Supporting Information

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SI Text

Gene Constructs and Rice Transformation. The *OsSKIPa*-overexpression construct (S58S) was constructed by directionally inserting the full cDNA sequence first into the entry vector pDONR207 and then into the destination vector pCB2004H (1) using the Gateway recombination reaction (Invitrogen). To make a dsRNAi construct of *OsSKIPa* (S59R), a 570-bp fragment of *OsSKIPa* (nucleotides 1534–2104) was generated by PCR with primers *SKIP*-RNAi and was cloned into pHellsgate2 (2) through *att*B × *att*P (BP) recombination cloning. The *attB1* and *attB2* are the 2 sequences for the BP recombination reaction (Invitrogen). The constructs were transformed into the *japonica* rice cv. Zhonghua 11 by the *Agrobacterium*-mediated transformation method (3).

Plant Growth, Stresses Treatment, and Measurement. Rice seeds of cultivar Zhenshan 97 (*O. sativa* L. ssp. *indica*) were germinated and grown in Hoagland hydroponic culture medium for 18–20 days under normal growth conditions for rice. To measure the expression level of the *OsSKIPa* gene under various stresses, plants at the 4-leaf stage were treated with abiotic stresses, including drought (removing the water supply from the plants for the designated time), salt (addition of 200 mM NaCl in the hydroponic culture medium), cold (exposing plants to 4 °C for the designated time), wounding (crushing rice leaves with a hemostat), and phytohormones (100 μM ABA, 450 μM kinetin, 100 μM gibberellic acid, 50 μM indole-3-acetic acid, 100 μM jasmonic acid, 1 mM salicylic acid, 1 mM ethephon, or 10 μM brassinosteroid).

Positive transgenic plants of S58S T_1 or T_2 families were selected by germinating seeds on MS medium containing 50 mg/L hygromycin. After germination, the positive seedlings were transplanted in MS medium containing 3 μM ABA, 150 mM NaCl, or 200 mM mannitol and grown for 10 days. S58S transgenic plants (at the 4-leaf stage) growing in sandy soil were drought-stressed (no watering for 7 days), followed by recovery. The drought stress at the panicle development stage was applied to plants growing in PVC tubes (1-m height, 20-cm diameter) by following the protocol of Yue et al. (4); genotypes of the plants were checked by PCR using hygromycin resistance gene-specific primers. Each stress test was repeated 3 or 4 times.

SOD activity was determined according to the methods described previously (5). The reaction mixture consists of 50 mM potassium phosphate (pH 7.8), 13 mM methionine, 0.01 mM EDTA, 0.002 mM riboflavin, and 0.075 mM nitroblue tetrazolium. SOD activity was determined by monitoring the inhibition of the reduction rate of nitroblue tetrazolium in the reaction mixture and the control without protein extract at 560 nm.

Gene Expression Analysis. Total RNA was isolated from rice leaves using TRIzol reagent (Invitrogen). For RNA gel blotting, 15 μg of total RNA from each sample was separated on a 1.2% (vol/vol) agarose gel containing 1% formaldehyde and then transferred onto a nylon membrane. The RNA gel blot was hybridized with α-^{32}P-dCTP–labeled *OsSKIPa* gene-specific probe overnight using modified Church buffer [7% SDS (wt/vol), 0.5 M phosphate buffer (pH 7.2), 10 mM EDTA] at 65 °C. Blots were washed using 2× SSC/0.1% SDS for 10 min at 65 °C. The blot was briefly air-dried and then subjected to radiography.

Real-time quantitative RT-PCR was performed on a 7500 Real-Time PCR System (Applied Biosystems) using SYBR Green PCR Master Mix Reagent (Applied Biosystems). Rice *Actin1* gene was used as the endogenous control. The relative expression levels were determined as described previously (6).

Western Blot Analysis. Nuclear protein (15 μg) was separated on 10% (vol/vol) SDS/PAGE gels and transferred to polyvinylidene difluoride membrane, followed by Western blot analysis. In brief, 2% (wt/vol) BSA in PBS containing 0.05% Tween 20 was used to block nonspecific binding. The blot was subsequently incubated with anti-OsSKIPa rabbit polyclonal antibody (New-East Biosciences) and with secondary antibody (SouthernBiotech). After antibody incubation, blots were extensively washed in PBS. An ECL kit (Pierce) was used for detection according to the manufacturer's instructions.

Yeast Two-Hybrid Screening and GST Pull-Down Assay. The yeast two-hybrid assay was performed using the ProQuest Two-Hybrid System (Invitrogen). The coding region of OsSKIPa was amplified with primers *SKIP*-Y2H. The PCR product was cloned into the entry vector pDONR221 using the BP reaction and then into the vector pDEST32 using the *att*L × *att*R reaction to generate bait vector with *OsSKIPa* fused to the *GAL4* DNA binding domain. A prey cDNA library of rice was constructed by fusing cDNAs with the *GAL4* activation domain in the pEXP-AD502 vector (Invitrogen) according to the manufacturer's instructions. The yeast strain Mav203 (*MAT*α; *leu2–3,112*; *trp1–901*; *his3*Δ*200*; *ade2–101*; *gal4*Δ; *gal80*Δ; *SPAL10*::*URA3*; *GAL1*::*lacZ*; *HIS3*$_{UAS\ GAL1}$::*HIS3@LYS2*; *can1*^{R}; *cyh2*^{R}) was transformed with the bait plasmid, and the cells containing the bait were transformed with the plasmid DNA of the prey cDNA library according to the method described previously (7). A total of 2.75×10^5 transformants were selected on synthetic complete selection medium containing 15 mM 3-AT (3-amino-1, 2, 4-Triazole) and lacking Leu, Trp, and His. Large yeast clones appearing within 7 days were picked out for testing of the LacZ reporter gene. Positive clones were isolated and cotransformed with pDEST32 to test their self-activation activities.

The cDNAs of *OsSKIPa*-interacting proteins identified from yeast two-hybrid assay were constructed in fusion with N-terminal GST tag in pDEST15 (Invitrogen) through recombination reactions with pDONR221 (Invitrogen) as an entry vector. The GST fusion proteins were expressed in *Escherichia coli* strain BL-21 for GST pull-down assay. The same fragment of *OsSKIPa* as used in the yeast two-hybrid assay was cloned into pDEST17 for expression of ^{35}[S]-labeled OsSKIPa protein. The GST pull-down assay was performed using the MagneGST Pull-Down System (Promega) according to the manufacturer's instructions.

Microscopic and in Situ Hybridization Analyses. The shoots and roots of S58S and S59R plants were collected 10 days after germination and fixed in FAA (50% (vol/vol) ethanol, 5% (vol/vol) acetic acid, 3.7% (vol/vol) formaldehyde). The procedures of dehydration, clearing, infiltration, and embedding were carried out as described by Dai et al. (8). The microtome sections (8 μm) were stained with Safranin and Fast Green before mounting on glass slides for imaging.

A TUNEL assay was performed according to the manufacturer's instructions (Takara). The FITC signals were observed in a fluorescence microscope equipped with a CCD (Leica).

The cDNA of N-terminal *OsSKIPa* was constructed in frame with the C-terminal of GFP in the CaMV 35S-GFP-NOS cassette vector. Plasmid DNA was precipitated onto gold par-

ticles using $CaCl_2$ and spermidine, and 5 μg of DNA was used to bombard the inner epidermal layers of onion using the Biolistic PDS-1000/He Particle Delivery System (Bio-Rad). The bombarded tissue was incubated in darkness for 20 h and then soaked in solution with 2 μg/μL DAPI, and florescence signal was captured through a confocal microscope (Leica).

The in situ RNA hybridization was performed according to the method of Dai et al. (8). The probe was amplified using OsSKIPa-specific primers *SKIP*-ISH. The PCR fragments were inserted into pGEM-T vector (Promega). DIG-labeled sense and antisense RNA probes were produced by T7 and Sp6 transcriptase (Roche), respectively.

Microarray Analysis. Two independent transgenic lines for S59R and S58S, respectively, were used for microarray analysis. One-month-old whole plants were collected for microarray analysis. RNA sample preparation and hybridization were performed following the standard protocol of Affymetrix Gene Chip service (CapitalBio). Signal was normalized and estimated using the gcRMA package of Bioconductor (9). Analysis of differential gene expression was performed using the LIMMA package (10). The differential expression genes were filtered according to the following criteria: (*i*) assignment present at least in 2 chips by MAS5.0 (Affymetrix); (*ii*) average log-transformed expression value by gcRMA larger than 3; and (*iii*) log-transformed changed fold more than 1 with expect value less than 0.05 by LIMMA (10). The annotations of the probe sets, downloaded from Affymetrix and modified based on protein–protein BLAST analysis, were used for gene ontology analysis. Overrepresentation of GO category was calculated by the BiNGO software (11).

Putative promoter sequences of the expression-level-changed genes were downloaded from the KOME web site (http://cdna01.dna.affrc.go.jp/cDNA/). The *cis*-element enrichment analysis followed the previous report (12). The annotation of *cis*-elements was downloaded from the PLACE database (13).

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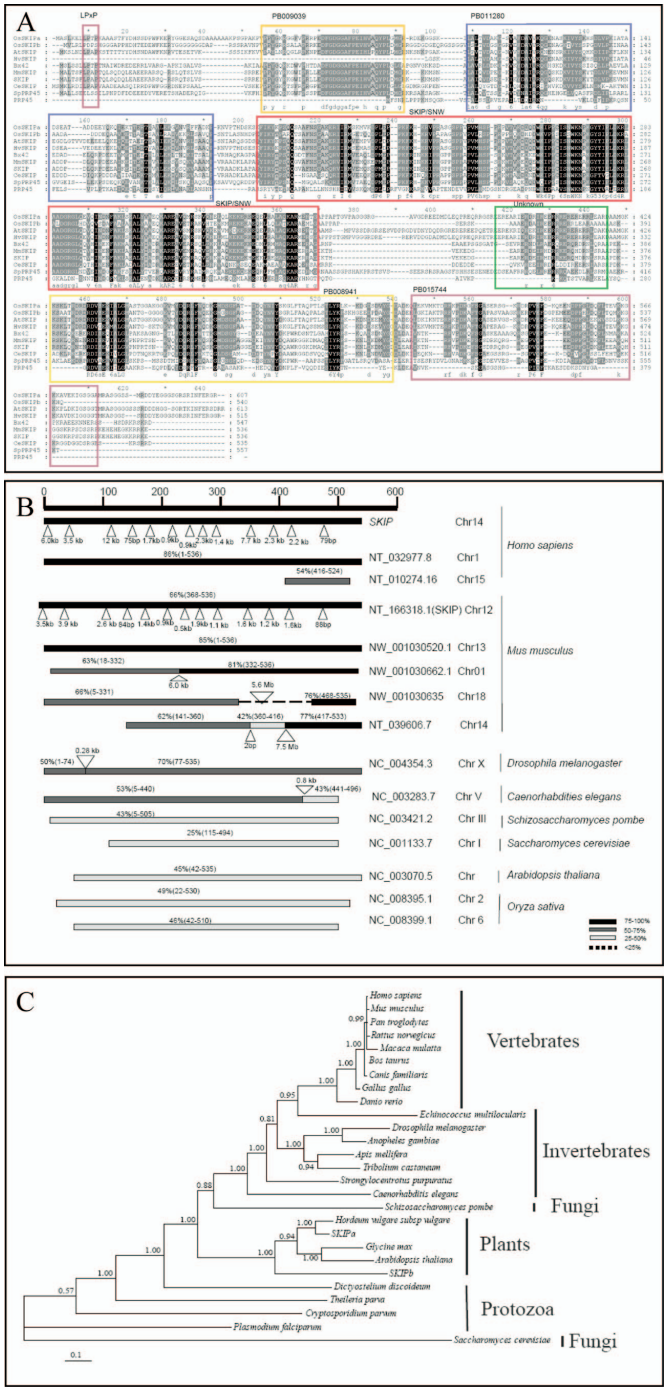

Fig. S1. Multiple sequence alignment, sequence and structure comparison, and phylogenetic tree of SKIPs from different species. (*A*) Multiple sequence alignment of SNW/SKIP proteins from rice (OsSKIPa and OsSKIPb), *Arabidopsis* (AtSKIP, O80653), wheat (HvSKIP, Q84UD2), *Drosophila* (Bx42, P39736), mouse (MmSKIP, Q9CSN1), humans (SKIP, Q13573), *Caenorhaabditis elegans* (CeSKIP, Q22836), *Schizosaccharomyces pombe* (SpPRP45, Q09882), and *Saccharomyces cerevisiae* (PRP45, P28004). The conserved motifs or domains are labeled with rectangular boxes in different colors with the PFAM accession numbers shown on the top of the boxes. (*B*) Sequence and structure comparison of *SKIP* with its homologous genes in humans, mouse, fruit fly, *C. elegans*, yeast, *Arabidopsis*, and rice. The scale indicates the length of the protein sequence. The protein sequence similarity to SKIP, with the compared region indicated in brackets, is indicated on the top of each *SKIP* homolog. The positions of introns are indicated by triangles with the length of introns (kb). The legend indicates the degree of sequence similarity. (*C*) Phylogenetic tree of SNW/SKIP members from different species. Accession numbers are as follows: *Homo sapiens*, NP_036377 (SKIP); *Mus musculus*, NP_079783; *Rattus norvegicus*, XP_576077; *Bos Taurus*, NP_001071302; *Pan troglodytes*, XP_001165674; *Canis familiaris*, XP_868304; *Macaca mulatta*, XP_001096395; *Danio rerio*, NP_001002864; *Gallus gallus*, XP_421294; *Drosophila melanogaster*, NP_511093; *Apis mellifera*, XP_623623; *Anopheles gambiae*, XP_313821; *Tribolium castaneum*, XP_971504; *Caenorhabditis elegans*, NP_505950; *Strongylocentrotus purpuratus*, XP_001188665; *Echinococcus multilocularis*, CAI59265; *Dictyostelium discoideum*, XP_646059; *Cryptosporidium parvum*, XP_627326; *Plasmodium falciparum*, XP_001349691; *Theileria parva*, XP_765077; *Arabidopsis thaliana*, NP_565151; *Glycine max*, AAZ38969; *Hordeum vulgare subsp. Vulgare*, AAO25542; *Saccharomyces cerevisiae*, NP_009370; and *Schizosaccharomyces pombe*, NP_588213.

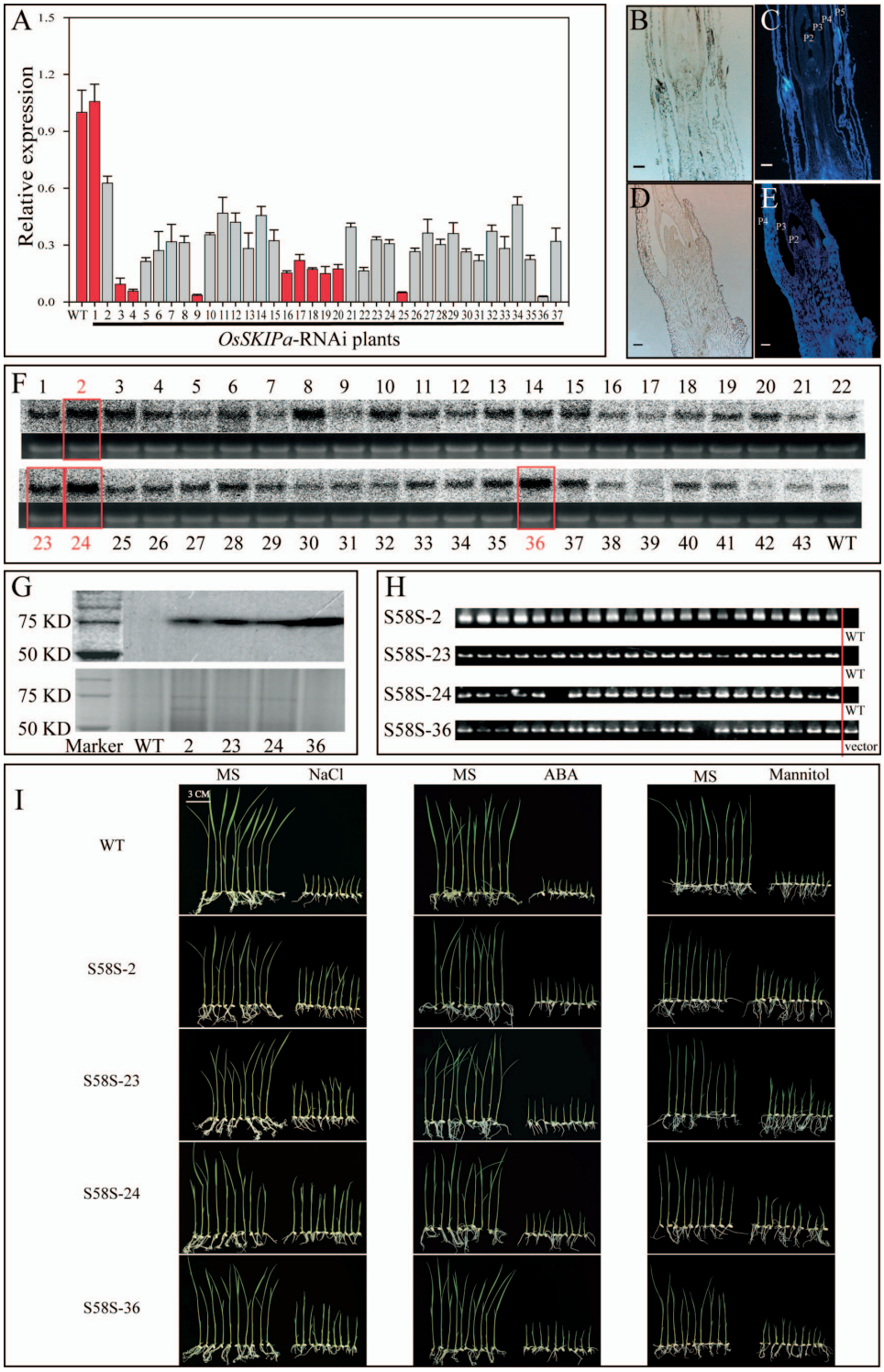

Fig. S2. Expression level of *OsSKIPa* in the *OsSKIPa*-suppressed (S59R) and *OsSKIPa*-overexpressed (S58S) plants and the performance of the transgenic plants. (*A*) The relative expression level of *OsSKIPa* in the T_0 generation transgenic plants (1–37) was compared with WT by real-time PCR analysis. Transgenic line 1 was used as negative control. The lines used for further analysis are labeled in red. TUNEL assay of WT (*B* and *C*) and S59R (*D* and *E*) seedling sections. (*B* and *D*) Image in light field. More TUNEL-positive cells are found in the leaf primordia and hypocotyl of S59R (*E*) than in WT (*C*). P2–P5: leaf primordia. Bars = 100 μm. (*F*) RNA gel blot analysis of the *OsSKIPa*-overexpressed plants. The 4 lines used for further analysis are labeled with red rectangles. (*G*) Western blot analysis of the *OsSKIPa*-overexpressed (S58S) plants using anti-OsSKIPa antibody. (*H*) Positive check of *OsSKIPa*-overexpressed (S58S) plants. Positive transgenic plants of S58S T_1 or T_2 families were selected by germinating seeds on MS medium containing 50 mg/L hygromycin, and the genotypes of the plants were then confirmed by PCR. (*I*) Performance of 4 independent *OsSKIPa*-overexpressing transgenic lines (S58S-2, S58S-23, S58S-24, and S58S-36) in MS medium containing 3 μM ABA, 150 mM NaCl, or 200 mM mannitol.

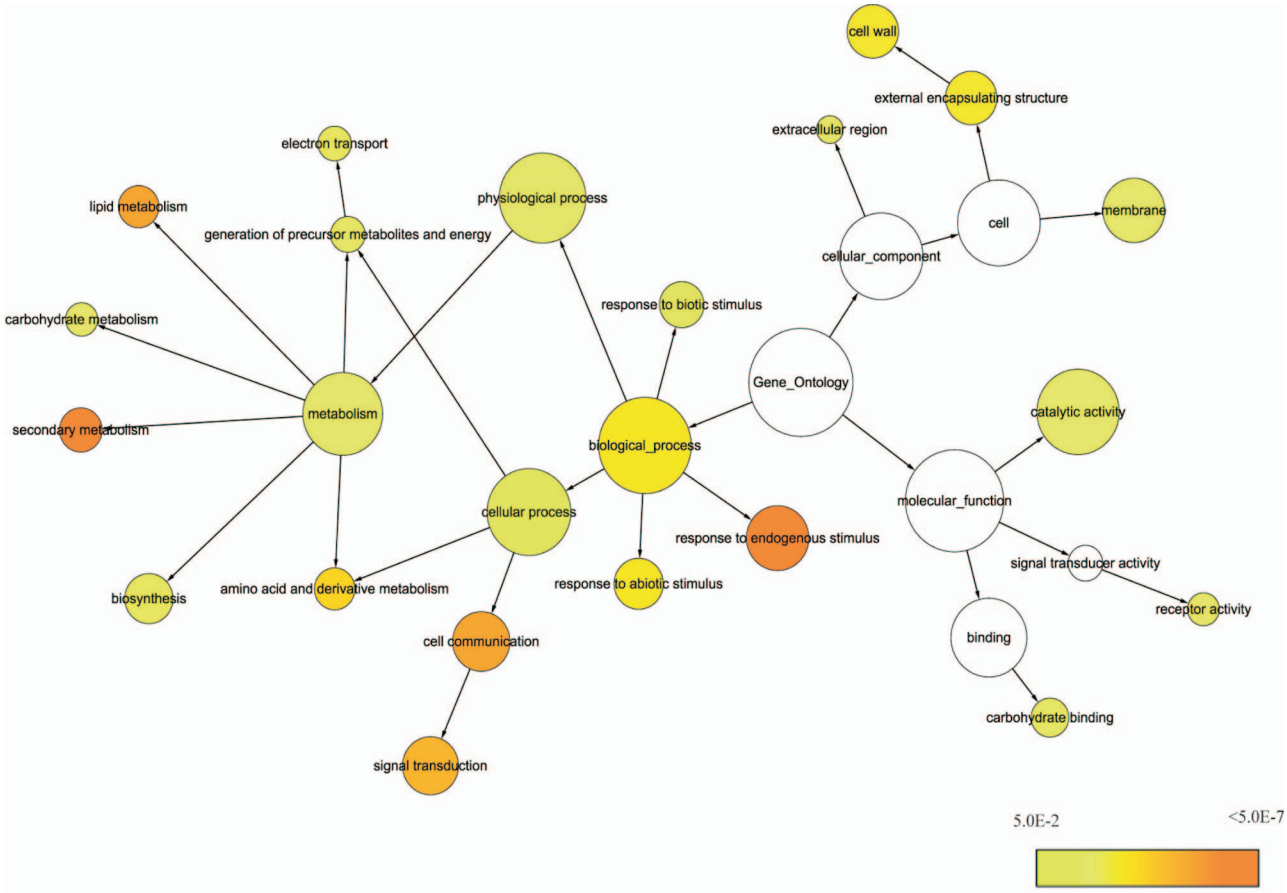

Fig. S3. Overrepresented categories of GO slims in *OsSKIPa*-suppressed and *OsSKIPa*-overexpressed lines. The size of the cycle indicates the number of genes assigned to the category. The orange color indicates the hypergeometric test, with the scale of *P* value indicated at the bottom.

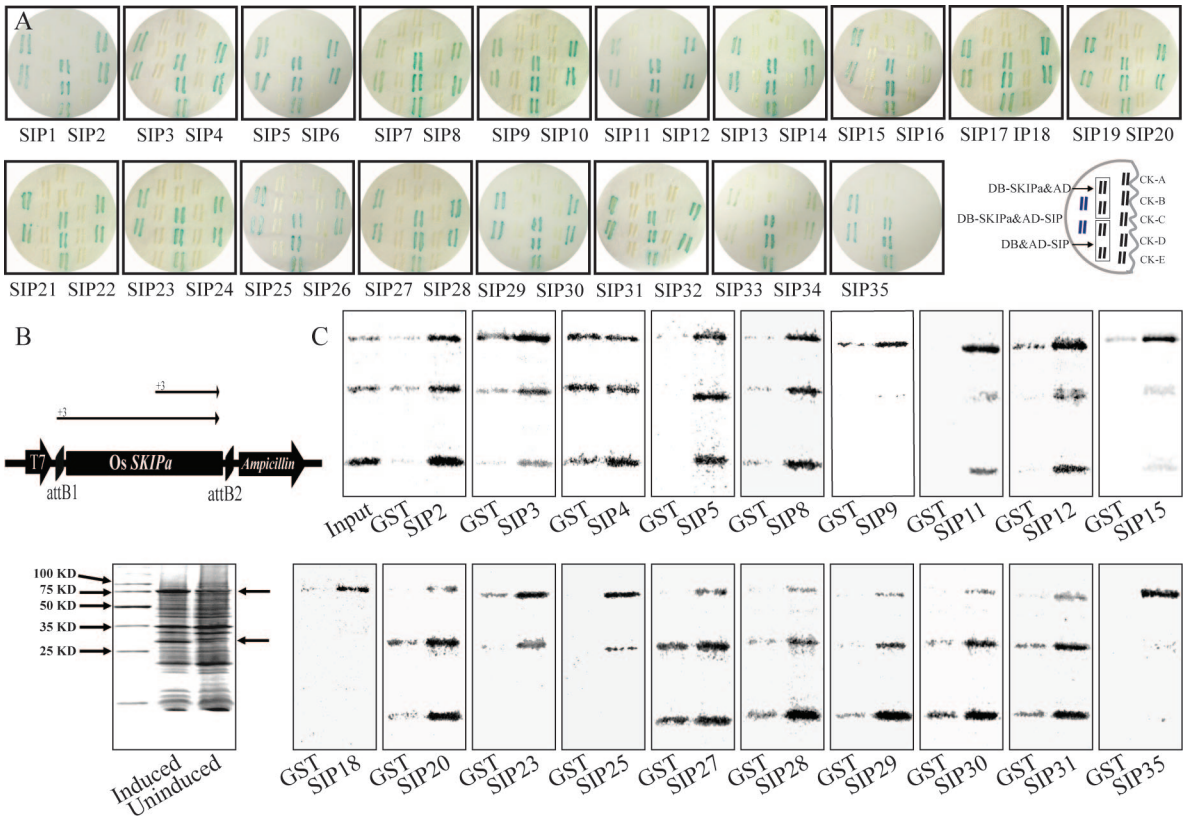

Fig. S4. SIPs identified by yeast two-hybrid and GST pull-down assays. (*A*) The X-gal assay of OsSKIPa-SIP interaction in yeast. Each membrane was patched 2 SIPs with control strains, and the patching method is shown at the end of panels. The control strains with different interacting activity (CK-A to CK-E, weak to strong) were patched in the middle of each panel. (*B*) Construct for in vitro expression of OsSKIPa protein. There are 2 ORFs (+3, indicated by the arrow lines) with 2 proteins expressed corresponding to the 75-kDa band and 30-kDa band (indicated by arrows). (*C*) GST pull-down assay of 19 pairs of OsSKIPa-SIP interactions. Each panel contains a GST-SIP fused protein and GST as control.

Table S1. Growth performance of the *OsSKIPa*-suppressed plants (S59R)

Line[†]	*N*[‡]	Shoot height (cm)[§]	Root length (cm)[¶]	Leaf grow rate[‖]	Leaf no. (20 DAG)	Growth rate (cm·d^{-1})[††]	Biomass (g)	Tiller no.[‡‡]
S59R-3	15	18.7 ± 3.2**	3.8 ± 0.4**	0.19 ± 0.03**	3.0 ± 0.5**	0.9 ± 0.2*	26.45 ± 6.89**	9.0 ± 2.3*
S59R-4	15	18.7 ± 1.7**	5.0 ± 0.4**	0.20 ± 0.02**	3.5 ± 0.3**	0.7 ± 0.1**	43.47 ± 19.11*	12.0 ± 2.0*
S59R-9	16	21.2 ± 2.6**	4.3 ± 0.3**	0.19 ± 0.03**	3.0 ± 0.5**	1.0 ± 0.2*	50.02 ± 12.84**	15.3 ± 4.7**
S59R-16	16	23.3 ± 1.8**	4.6 ± 0.3**	0.27 ± 0.02*	4.3 ± 0.4*	1.1 ± 0.1*	46.01 ± 5.45**	12.3 ± 1.3*
S59R-17	16	26.2 ± 1.9*	4.9 ± 0.4**	0.23 ± 0.03**	4.2 ± 0.4*	1.2 ± 0.1	44.78 ± 5.97**	12.3 ± 1.6*
S59R-18	16	18.3 ± 2.0**	4.6 ± 0.3**	0.25 ± 0.02**	3.9 ± 0.3**	0.9 ± 0.1**	30.82 ± 4.74**	7.7 ± 1.1**
S59R-19	16	19.4 ± 2.7**	4.3 ± 0.5**	0.21 ± 0.03**	3.4 ± 0.5**	1.0 ± 0.2*	42.95 ± 8.12*	10.0 ± 1.9*
S59R-20	14	21.6 ± 1.9**	5.0 ± 0.5**	0.23 ± 0.02**	3.7 ± 0.3**	1.1 ± 0.1*	30.88 ± 2.08**	8.0 ± 0.6*
S59R-25	12	27.4 ± 2.2	5.1 ± 0.4**	0.24 ± 0.03**	4.1 ± 0.5*	1.1 ± 0.1*	14.85 ± 4.51**	6.8 ± 1.7**
WT	24	30.9 ± 1.3	7.4 ± 0.4	0.30 ± 0.01	4.8 ± 0.1	1.4 ± 0.1	78.96 ± 8.18	18.9 ± 2.0
NC	15	30.1 ± 1.3	5.8 ± 0.5	0.29 ± 0.01	4.8 ± 0.1	1.3 ± 0.1	74.90 ± 8.08	18.9 ± 2.0

The data on shoot height, root length, leaf number, growth rate, and tiller number are shown as mean ± SE. DAG, days after germination; NC, negative transgenic control. **t* test, $P < 0.05$; ***t* test, $P < 0.01$.

[†]Relative expression level of *OsSKIPa* is shown in Fig. S2*A*.

[‡]Number of positive T_1 plants tested.

[§]Length of the shoot at 30 DAG.

[¶]Length of the root at 15 DAG.

[‖]Rate of leaf initiation per day at the seedling stage.

[††]Elongation of new leaves per day at seedling stage.

[‡‡]The tiller number at flowering stage.

Table S2. Enriched *cis*-elements in promoters of the differentially expressed genes in the overexpression (OE) and RNAi transgenic plants

Name of *cis*-element	Motif	Count*	Exp†	*P* value	TF‡	Stimulus/Tissue§
ACGT element						
ACGTATERD1	ACGT	727	600	0.00	ERD1	Light
ABRELATERD1	ACGTG	235	180	0.00	NACR	Drought
ACGTABREMOTIFA2OSEM	ACGTGKC	41	27	0.01		ABA, drought
BOXIIPCCHS	ACGTGGC	27	16	0.01	bZIP	ABA
ABREATCONSENSUS	YACGTGGC	15	9	0.02	ABF/bZIP	ABA
ACGTTBOX	AACGTT	52	39	0.03		
TGACGTVMAMY	TGACGT	56	37	0.00		Seed
ACGTABOX	TACGTA	79	47	0.00		Sugar (repression)
Core *cis*-elements						
CCAATBOX1	CCAAT	310	279	0.04		
−300ELEMENT	TGHAAARK	149	127	0.02		
TATABOX3	TATTAAT	79	61	0.01		
TATABOX4	TATATAA	105	77	0.00		
TATABOXOSPAL	TATTTAA	86	67	0.02	OsTBP2	
Other *cis*-elements						
IBOXCORE	GATAA	362	320	0.01		Light
GATABOX	GATA	1,113	1,028	0.01		
ASF1MOTIFCAMV	TGACG	187	153	0.01	ASF	Stress, auxin,
AMMORESIIUDCRNIA1	GGWAGGGT	11	6	0.02		Ammonium
DOFCOREZM	AAAG	1,616	1,505	0.01	Dof	
GAGA8HVBKN3	(GA)8	25	9	0.01		
GAGAGMGSA1	(GA)9	20	6	0.01		
MARARS	WTTTATRTTTW	18	10	0.01		
MYCCONSENSUSAT	CANNTG	1,283	1,187	0.01	MYC	ABA, cold
NAPINMOTIFBN	TACACAT	39	29	0.03		Seed
NTBBF1ARROLB	ACTTTA	134	99	0.00	Dof	Auxin
POLASIG2	AATTAAA	109	83	0.01		
ROOTMOTIFTAPOX1	ATATT	903	769	0.00		
RYREPEATGMGY2	CATGCAT	66	49	0.01		
RYREPEATLEGUMINBOX	CATGCAY	88	70	0.03		Seed
TAAAGSTKST1	TAAAG	326	284	0.01		Guard cell

*Actual number of the motif existing in the 500-bp region upstream of the transcription start site.
†Average expected (Exp) number of the motif for 1,000 randomly selected genes.
‡Predicted or evidenced transcription factor (TF) binding to the *cis*-element.
§To which stimulus or in which tissue the *cis*-element is responsive or specifically expressed.

Table S3. OsSKIPa-interacting proteins identified by yeast two-hybrid screening

ID	Locus*	cDNA†	Domains‡	Expect value§	Description¶
Cell cycle/cytoskeleton					
SIP1	LOC_Os01 g61760	AK071045			Probable myosin heavy chain
SIP30	LOC_Os07 g32450	AK069914			Myosin-like protein
SIP2	LOC_Os06 g27970	AK242820			Similar to AT3G54170 (*FIP37*)
SIP6	LOC_Os03 g17930	AK101532	COG1196: Smc	1e-04	Muscle derived-like protein
SIP12	LOC_Os08 g44520	AK072675	PF00160: cyclophilin type peptidyl-prolyl *cis-trans* isomerase/CLD	6.4e-68	Rice cyclophilin
SIP13	LOC_Os10 g36880		PF00225: kinesin motor domain	1.4e-91	Similar to AT4G39050(*MKRP2*)
SIP18	LOC_Os04 g28260	AF210816	PF06548: kinesin-related PF00225: kinesin motor domain	0 6e-13	Similar to AT3G23670(*PAKRP1L*)
SIP24	LOC_Os10 g36060		COG1196: Smc	2e-09	
SIP26	LOC_Os02 g53520	AK121333	PF00225: kinesin motor domain	1.9e-156	Similar to AT5G06670
SIP27	LOC_Os02 g28850		PF06548: kinesin-related PF00225: kinesin motor domain	3.2e-211 1.1e-81	Similar to AT3G23670(*PAKRP1L*)
Ubiquitin-ligase complex					
SIP20	LOC_Os04 g46450	AK067475	PF00097: C3HC4 type RING finger	2.2e-08	Similar to AT2G44950(*HUB1*)
SIP14	LOC_Os02 g19140	AK072985	PF03145: seven in absentia protein family	1.4e-130	Putative ubiquitin ligase SINAT5
SIP17	LOC_Os12 g41910		PF03000: NPH3 family PF00651: BTB/POZ domain	8.6e-124 9.6e-4	AT1G30440
SIP19	LOC_Os11 g02054	AK061388	PF00651: BTB/POZ domain	6.6e-12	Weak similar to At3 g26744(*ICE1*, inducer of CBF expression1)
SIP28	LOC_Os10 g16440		PF02845: CUE domain	2e-4	Unknown protein
SIP31	LOC_Os03 g46570	CT828890			Similar to AT1G79110: ubiquitin protein ligase/zinc ion binding
SIP33	LOC_Os05 g14860		PF03145: seven in absentia protein family	6.6e-130	Putative ubiquitin ligase SINAT5
Signal transduction					
SIP35	LOC_Os03 g60650	AK071722	PF00481: protein phosphatase 2C	3.2e-8	Similar to AT2G28890 (*PLL4*)
SIP4	LOC_Os03 g48170		cd02859: AMPK beta_GBD_like	2e-20	Similar to AT1G27070: 5¢ -AMP-activated protein kinase-related
SIP11	LOC_Os07 g46450	AK103870	PF00169: PH PF00620: RhoGAP	4e-18 1e-43	Similar to AT5G19390
SIP21	LOC_Os07 g04550	AK059496	PF00169: PH domain	3.2e-11	Similar to AT2G30880
Transcription regulation					
SIP5	LOC_Os06 g41730	AK064549	PF01388: ARID/BRIGHT DNA-binding domain	2.9e-08	Similar to AT2G14710
SIP22	LOC_Os12 g41860	AK102183	PF08670: MEKHLA domain PF01852: START domain PF00046: homeobox domain	8.4e-86 2.3e-63 2.9e-16	Similar to AT2G34710 (*PHB*)
SIP25	LOC_Os05 g48620	AK062036			Similar to TMF1 (TATA element modulatory factor 1)
Unknown					

ID	Locus*	cDNA†	Domains‡	Expect value§	Description¶
SIP8	LOC_Os10 g27480	AK100246	PF04576: protein of unknown function, DUF593	1.1e-43	Similar to AT1G08800
SIP10	LOC_Os05 g07860		PF04379: protein of unknown function, DUF525	1.1e-47	Similar to AT1G27510
SIP15	LOC_Os12 g31790				Similar to AT5G64180
SIP16	LOC_Os02 g58470	AK122003			Similar to AT4G09060
SIP23	LOC_Os04 g33030	AK120702			Similar to AT1G79110
SIP3	LOC_Os08 g37500				Similar to AT4G40020
SIP7	LOC_Os02 g15980				Similar to AT5G41620
SIP9	LOC_Os02 g02690				Similar to AT1G51710
SIP29	LOC_Os04 g07830				
SIP32	LOC_Os03 g18300				Similar to AT4G18570
SIP34	LOC_Os01 g02150	AK103326			

*Locus identification of TIGR rice annotation release 5 (http://rice.tigr.org).
†Accession numbers of full-length cDNAs from KOME database (http://cdna01.dna.affrc.go.jp/cDNA/) are listed if available. The cDNA sequences of SIPs obtained in this study were submitted to the National Center for Biotechnology Information (NCBI).
‡Accession numbers of domains are based on the sequence search against the PFAM database (release 22) and NCBI CCD database (v2.11).
§Expect value of domain search in Pfam.
¶Descriptions of SIPs according to TIGR pseudomolecular annotation or homologous gene in *Arabidopsis*.

Table S4. Putative SKIP-interaction proteins in different species

No.	Accession no.	Description	Putative domains	Accession no. (homologs in rice)	Identities
Putative SKIP-interacting proteins (human)					
1	Q9H1I8	ASC 1 complex subunit p100	CUE	NP_001049312	19%
2	P12755	C Ski	Ski, c-SKI_SMAD_bind		
3	Q06330	J kappa-recombination signal-binding protein	Beta-trefoil, beta-trefoil LAG1, DNA binding, IPT/TIG domain		
4	P46531	Notch 1	EGF-like domain, ankyrin repeat, Notch (DSL) domain	NP_001062603	20%
5	Q9UM47	Notch3	EGF-like domain, ankyrin repeat, Notch (DSL) domain	NP_001062606	21%
6	Q9Y618	Nuclear receptor corepressor 2	Myb-like DNA-binding domain	NP_001054527	10%
7	8106 (Entrez gene)	Poly adenylate-binding protein 2		NP_001057163	46%
8	P06400	Retinoblastoma 1	Retinoblastoma-associated protein A domain, Rb C-terminal domain, retinoblastoma-associated protein B domain	NP_001062372	24%
9	P28749	Retinoblastoma-like 1	Retinoblastoma-associated protein A domain, retinoblastoma-associated protein B domain	NP_001062372	23%
10	Q08999	Retinoblastoma-like 2	Retinoblastoma-associated protein A domain, retinoblastoma-associated protein B domain	NP_001062372	22%
11	P10276	Retinoic acid receptor alpha	Zinc finger, C4 type (2 domains), Hormone_recep Ligand-binding domain of nuclear hormone 7		
12	Q15796	SMAD, mothers against DPP homolog 2 (*Drosophila*)	MH2 domain		
13	P11473	Vitamin D (1,25-dihydroxyvitamin D_3) receptor	Zinc finger, C4 type		
14	Q09472	E1A-binding protein p300	Domain of unknown function, (DUF906), TAZ zinc finger, Creb binding, KIX domain, bromodomain, domain of unknown function (DUF902), zinc finger, ZZ type	NP_001045830	22%
15	P43355	MAGE1	MAGE family	NP_001058903	18%
16	4088(Entrez gene)	SMAD3	Tubulin-tyrosine ligase family		
17	Q92769	Histone deacetylase 2	Histone deacetylase domain 1	NP_001057943	60%
18	9541(Entrez gene)	CBF1 interacting corepressor		NP_001062154	21%
19	55805(Entrez gene)	Megalin-binding protein		NP_001053077	21%
20	122953(Entrez gene)	Jun dimerization protein 2	Hemagglutinin	NP_001044866	19%
21	Q9Y3C6	Peptidyl prolyl isomerase like 1	Pro_isomerase Cyclophilin type peptidyl-prolyl *cis*-trans isomerase	NP_001062502 (SIP12)	63%
Putative PRP45-interacting proteins (yeast)					
1	Q09882	PRP45_SCHPO pre-mRNA-processing protein 45		NP_001048184	43%
2	Q08817	SOG2_YEAST, Leucine-rich repeat-containing protein SOG2	Leucine-rich repeat	NP_001062214	17%
3	Q06411	SP382_YEAST, pre-mRNA-splicing factor SPP382	G-patch domain	NP_001067277	17%

No.	Accession no.	Description	Putative domains	Accession no. (homologs in rice)	Identities
4	Q06091	SN309_YEAST, pre-mRNA-splicing factor SNT309			
5	Q03654	CEF1_YEAST, pre-mRNA-splicing factor CEF1	Myb-like DNA-binding domain	NP_001052521	31%
6	Q02821	IMA1_YEAST, Importin subunit alpha	Armadillo/beta-catenin-like repeat, Importin beta-binding domain	NP_001054692	14%
7	P46951	YG4B_YEAST, Uncharacterized protein YGR198W			
8	P39964	CEF1_SCHPO pre-mRNA-splicing factor cef1, *Schizosaccharomyces pombe*	Myb-like DNA-binding domain	NP_001052521	41%
9	P38217	IMB2_YEAST, Importin subunit beta-2	HEAT repeat	NP_001054359	30%
10	P32357	AAR2_YEAST, A1 cistron-splicing factor AAR2	AAR2 protein	NP_001052095	22%
11	P28320	CWC16_YEAST, protein CWC16	Family of unknown function (DUF572)	NP_001043437	26%
12	P04147	PABP_YEAST, polyadenylate-binding protein, cytoplasmic and nuclear	RNA recognition motif, poly-adenylate-binding protein, unique	NP_001062583	45%
13	P32524	PRP21_YEAST, pre-mRNA-splicing factor PRP21	Surp module	NP_001046418	18%
14	P32589	HSP7F_YEAST, heat shock protein homolog SSE1	Hsp70 protein	NP_001042210	38%
15	P49955	SF3B1_YEAST, U2 snRNP component HSH155	HEAT repeat	NP_001045883	48%
16	P32523	PRP19_YEAST, pre-mRNA-splicing factor 19	Prp19/Pso4-like	NP_001064804	22%
17	P32854	PEP12_YEAST, syntaxin PEP12	SNARE domain	NP_001042620	29%
18	Q06137	YL345_YEAST, putative 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase YLR345W	6-phosphofructo-2-kinase, phosphoglycerate mutase family	NP_001049815	27%
19	P33334	PRP8_YEAST, pre-mRNA-splicing factor 8	PROCN (NUC071) domain	NP_001054734	62%
20	P40968	PRP17_YEAST, pre-mRNA-processing factor 17	WD domain, G-beta repeat	NP_001050302	34%
21	P36048	SN114_YEAST, 114-kDa U5 small nuclear ribonucleoprotein component	Elongation factor Tu GTP-binding domain, elongation factor G C-terminus	NP_001058038	33%
22	P53131	PRP43_YEAST, pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43	Domain of unknown function, helicase-associated domain (HA2), helicase-conserved C-terminal domain	NP_001049931	62%
23	P53333	CWC22_YEAST, pre-mRNA-splicing factor CWC22	MIF4G domain, MA3 domain	NP_001066507	30%
24	Q12046	CWC2_YEAST, pre-mRNA-splicing factor CWC2		NP_001059374	20%
25	Q12417	PRP46_YEAST, pre-mRNA-splicing factor PRP46	WD domain, G-beta repeat	NP_001050058	43%

No.	Accession no.	Description	Putative domains	Accession no. (homologs in rice)	Identities
26	Q08963	RU2A_YEAST, U2 small nuclear ribonucleoprotein A¢		NP_001046383	26%
27	P52868	CWC23_YEAST, pre-mRNA-splicing factor CWC23	DnaJ domain	NP_001048897	18%
28	P32639	BRR2_YEAST, pre-mRNA-splicing helicase BRR2	Sec63 Brl domain, DEAD/DEAH box helicase, helicase-conserved C-terminal domain	NP_001049362	29%
29	Q06410	ATG17_YEAST, Autophagy-related protein 17	Autophagy protein Apg17		
30	Q04048	SYF1_YEAST, pre-mRNA-splicing factor SYF1		NP_001060448	23%
31	Q12309	CLF1_YEAST, pre-mRNA-splicing factor CLF1	HAT (half-a-TPR) repeat, TPR repeat	NP_001055097	36%
32	Q04693	RSE1_YEAST, pre-mRNA-splicing factor RSE1	CPSF A subunit region	NP_001045829	23%
33	P10592	HSP72_YEAST, heat shock protein SSA2	Hsp70 protein	NP_001055754	72%
34	O94084	O94084_YEAST, Ylr338wp			
Putative BX42-interacting proteins (*Drosophila*)					
1	Q9VJE7		Protein phosphatase inhibitor 2 (IPP-2)		
2	Q9VCU7		Tudor domain		
3	Q9VB22		TPR repeat, GoLoco motif	NP_001048326	15%
4	Q06330	SUH_HUMAN Recombining binding protein suppressor of hairless, *Homo sapiens*			
5	P52485	UBCD2_DROME Ubiquitin-conjugating enzyme E2–24 kDa, *Drosophila melanogaster*	Ubiquitin-conjugating enzyme	NP_001043763	63%
6	P46531	NOTC1_HUMAN Neurogenic locus notch homolog protein 1 precursor, *H. sapiens*		NP_001062603	20%
7	Q9VV87	Q9VV87_DROME CG3971-PA, isoform A, *D. melanogaster*	GNS1/SUR4 family	NP_001051002	23%
8	Q9V4G9			NP_001064999	21%
9	Q9V4M7			NP_001051912	44%
10	Q9VKC5	Q9VKC5_DROME CG6770-PA, *D. melanogaster*			
11	P19109	RM62_DROME ATP-dependent RNA helicase p62, *D. melanogaster*	DEAD/DEAH box helicase, helicase-conserved C-terminal domain	NP_001042298	53%
12	P17886	CRN_DROME Protein crooked neCK, *D. melanogaster*	HAT (half-a-TPR) repeat, TPR repeat	NP_001055097	54%
13	O46052	O46052_DROME EG:152A3.3 protein, *D. melanogaster*			
Putative CeSKIP-interacting proteins (*Caenorhabditis elegans*)					

No.	Accession no.	Description	Putative domains	Accession no. (homologs in rice)	Identities
1	Q18239	Q18239_CAEEL Dishevelled related protein 2, *C. elegans*	DIX domain, domain found in Dishevelled, Egl-10, and Ple; PDZ domain (also known as DHR or GLGF)		
2	P46531	NOTC1_HUMAN Neurogenic locus notch homolog protein 1 precursor, *H. sapiens*		NP_001062603	20%
3	Q06330	SUH_HUMAN Recombining binding protein suppressor of hairless, *H. sapiens*			
4	Q19872	Q19872_CAEEL Hypothetical protein, *C. elegans*			
5	P39745	SUR1_CAEEL Mitogen-activated protein kinase mpk-1, *C. elegans*	Protein kinase domain	NP_001056846	48%

TPR, tetratricopeptide.

Table S5. Primers used in this study

	Forward primer	Reverse primer
SKIP-QTR	TACAGATGCGATCCAAGGTG	AGTGCCCTTAGCTCTTGCTC
Actin1	TGGCATCTCTCAGCACATTCC	TGCACAATGGATGGGTCAGA
SKIP-Y2H	*attB1*-CTCGTTCTACGACCACAGCAGC	*attB2*-GTGCATGGAGAAACTTCTGAACA
SKIP-ISH	CTAGCTTTTCCTCTTCGATTC	AAGATGCCCCTTGGAAGTAGA
Hpt	CTGCTCCATACAAGCCAACC	TGACATTGGGGAGTTTAGCG
SNAC1	CATGGTCCCGTTCTGAGGTG	CACACGTTGCAGCATCGATC
04 g46440 (CBF2)	GAGCCCATGCTGTGGGATT	CGATCTAATACACGGAAGCATGAC
09 g15670 (PP2C)	CGCAGCTCCGACAACATCT	GCTGGGTGACACTCTCTCTACAAG
06 g19800 (RD22)	GGAATGGATCATGGACGCC	GATGACGGAGCCCGGC
11 g26760 (RAB16c)	TTCCCGGCCAGCACTAAAT	AAACTGCACGTACATCACGACAT
01 g40094 (ABI2)	TGGATCATCCCCGTTTTCTG	TGGCCCAGCTTAACAAAAAGAAT
01 g22249 (POD)	AACGGAGTGGAAGCAGCGT	CAGCACCTCTATGTTGCCCA
09 g28210	GCTCCGAGCTTTTGTTGGAC	GCCTACGGTCGAATGAAACG
10 g25230	ACACGTCAGCTTTAATCCCATAATT	GAATAATCGTGCACTGTACAAATGC
10 g25290	TGCCGATCGCGAGGAA	GGTTCGCTCGTTGTCGTGAT
01 g03320	TGTTCTAGCTTGTTCGTATTCGTACA	ACATAACACGCATACCAACATCAA
03 g08320	CAGCCTTGCCTACCAGACATG	GACGATCCTGTTCTTCCTCTTCTC
06 g44190	CATGGTAGTCACATGGTGTGCTAGT	CCGTTACTTACATACAGAGACGAACAG
03 g08310	TCGCCGAGCCTGACCTT	CGCGATAACTAGGGTAACTGCTAATC
02 g41954	CCGTGAACATATTCCGGGC	CAAAGCGTGACGCTGCAA
RAB21	CACACCACAGCAAGAGCTAAGTG	TGGTGCTCCATCCTGCTTAAG