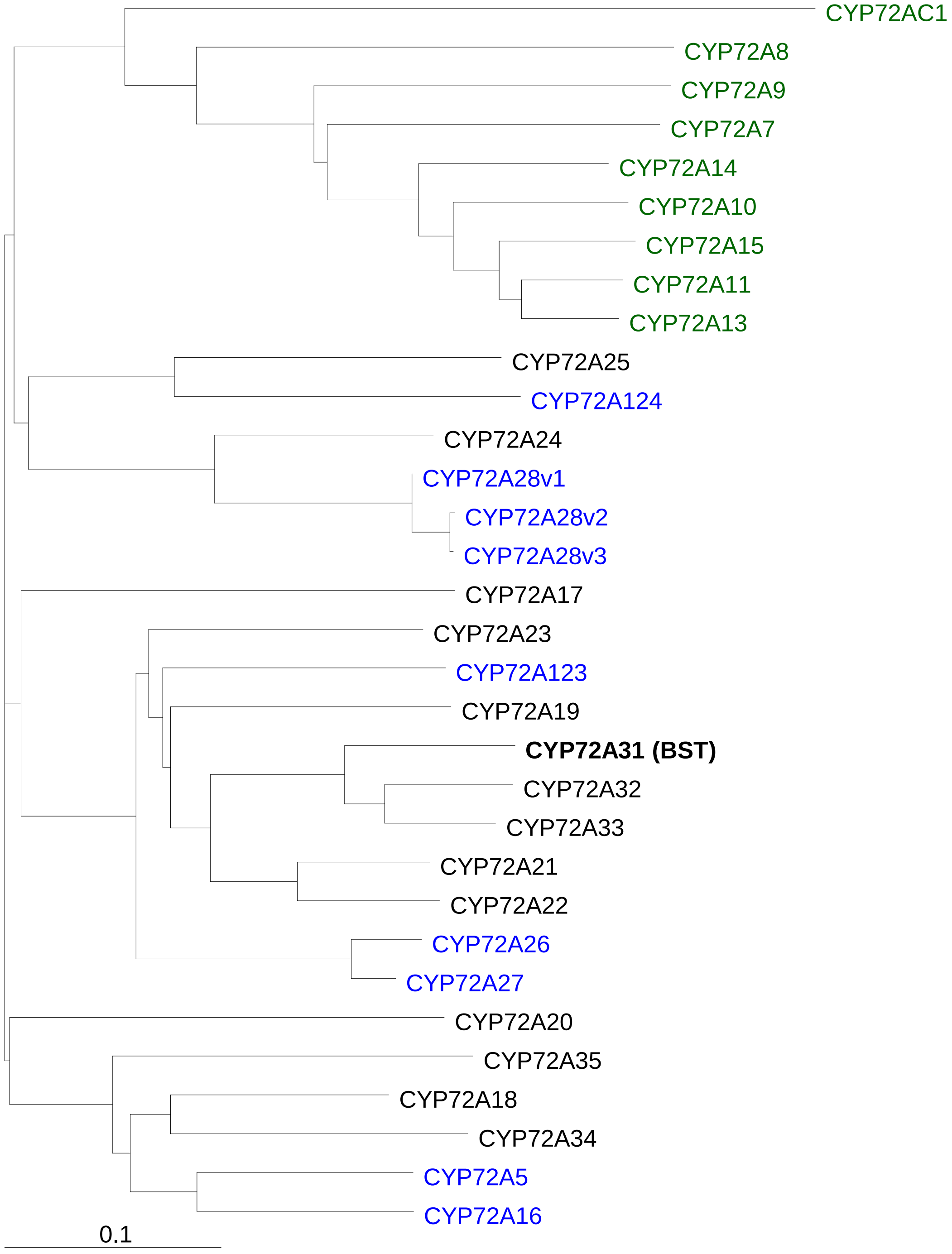

Supplemental Figure S1. The phylogenic tree of CYP72A protein in rice, maize and Arabidopsis.
The phylogenic tree was generated by the CLUSTAL W algorithm. Black, blue and green characters indicate CYP72A proteins of rice, maize and Arabidopsis, respectively. Rice and maize P450 deduced amino acid sequences were used in RAP-DB (http://rapdb.dna.affrc.go.jp/) or Rice Genome Annotation Project (http://rice.plantbiology.msu.edu/index.shtml) based on the information listed in Cytochrome P450 Homepage (http://drnelson.uthsc.edu/CytochromeP450.html). Arabidopsis P450 sequences were used in The *Arabidopsis* Cytochromes P450, Cytochromes b$_5$, P450 reductase, β-Glucosidase, and Glycosyltransferase Site (http://www.p450.kvl.dk/At_cyps/types.shtml).

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CYP72A32(Kas)    1  MVLGGWLLMWAPASSPTILVAFGLLFGLVLAWQAGLQLHRLWWRPRRLEKALRARGLRGS
CYP72A32(NB)     1  MVLGGWLLMWAPASSPTILVAFGLLFGLVLAWQAGLQLHRLWWRPRRLEKALRARGLRGS
CYP72A33(Kas)    1  --------MWAPASSPTILAAFG-LVGLVLAWQAGLQLHRLWWRPRRLEKALRARGLRGS
CYP72A33(NB)     1  --------MWAPASSPTILAAFG-LVGLVLAWQAGLQLHRLWWRPRRLEKALRARGLRGS
CYP72A31(Kas)    1  MVFRG-WLMWAPAS-APVLVVFGLLFGLALVWQAGRLLHRLWWRPRRLEKALRARGLRGS

CYP72A32(Kas)   61  SYRFLTGDLAEESRRRKEAWARPLPLRCHDIAPRIEPFLHDAVVRPEQHYGKPCITWLGP
CYP72A32(NB)    61  SYRFLTGDLAEESRRRKEAWARPLPLRCHDIAPRIEPFLHDAVVRPEQHYGKPCITWLGP
CYP72A33(Kas)   52  RYRFLTGDLAEESRRRKEAWARPLPLRCHDIAPRVEPFLHGAVG-VGAAHGKPRITWFGP
CYP72A33(NB)    52  RYRFLTGDLAEEGRRRKEAWARPLPLRCHDIAPRVEPFLHGAVG-VGAAHGKPRITWFGP
CYP72A31(Kas)   59  SYRFLTGDLAEESRRRKEAWARPLPLRCHDIAPRIKPFLHDTLG-EHGKQRQPCITWFGP

CYP72A32(Kas)  121  TPEVHVTDPELAKVVMSNKFGHFEKIRFQALSKLLPQGLSYHEGEKWAKHRRILNPAFQL
CYP72A32(NB)   121  TPEVHVTDPELAKVVMSNKFGHFEKIRFQALSKLLPQGLSYHEGEKWAKHRRILNPAFQL
CYP72A33(Kas)  111  TPEVHVADPELARVVLSNKFGHFEKVSFPELSKLIPQGLSAHEGEKWAKHRRILNPVFQL
CYP72A33(NB)   111  TPEVHVADPELARVVLSNKFGHFEKVSFPELSKLIPQGLSAHEGEKWAKHRRILNPVFQL
CYP72A31(Kas)  118  TPEVNITDPELAKVVLSNKFGHLERVRFKEVSKLLSQGLTYHEGEKWVKHRRIINPAFQL

CYP72A32(Kas)  181  EKLKLMLPVFSACCEELISRWMGAIGSDGSYEVDCWPELKSLTGDVISRTAFGSSYLEGR
CYP72A32(NB)   181  EKLKLMLPVFSACCEELISRWMGAIGSDGSYEVDCWPELKSLTGDVISRTAFGSSYLEGR
CYP72A33(Kas)  171  EKLKLMLPVFSACCEELISRWMGSIGSDGSYEVDCWPEFKSLTGDVISRTAFGSSYLEGR
CYP72A33(NB)   171  EKLKLMLPVFSACCEELISRWMGSIGSDGSYEVDCWPEFKSLTGDVISRTAFGSSYLEGR
CYP72A31(Kas)  178  EKLKLMLPAFSACCEELISRWIGSIGCDGSYEVDCWPELKSLTGDVISRTAFGSSYLEGR

CYP72A32(Kas)  241  RIFELQGELFERVMKSVEKIFIPGYMYLPTENNRKMHQINKEIESILRSMIGKRMQAMKE
CYP72A32(NB)   241  RIFELQGELFERVMKSVEKIFIPGYMYLPTENNRKMHQINKEIESILRSMIGKRMQAMKE
CYP72A33(Kas)  231  RIFELQGELFERVIKSIQKMFIPGYMYLPTENNRKMHQMNKEIESILRGMIGKRMQAMKE
CYP72A33(NB)   231  RIFELQGELFERVIKSIQKMFIPGYMYLPTENNRKMHQMNKEIESILRGMIGKRMQAMKE
CYP72A31(Kas)  238  RVFELQAEQFERAMKCMQKISIPGYMSLPIENNRKMHQINKEIESILRGIIGKKMQAMKE

CYP72A32(Kas)  301  GESTKDDLLGILLESNMRHTEENSQSSQGLTIKDIMEECKLFYFAGADTTSVLLTWTILL
CYP72A32(NB)   301  GESTKDDLLGILLESNMRHTEENSQSSQGLTIKDIMEECKLFYFAGADTTSVLLTWTILL
CYP72A33(Kas)  291  GESTKDDLLGILLESNTRHMEVNGQSNQGLTIKDIMEECKLFYFAGADTTSVLLTWTMLL
CYP72A33(NB)   291  GESTKDDLLGILLESNTRHMEVNGQSNQGLTIKDIMEECKLFYFAGADTTSVLLTWTMLL
CYP72A31(Kas)  298  GESTKDDLLGILLESNTKHMEENGQSSQGLTMKDIVEECKLFYFAGAETTSVLLTWAMLL

CYP72A32(Kas)  361  LSMHPEWQDRARKEILGLFGKNKPEYDGLSHLKIVTMILYEVLRLYPPFIELKRRTYKEM
CYP72A32(NB)   361  LSMHPEWQDRARKEILGLFGKNKPEYDGLNNLKIVTMILYEVLRLYPPFIELKRRTYKEM
CYP72A33(Kas)  351  LSMHPEWQDRAREEILGLFGKNKPDYDGLSRLKIVTMILYEVLRLYPPFIELTRKTYKEM
CYP72A33(NB)   351  LSMHPEWQDRAREEILGLFGKNKPDYDGLSRLKIVTMILYEVLRLYPPFIELTRKTYKEM
CYP72A31(Kas)  358  LSMHPEWQDRAREEILGLFRKNKPDYEGLSRLKIVTMILYEVLRLYPPFIEIGRKTYKEM

CYP72A32(Kas)  421  KIGGVTYPAGVIINLPVLFIHHDLEIWGSDVHEFKPERFSEGISKASKDPGAFLPFGWGP
CYP72A32(NB)   421  KIGGVTYPAGVIINLPVLFIHHDLKIWGSDVHEFKPERFSEGISKASKDPGAFLPFGWGP
CYP72A33(Kas)  411  EIGGITYPAGVIINLPVMFIHHDPEIWGSDVHEFKPERFSEGISKASKDPGAFLPFGWGP
CYP72A33(NB)   411  EIGGITYPAGVIINLPVMFIHHDPEIWGSDVHEFKPERFSEGISKASKDPGAFLPFGWGP
CYP72A31(Kas)  418  EIGGVTYPAGVSIKIPVLFIHHDPDTWGSDVHEFKPERFSEGISKASKDPGAFLPFGWGP
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CYP72A32(Kas)  481 RICIGQNFALLEAKMALCLILQRLEFELAPTYTHAPHTMITLHPMHGAQIKIRAI-----
CYP72A32(NB)   481 RICIGQNFALLEAKMALCLILQRLEFELAPTYTHAPHTMITLHPMHGAQIKIRAI-----
CYP72A33(Kas)  471 RICIGQNFALLEAKMALCLILQRLEFELATSYTHAPHTIISLHPMHGAQIKVKSYMTISD
CYP72A33(NB)   471 RICIGQNFALLEAKMALCLILQRLEFELATSYTHVPHTIISLHPMHGAQIKVKSYMTISD
CYP72A31(Kas)  478 RICIGQNFALLEAKMALCLILQRLEFELAPSYTHAPHTMVTLHPMHGAQIKVRAI-----

CYP72A32(Kas)        -----
CYP72A32(NB)         -----
CYP72A33(Kas)  531  YSVFY
CYP72A33(NB)   531  YSVFY
CYP72A31(Kas)        -----
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Supplemental Figure S2. Alignment of CYP72A31, 32 and 33 protein in Nipponbare and Kasalath.

The deduced amino acid sequences of CYP72A32 and 33 in Nipponbare (NB) were taken from RAPDB (http://rapdb.dna.affrc.go.jp/) or the Rice Genome Annotation Project (http://rice.plantbiology.msu.edu/index.shtml) based on information listed on the Cytochrome P450 Homepage (http://drnelson.uthsc.edu/CytochromeP450.html). The deduced amino acid sequences of CYP72A31, 32 and 33 in Kasalath (Kas) were searched for in the genomic sequence of chromosome 1 of Kasalath based on information in the databases mentioned above. The alignments were generated by the CLUSTAL W algorithm. Black and grey boxes represent identical and similar residues, respectively.

A

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Kasalath       1 ATGGTTTTCAGAGGGTGGTTGATGTGGGCTCCGGCCTCAGCGCCAGTCCTCGTGGTGTTC
Koshihikari    1 ATGGTTTTCAGCGGGTGGTTGATGTGGGCTCCGGCCTCAGCGCCAGTCCTCGTGGTGTTC

Kasalath      61 GGTCTCCTCTTCGGCCTCGCCCTCGTGTGGCAGGCCGGCCGCCTGCTTCACCGGCTGTGG
Koshihikari   61 GGTCTCCTCTTCGGCCTCGCCCTCGCGTGGCAGGCCGGCCGCCTGCTTCACCGGCTGTGG

Kasalath     121 TGGCGGCCGCGGCGGCTGGAGAAGGCGCTGCGCGCGCGGGGCCTCCGCGGCTCGTCCTAC
Koshihikari  121 TGGCGGCCGCGGCGGCTGGAGAAGGCGCTGCGCGCGCGGGGCCTCCGCGGCTCGTCCTAC

Kasalath     181 CGCTTCCTCACCGGCGACCTCGCGGAGGAGAGCCGGCGGAGGAAGGAGGCCTGGGCGAGG
Koshihikari  181 CGCTTCCTCACCGGCGACCTCGCGGAGGAGAGCCGGCGGAGGAAGGAGGCCTGGGCGAGG

Kasalath     241 CCGCTGCCGCTGCGGTGCCACGACATCGCGCCGCGCATCAAGCCGTTCCTCCACGACACC
Koshihikari  241 CCGCTGCCGCTGCGGTGCCACGACATCGCGCCGCGCATCAAGCCGTTCCTCCACGGCACC

Kasalath     301 CTCG------GGGAGCACGGCAAGCAGCGGCAGCCGTGCATCACCTGGTTCGGCCCGACG
Koshihikari  301 GTCGTCAGGGAGCAGCACGGCAAGCGGCGGCAGCCGTGCATCACCTGGTTCGGCCCGACG

Kasalath     355 CCGGAGGTGAACATCACCGATCCCGAGCTGGCCAAGGTCGTCCTGTCCAACAAGTTCGGC
Koshihikari  361 CCGGAGGTGAACATCACCGATCCCGAGCTGGCCAAGGTCGTCCTGTCCAACAAGTTCGCC

Kasalath     415 CACTTGGAGAGGGTCAGGTTCAAGGAGGTGTCGAAGCTGCTATCCCAAGGCCTCACCTAC
Koshihikari  421 CACTTGGAGAGGGTCAGGTTCAAGGAGGTGTCGAAGCTGCTATCCCAAGGCCTCTCCTAC

Kasalath     475 CACGAGGGCGAGAAGTGGGTCAAGCACAGGAGGATCATCAACCCGGCTTTCCAGCTCGAG
Koshihikari  481 CACGAGGGCGAGAAGTGGGTCAAGCACAGGAGGATCATCAACCCGGCTTTCCAGCTCGAG

Kasalath     535 AAGCTCAAGCTCATGCTGCCAGCGTTTTCTGCATGCTGCGAGGAACTGATAAGCAGGTGG
Koshihikari  541 AAGCTCAAGCTCATGCTGCCAGCGTTTTCTGCATGCTGCGAGGAACTGATCAGCAGGTGG

Kasalath     595 ATAGGGTCCATTGGCTGTGATGGCTCGTACGAGGTGGATTGCTGGCCGGAGCTCAAGAGC
Koshihikari  601 ATAGGGTCCATTGGCTCTGATGGCTCGTACGAGGTGGATTGCTGGCCGGAGATGAAGAGC

Kasalath     655 CTCACCGGAGATGTCATCTCGCGCACCGCGTTCGGAAGCAGCTATCTTGAAGGAAGAAGG
Koshihikari  661 CTCACCGGAGATGTCATCTCGCGCACCGCGTTCGGAAGCAGCTATCTTGAAGGAAGAAGG

Kasalath     715 GTCTTCGAGCTGCAGGCCGAGCAATTTGAGCGCGCAATGAAATGCATGCAGAAGATTTCC
Koshihikari  721 GTCTTCGAGCTGCAGGCCGAGCAATTTGAGCGCGCAATGAAATGCATGCAGAAGATTTCC

Kasalath     775 ATCCCGGGTTACATGTCTTTGCCTATTGAGAACAACCGGAAGATGCATCAAATAAATAAA
Koshihikari  781 ATCCCGGGTTACATGTCTTTGCCTATTGAGAACAACCGGAAGATGCATCAAATAAATAAA

Kasalath     835 GAGATCGAATCGATTCTAAGAGGTATAATTGGGAAAAAATGCAAGCTATGAAAGAAGGT
Koshihikari  841 GAGATCGAATCGATTCTAAGAGGTTTAATTGGGAAAAGAATGCAAGCTATGAAAGAAGGT

Kasalath     895 GAAAGCACAAAAGATGATTTACTTGGCATATTGCTTGAGTCAAACACAAAGCACATGGAA
Koshihikari  901 GAAAGCACAAAAGATGATTTACTTGGCATATTGCTTGAGTCAAACACAAAGCACATGGAA

Kasalath     955 GAGAATGGTCAATCAAGCCAGGGGTTGACAATGAAGGATATCGTGGAGGAGTGCAAGCTG
Koshihikari  961 GAGAATGGTCAATCAAGCCAGGGGTTGACAATCAAGGATATCGTGGAGGAGTGCAAGCTG
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Kasalath    1015 TTCTACTTTGCAGGAGCGGAGACAACATCAGTGCTTCTCACATGGGCCATGCTGCTATTA
Koshihikari 1021 TTCTACTTTGCAGGAGCGGAGACAACATCAGTGCTTCTCACATGGACCATGCTGCTATTA

Kasalath    1075 AGCATGCACCCGGAGTGGCAGGACCGTGCAAGGGAAGAGATCCTGGGATTATTTAGGAAG
Koshihikari 1081 AGCATGCACCCGGAGTGGCAGGACCGTGCAAGGGAAGAGATTATGGGATTATTTAGGAAG

Kasalath    1135 AACAAACCTGACTACGAAGGCTTGAGCCGCCTCAAAATTGTGACGATGATCCTCTACGAG
Koshihikari 1141 AACAAACCTGACTACGAAGGCTTGAGCCGCCTCAAAATTGTGACAATGATCTTCTACGAG

Kasalath    1195 GTTCTTCGGTTGTACCCACCGTTCATCGAGATTGGTCGGAAAACATACAAAGAGATGGAG
Koshihikari 1201 GTTCTTCGGTTGTACCCACCGTTCATCGAGATTGGTTGGAAAACAT-CAAAGAGATGGAG
                                                               ▲
Kasalath    1255 ATAGGAGGAGTCACTTACCCAGCTGGTGTCAGCATTAAAATCCCCGTGTTGTTCATCCAC
Koshihikari 1260 ATAG--------------------------------------------------------

Kasalath    1315 CATGATCCGGACACCTGGGGAAGTGATGTGCATGAGTTCAAACCTGAGAGGTTCTCTGAG
Koshihikari      ------------------------------------------------------------

Kasalath    1375 GGGATCTCTAAGGCGTCTAAGGATCCGGGTGCATTCCTCCCGTTCGGTTGGGGGCCACGA
Koshihikari      ------------------------------------------------------------

Kasalath    1435 ATCTGCATCGGCCAAAACTTCGCGCTGCTTGAGGCCAAGATGGCATTGTGCCTGATTCTT
Koshihikari      ------------------------------------------------------------

Kasalath    1495 CAACGCTTGGAGTTTGAGCTTGCGCCATCGTATACTCATGCGCCGCATACTATGGTAACT
Koshihikari      ------------------------------------------------------------

Kasalath    1555 CTGCATCCAATGCACGGTGCACAGATTAAAGTTAGAGCTATATGA
Koshihikari      ---------------------------------------------
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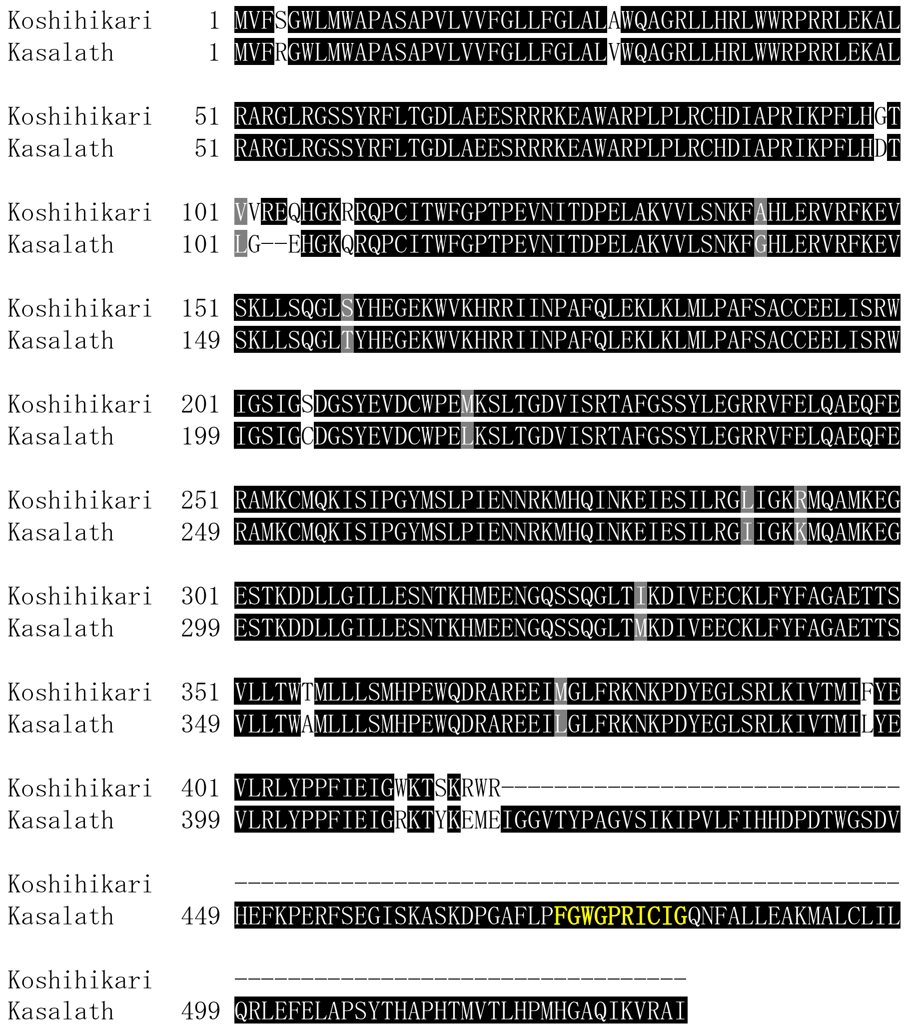
B



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Koshihikari     1 MVFSGWLMWAPASAPVLVVFGLLFGLALAWQAGRLLHRLWWRPRRLEKAL
Kasalath        1 MVFRGWLMWAPASAPVLVVFGLLFGLALVWQAGRLLHRLWWRPRRLEKAL

Koshihikari    51 RARGLRGSSYRFLTGDLAEESRRRKEAWARPLPLRCHDIAPRIKPFLHGT
Kasalath       51 RARGLRGSSYRFLTGDLAEESRRRKEAWARPLPLRCHDIAPRIKPFLHDT

Koshihikari   101 VVREQHGKRRQPCITWFGPTPEVNITDPELAKVVLSNKFAHLERVRFKEV
Kasalath      101 LG--EHGKQRQPCITWFGPTPEVNITDPELAKVVLSNKFGHLERVRFKEV

Koshihikari   151 SKLLSQGLSYHEGEKWVKHRRIINPAFQLEKLKLMLPAFSACCEELISRW
Kasalath      149 SKLLSQGLTYHEGEKWVKHRRIINPAFQLEKLKLMLPAFSACCEELISRW

Koshihikari   201 IGSIGSDGSYEVDCWPEMKSLTGDVISRTAFGSSYLEGRRVFELQAEQFE
Kasalath      199 IGSIGCDGSYEVDCWPELKSLTGDVISRTAFGSSYLEGRRVFELQAEQFE

Koshihikari   251 RAMKCMQKISIPGYMSLPIENNRKMHQINKEIESILRGLIGKRMQAMKEG
Kasalath      249 RAMKCMQKISIPGYMSLPIENNRKMHQINKEIESILRGIIGKKMQAMKEG

Koshihikari   301 ESTKDDLLGILLESNTKHMEENGQSSQGLTIKDIVEECKLFYFAGAETTS
Kasalath      299 ESTKDDLLGILLESNTKHMEENGQSSQGLTMKDIVEECKLFYFAGAETTS

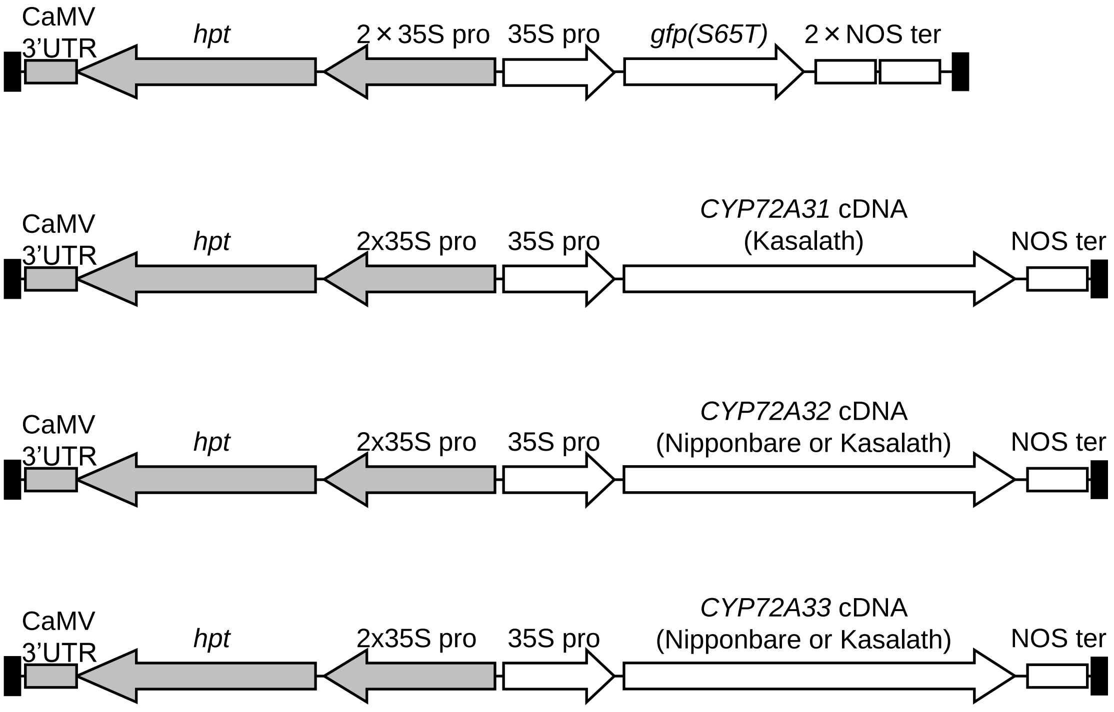
Koshihikari   351 VLLTWTMLLLSMHPEWQDRAREEIMGLFRKNKPDYEGLSRLKIVTMIFYE
Kasalath      349 VLLTWAMLLLSMHPEWQDRAREEILGLFRKNKPDYEGLSRLKIVTMILYE

Koshihikari   401 VLRLYPPFIEIGWKTSKRWR------------------------------
Kasalath      399 VLRLYPPFIEIGRKTYKEMEIGGVTYPAGVSIKIPVLFIHHDPDTWGSDV

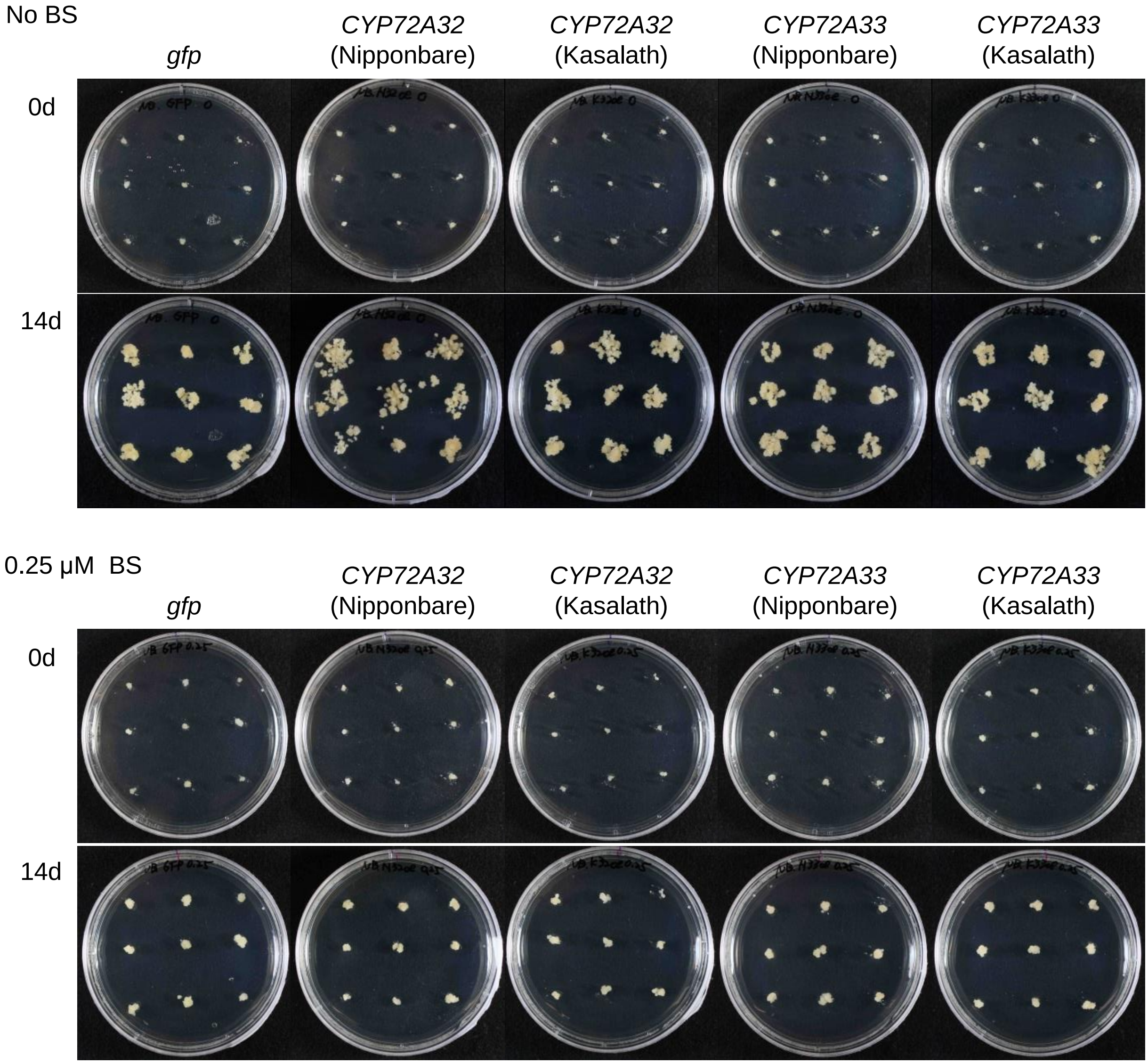
Koshihikari       --------------------------------------------------
Kasalath      449 HEFKPERFSEGISKASKDPGAFLPFGWGPRICIGQNFALLEAKMALCLIL

Koshihikari       ----------------------------------
Kasalath      499 QRLEFELAPSYTHAPHTMVTLHPMHGAQIKVRAI
```

Supplemental Figure S3. The alignment of *CYP72A31* in Koshihikari and Kasalath.
A The cDNA sequences of *CYP72A31* in Koshihikari and Kasalath. The cDNA sequence of *CYP72A31* in Koshihikari was determined by RT-PCR amplified with total RNA extracted from callus as a template. The cDNA sequence of *CYP72A31* in Kasalath was determined by RT-PCR amplified with total RNA extracted from shoots as a template. An pink arrowhead shows -1 frame-shift mutation in Koshihikari. **B** The deduced amino acid sequences of CYP72A31 in Koshihikari and Kasalath. Yellow and bold character shows the cytochrome P450 cysteine heme-iron ligand signature. Details are same as Supplemental Figure S2.

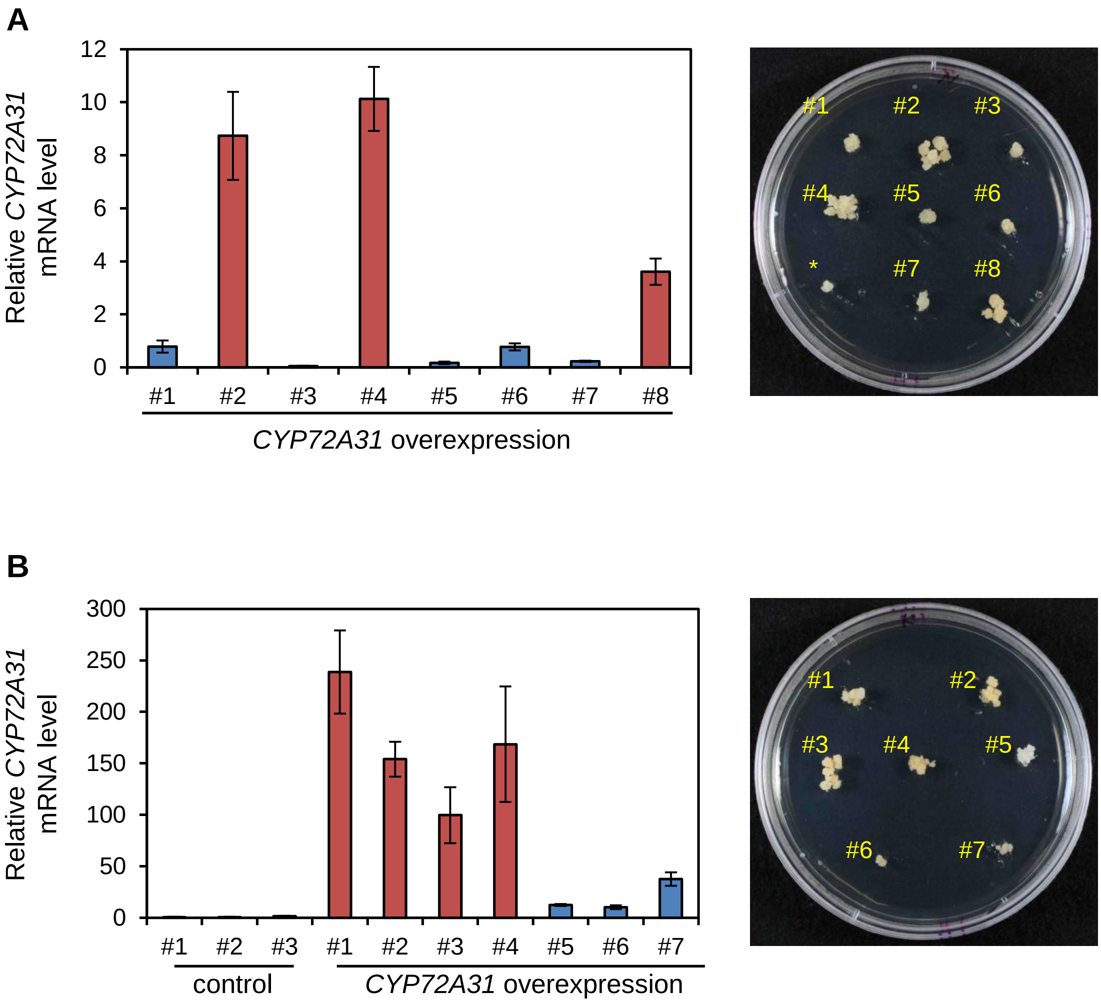


Supplemental Figure S4. Structure of *CYP72A31, 32* and *33* overexpression vectors.
The *gfp, CYP72A31, CYP72A32* and *CYP72A33* expression cassettes were cloned in the binary vector pCAMBIA1390. These genes are under the control of the CaMV 35S promoter (35S pro) and nopaline synthase terminator (NOS ter); *hpt* expression was directed by a duplicated 35S promoter (2×35Spro) and the CaMV 35S polyA (CaMV 3'UTR). In these vectors, a Kasalath *CYP72A31* cDNA fragment, and Nipponbare and Kasalath *CYP72A32* or *CYP72A33* cDNA fragments were used.

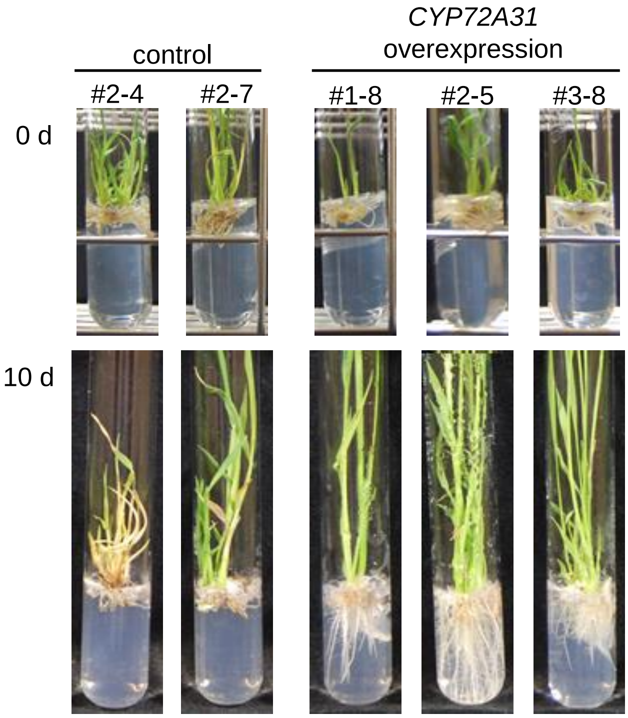


Supplemental Figure S5. BS sensitivity of overexpression of *CYP72A32* and *CYP72A33* genes in Nipponbare.

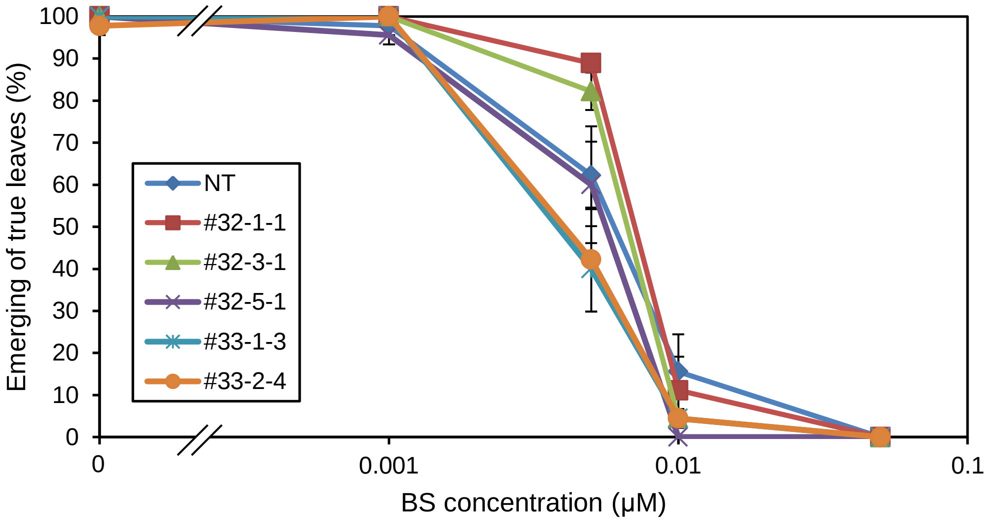
Rice calli in T_0 generation were transferred to fresh medium containing 0.25 μM BS and cultivated for 14 days. Transgenic calli overexpressing *CYP72A32* or *CYP72A33* gene showed BS sensitivity similar as control calli transformed with *gfp* expressing vector.



Supplemental Figure S6. Correlation of *CYP72A31* expression levels and BS tolerance in rice callus.
BS sensitivity test in *CYP72A31* overexpressing callus of Nipponbare (A) and Kasalath (B). In graphs, red and blue bars indicate the lines that showed tolerant and sensitive to 0.75 μM BS, respectively. The y axis shows relative *CYP72A31* mRNA levels normalized to the *OsActin1* mRNA level as a control. In B, mRNA levels are presented as a ratio of that in the average of control samples (#1-3). The photo shows the calli grown on the medium containing 0.75 μM BS for 14 days. The lines #4 and #6 in A are same as shown in Fig. 4. It is suggested that *CYP72A31* expression level in #6 is sufficient to confer tolerance to 0.25 μM BS, although it is not sufficient to confer tolerance to 0.75 μM BS. The callus line marked an asterisk in A is not tested. We estimated that the line #5 in B was BS sensitive because it was bleached on the medium containing BS.

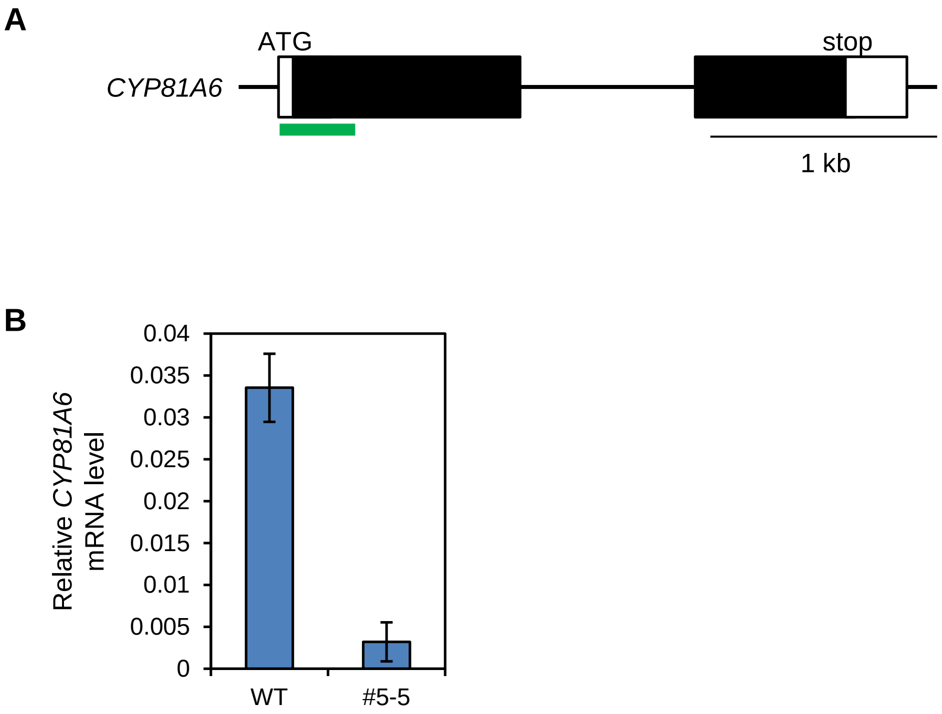


Supplemental Figure S7. Overexpression of *CYP72A31* gene confers BS tolerance in regenerated seedlings of Nipponbare.
Regenerated plantlets were transferred to fresh medium containing 1 μM BS and cultivated for 10 days. The roots of transgenic plants overexpressing *CYP72A31* gene grew vigorously, although control plants stopped growth.



Supplemental Figure S8. BS sensitivity of overexpression of *CYP72A32* and *CYP72A33* genes in Arabidopsis.

Transgenic Arabidopsis seedlings overexpressing *CYP72A32* (#32-1-1, #32-3-1 and #32-5-1) or *CYP72A33* (#33-1-3 and #33-2-4) gene showed BS sensitive similar as wild-type plants. Data show mean±SE of three experiments.



Supplemental Figure S9. *CYP81A6* knock-down rice plants.
A. Schematic representation of *CYP81A6* gene (Os03g0760200). Black and white boxes show the putative untranslated region and coding region of *CYP81A6*, respectively. Green bar shows the region used as a 326-bp inverted repeat sequence of *CYP81A6* for RNAi. Bar = 1 kb. B. Relative mRNA levels of *CYP81A6* gene in wild-type (WT) and *CYP81A6* knock-down line (#5-5).

Supplemental Table S1 Putative QTL for BS tolerance detected through composite interval mapping using 183 BILs (Koshihikari/Kasalath//Koshihikari)

Chr	Marker interval	(Mb)[a]	LOD[b]	a[c]	r^2 [d]
1	C178-C122	15.9-28.6	17.3	-0.4	37.4

[a] According to IRGSP build 5.

[b] LOD values >3.3 are shown.

[c] Additive effect of the Kasalath allele.

[d] Percentage of the total phenotypic variance explained.

Supplemental Table S2 Primers used in this study

For vector construction

primer name	sequence (5'-3')
CYP72A31 F	ATCAGCAGCATCTTTTCACCCCCTTCT
CYP72A31 R	CAAAGGTACAAATATCACAACTCACAACCA
CYP72A32 F	GCTTCTTTTCACTTCATTCCCCCTGTTC
CYP72A32 F2	TACTTACAGGtcGAcCACGGCCAGTAGTAG
CYP72A32 R	TCCTATGCCACTTTTATTCCAAAGGTACAA
CYP72A33 F	CTTCTTTTTCACCCTGGTTTTCGCTTGT
CYP72A33 R	CAAAGGTACAAATGGTATAACCCAACCA
CYP81A6 F	CACCGAGTGCACCAGAGTCACAGAAACACATCACAC
CYP81A6 R	CGGTGAAGCACTCCCTGGCGCAC
M13 Rv	GGAAACAGCTATGACCATGATTACGC

For real time RT-PCR

primer name	sequence (5'-3')
CYP72A31 RT-F	GAAGAACAAACCTGACTACGAAGGCT
CYP72A31 RT-R	CTCCATCTCTTTGTATGTTTTCCGACCAAT
CYP72A32 RT-F	GAAGAACAAACCTGAGTACGATGGCT
CYP72A32 RT-R	TTCATCTCCTTGTATGTTCTCCGCTTAAG
CYP72A33 RT-F	GGAAGAATAAACCAGACTATGATGGCC
CYP72A33 RT-R	CTCCATCTCCTTGTATGTTTTTCGAGTAAG
OsAct1 RT-F	AGGCCAATCGTGAGAAGATGACCCA
OsAct1 RT-R	GTGTGGCTGACACCATCACCAGAG
AtEF1αA4 RT-F	AGGCTGGTATCTCTAAGGATGGTCA
AtEF1αA4 RT-R	TTGTATCCGACCTTCTTCAGGTATG
CYP81A6 RT-F	TGTTCTTCGCGAGCTCGTCT
CYP81A6 RT-R	TGCTCACGAGAAGCTTATTTGCTAC
CA000683_F	CCCAAGAATGCTAAGCCAAGAG
CA000683_R	TGATAACAGATAGGCCGGTTGAA

For genotyping

primer name	sequence (5'-3')
*RM9 F	GGCCCTCATCACCTTCGTAGC
*RM9 R	CGTCCTCCCTCTCCCTATCTCC
*RM11288 F	CAATATCAGCCTAGCACAAAGG
*RM11288 R	CTATCCAACCAGCCATTTATCC
41834-50 F	ACTAATTACTGAAACATACAAATAGCACCA
41834-50 R	TTCAACCAAATAAACTTAATGTTTCACA
*RM11302 F	CTTAGGCCCACATTTGATGTCC
*RM11302 R	CCCATCGTTTGCTCATATTCC

*Matsumoto et al. (2005) *Nature* 436:793-800