

Supplementary Information File

Map-based Cloning and Characterization of a Brown Planthopper

Resistance Gene *BPH26* from *Oryza sativa* L. ssp. *indica* Cultivar ADR52

Yasumori Tamura^{1*}, Makoto Hattori¹, Hirofumi Yoshioka², Miki Yoshioka², Akira Takahashi³, Jianzhong Wu⁴, Naoki Sentoku⁵ and Hideshi Yasui^{6*}

*To whom correspondence should be addressed.

E-mail: Yasumori Tamura: yasumori@affrc.go.jp

Hideshi Yasui: hyasui@agr.kyushu-u.ac.jp

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Supplementary Fig. S1 Genomic sequences containing the ORF regions of *BPH26*.

- (a) The genomic sequence of ADR52. The ORF region of *BPH26* is shown in red-color font.
- (b) The genomic sequence of Nipponbare. The ORF region of *BPH26* is shown in red-color font. The blue border indicates Os12g0559600 and the yellow border indicates Os12g0559400. Both Os12g0559600 and Os12g0559400 are putative genes. Both putative genes partially overlapped with the ORF of *BPH26*.

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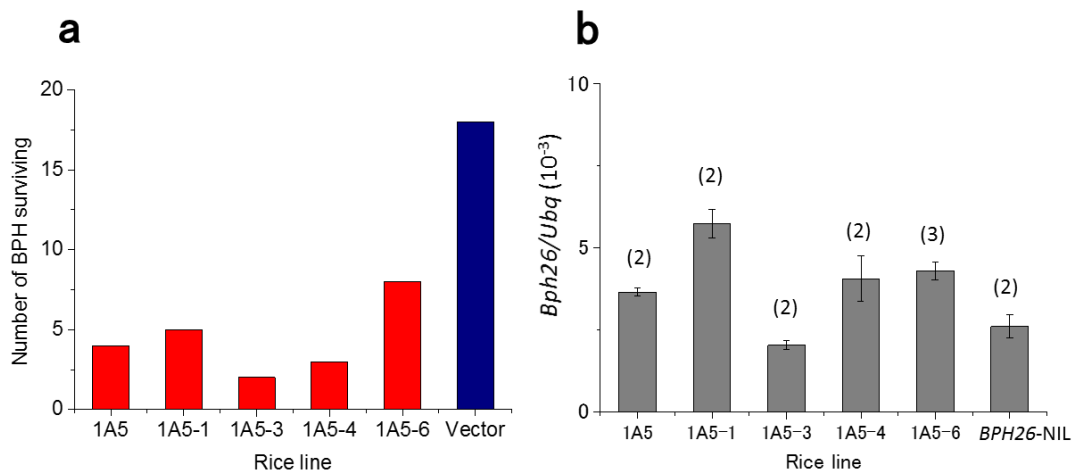
Supplementary Fig. S1 a Continued.

b

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ATTCTACCTTGGCACACGTTCTTCACTAGATGTACAACCGTTGCTTACAGGTTCTGGGATTTTGTGTTCTCGTTATTTTATTGTTGTTGATTGCACGAAGCATGAGAAGTGGAT
CATGATCCATGTGGTCTGGGCGACCTTAGGCCTTTGCAAGTGGTGTAAAGTTGGTACTTACTATTGAGTGGAAAAAGAAAAATCAAAATTTGTTGACCTAAAACTCTCTATGCAGCTT
TAAAAATTTAATTTATTTTCTTGAAGTTGAAATAAATTAATTTAAATTTAACCAAAATTTGAAACTTTATGCAAAATGAGAATCTGCTATAGAAAAATTTAAAAAATCTAAA
AAAAATCAAAACATCAACTCAAAATAACAAACTTCTCAGATTTTAAGGCTTCTACCCAAACTTTATAACTTTCAACTCAAAATCTGAAATTTTCAAGTCAAAATTTGTAACCTTTGAAG
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TGAGAAAGTTGAGCAATCAATTTGATGAGAAAAACTAGACGAAACTTGTGCCGGGCGACTAAGCCATGGTGCAGATGTACTTACCTCCTATACAGTACGCGTATTAGCAACA
CCTACCACCAAGGTAATCATAGTATGATGGTGCATGCCTAGTGTGCACGCTGTGCAGGGTACGGATAAGGCATACCTCACTACGACTTATGGAATATACCGATAAGGT
ATACCTTACGATATAGGATGCTTCTGCAAAATCGTACAAAAACGCCCAAATTAAGAAAAATCTCCACAGTCAAGTATTCTAAAGTCTACAGGAGGGGATAGAAATTCGG
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GTAGCTGTGGCAGCACCCTTCTCCCATCTACAGCCAAAGCATTTCAGCAACAGAGCTCCACACACATGGTCAACACCGAGGTTCCCTGCTCCCTCCGCCACCCATCGAAGCCCG
AACCTGTTGCTCCGTATGACACCTACGACCCCATGGCTCAACGCCGCGACGGTGAAGTATGGCAGAGGTTGGATGGTGGCTTCAAACTCACAATGGAAGTGGTGAAGTCAACGGCGA
GATCCACAACCTCAACACCGCTGCATCCACTATCTGTGACGGTGCCTCACTTCTGACCTCAGTTTTGCTCCTCTGTTAGTCCACTGCCTGTCACCCATAATCTCAGCG
CTGCTTCTTGGCTTGGCTTGGTCCGTCGATGCTGGGAGATGGTCAACGCCGAGTACGTCAGATCGAGCGAAAGAGAGGATGGGAGAAAGAGAGGACTGGGTCACAATGGGTC
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TGTAATTTAGTGGGGTGGGGTAAATCGAACGGACGATAGGGTAATTCAGACTTTTCTTTATTTGGCTACACCAGCAAGGAAACACATAAGTATGCTGTGAGTGCCTGAGG
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TCTGACAAGATGAGGTTGTTGCGTGTGCTGACTTGAAGACACAAAAGTGTACGTAATCACCATAATTAAGCAAAATAGGGAGCTTCTTCACTTATAGTACTTCTTCAAGAGGATGTA
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TCTCCGTGCAATTTAGACAAAATCACCTATGAAGAAATAGCAGAGGAACTACCAGAGGTCATGAGGAACTGCTATGCATTTTACCCTGCGTGTGTTGCTTGTGCTGGCATGCACA
ACAAGTCAATTTGATGCTGGATGATGAGATTAATACCCGTGAGATGTGCTCCTGTTTTGCTGAGATTCTCCCTAGCATTGCTATGCGCTCCAAAGGAAATGGTGTAGTAGCACAA
GAGGGCTGAGGAGACTGACAGCCCTGCACAGCTAGGTGTGGTGGACATCTCATGGGAATCATCAGTTTTACAGGATCTCAAGAACTCACTAGCTGCGCAAAATGGAAGTACCCGTGT
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TTTTACCACCTAAGGATGTCAAGAGCCTGAAGCTGCAAGGCAACCTGGTTGAGTTGCCAAATGGATCAAGCAGCTCAACAATCTGTTGAGGTTGAAAGTCACTAAAGG
ATCATGATGCTGCTATACAAGCTTGGTATGCTACCAACCTGACCCTCATGCTGTCGCTGAGTGGTTCACTCGCTGAGGGTGAAGAACTCAATTTCTCGAGGGATCTTTCAA
AAGCCTGGTGGTCTCGAGCTCAACTCAGTGGGAGCAATGTGTCAAGTTTGAACAAGGAGCGTCTCCTCAATCTTGGAGTACTGCTGTTTCACTTACTATGAAGAGTTGAAACTAAG
TTCTCTGGGCTAGAATTTCTCAAGAGCTCAAGGAGTCCAGATCGATGTTTATGCCAAATAGGAAAGGATTGAAGAAAGACTTGTGGTCCAGCTTCTCAGAAATCAAGAAACCCT
TTCTGAAGACTGGCCGTAATTTTTAA

Supplementary Fig. S1 b Continued.



Supplementary Fig. S2 Functional complementation test of transgenic plants (T_1) that harbored the genomic region (1A5 fragment) of the candidate gene.

(a) Evaluation of resistance. The five 1A5 lines are the transgenic lines (T_1) carrying the candidate gene on the DNA fragment 1A5 in the background of Taichung 65. The vector line is the transgenic plant (T_1) with only the vector fragment in the background of Taichung 65. T_1 plants that harbored fragment 1A5 were selected by PCR and used in the assays. The two brown planthopper (BPH) individuals at the last instar larval stage that had been fasted for 24 h were released in a test tube containing a T_1 plant aged 13 days after germination, and the number of live BPH were recorded 5 days after their release. The tests were repeated 10 times (the total number of BPH was 20), and the total number of live BPH was summed accordingly.

(b) Expression levels of transformed *Bph26* mRNA. Relative mRNA levels were determined by real-time quantitative RT-PCR. The average values and standard deviation (s.d.) were calculated from three PCR measurements derived from one T_1 plant. The number in parentheses at the top of each bar graph show the copy number of transformed *Bph26* determined by real-time quantitative RT-PCR.

atccatccatcacacaagttactagcaatccacgagagagaacgccgaggagaggagagcaaa	60
agccatggaggccacggcggtgagcattggcagggtccgtgctgaagggagcggcttggcctt	120
cgccaaatccaccttgggtggaggagggtttccctgcagctcggcgctccagcgtgaccaggc	180
gttcatcaggacgagctggagatgatgaactccttcctgatggccgccaatgatgagaa	240
agatgacaacaaggtggtaaggacctgggtgaagcagggtccgcgacgtggccctacgacgt	300
tgaggactgcctccaggacttcgccgtccgcttggggggggaagagttcaacctgggtggct	360
cagccctcacacgctgtgggagcggcgccgcatcgccaagcagatgaaggagctgaggggg	420
caaggttgaggatgtcagccagaggaacatgcgctatcaactcatcaagggctccaagcc	480
tactgtagctaccaatgtcacacccagcagcactgccgtgcgaccatgtctggcgcgca	540
tgaagaacgggtggcagcatgagaaggcaatagatcatctgggttcggctggtcaaaaccaa	600
agtcgatgaacgtagagtgatcgcggtgtggggaaacaagttggtgatatacagggaaatgtc	660
catcttgaggagggcctatgatcatctcaagagaaacaacaagtttgagtgctatgcctg	720
ggttaatttgatgcatcctctgaacccaacaaagctcctgcaaacattgttaggcaatt	780
ctatgtaagatctcttcaggaggctggcaaaagcaactccgctcgtgtcaaatcttgagtag	840
catgttgataaaggaagatcaggggtttgggggttaggggtctgaggagcatgctgatgaa	900
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gcttaatgacctatcgaccgctgaagagtggaaagc aaattaaaatgctcttcccagacaa	1020
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taggacagaggagggtggcaccggagcacatgacagttgtttgctgatcagactctttatgc	1140
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cgaagacactacatacaacgctgtagaaggaaagagcctcactcgcacataattcaatggt	1260
aactgctttcaaggaatctgagatcgttggcgagttgatgaaataaaggagattattga	1320
actgatttcaaaaggtagccaacaacttgagaaagatctcagttggtgggaaatgggtggtat	1380
tgggaaaaccactctaattcaaaatgtctacaggaagcggataaataaccacaagcttaaa	1440
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agttaggcaactagaagattcaaaaacttctggaggaaaggagttggttagcattttaga	1560
aggaaagaaatacttgattgttcttgatgatgtattattcaacaacagaatgggatgctat	1620
agaatcatatttcccagcaacaggaaacaggaaagccggatcataataaccacaagcattga	1680
aagtattgctaagcattgttcaggggatcaacaaggcaaaatgtatcaactcaatcgtct	1740
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ggccatcagagctgtccttaataataagctacgatggattaccttatcaccctcaagctctg	2040
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cggtgaattgaagacaacagtagacatgtcccgaataagatcattaacagtggtttggggga	2460
gtggaggccaattttcatttctgacaagatgagggttgttgcgctgtgctcgcacttgggaaga	2520
cacagaagggtgtacgtaatcaccatattaaagcaaataggggagcttcttacccttagata	2580
cttctcctaaagagatgtacgcacattgtctcaacagcctgattcttgggtaacctaaag	2640
gcaactggagacactagatgtcagagatacgttcaactcagggttgccaaagaccatcac	2700
taatctttgcaagctgaagtatctccgctgcaagtaaaagaccctcaacttctatgaaggcat	2760
aagagagaaactaccagagctcatgaggaaacaggctatgcatttttaccgctgctgtgct	2820
ggggctttgtctggcattgctcagctagtgcgattggtaagtttgatgaagagattaatac	2880
ccgtgatgtctgcaccatgtgttgcctgacgtattctcccctagcattgctatgctgcccctca	2940
agggaaatgggtgtagtagcacc aagagggtgaggatcaggagagactgacagccctgcacac	3000
gctaggtgtgggtggacatttcatggcagccatcaattttacaagatatacaagaggctcat	3060
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tctctggggctgtctggatgctgaagaaaagtttctgccaccctaagaatctcaagactct	3240
gaagcttcaaggcaacctgggttgagctgcca aaatggatcgggaagctcaacaatcttgt	3300
taagctgaagctatcaaaaatccaggctcaaggatcatgatgctgctatacaagctccttgg	3360
tatgctaccaaaacctgaccatcctatgcctgcccgcgaagtcatttcaactcgtttagggg	3420
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cagttgggagcaaaagggtgttacgtttcaacaaggagcattccgcaaaactagagctgttatt	3540
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catcaaggaagttcagatc gatggttattgccc aaacgaggaaggattgaagaaagactt	3660
gctggtccaactttctcaaaaatccaaagaaaccttcttgaagatcgacgggttatttt	3720
agctgactctgatgttggggctaatgttctcctctgtgctgcttgggttgttgtcaact	3780
tct	3840
tttggcgtttttatccaaactttactgaagcttctccttaatcatgtgtggtgctgctc	3900
caaatgaagtgatcaggaaagctctactagtagtactgttagtgatgctagtgcataaat	3960
aatatactccctccatattttaatgtatgacgctgttgactttttg	4006

Supplementary Fig. S3 cDNA sequence of *Bph26*. Bases painted yellow show initiation codon and stop codon in order.

ADR52	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
ASD7	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
Nor in-PL4	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
IR1154-243	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
Rathu Heenati	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
Babawee	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
T65	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
Nipponbare	MEATAVS IGRSVLKGALGFAKSTLVEEVSLQLGVQRDQAF IRDELEMMNSFLMAANDEKD
ADR52	DNKVVRTVVKQVRDVAYDVEDCLQDFAVRLGGKSSTWWLSPHTLWERRR IAKQMKELRGK
ASD7	DNKVVRTVVKQVRDVAYDVEDCLQDFAVRLGGKSSTWWLSPHTLWERRR IAKQMKELRGK
Nor in-PL4	DNKVVRTVVKQVRDVAYDVEDCLQDFAVRLGGKSSTWWLSPHTLWERRR IAKQMKELRGK
IR1154-243	DNKVVRTVVKQVRDVAYDVEDCLQDFAVRLGGKSSTWWLSPHTLWERRR IAKQMKELRGK
Rathu Heenati	DNKVVRTVVKQVRDVAYDVEDCLQDFAVRLGRKSSWWLSPHTLWERRR IAKQMEELRGK
Babawee	DNKVVRTVVKQVRDVAYDVEDCLQDFAVRLGRKSSWWLSPHTLWERRR IAKQMEELRGK
T65	DNKVVRTVVKQVRDVAYDVEDCLQDLAVRLGRKSSWWLSPHTLWERRR IAKQMKELRGK
Nipponbare	DNKVVRTVVKQVRDVAYDVEDCLQDLAVRLGRKSSWWLSPHTLWERRR IAKQMKELRGK
ADR52	VEDVSQRNMRYQL IKGSKPTVATNVTSPSTARATMSGAEERWQHEKA IDHLVRLV-KTK
ASD7	VEDVSQRNMRYQL IKGSKPTVATNVTSPSTARATMSGAEERWQHEKA IDHLVRLV-KTK
Nor in-PL4	VEDVSQRNMRYQL IKGSKPTVATNVTSPSTARATMSGAEERWQHEKA IDHLVRLV-KTK
IR1154-243	VEDVSQRNMRYQL IKGSKPTVATNVTSPSTARATMSGAEERWQHEKA IDHLVRLV-KTK
Rathu Heenati	VEDVSQRNMRYQL IKGSKPTVATNVAPSSTARATMSGAEERWQHEKA IDHLVRLV-KTK
Babawee	VEDVSQRNMRYQL IKGSKPTVATNVAPSSTARATMSGAEERWQHEKA IDHLVRLV-KTK
T65	VEDVSQRNMRYQL IKGSKPTVATNVAPSSTARATMSGVHEERWQHDKAVAGL VRLV I KTK
Nipponbare	VEDVSQRNMRYQL IKGSKPTVATNVAPSSTARATMSGVHEERWQHDKAVAGL VRLV I KTK
ADR52	VDERRVI AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
ASD7	VDERRVI AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
Nor in-PL4	VDERRVI AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
IR1154-243	VDERRVI AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
Rathu Heenati	VDERRVI AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
Babawee	VDERRVI AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
T65	VDELRV I AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
Nipponbare	VDELRV I AVWGTSGD IREMS I VGGAYDHLKRNNKFECYAWVNLMHPLNPTKLLQT I VRQF
ADR52	YVRS LQEAGKATPSCQ I LSSML I KEDQGLGFRVLR SMLMKEDHLNDEFNKYLSDKCYL I V
ASD7	YVRS LQEAGKATPSCQ I LSSML I KEDQGLGFRVLR SMLMKEDHLNDEFNKYLSDKCYL I V
Nor in-PL4	YVRS LQEAGKATPSCQ I LSSML I KEDQGLGFRVLR SMLMKEDHLNDEFNKYLSDKCYL I V
IR1154-243	YVRS LQEAGKATPSCQ I LSSML I KEDQGLGFRVLR SMLMKEDHLNDEFNKYLSDKCYL I V
Rathu Heenati	YVRS LQEAGKATPSCQ I LSSML I KEDQGLGFRVLR SMLMKEDHLNDEFNKYLSDKCYL I V
Babawee	YVRS LQEAGKATPSCQ I LSSML I KEDQGLGFRVLR SMLMKEDHLNDEFNKYLSDKCYL I V
T65	YVRS LQEAGKATPSCQ I L S-----SML I KEDHLNDEFN E YLSDKCYL VM
Nipponbare	YVRS LQEAGKATPSCQ I L S-----SML I KEDHLNDEFN E YLSDKCYL VM
ADR52	FHCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
ASD7	FHCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
Nor in-PL4	FHCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
IR1154-243	FHCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
Rathu Heenati	FHCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
Babawee	FHCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
T65	FRCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E
Nipponbare	FRCKGAKDGVDSMEDSSNLNEDTTYNAVEGKSLTRTYSMVTAFKESE I VGRVDE I KE I I E

Supplementary Fig. S4 Alignment of amino acid sequences of BPH26 in some rice varieties. The amino acid sequences of ADR52, ASD7, and Norin-PL4 were deduced from the cDNA sequences, and those of IR1154-243, Rathu Heenati, Babawee, Taichung65 (T65), and Nipponbare were deduced from its genomic sequences. The ORF sequences based on the genomic sequences of ADR52 and ASD7 have been confirmed to be the same as those of the cDNA sequences. A yellow border indicates that the amino acid sequence is the same as that of ADR52, and green and blue borders indicate that the sequence is different from that of ADR52. The repetitive amino acids in the deduced leucine-rich repeat (LRR) are shown in red-color font.

ADR52 LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
ASD7 LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
Nor in-PL4 LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
IR1154-243 LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
Rathu Heenati LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
Babawee LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
T65 LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL
Nipponbare LISKGSQQLEKISVWGMGGIGKTTLIQNVYRSEKVKKMFDKHACVTIMRPFNLNDLLMSL

ADR52 VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
ASD7 VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
Nor in-PL4 VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
IR1154-243 VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
Rathu Heenati VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
Babawee VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
T65 VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE
Nipponbare VRQLEDKSTSGGKELVSILEGKKYLIVLDDVLFTEWDAIESYFPATETGSRIIITTRHE

ADR52 SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
ASD7 SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
Nor in-PL4 SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
IR1154-243 SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
Rathu Heenati SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
Babawee SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
T65 SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG
Nipponbare SIAKHCSGDQQGKMYQLNRLGDNDAKNLF AKKVFKE SVNLDQQDLEL I KEAKP I LKKCNG

ADR52 LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
ASD7 LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
Nor in-PL4 LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
IR1154-243 LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
Rathu Heenati LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
Babawee LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
T65 LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC
Nipponbare LPLAIVTIGGFLASRPKTTLEWRKLNHISAELETNPGLA I RAVLN I SYDGLPYHLKSC

ADR52 FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
ASD7 FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
Nor in-PL4 FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
IR1154-243 FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
Rathu Heenati FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
Babawee FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
T65 FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS
Nipponbare FLYLSIFPEDDKISRKRLVLRWCAEGYSRELWDKSAEEIANNYFFELIDRSMI-LPTQKS

ADR52 TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
ASD7 TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
Nor in-PL4 TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
IR1154-243 TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
Rathu Heenati TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
Babawee TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
T65 TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD
Nipponbare TYSNRGADSCQVHDMREIAISKSKEENLVLREGGRRLHNHDI VRHLSITNSSEDWETD

ADR52 VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
ASD7 VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
Nor in-PL4 VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
IR1154-243 VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
Rathu Heenati VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
Babawee VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
T65 VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR
Nipponbare VGELKTTVDMSRIRSLTVFGEWRPFI SDKMRLLRVLDLEDTEGVRNHHIKQIGELHLR

Supplementary Fig. S4 Continued.

ADR52 YLSLRGCTHIAYMPDSLGNLRQLETLDVRDTFILRLPKTI TNLCKLYLRASKDLNFYEG
ASD7 YLSLRGCTHIAYMPDSLGNLRQLETLDVRDTFILRLPKTI TNLCKLYLRASKDLNFYEG
Nor in-PL4 YLSLRGCTHIAYMPDSLGNLRQLETLDVRDTFILRLPKTI TNLCKLYLRASKDLNFYEG
IR1154-243 YLSLRGCTHIAYMPDSLGNLRQLETLDVRDTFILRLPKTI TNLCKLYLRASKDLNFYEG
Rathu Heenati YLSLRGCTDIAYLPDSLGNLRQLETLDVRDTFILRLPKTI TNLRKLYLRASIDLMIVEV
Babawee YLSLRGCTDIAYLPDSLGNLRQLETLDVRDTFILRLPKTI TNLRKLYLRASIDLMIVEV
T65
Nipponbare -----

ADR52 IREKLPPELNRRLCIFTAALLGLCLACSASAIKGFDEEINTRDVCTMCCCSILPSIAMRL
ASD7 IREKLPPELNRRLCIFTAALLGLCLACSASAIKGFDEEINTRDVCTMCCCSILPSIAMRL
Nor in-PL4 IREKLPPELNRRLCIFTAALLGLCLACSASAIKGFDEEINTRDVCTMCCCSILPSIAMRL
IR1154-243 IREKLPPELNRRLCIFTAALLGLCLACSASAIKGFDEEINTRDVCTMCCCSILPSIAMRL
Rathu Heenati IIEKLPPELNRRLCIFTAALLFLCLACTTSSIGMLNGGINTRDVCTLGCCSFLPSIAMLL
Babawee IIEKLPPELNRRLCIFTAALLFLCLACTTSSIGMLNGGINTRDVCTLGCCSFLPSIAMLL
T65
Nipponbare -----

ADR52 QGNGVVAPRGLRIRRLTALHTLGVVDISWQPSIQDIKRLIQLRKLEVTGVNKKNSKKLF
ASD7 QGNGVVAPRGLRIRRLTALHTLGVVDISWQPSIQDIKRLIQLRKLEVTGVNKKNSKKLF
Nor in-PL4 QGNGVVAPRGLRIRRLTALHTLGVVDISWQPSIQDIKRLIQLRKLEVTGVNKKNSKKLF
IR1154-243 QGNGVVAPRGLRIRRLTALHTLGVVDISWQPSIQDIKRLIQLRKLEVTGVNKKNSKKLF
Rathu Heenati DGSVVAPRGLRIRRLTALHTLGVVDISWESSIQDIIKRLIQLRKLEVTGVNKKNSKKFF
Babawee DGSVVAPRGLRIRRLTALHTLGVVDISWESSIQDIIKRLIQLRKLEVTGVNKKNSKKFF
T65
Nipponbare -----

ADR52 SALAALSQLESLSLFSKWKPGLWGCLDAEEKFSPPKNLKTLLQGNLVELPKWIGKLNLL
ASD7 SALAALSQLESLSLFSKWKPGLWGCLDAEEKFSPPKNLKTLLQGNLVELPKWIGKLNLL
Nor in-PL4 SALAALSQLESLSLFSKWKPGLWGCLDAEEKFSPPKNLKTLLQGNLVELPKWIGKLNLL
IR1154-243 SALAALSQLESLSLFSKWKPGLWGCLDAEEKFSPPKNLKTLLQGNLVELPKWIGKLNLL
Rathu Heenati SALAALSRLLESLSLFSKWKPGLWGCLDAEEKFSPPKDLKSLKQGNLVELPKWIRQLNLL
Babawee SALAALSRLLESLSLFSKWKPGLWGCLDAEEKFSPPKDLKSLKQGNLVELPKWIRQLNLL
T65
Nipponbare -----

ADR52 VKLKLKSKSRLKDHDAAIQVLMPLNLTILCLPRKSFHSLEGGELNFSEGSFKSLLVLELD
ASD7 VKLKLKSKSRLKDHDAAIQVLMPLNLTILCLPRKSFHSLEGGELNFSEGSFKSLLVLELD
Nor in-PL4 VKLKLKSKSRLKDHDAAIQVLMPLNLTILCLPRKSFHSLEGGELNFSEGSFKSLLVLELD
IR1154-243 VKLKLKSKSRLKDHDAAIQVLMPLNLTILCLPRKSFHSLEGGELNFSEGSFKSLLVLELD
Rathu Heenati VKLKLSETMLKDHDAAIQVLMPLNLTILCLSRFSFHSLEGGELNFSEGSFKSLVVLKLF
Babawee VKLKLSETMLKDHDAAIQVLMPLNLTILCLSRFSFHSLEGGELNFSEGSFKSLVVLKLF
T65
Nipponbare -----

ADR52 FSGSKGVTFQQGAFRKELELLSVHSEEVQSKLSGLEFLQSIKEVQIDGYCPNEEGLKGD
ASD7 FSGSKGVTFQQGAFRKELELLSVHSEEVQSKLSGLEFLQSIKEVQIDGYCPNEEGLKGD
Nor in-PL4 FSGSKGVTFQQGAFRKELELLSVHSEEVQSKLSGLEFLQSIKEVQIDGYCPNEEGLKGD
IR1154-243 FSGSKGVTFQQGAFRKELELLSVHSEEVQSKLSGLEFLQSIKEVQIDGYCPNEEGLKGD
Rathu Heenati FGGSKCVKFQQGAFHDELELLSVYSEEVETKFSGLEFLQSIKEVQIDGYYPNWKGLKGD
Babawee FGGSKCVKFQQGAFHDELELLSVYSEEVETKFSGLEFLQSIKEVQIDGYYPNWKGLKGD
T65
Nipponbare -----

ADR52 LLVQLSQNPKKPFLKIDGYF
ASD7 LLVQLSQNPKKPFLKIDGYF
Nor in-PL4 LLVQLSQNPKKPFLKIDGYF
IR1154-243 LLVQLSQNPKKPFLKIDGYF
Rathu Heenati LLVQLSQNPKKPFLKTGRNF
Babawee LLVQLSQNPKKPFLKTGRNF
T65
Nipponbare -----

Supplementary Fig. S4 Continued.

P-loop

BPH26 K I S V W G M G G I G K T T L I Q N V Y R
 BPH14 V L P I V G M G G M G K T T L A Q L I Y N
 PIB V I S V W G M G G L G K T T L V S G V Y Q

RNBS-I

BPH26 F D K H A C V T I M R P F N L N D L L M
 BPH14 F Q L L L W V C V S D N F D V D L L A K
 PIB F D K Y V F V T I M R P F I L V E L L R

Kinase-2

BPH26 K K Y L I V L D D V
 BPH14 Q R Y L L V L D D V
 PIB K S C L I V L D D F

RNBS-II

BPH26 G S R I I I T T R H E S I A K
 BPH14 G S S V L T T T R D Q E V A Q
 PIB T S R I I V T T R K E N I A N

RNBS-III

BPH26 Y Q L N R L G D N D A K N L F
 BPH14 Y D L K R L K E S F I E E I I
 PIB H N L K V L K H N D A L C L L

GLPL

BPH26 I L K K C N G L P L A I V T I
 BPH14 I A K K C S G S P L A A T A L
 PIB I L K K C D G L P L A I V V I

RNBS-IV

BPH26 P G L E A I R A V L N I S Y D G L P Y H L
 BPH14 D E E N G I L P I L K L S Y N C L P S Y M
 PIB P E L G M I R T V L E K S Y D G L P Y H L

RNBS-V

BPH26 K S C F L Y L S I F P E D D K I S R K R L V L R W C A E G Y S R E
 BPH14 R Q C F S F C A I F P K D H E I D V E M L I Q L W M A N G F I P E
 PIB K S C F L Y L S I F P E D Q I I S R R R L V H R W A A E G Y S T A

RNBS-VI

BPH26 A N N Y F F E L I D R S M I L
 BPH14 G K R I F S E L V S R S F F Q
 PIB A N G Y F M E L K N R S M I L

MHDV

BPH26 C Q V H D I M R E I A I S K S
 BPH14 C K I H D L M H D V A Q S S M
 PIB C K V H D L M R D I A I S K S

NL17

BPH26 E E N L V L R L E G G
 BPH14 E G S F L I P K Y H H
 PIB E E N L V F R V E E G

Supplementary Fig. S5 Alignment of main motifs in CC-NBS domains of BPH26 in *O. sativa* cv. ADR52, BPH14 in *O. officinalis* and PIB in *O. sativa* cv. Engkatek.

<BPH26 LRR>

-----IKQIGELHLRYLSLRGCTHIAY
-----MPDSLGNLRQLLETLDVRDTFILR
-----LPKTI TNLCYLKYL RASKDLNFYEGIREKLPELMRN
-----RLCIFTAALLGLCLACSASAIGKFDEEINTRDVCTMCCCSILPSIAMRLQGNGVVAPRGLR
-----IRRLTALHTLGVVDISWQPS
-----ILQDIKRLIQLRKLEVTGVNKKNSKK
-----LFSALAAALSQLESLSLFSKWKPGWGLDAE
-----EKFSPPKNLKTLKQ
GNLVELPKWIGKLNVLKLSKSRDKHDAA
-----IQVLGMLPNLTI LCLPRKSFHSLEGGELN
-----FSEGSFKSLLVLELDFSGSKG
-----VTFQQGAFRKELELLSVHSEEVQS
-----KLSGLEFLQS I KEVQIDGYCPNEEGLKDLLVQLSQNPKKPFLKIDGYF

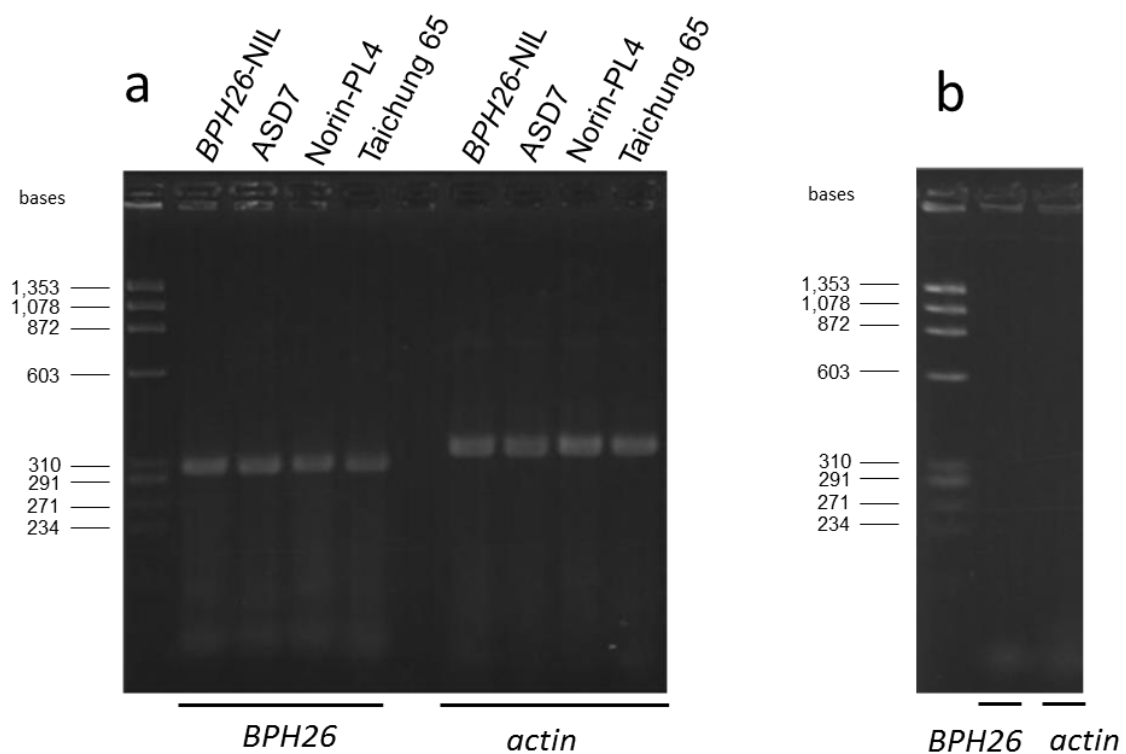
<BPH14 LRR>

-----LIPKYHHHLRYLDLSESEIKA
-----LPEDISILYHLQTLNLSRCLSLRRLPKGMKYMALRHLYTHGCWSLGSMP
-----PDLGHLTCLQTLTCFVAGTCSGC
-----SDLGE LRQLDLGGRELRKLENTKADAKA
-----ANLGKKEKLTCLTITWDQEYKEAQSNNHKEVL
-----EGLTPHEGLKVLSTYHCGSSTCPTWMNKL RDMVGLLELNGC
-KNLEKLPPLWQLPALQVLC
-----EGLGSLNCLFNCDTHTPFTF
-----CRLKELTLDMTNFETWWDTNEVQGEELMF
-----PEVEKLSIESCHRALTALPKASNAISESSGEVSTVCRSAFPALKE
-----MKLYDLRIFQKWEAVDGT
-----PREEATFPQLDKLEIRQCELTTLPEAPKLSDEISKGNQQISLQAAS
-----RHITSLSSLVHLSTDDTETASVAKQDSSDLVIEDEKWSHKSPLELMVLSRCNLLFSHPALALWTCFA
-----LDLKI RYDALVSWPEE
-----VFQGLVSLRKEISVCENLTGHTQARGQSTPAPS
-----ELLPRLSELEITCCDSIVEVPN
-----LPASLKLLEIRGCPGLESIVFNQQDRTMLVSAESFAEQDKSSLISGSTSETND
-----HVLPRLESVINWCDRLE
-----VLHLPSTKKGISYCEKLRSL
-----LSVKLDAVRELSIRHCGSLKS
-----LESCLELASLQQLKLFDCSLES LKPGPQAY
-----SSLTSLEIRGCSGIKVLPSSLQQLDDIEDKELDACYEAEAEPKSRHRQSAISRLMCLK

<PIB LRR>

-----GAI RHLA I SSNWKGDKSEF
-----EGIVDL SRIRSLSLFGDWKPFV
-----KMRFIRVLD FEGTRGLEYYH
-----LDQIWKLNHLKFLSLRGCYRIDL
-----LPDLLGNLRQLQMLDIRGTYVKA
-----LPKTIKQLQYIHAGRKTDYVWEEKHSLMQRCKVGCICATCCLPLCEMYGPLHKALARRDAWTFACCVKFPSIMTGVEEEGA
-MVPSGIRKLDLHTLRNINVGRGN
-----AILRDI GMLTGLHKLGVAGINKKNGRAFR
-----LAISNLNKLESLSVSSAGMPGLCGCLDDISSPP
-----ENLQSLKLY
GSLKTLPEWIKELQHLVKLKL VSTRLEHDVAM
-----EFLGELPKVEILVISPFKSEEIHFKPPQTG
-----TAFVSLRVLKL AGLWGIKS
-----VKFEEGTMPKLERLQVQGR IENEIGF
-----SGLEFLQNI NEVQLSVWFPTDHDRIRARAAGADYETAWEEVQEARRKGGELKRKIREQLARNPNQPIIT

Supplementary Fig. S6 Amino acid sequences of the deduced leucine-rich repeat (LRR) of BPH26 in *O. sativa* cv. ADR52, BPH14 in *O. officinalis* and PIB in *O. sativa* cv. Engkatek. The repetitive amino acids in the LRR are shown in red-color font.



Supplementary Fig. S7 Full-length gel of Figure 4a and that of negative control.

(a) Gene expression analysis of *BPH26* in some rice varieties by using reverse transcriptase (RT)-PCR. Actin primers were used in the control amplification. ϕ X174 - *Hae* III digest was used as a molecular-weight size marker. Fragments sizes are marked on the left, in base pairs.

(b) Negative control of (a). One step RT-PCR was conducted without total RNA.

Supplementary Table S1

Predicted genes by rice annotation project database in the candidate region of the *japonica* cultivar Nipponbare.

1	Os12g0558366	Similar to F-box domain-containing protein
2	Os12g0558400	Similar to F-box domain-containing protein
3	Os12g0559000	Hypothetical conserved gene
4	Os12g0559100	Conserved hypothetical protein
5	Os12g0559250	Non-protein coding transcript
6	Os12g0559200	Lipoxygenase (EC 1.13.11.12)
7	Os12g0559300	Similar to leucine-rich repeat family protein
8	Os12g0559400	Similar to leucine-rich repeat family protein
9	Os12g0559600	Similar to resistance protein RGA2

Supplementary Table S2

PCR primers used in this study

Primer name	Forward primer (5'-3')	Reverse primer (5'-3')	Purpose
High-resolution mapping			
RM28449	CACCCATTGATGTGAAACTCTGG	GGATTCATGATACAGTGTGCAACG	SSR marker
RM3813	ACCGTTAGATGACACAAGCAACG	GGTTAGCAAGACTGGAGGAGACG	SSR marker
ID-28L4	GAAGGGAAATGGAAGCATGA	TACACCCGACAAGGAACACA	InDel marker
ID-174	TGCTCGTACGATGGAGTCAT	CGGGCTTCATTCATCGTTA	InDel marker
ID-161	CTGTCAAATTGCGTTCGAT	CATCCCCTGAATTTGAAACA	InDel marker
ID-161-2	ATCCTTTTCGGACAGGGTGAT	GGACGGGATGATACCTCAGA	InDel marker
DS-L74	AGCGGATGCTAAAAGCAAAA	AATAGACGGGGCAAGGGTAG	SNP marker
DS-72B4	AAAGTGCGCAGCAGTACAGA	GGATGCAGATCGAACACTGA	SNP marker
DS-173B	TCACGACGTTATTCATGTTTCA	TCCCATGCCAATCAATATCA	SNP marker
Comparison of alleles from some varieties			
BPH26-Exson1	TAGCATCAGTCCCTTGCTTGTTC	ATTGATTTAATTAGCAGACAAGTTG	Sequencing
BPH26-Exson2	AACTCTCGTCTCGTCTTAAAATATA	AGTAGTAATGTGCGTAGCAATGGAG	Sequencing
BPH26-Exson3	CTAGTGCCAGTTACTCCGATAAATAT	TATGCACTAGCATCACTACA	Sequencing
Gene expression analysis			
BPH26-RT-PCR	GCTACCAAACCTGACCATCC	AGCAAGTCTTTCTTCAATCCTT	RT-PCR
Actin-RT-PCR	TCCATCTTGGCATCTCT	GTACCCGCATCAGGCATCTG	RT-PCR
<i>In situ</i> hybridization analysis			
BP26-insitu-AP	<u>ATTAACCCTCACTAAAGGGAA-</u> GGAAGTTCAGATCGATGGTT	TGGATAAAACGGCAAATTA	Probe
BP26-insitu-SP	<u>ATTAACCCTCACTAAAGGGAA-</u> TGGATAAAACGGCAAATTA	GGAAGTTCAGATCGATGGTT	Probe
Confirmation of the insertion site in T ₁ transgenic lines			
pPZP2H-lac-D	ACTATCCTTCGCAAGACCCT	GATCAGCAATCGCGCATATG	Detection
Real-time quantitate RT-PCR analysis			
BPH26-qPCR	CCAAACGAGGAAGGATTGAA	AGCCCCAACATCAGAGTCAG	Real-time PCR
UBQ-qPCR	GAGCCTCTGTTCGTCAGTA	ACTCGATGGTCCATTAAACC	Real-time PCR

The *in situ* hybridization probe: T3 promoter sequence (underlined) was attached to the top sequence of the forward primer.

SSR, simple sequence repeat. InDel, insertion-deletion mutation. SNP, single nucleotide polymorphism. RT-PCR, reverse-transcription PCR.