

Supplementary Table S1. List of primers used in this study.

Purpose	Gene	TIGR locus ID	Sense primer (5'→3')	Anti-sense primer (5'→3')
OE construct	<i>SNAC3</i>	LOC_Os01g09550	TTggtaccCTCGTCCTCTTTGCTCT	TTggtaccCTTCTCCCAACCGTAGT
RNAi construct	<i>SNAC3</i>	LOC_Os01g09550	TCGactagtgtaccTGCCAGCAATCCTTCT	TTAgagctcgatccCCAACCGTAGTACATACA
Promoter construct	<i>SNAC3</i>	LOC_Os01g09550	AAgtcgacCTGGAAACCGTGAGAC	AAgtcgacGCTGCTTTCACAAGTTTA
Subcellular location constructs	<i>SNAC3</i> (pH7WGF2.0) <i>SNAC3</i> (HBT)	LOC_Os01g09550	<i>attB1</i> -TGAATAGGGGGCACATCA TTtctagaATGAATAGGGGGCACAT	<i>attB2</i> -TGGTTAGTTTTCTTTTGGTATTG TTtctagaTCCATGATGATCCTGGTT
QPCR	<i>SNAC3</i>	LOC_Os01g09550	GCACGTCTTCGAGCACAAAA	TGGCTGGTAAGGCCATTCTG
	<i>R1</i> (CATA)	LOC_Os02g02400	CCCCAAGGTCTCCCCTGA	AACGACTCATCACACTGGGAGAG
	<i>R2</i> (CATB)	LOC_Os06g51150	GCTGGTGAGAGATACCGGTCA	TCAACCCACCGCTGGAGA
	<i>R3</i> (CATC)	LOC_Os03g03910	CGAAGCCGAGCATGTAAGGA	GGCTGAGGCCTTCCGTG
	<i>R4</i> (APX1)	LOC_Os03g17690	TCCACCCAGGAAGGGAGG	TTGGTAGCATCAGGAAGACGG
	<i>R5</i> (APX2)	LOC_Os07g49400	TCCCCTACCCTGCTGCATC	ACCAGCCAACCACTCGCA
	<i>R6</i> (APX3)	LOC_Os04g14680	AGCACTCTCAGGCGGCC	AGGCACCATCAAATCCTGATCT
	<i>R7</i> (APX4)	LOC_Os08g43560	CGGCCCTGCATCTACGAA	CAGCTACCCCGACAGCACTC
	<i>R8</i> (APX5)	LOC_Os12g07830	CCGGTGGCCCCAAGAT	GGTGGGCATTCTTACCATC
	<i>R9</i> (APX6)	LOC_Os12g07820	CCCCAAGATCCCCATGATCTA	CCTCTGGCGGGCATTG
	<i>R10</i> (APX7)	LOC_Os04g35520	TTCACGTTGGACGGTTAATGC	TTTCTGTAAAAGTGGTTGGCCA
	<i>R11</i> (APX8)	LOC_Os02g34810	ATCATCGCCAGCGGATGA	GCAGCGACGAAGGGCTC
	<i>R12</i> (putative copper/zinc superoxide dismutase)	LOC_Os03g11960	CAGATTTACTAAGCGGGCC	CTTCCTAGGTCATCAGAATCAGCA
	<i>R13</i> (SodCc1)	LOC_Os03g22810	TGCGCATGGTTTTTGGTG	CATAGTTCATTGGGCGCCA
	<i>R14</i> (putative copper chaperone for superoxide dismutase)	LOC_Os04g48410	AGATCAGATCCTGGCATTGCA	TTCTTGTAGTTCTCGCCAACCC

Purpose	Gene	TIGR locus ID	Sense primer (5'→3')	Anti-sense primer (5'→3')
QPCR	<i>R15</i> (SodA1)	LOC_Os05g25850	CCGCCATCGTGCACCT	TCGAATGATTGACATGGCCTC
	<i>R16</i> (putative superoxide dismutase)	LOC_Os06g02500	CGGAGCCAAGTAAGCTACGG	TGTTACAAGTCCATCATCCCCA
	<i>R17</i> (Fe-SOD)	LOC_Os06g05110	CGACGCCGAGGAATTTCTAG	AGGTGGTGTAAGTGTCTCTCATGC
	<i>R18</i> (SodCc2)	LOC_Os07g46990	ATTCCATGTGCACGCGC	GGATTGAAGTGTGGTCCAGTTG
	<i>R19</i> (plastidic Cu/Zn-SOD)	LOC_Os08g44770	TGTGACGGGACTTACTCCTGG	CACCCATTCGTAGTATCGCCA
	<i>R45</i> (RbohF)	LOC_Os08g35210	GCCCTCAGCCATCGTCTATC	CCATATATAGTATCACTGCGCAATGC
	<i>R54</i> (Prx IIE2)	LOC_Os02g09940	GCGCTCTGAAGATGGAATCC	TCACAACGACGACGCTACTCA
	<i>Ubiquitin</i>	LOC_Os03g13170	AACCAGCTGAGGCCCAAGA	ACGATTGATTTAACCAGTCCATGA
Yeast one-hybrid constructs	<i>SNAC3</i>	LOC_Os01g09550	CAGgaattcGGCATGAATAGGGGGCAC	CAGggatccTGGTTAGTTTTCTTTTGGTATTG
	<i>R1</i> (CATA)	LOC_Os02g02400	ATAgaattcATAACGAGGGTGTAGC	ATAgagctcGAGGTGGTGAGGAGCA
	<i>R6</i> (APX3)	LOC_Os04g14680	ATAgaattcGCCGAGTAGGGCTGAA	ATAgagctcGGCAAGGGATGTCTCC
	<i>R11</i> (APX8)	LOC_Os12g07830	ATAgaattcCATCGGTGGCTAACGG	ATAgagctcGAAGGTTTCGGCAAGG
	<i>R45</i> (RbohF)	LOC_Os08g35210	ATAgaattcCCTGCTTTGGTAATGG	ATAgagctcCAAGAGGACGGAGATA
	<i>R54</i> (Prx IIE2)	LOC_Os02g09940	ATAgaattcGGAGCAGCCAGAGGTCA	ATAgagctcCCGCAAGGGCGATTTT
BiFC assay	<i>SNAC3</i>	LOC_Os01g09550	AGTggatccATGAATAGGGGGCACATC	GAGggtaccTCCATGATGATCCTGGTTG
	<i>SNAC3IP1</i>	LOC_Os03g01180	CCactagtAGACGCTGCTGGAGTAG	GAgtcgacGTCGGGGACCTCAGATG
	<i>SNAC3IP2</i>	LOC_Os01g63900	AGTggatccTTCTTCGAGCAGGTGAG	GAGggtaccTTTCTTGAAAAGTCTGTTC
	<i>SNAC3IP3</i>	LOC_Os01g72880	AGTggatccACCCTCGACGGAACCGC	CTgtcgacTCCTGATTCTGGGGCG
	<i>SNAC3IP4</i>	LOC_Os05g33600	AGTggatccGAGTGAGTCCCGACCA	GAGggtaccACACCTTTCAAAAATCTTG
	<i>SNAC3IP5</i>	LOC_Os06g39600	AGTggatccGCCAATCCTACCACATCC	GAGggtaccGTTGCCACCAGACTCCT
	<i>SNAC3IP6</i>	LOC_Os04g52870	AGTggatccAAATCGGAACCCTAACC	GAGggtaccATCAGCCAAGCTATCAAGA
	<i>SNAC3IP7</i>	LOC_Os10g27340	CCactagtAGGCTGCTCCCATCCTC	GACctcgagTTTCTTCTTGGCGGCAG
	<i>SNAC3IP8</i>	LOC_Os02g43930	CCactagtGGTCGCTTCTTCCTCTT	GAGggtaccCTGCTGGGCACACTGTA

Supplementary Table S2. Correlation between *SNAC3* and the ROS genes.

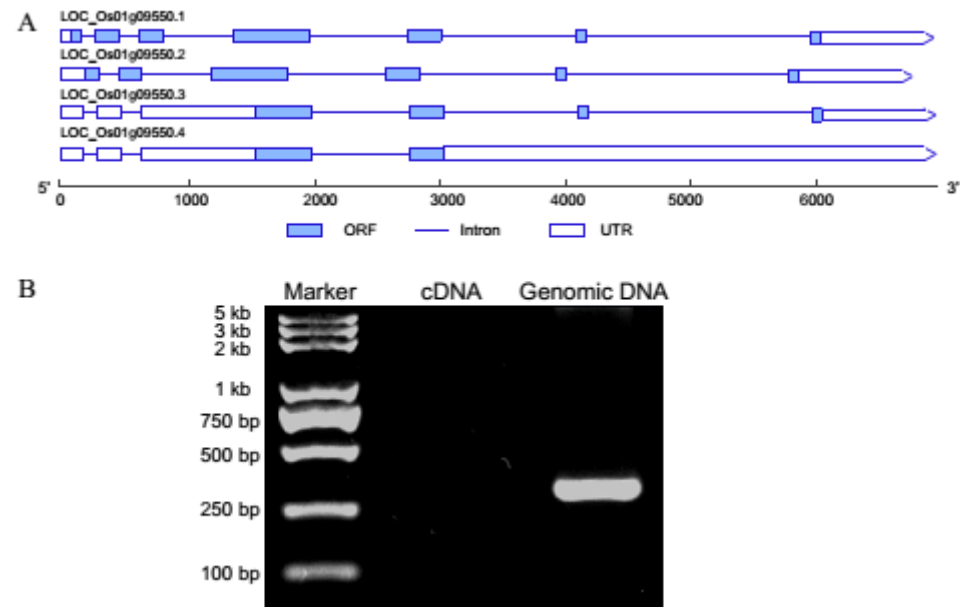
SNAC3	Normal condition	Abiotic stress	Biotic stress
R1		√ (0.5022)	√ (0.6330)
R6	√ (0.5076)		√ (0.6604)
R11			
R45	√ (0.5434)		√ (0.5404)
R54	√ (0.5076)		

Supplementary Table S3. Distribution of NACRS and CDBS elements in the ROS genes.

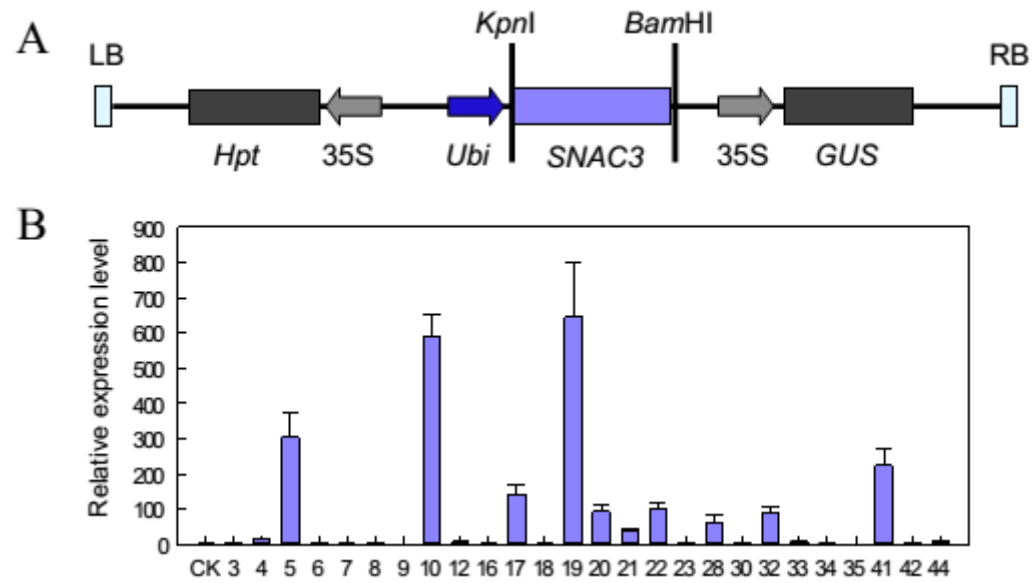
Promoter	Fragments length	NACRS number	CDBS number
R1	498 bp	2	2
R6	913 bp	3	3
R11	820 bp	1	8
R45	1376 bp	2	5
R54	1525 bp	1	17

Supplementary Table S4. Information of putative SNAC3-interacting proteins.

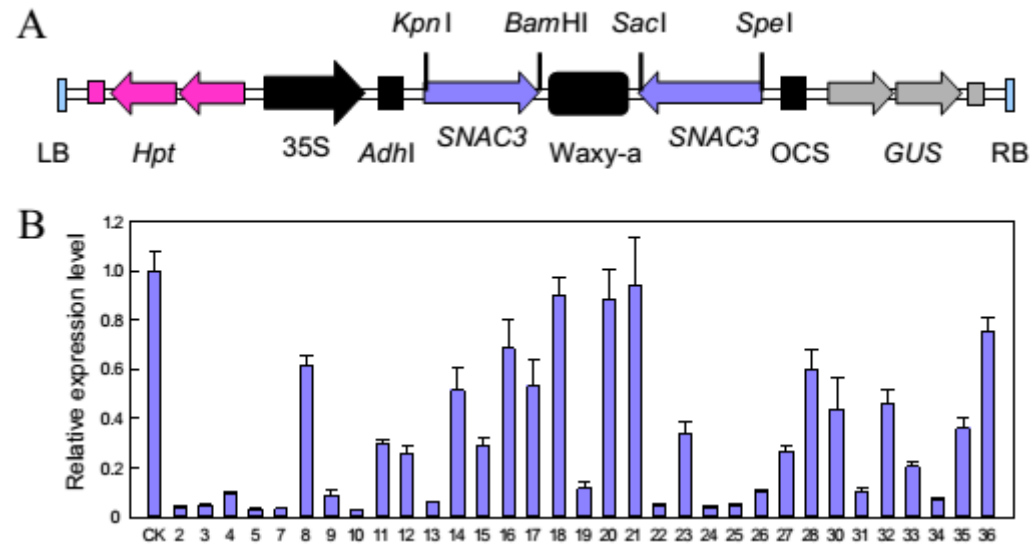
Name	TIGR locus ID	Annotation
SNAC3IP1	LOC_Os03g01180	Phosphoglycerate mutase
SNAC3IP2	LOC_Os01g63900	WD domain, G-beta repeat domain containing protein
SNAC3IP3	LOC_Os01g72880	DNA mismatch repair protein MLH1
SNAC3IP4	LOC_Os05g33600	Cytochrome P450 72A1
SNAC3IP5	LOC_Os06g39600	Protein phosphatase 2C
SNAC3IP6	LOC_Os04g52870	OsFBW1, F-box domain and WD40 repeat containing protein
SNAC3IP7	LOC_Os10g27340	Oxidoreductase
SNAC3IP8	LOC_Os02g43930	Chaperone protein dnaJ



Supplementary Figure S1 Schematic diagram of *SNAC3* gene structure. (A) Putative transcripts of *SNAC3*. (B) N-terminus PCR of LOC\_Os01g09550.1. “cDNA” indicated PCR from the cDNA template, and “Genomic DNA” indicated PCR from the genomic DNA template.



Supplemental Figure S2 Overexpression of *SNAC3*. (A) Schematic diagram of *SNAC3* overexpression construct. (B) Expression level analysis of *SNAC3* in transgenic plants by qPCR.



Supplementary Figure S3 Suppression of *SNAC3* by RNAi. (A) Schematic diagram of *SNAC3* RNAi construct. (B) Expression level analysis of *SNAC3* in RNAi transgenic plants by qPCR.