature. The protoplasts were gently resuspended and washed twice in KMC solution (117 mM KCl, 82 mM $MgCl_2$, and 85 mM $CaCl_2$). The protoplast concentration was quantified using a hemocytometer and a light microscope. Almost all protoplasts were observed in their usual healthy and round shape. Before PEG-mediated transformation, the protoplasts were centrifuged and resuspended at 2 x 10^5 cells/ml in MMg solution (0.3 M

mannitol, 15 mM $MgCl_2$, and 4 mM MES-KOH, pH 5.7). The protoplast suspension (0.2 ml, 4 x 10^4 cells) was mixed with ~20 µl of the DNA solution. An equal volume of PEG solution (40 % (v/v) PEG 4000 (Fluka, Buchs, Switzerland), 0.2 M mannitol, and 0.1 M $CaCl_2$) was added and gently mixed. After incubating 10 min at room temperature, protoplasts were diluted with 0.8 ml of KMC solution and centrifuged at 80*g* for 3 min at room temperature. After removing the supernatant, the protoplasts were suspended in 0.2 ml KMC solution and incubated for 16 h at 30°C before assaying.

Nuclei purification and imunoblot analysis

Rice protoplasts were transformed with each suitable vector and cultured for 12 or 24 h at 30°C. Transformed protoplasts were broken by resuspension in a burst buffer (5 mM MES pH5.6, 5mM $MgCl_2$, 10 mM KCl, 0.4% (w/v) Triton X-100, 0.35 M sucrose, 20% (w/v) glycerol, 1 x Roche proteinase inhibitor, 5 mM 2-mercaptoethanol). Nuclei were separated from cytosol fraction by filtration using a 70 µm cell strainer and collected by centrifugation at 3,500*g* for 5 min at 4°C. Isolated nuclei was washed by washing buffer containing 5 mM MES pH5.6, 5mM $MgCl_2$, 10 mM KCl, 0.35 M sucrose, 20% (w/v) glycerol, 1 x Roche proteinase inhibitor, 5 mM 2-mercaptoethanol and collected by centrifugation at 2,000*g* for 5 min. Nuclear protein was extracted by resuspension in isolation buffer (50 mM HEPES-KOH pH 8.0, 1% SDS, 2 mM EDTA, 1 mM DTT).

To generate the specific anti-OsNAC4 antibody, the C-terminal region of OsNAC4, encompassing the region from His-201 to Phe-318, was cloned in–frame into the pET-28(a)+ vector (Novagen, Madison, WI). The resulting His tag fusion protein was overproduced in the BL21 (DE3) strain of *E. coli* (Novagen) and purified using a HisTrap Kit according to the manufacturer's protocol (GE Healthcare). The purified recombinant protein (10 mg) was used to immunize rabbits. Antiserum was further purified by affinity chromatography with a HiTrap N-hydroxysuccinimide-activated column coupled to recombinant OsNAC4.

Isolated nuclear fraction and cytosol fraction were separated by SDS-polyacrylamide gels (12.5%). Separated proteins were electrophoretically transferred to a nitrocellulose membrane (Millipore, Bedford, USA) with a Bio-Rad semidry blotter (Bio-Rad). Nonspecific binding was blocked with 3% BSA in PBS buffer for 1 h at room temparature. Immunoreactive polypeptides were detected using a peroxidase-conjugated goat antibody raised against rabbit IgG (Medical & Biological Laboratories, Nagoya, Japan) and visualization was performed with an enhanced immunochemiluminescence kit (ECL-plus, GE Healthcare) and

chemiluminescence was detected by LAS-1000 (Fujifilm, Tokyo, Japan). Phosphorylated OsNAC4 was detected using phosphoserine antibody (ab6639) (Abcam, Cambridge, UK). The purity of the isolated nuclei and cytosol were analyzed by Western blotting using an anti-histon H3 antibody (nucleus-specific antibody) and an anti-OsUSP antibody (cytosol-specific antibody).

Immunoprecipitation

Isolated cytosol and nuclei fractions were passed through a NAP-5 column (GE Healthcare) equilibrated with binding buffer (20 mM HEPES-KOH, pH 8.0, 15 mM Sucrose, 35 mM KCl, 15 mM NaCl. 4 mM $MgCl_2$, 0.2 mM DTT, 0.2 mM EDTA, 0.1% Triton X-100). To test for any non-specific binding of proteins to Protein A-sepharose (GE Healthcare), the cytosol and nuclei fractions were mixed with Protein A-sepharose by shaking for 1 h at 4°C. Following pre-mixing, Protein A-sepharose was removed by centrifugation at 500*g* for 5 min. Anti-OsNAC4 antibody were added to the supernatant solution and incubated for 6 h, followed by the addition of Protein A-sepharose and incubation for an additional 1 h at 4°C. Treated samples were then centrifuged at 3,000*g* for 1 min to yield protein A-sepharose precipitated portions. The protein A-sepharose precipitates were further washed with binding buffer three times for removing any non-specific protein binding, resuspended in 30 μl Laemmli sample buffer and boiled at 95 for 5 min to collect for interacted proteins. Equal quantities of protein samples were loaded on SDS-PAGE gel and analyzed by immunoblotting.

Quantitative real-time RT-PCR

Quantitative real-time RT-PCR was performed on an Opticon2 (Bio-Rad, Hercules, CA) using a QuantiTect SYBR Green RT-PCR Kit (QIAGEN) with the following gene-specific primers. *OsNAC4*: forward, 5'-GGTGAAGGAGGACAACGACT-3' and reverse, 5'-TCAGAATGGTGGCAGGATTGT-3'. OsHSP90: forward, 5'-CAGGGCAGAAGGACATCTTTT-3' and reverse, 5'-CGTCAACAGGGTCAGTGAAG-3'. *IREN*: forward, 5'-CTGCCAGGCACTTTGTCAGT-3' and reverse, 5'-TCTTGGCTGCAGCATGTAGG-3'. To eliminate DNA contamination during qRT-PCR, all primer sets used for real-time RT-PCR were designed across an intron. The sizes of the PCR products were checked to confirm that only products from mRNA were amplified in all real-time RT-PCR experiments. The fluorescence data produced sigmoidal amplification plots

in which the number of cycles was plotted against fluorescence. Quantification of each mRNA was calculated with calibration curve which was prepared using standard gene of known template amounts (1 ng-0.1 pg) and corrected with reference data of *Act-1* gene.

22K oligo array data analysis

We used a long oligonucleotide array (60-mer; Agilent Technologies, 22K) designed by the Institute for Genomic Research from tentative consensus sequences. RNA was isolated from controls cell lines and those expressing an *OsNAC4*-specific RNAi in three independent transformation experiments. cRNAs were synthesized from 8.25 mg total RNA for each replicate using an T7 primer and labeled by the Cy3 or Cy5 dyes. Microarrays were scanned using a scanning laser microscope (model ScanArray4000XL; GSI Lumonics, Billerica, MA, USA). Separate images were acquired for each fluorescence at a resolution of 10 μm per pixel. We used ArrayVision 5.1 (Amersham) and GeneSpring GX 7.3 (Silicon Genetics, Redwood, CA, USA) software for microarray data analysis. Local background fluorescence was subtracted from the value assigned to each spot on the array. Spots obscured by dust particles, missing spots, spots with low signal intensity, and spots with high local background fluorescence were flagged for exclusion after further analysis. Normalization between the Cy3 and Cy5 emission channels was achieved by calculating the ratio of the total Cy3 signal intensity from all spots in relation to the total Cy5 signal intensity from all spots.

Supplementary Figure legends

Figure S1 Immuno blot analysis of OsNAC4 in rice cultured cells using the specific anti-OsNAC4 antibody. Lane 1, 5 μg of total cell extract proteins; lane 2, 10 μg of total cell extract proteins; lane 3, 20 μg of total cell extract proteins; lane 4, 30 μg of total cell extract proteins. The C-terminal region of OsNAC4, encompassing the region from His-201 to Phe-318, was cloned in–frame into the pET-28(a)+ vector. The resulting His tag fusion protein was overproduced in the BL21 (DE3) strain of *E. coli* and purified using a HisTrap Kit. The purified recombinant protein (10 mg) was used to immunize rabbits. Antiserum was further purified by affinity chromatography with an OsNAC4-coupled HiTrap NHS-activated sepharose column.

Figure S2 H_2O_2 generation in OsNAC4-RNAi line, NR2-2 (open circle) and control line (solid circle) after treatment with flagellin (0.5 μM) from the avirulent N1141 strain. H_2O_2 generation was analyzed by luminol-chemiluminescence. Each data point represents the average of three independent experiments. Bars indicate the standard errors.

Figure S3 Functional Categories of 139 genes. **(A)** Classification of genes whose expression is differed in *OsNAC4* knock-down line and control line following the HR-cell death induction. Ratios of *OsNAC4* knock-down line to control line gene expressions were obtained from microarray experiments. Numbers represent groups of genes with unknown function (1), and those involved in metabolism (2), transcription (3), cellular communication/signal transduction (4), cellular transport and transport mechanisms (5), protein destination (6), cell rescue, defense, cell death and ageing (7), cell growth, cell division and DNA synthesis (8), protein synthesis (9), development (10), and cellular organization (11). **(B)** Predicted topology of IREN. Hashed bar indicates endonuclease domain, and filled bar indicates EF-hand motif.

Figure S4 Exogenous expression of OsNAC4 in *Nicotiana benthamiana* leaves by viral transduction. Full length of OsNAC4 were subcloned into *TogJ* vector and the vector template DNA was linearized with *MluI* prior to in vitro transcription to make a run-off transcription. The in vitro transcription reaction was performed with linearized vector

DNA using T7 RNA polymerase. The transcripts were inoculated to six-week old *N. benthamiana* with carborundum. Seven days after inoculation, lesions resulted from HR cell death were observed in left leaf. Right leaf is control leaf transfected by empty *TogJ* vector

Figure S5 Model for HR cell death induced by OsNAC4.

Figure S1
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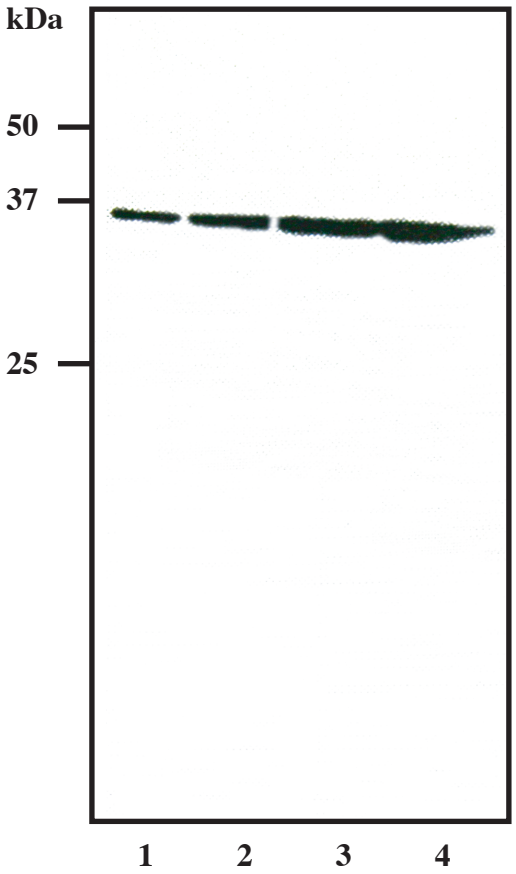

Figure S2
Kaneda et al.

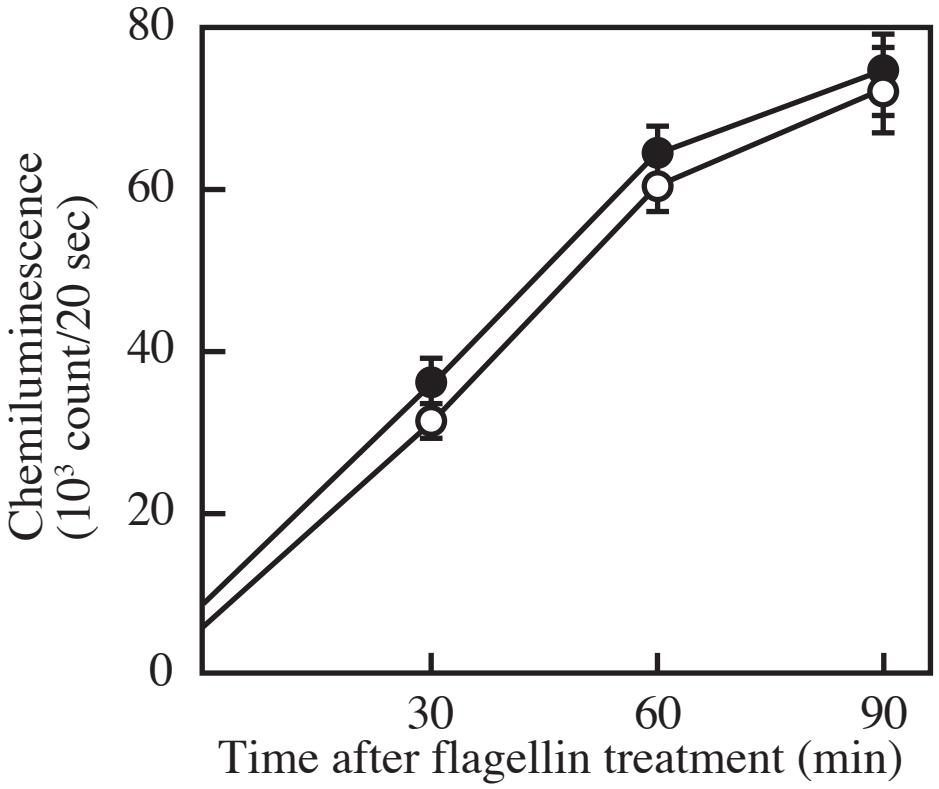

Figure S3
Kaneda et al.

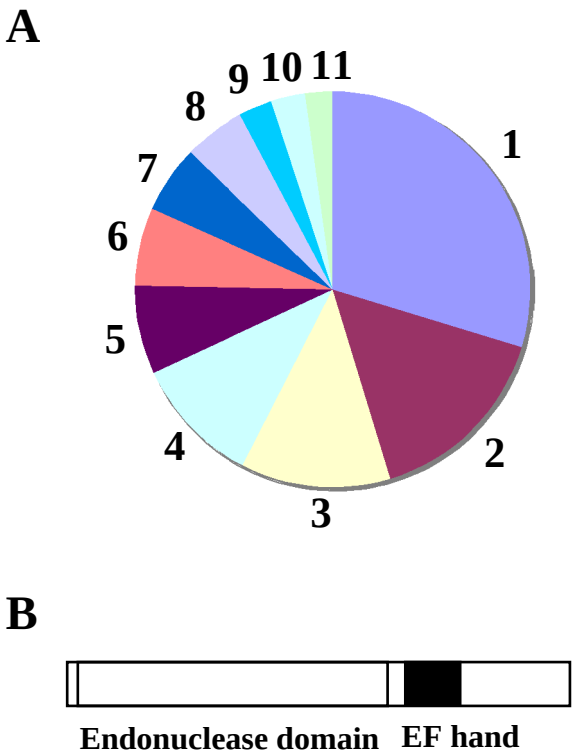

Figure S4
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Figure S5
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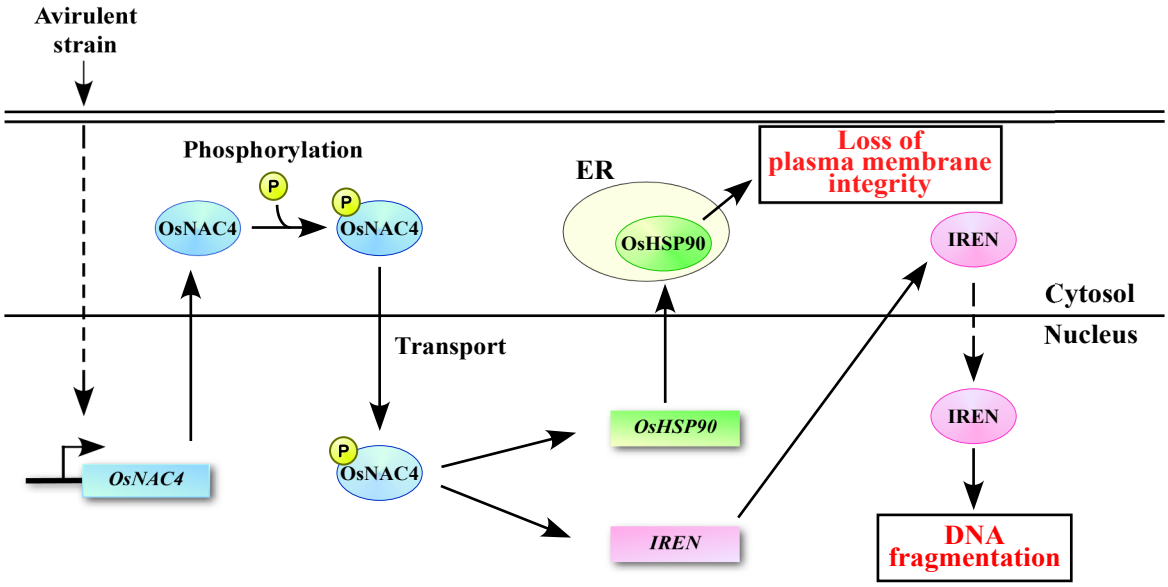

Table S1. Differentially expressed transctipts between cultured rice cells and OsNAC4 RNAi line, NR2-4, inoculated with the incompatible N1141 at different time points.

Accession	Putative gene identification	NR2-4 line				Wild type			
		0	1	3	6	0	1	3	6 (hr)
AK060274	Putative UDP-galactose/UDP-glucose transporter	0.95	0.87	1.03	1.44	1.12	1.42	8.27	5.24
AK063898	Hypothetical protein	0.88	0.64	1.50	1.01	0.86	2.51	7.96	7.47
AK065588	Putative CBL-interacting protein kinase	0.97	0.74	0.99	1.08	0.94	1.27	4.97	6.73
AK058409	Putative arm repeat-containing protein	0.88	0.93	0.90	1.25	0.97	1.27	3.70	5.46
AK067860	Hypothetical protein	0.94	0.96	1.06	1.38	1.10	1.51	6.50	6.34
AK100148	Hypothetical protein	0.83	1.11	1.27	1.04	0.93	1.30	5.75	5.85
AK103383	Actin-like protein 3	1.02	0.93	1.07	1.15	0.92	1.53	4.91	4.13
AK064143	BTB/TAZ domain protein	0.91	0.80	1.34	1.20	1.19	1.27	8.02	13.48
AK058319	Polyubiquitin.	0.80	0.91	1.07	1.16	0.94	2.02	3.71	3.14
AK100224	Putative ubiquitin.	1.07	0.99	1.04	1.48	1.01	1.60	3.25	2.46
AK072505	Serine/threonine protein kinase.	0.92	1.02	2.18	1.03	1.29	1.46	5.35	6.38
AK066397	Receptor protein kinase	0.83	1.28	1.34	0.67	0.96	1.88	11.29	5.72
AK063871	Putative UDP-glucose 4-epimerase.	0.85	1.03	1.10	1.31	1.07	1.70	4.96	2.92
AK063428	Aluminum-activated malate transporter	0.67	0.95	1.14	0.84	0.85	1.49	8.90	17.25
AK106226	Hypothetical protein	0.97	0.83	0.89	1.51	0.90	1.35	3.13	3.55
AK060598	Transmembrane amino acid transporter protein	1.03	0.94	0.65	0.50	1.01	1.30	7.85	8.02
AK064554	Lipase-like protein.	0.90	1.05	0.96	1.36	1.00	1.13	6.50	7.35
AK062718	Hypothetical protein	0.96	1.07	1.04	1.60	1.05	1.42	7.48	4.88
AK070399	Hypothetical protein	1.20	1.16	1.18	1.05	1.01	1.95	4.76	4.98
AK064074	LEA protein.	1.80	0.48	1.20	1.01	1.12	0.89	8.86	8.15
AK069950	Hypothetical protein	0.83	1.26	1.12	1.12	1.05	1.36	4.66	4.37
AK060275	Proline-rich protein	1.30	0.75	1.26	1.31	0.97	1.24	4.46	3.85
AK099485	Hypothetical protein	0.89	1.01	1.11	1.42	0.88	1.81	3.10	3.02
AK071729	Hypothetical protein	0.88	1.10	1.24	0.90	1.22	1.38	6.69	8.71
AK065831	Putative regulatory protein.	1.16	0.98	1.04	1.28	1.29	1.72	6.43	5.14
AK059734	Type A response regulator 6.	0.81	0.91	0.86	0.52	1.16	1.35	6.91	8.24
AK109040	Protein kinase-like.	1.11	1.12	1.30	1.14	1.11	2.24	6.99	4.79

AK100514	Endonuclease, putative.	0.97	1.11	0.95	0.93	0.98	1.11	4.17	4.62
AK061327	Transferase family	0.91	1.01	1.11	1.21	1.07	1.23	7.78	17.22
AK109902	Putative trehalose-6-phosphate phosphatase	0.69	1.11	0.87	0.87	1.20	1.27	8.56	11.08
AK109325	Putative nuclear protein.	1.04	0.81	1.64	1.83	1.29	1.10	9.04	10.84
AK102478	Heat shock protein 90.	0.97	1.00	0.90	1.07	1.03	1.29	5.71	3.85
AK105877	Putative AP2-domain DRE binding factor	1.21	1.04	0.98	1.03	1.12	1.84	3.52	3.06
AK102970	Putative antifungal thaumatin-like protein	0.91	0.80	0.83	1.54	0.99	1.34	3.30	4.43
AK103071	Retrotransposon protein,	1.20	0.84	1.30	1.59	1.16	1.68	6.44	5.90
AK100379	GCIP-interacting family protein-like.	1.40	1.17	1.59	1.68	1.01	2.45	6.83	4.75
AK063625	Caleosin	1.85	0.45	0.75	0.75	0.89	0.88	6.88	12.54
AK070672	Hypothetical protein	0.84	1.09	1.16	1.44	1.07	1.33	6.47	5.44
AK065743	Putative dnaK-type molecular chaperone	1.05	0.86	0.92	1.37	1.04	1.48	9.09	6.37
AK103321	Hypothetical protein	1.16	1.03	0.79	0.62	0.78	3.16	5.96	6.93
AK061174	Putative harpin inducing protein.	1.12	1.10	0.90	0.77	0.92	1.52	5.35	2.81
AK067056	Hypothetical protein	0.82	1.21	1.16	1.96	0.97	4.06	6.04	11.56
AK101170	Phosphate transporter - HvPT4	1.17	0.81	0.80	1.28	0.68	3.65	8.10	7.56
AK107893	Hypothetical protein	1.44	1.12	0.90	1.68	1.20	1.43	10.49	13.03
AK104746	Aldehyde dehydrogenase	1.25	1.16	1.16	1.87	0.99	1.93	8.29	12.21
AK107530	Hypothetical protein	0.80	0.91	1.04	1.50	1.15	4.46	22.04	26.48
AK063715	ZF-HD protein dimerisation region	1.22	0.93	1.09	1.46	0.82	2.04	11.85	12.70
AK058426	Thioredoxin-like 1.	1.35	1.26	1.29	1.50	1.09	1.98	6.80	7.15
AK060392	Remorin, C-terminal region,	1.30	0.91	1.61	1.36	1.18	2.43	8.35	10.74
AK071968	Putative choline kinase CK2.	1.09	0.95	1.64	1.49	0.93	3.10	15.05	13.14
AK065194	Hypothetical protein	1.18	1.01	1.13	1.87	0.92	3.28	7.63	10.25
AK111746	Putative CBL-interacting protein kinase	1.12	1.03	1.98	1.91	0.98	2.47	17.51	9.92
AK070177	Putative mannose-6-phosphate isomerase	1.08	1.07	0.95	0.89	0.94	6.05	10.69	13.01
AK099079	Putative glucose transport protein STP1	1.13	1.16	1.42	1.72	1.06	2.91	11.26	20.67
AK065989	Putative NAM protein	1.15	0.97	1.29	1.57	1.04	2.00	6.85	7.08
AK073507	Putative serine/threonine-specific receptor protein	1.08	1.16	1.54	1.66	1.00	2.62	4.80	5.22
AK111294	Hypothetical protein	1.35	1.35	1.58	1.52	1.23	2.50	10.21	3.31
AK065329	Hypothetical protein	0.97	1.19	1.30	1.56	0.86	2.63	6.25	5.22
AK107983	Hypothetical protein	1.04	1.21	1.45	1.53	0.92	3.24	6.63	5.66

AK065359	Lustrin A-like.	1.27	1.01	1.51	1.78	1.06	3.32	8.17	5.11
AK108304	NHL repeat-containing protein-like.	0.87	0.89	1.56	1.46	0.94	2.59	4.63	5.98
AK060684	Putative myb-related protein	0.95	1.08	1.36	1.48	0.89	2.79	4.69	3.67
AK107964	Hypothetical protein	0.99	1.06	1.47	1.73	1.14	2.30	4.06	4.07
AK100767	Alcohol dehydrogenase	0.74	1.08	0.70	1.35	0.66	14.70	7.74	9.05
AK101103	Putative beta-ketoacyl-CoA synthase.	0.97	0.99	1.18	1.42	0.99	2.37	3.53	3.21
AK107989	Ethylene-responsive element binding protein	1.02	1.69	1.95	1.82	1.04	13.90	34.30	7.72
AK105596	Putative NAC domain protein NAC1.	1.13	1.20	1.44	1.91	0.89	6.03	7.62	5.94
AK111415	Putative chitinase.	0.95	1.21	1.91	1.89	1.13	6.39	17.93	6.98
AK068151	Wound-induced protein	1.01	0.94	0.99	0.99	1.09	7.35	6.36	5.32
AK058853	Enzyme of the cupin superfamily.	1.05	1.31	1.48	1.49	1.15	4.23	4.34	2.93
AK109116	Putative hydroxycinnamoyl transferase.	1.04	0.91	2.52	4.92	1.06	13.52	17.92	11.83
AK064946	BHLH protein-like.	1.15	1.52	2.24	2.00	1.12	9.82	6.89	7.14
AK100238	Zinc finger-like.	0.96	1.45	1.81	2.86	1.15	5.16	7.27	8.57
AK072729	Myristoyl-acyl carrier protein thioesterase	0.91	1.39	1.08	2.63	0.96	3.71	4.79	4.55
AK101182	Putative heat shock factor.	1.03	0.98	1.38	2.64	0.83	5.43	4.32	5.05
AK107493	Sialyltransferase-like protein.	0.88	1.15	1.04	1.54	1.05	2.42	5.02	3.53
AK070719	Sialyltransferase-like protein.	0.96	1.26	1.10	1.17	1.03	5.50	4.07	2.07
AK066063	Receptor-like protein kinase	1.02	1.32	1.03	1.79	0.90	8.10	5.23	10.62
AK061011	Hypothetical protein	0.97	0.92	1.35	1.50	0.95	2.91	4.51	3.78
AK109344	Putative GTP-binding protein.	0.84	0.79	0.94	0.82	0.99	1.55	3.04	1.73
AK100906	Diacylglycerol kinase 1.	0.83	0.91	1.07	0.78	0.90	1.51	5.31	3.95
AK064265	Hypothetical protein	0.81	0.96	0.95	1.17	1.08	2.16	5.02	2.43
AK070197	Putative cold acclimation protein	1.18	0.71	0.85	0.68	1.42	0.95	4.97	3.11
AK059764	Putative fiber protein Fb2.	0.85	0.88	1.07	1.02	0.89	1.33	2.78	2.22
AK072284	Hypothetical protein	0.87	0.78	1.09	0.89	0.94	1.47	4.20	2.77
AK103072	Putative elicitor inducible beta-1,3-glucanase	1.30	0.49	0.83	1.32	0.97	1.89	2.76	2.26
AK101596	Hypothetical protein	0.80	0.74	0.88	0.63	1.03	1.14	3.69	3.87
AK063711	Hypothetical protein	0.76	0.67	1.05	0.79	0.78	0.97	2.87	2.93
AK107774	Putative oleosin.	1.85	0.36	0.61	0.73	0.97	0.96	4.39	10.29
AK069824	Hypothetical protein	0.84	1.00	1.10	1.22	1.03	1.39	3.45	2.66
AK107760	Putative reversibly glycosylated polype.	1.45	1.03	0.96	1.31	0.88	4.18	3.60	2.59

AK060706	2-hydroxyisoflavanone dehydratase	0.85	0.81	0.77	0.90	0.67	1.97	3.19	2.57
AK071777	Putative CDP-diacylglycerol synthetase	0.91	0.86	0.92	1.26	0.89	1.68	3.33	2.86
AK069118	Calnexin homolog precursor.	0.87	0.84	0.88	0.91	1.08	1.11	3.52	2.01
AK071527	Putative DHHC-type zinc finger domain-containing protein	0.99	0.86	1.12	1.27	0.89	2.12	3.12	2.33
AK100034	12-oxo-phytodienoic acid reductase.	1.15	0.70	1.04	1.00	0.77	2.41	5.00	4.39
AK108264	Hypothetical protein	0.84	1.08	0.40	0.58	1.09	1.39	4.50	4.14
AK107295	Hypothetical protein	0.95	0.88	1.17	0.78	0.96	1.74	4.15	3.89
AK072910	Membrane protein CH1-like.	1.13	0.96	1.05	1.12	1.08	1.29	3.71	4.58
AK061082	Putative GRAS family transcription factor	1.06	0.90	0.99	1.23	0.87	2.34	4.06	4.53
AK071680	Putative purine permease.	0.92	1.20	1.23	0.81	1.03	1.39	4.33	2.27
AK062254	Protein disulfide isomerase.	0.76	0.91	0.68	1.00	0.94	0.87	4.37	3.45
AK068075	Ring-H2 zinc finger protein-like.	0.99	0.87	1.13	0.93	0.97	1.62	5.63	3.52
AK074014	Putative splicing regulatory protein.	0.82	0.97	0.77	0.73	0.87	1.46	4.04	1.86
AK061872	Putative ubiquitin.	1.11	1.05	1.08	1.42	1.12	1.59	3.38	2.86
AK107193	SF16 protein-like.	0.75	0.89	0.52	0.48	1.02	1.92	4.52	3.21
AK101234	Hypothetical protein	1.04	0.99	0.82	0.96	0.94	1.12	4.01	4.80
AK072705	Putative CENP-E like kinetochore protein	0.91	1.08	1.07	1.05	1.01	2.48	3.78	2.15
AK070712	Putative calreticulin.	0.90	1.03	0.64	0.41	1.16	1.24	3.73	2.64
AK108172	F-box domain, putative.	0.92	1.07	1.06	0.51	1.14	1.46	3.77	2.12
AK071151	Oxysterol-binding protein-like.	1.12	0.92	0.72	0.69	0.93	1.20	3.95	4.90
AK073109	Hypothetical protein	1.52	0.52	0.62	0.86	1.28	0.94	5.46	5.23
AK100997	Putative HSP protein.	1.02	0.84	0.85	0.91	0.91	0.98	2.91	2.47
AK061570	Hypothetical protein	0.86	1.03	0.84	0.87	0.82	2.23	3.54	3.15
AK071491	Heavy-metal-associated domain	0.68	0.55	1.68	1.52	0.88	1.08	3.99	4.49
AK109491	Hypothetical protein	0.97	1.02	1.07	1.11	1.08	1.36	3.64	3.06
AK063647	Phytosulfokines 4 precursor	1.39	0.98	1.45	2.13	1.15	1.91	4.12	3.74
AK069826	Putative regulatory protein.	0.92	0.75	1.81	1.89	0.94	2.33	3.85	4.75
AK102658	Putative zinc finger protein.	1.18	0.55	1.21	2.46	0.91	2.68	3.45	3.14
AK065106	Zinc finger (C3HC4-type RING finger)-like protein	0.83	0.95	1.08	1.91	1.13	1.85	4.38	7.28
AK106955	Putative serine/threonine protein kinase	0.98	0.90	1.05	1.47	0.83	3.06	4.87	3.11
AK069779	ABA-responsive protein-like.	0.85	0.74	1.04	1.72	0.74	1.77	3.72	3.56
AK111073	Hypothetical protein.	1.01	0.81	1.43	1.81	0.95	1.82	3.05	4.49

AK106276	F-box protein-like.	0.72	0.81	1.81	3.05	0.99	2.22	5.26	9.08
AK106598	Epstein-Barr virus EBNA-1-like.	0.72	0.97	1.31	1.45	0.96	1.72	3.70	5.13
AK065638	Putative histone H1flk.	0.88	0.75	0.79	1.31	0.92	2.39	3.42	5.61
AK066981	MAPK activating protein-like.	0.81	0.70	1.51	1.33	0.81	1.97	3.55	3.88
AK100658	Putative translation elongation factor	0.89	0.95	1.21	1.27	0.96	1.64	3.82	4.07
AK105720	Function unknown		0.98	1.08	1.57	1.07	1.40	5.02	3.98
AK106044	probable amine oxidase	0.86	0.72	1.00	1.61	0.99	1.16	3.81	3.90
AK071047	Putative senescence-associated-like protein	0.95	1.04	0.98	1.74	1.06	1.52	3.64	3.25
AK105755	NADH-dependent Glu synthase	0.77	0.77	0.68	1.35	1.15	1.24	3.18	5.96
AK100248	Leucine zipper protein-like.	0.98	1.29	1.08	1.16	0.96	2.12	7.61	2.54
AK063558	Lipase class 3 protein-like.	0.90	0.99	1.36	1.22	0.94	1.51	3.69	4.07
AK062189	Putative glycolate oxidase	0.98	1.02	1.36	1.47	1.11	1.43	5.08	4.18
AK069864	Putative male sterility 1 protein.	0.99	1.07	1.03	1.88	0.93	2.53	3.38	2.64
AK069810	MAD, mothers against decapentaplegic homolog	1.01	1.03	1.32	1.45	1.11	1.81	3.89	3.43
AK067907	Fatty acidhydrolase	0.80	1.70	2.08	3.00	1.02	8.20	40.92	32.81
AK101060	Bax inhibitor 1 (BI-1) (OsBI-1).	0.99	1.04	1.49	2.11	0.99	1.43	5.47	4.25

Median value are given.
Each values represents the ratio of avirulent strain-inoculated cells/water-treated cells