

Supplementary Figure

(A)

| | ATHB-1 | |
|------------|---|-----|
| JHN | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 358 |
| ARC10550 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 353 |
| ASD7 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 353 |
| TN1 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 356 |
| PTB33 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 353 |
| RH | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 355 |
| IL162 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 356 |
| IL302 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 347 |
| IL308 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 357 |
| Mudgo | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 358 |
| Pokkali | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 340 |
| Nipponbare | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 343 |
| IL143 | TTTGACA AA TTAATTATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 357 |
| PK3 | TTTGACA AA TT CATT ATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 356 |
| RBR | TTTGACA AA TT CATT ATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 346 |
| HCS | TTTGACA AA TT CATT ATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 358 |
| PK2 | TTTGACA AA TT CATT ATTGCTAGAACTGTTTCATGAATATTGTAATGTTATTTTCACAAAG | 355 |
| | ***** | |

(B)

| | SBF-1 | |
|------------|--|-----|
| JHN | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 418 |
| ARC10550 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 413 |
| ASD7 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 413 |
| TN1 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 416 |
| PTB33 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 413 |
| RH | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 415 |
| IL162 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 416 |
| IL302 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 407 |
| IL308 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 417 |
| Mudgo | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 418 |
| Pokkali | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 400 |
| Nipponbare | CTT- GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 402 |
| IL143 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 417 |
| PK3 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 416 |
| RBR | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 406 |
| HCS | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 418 |
| PK2 | CTTT GCGTGGTTAATAAT CTCTTTTGTGATAACTATAATAAATCAAACTCGTGAATCCAAC | 415 |
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(C)

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JHN      CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 478
ARC10550 CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 473
ASD7     CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 473
TN1      CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 476
PTB33    CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 473
RH       CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 475
IL162    CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 476
IL302    CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 467
IL308    CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 477
Mudgo    CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 478
Pokkali  CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 460
Nipponbare CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 462
IL143    CAACCAACCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 477
PK3      CAACTAACCCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 476
RBR      CAACTAACCCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 466
HCS      CAACTAACCCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 478
PK2      CAACTAACCCAGAGATCGGAAGAATGGATGAGGAAGAGAGCTGACGAGCTCAAGGAGAAAAGTCCG 475
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Supplementary Figure S1. Association between 4SNP at 5'upstream and expression of OsSTPS2 in 18 rice cultivars. Sequence alignment at ATHB-1 (A), SBF-1 (B) and P (C) transcription factor binding sites, consensus sequence of these elements are labeled in red color. The SNPs found in each element are labeled in blue color.

(A)

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KD          AAACTGTCCACCTACTATCTCCAGGAAGCCAAATGGTCACACCAGAGGCATAAACCAAGC
PK3         AAACTGTCCACCTACTATCTCCAGGAAGCCAAATGGTCACACCAGAGGCATAAACCAAGC
HCS         AAACTGTCCACCTACTATCTCCAGGAAGCCAAATGGTCACACCAGAGGCATAAACCAAGC
PK2         AAACTGTCCACCTACTATCTCCAGGAAGCCAAATGGTCACACCAGAGGCATAAACCAAGC
RBR         AAACTGTCCACCTACTATCTCCAGGAAGCCAAATGGTCACACCAGAGGCATAAACCAAGC
Mudgo      AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
TN1         AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
Pokkali    AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
ARC10550   AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
ASD7       AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
JHN        AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
PTB33      AAACTGTCCACCTACTATCTCCAGGAAGCTGAATGGTCACACCAGAGGCATAAACCAAGC
IL308      AAACTGTCCACCTACTATCTCCAGGAAGCTGAATGGTCACACCAGAGGCATAAACCAAGC
IL143      AAACTGTCCACCTACTATCTCCAGGAAGCTGAATGGTCACACCAGAGGCATAAACCAAGC
IL162      AAACTGTCCACCTACTATCTCCAGGAAGCTGAATGGTCACACCAGAGGCATAAACCAAGC
IL302      AAACTGTCCACCTACTATCTCCAGGAAGCTGAATGGTCACACCAGAGGCATAAACCAAGC
Nipponbare AAACTGTCCACCTACTATCTCCAGGAAGCTGAA-----CCAAGC
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(B)

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KD          AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
JHN         AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
TN1         AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
Mudgo      AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
Pokkali    AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
ARC10550   AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
ASD7       AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
Nipponbare AAGCTGAA-----CCAAGCTTCGGTGACCAGATTACTTT
IL143      AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
IL302      AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
IL162      AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
PTB33      AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
PL2        AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
IL308      AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
RH         AAGCTGAATGGTCACACCAGAGGCATAAACCAAGCTTCGGTGACCAGATTACTTT
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(C)

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JHN          EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
TN1          EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
Mudgo       EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
Pokkali     EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
ARC10550    EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
ASD7        EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
Nipponbare  EFQKLSTYYLQEA-----PSFGDQITLTAMSSVIPL
IL143       EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
IL302       EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
IL162       EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
PTB33       EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
PL2         EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
IL308       EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
RH          EFQKLSTYYLQEAESHQRHKPSFGDQITLTAMSSVIPL
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Supplementary Figure S2. Sequence alignment analysis. genomic (A), cDNA (B), amino acid (C) sequence alignments of 2SNPs, 21-bp, and 7-amino acid deletion respectively in several rice cultivars. A; The TG/CA SNPs in exon 5 genomic DNA is labeled by blue/red color. B and C; the rice cultivars with 21-bp and 7-amino-acid deletion are labeled in red color.