

Supplementary Data 1 Multiple DNA sequence alignment for predicted protein of LOC_Os07g12130

Sequence 1: Nipponbare 438 aa

Sequence 2: Peiai64S 441 aa

Sequence 3: 9311 441 aa

CLUSTAL W (1.81) multiple sequence alignment

Peiai64S MAAAGNSFLNQELVKVADGVSDWHLPSSSHGGTCHTNTRGAPITVGVPDLGCPVSSIGMA
9311 MAAAGNSFLNQELVKVADGVSDWHLPSSSHGGTCHTNTRGAPITVGVPDLGCPVSSIGMA
Nipponbare MAAAGNSFLNQELVKVADGVSDWHLPSSSHGGTCHTNTRGAPITVGVPDLGCPVSSIGMA

Peiai64S TSSSLMPKEGLTTASYNVAVFPVGATMVPQQQTQAAGSNDNPGLVKGWWTREEDVLR
9311 TSSSLMPKEGLTTASYNVAVFPVGATMVPQQQTQAAGSNDNPGLVKGWWTREEDVLR
Nipponbare TSSSLMPKEGLTTASYNVAVFPVGATMVPQQQTQAAGSNDNPGLVKGWWTREEDVLR

Peiai64S QMVRHHGDRKWAEIAKSLPGRVGKQCRERWTNHLHPDIKKDIWTEEDRMLIEAHQTYGN
9311 QMVRHHGDRKWAEIAKSLPGRVGKQCRERWTNHLHPDIKKDIWTEEDRMLIEAHQTYGN
Nipponbare QMVRHHGDRKWAEIAKSLPGRVGKQCRERWTNHLHPDIKKDIWTEEDRMLIEAHQTYGN

Peiai64S SWSAIAKQLPGRSENTIKNHWNATKRSLNSKRRLRKKNSEQTVPGQPSLLENYIRSCQHM
9311 SWSAIAKRLPGRSENTVKNHWNATKRSLNSKRRLRKKNSEQTVPGQPSLLENYIRSCQHM
Nipponbare SWSAIAKQLPGRSENTIKNHWNATKRSLNSKRRLRKKNSEQTVPGQPSLESYIRSCQHM

*****:*****:*****:*****:*****:*****:*****

Peiai64S LPNETVPPPPAPPAPFDISRYGNSGVIDASPTLPVVQEPGTSTPPGLVMFLDLLNQAIPH
9311 LPSETVPPPPAPPAPFDISRYGNSGVIASPTLPVQEPGTSTPPGLVMFLDLLNQAIPH
Nipponbare LPSETVPPP---PAPFDISRYGNSGVIASPTLPVVQEPGTSTPPGLVMFLDLLNQAIPH

*,***** *****:*****:*****:*****:*****:*****

Peiai64S PPQPETMDLFNMTPEVSHLNTSGYCLQLDAGGNLYGRLPVPAVQPHGISTQELQDTPH
9311 PPQPETMDLFNMTPEVSHLNTSGYCLQLDAGGNLYGRLPAPAVQPHGISTQELQDTPH
Nipponbare PPQPETMDLFNMTPEVSHLNTSGYCLQLDAGGNLYGRLPAPAVQPHGISTQELQDTPQ

*****:*****:*****:*****:*****:*****:

Peiai64S LSLYPLSSFAGSHTDGTVEFDHQLSNPDGGHYGEEAGPSSVAAGGSANGMDDNDVVQMA
9311 LSLYPLSSFAGSHTDGTVEFDHQLSNPNGGHYGEEAGPSSVAAGGSANGMDDNDVVQMA
Nipponbare LSLYPLSSFAGSHTDGTVEFNHQLSNPNGGHYGEEAGPSSVATGGSANGMDDNDVVQMA

*****:*****:*****:*****:*****:*****

Peiai64S SNQFMPSEDEGILDLARWIN

```

9311          SNQFMMPCEDEGILDLARWIN
Nipponbare    SNQFMMPSEDEGILDLARWIN
              *****

```

Note: 8 altered loci between Pei'ai64S and 9311 and six amino acids differences between Nipponbare and Pei'ai64S, and a deletion of three amino acids (PAP) in Nipponbare were found from the Supplementary Data 1.

Supplementary Data 2 Multiple DNA sequence alignment for LOC_Os07g12130 in Pei'ai64S S1, S2, and S3

```

Sequence 1: Pei'ai64S_2378_    2378 bp
Sequence 2: S3_1273_          1273 bp
Sequence 3: S1_2320_          2320 bp
Sequence 4: S2_1701_          1701 bp

```

CLUSTAL W (1.81) multiple sequence alignment

```

Pei'ai64S_2378_    TACACGCCAGGGTAGAGTTCAACTTCATTGGAGAAAAGAAAACTAAGAGATGATAATCAT
S1_2320_          -----AATCAT
S2_1701_          -----ATAATCAT
S3_1273_          -----AATCAT
                                   *****

```

```

Pei'ai64S_2378_    AATTGTTATTATTAATGGGTGATGGTTGGAAGTACTGCGAACAAGCATCAGTTGATCC
S1_2320_          AATTGTTATTATTAATGGGTGATGGTTGGAAGTACTGCGAACAAGCATCAGTTGATCC
S2_1701_          AATTGTTATTATTAATGGGTGATGGTTGGAAGTACTGCGAACAAGCATCAGTTGATCC
S3_1273_          AATTGTTATTATTAATGGGTGATGGTTGGAAGTACTGCGAACAAGCATCAGTTGATCC
                                   *****

```

```

Pei'ai64S_2378_    ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
S1_2320_          ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
S2_1701_          ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
S3_1273_          ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
                                   *****

```

```

Pei'ai64S_2378_    TTTGGACGACGTCATTGTCATCCATGCCATTGGCGCTGCCACCAGCGGCGACGCTACTTG
S1_2320_          TTTGGACGACGTCATTGTCATCCATGCCATTGGCGCTGCCACCAGCGGCGACGCTACTTG
S2_1701_          TTTGGACGACGTCATTGTCATCCATGCCATTGGCGCTGCCACCAGCGGCGACGCTACTTG
S3_1273_          TTTGGACGACGTCATTGTCATCCATGCCATTGGCGCTGCCACCAGCGGCGACGCTACTTG
                                   *****

```

Pei' ai64S_2378_ GGCCTGCCTCCTCACCATAGTGGCCGCCGTCGGGTTGGACAACTGGTGATCGAACTCCA
S1_2320_ GGCCTGCCTCCTCACCATAGTGGCCGCCGTCGGGTTGGACAACTGGTGATCGAACTCCA
S2_1701_ GGCCTGCCTCCTCACCATAGTGGCCGCCGTCGGGTTGGACAACTGGTGATCGAACTCCA
S3_1273_ GGCCTGCCTCCTCACCATAGTGGCCGCCGTCGGGTTGGACAACTGGTGATCGAACTCCA

Pei' ai64S_2378_ CAGTGCCATCCGTGTGGCTCCCGCAAATGATGACAGCGGGTAGTACAGGCTTAGGTGCG
S1_2320_ CAGTGCCATCCGTGTGGCTCCCGCAAATGATGACAGCGGGTAGTACAGGCTTAGGTGCG
S2_1701_ CAGTGCCATCCGTGTGGCTCCCGCAAATGATGACAGCGGGTAGTACAGGCTTAGGTGCG
S3_1273_ CAGTGCCATCCGTGTGGCTCCCGCAAATGATGACAGCGGGTAGTACAGGCTTAGGTGCG

Pei' ai64S_2378_ GAGTATCCTGCAGCTCCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTACTGGTA
S1_2320_ GAGTATCCTGCAGCTCCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTACTGGTA
S2_1701_ GAGTATCCTGCAGCTCCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTACTGGTA
S3_1273_ GAGTATCCTGCAGCTCCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTACTGGTA

Pei' ai64S_2378_ GCCGGCCATAATACAGGTTGCCCTGCATCGAGCTGTAGACAGTATCCACTGGTGTGA
S1_2320_ GCCGGCCATAATACAGGTTGCCCTGCATCGAGCTGTAGACAGTATCCACTGGTGTGA
S2_1701_ GCCGGCCATAATACAGGTTGCCCTGCATCGAGCTGTAGACAGTATCCACTGGTGTGA
S3_1273_ GCCGGCCATAATACAGGTTGCCCTGCATCGAGCTGTAGACAGTATCCACTGGTGTGA

Pei' ai64S_2378_ GGTGTGATACCTCCGGTGCATGTTGAACAAATCCATGGTCTCTGGCTGCGGTGGGTGCG
S1_2320_ GGTGTGATACCTCCGGTGCATGTTGAACAAATCCATGGTCTCTGGCTGCGGTGGGTGCG
S2_1701_ GGTGTGATACCTCCGGTGCATGTTGAACAAATCCATGGTCTCTGGCTGCGGTGGGTGCG
S3_1273_ GGTGTGATACCTCCGGTGCATGTTGAACAAATCCATGGTCTCTGGCTGCGGTGGGTGCG

Pei' ai64S_2378_ GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG
S1_2320_ GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG
S2_1701_ GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG
S3_1273_ GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG

Pei' ai64S_2378_ GCTCCTGCACAACGGGTAGAGTTGACTTGATCTATCACCCCACTATTGCCATACCTGC
S1_2320_ GCTCCTGCACAACGGGTAGAGTTGACTTGATCTATCACCCCACTATTGCCATACCTGC
S2_1701_ GCTCCTGCACAACGGGTAGAGTTGACTTGATCTATCACCCCACTATTGCCATACCTGC
S3_1273_ GCTCCTGCACAACGGGTAGAGTTGACTTGATCTATCACCCCACTATTGCCATACCTGC

Pei' ai64S_2378_ TGATGTCAAATGGTGCGGGCGGCCGGGTTGGCGGTACAGTTTCATTGGGAAGCATGT
S1_2320_ TGATGTCAAATGGTGCGGGCGGCCGGGTTGGCGGTACAGTTTCATTGGGAAGCATGT

S2_1701_ TGATGTCAAATGGTGC GGCGCGGCCGCGGTGGCGGTACAGTTTCATTGGGAAGCATGT
S3_1273_ TGATGTCAAATGGTGC GGCGCGGCCGCGGTGGCGGTACAGTTTCATTGGGAAGCATGT

Pei' ai64S_2378_ GCTGGCAGCTACGGATGTAATTTCAAGGAGGGAAGGCTGCCCGGCACAGTTTGCTCGC
S1_2320_ GCTGGCAGCTACGGATGTAATTTCAAGGAGGGAAGGCTGCCCGGCACAGTTTGCTCGC
S2_1701_ GCTGGCAGCTACGGATGTAATTTCAAGGAGGGAAGGCTGCCCGGCACAGTTTGCTCGC
S3_1273_ GCTGGCAGCTACGGATGTAATTTCAAGGAGGGAAGGCTGCCCGGCACAGTTTGCTCGC

Pei' ai64S_2378_ TGTTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGTTGCATTCCAATGGT
S1_2320_ TGTTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGTTGCATTCCAATGGT
S2_1701_ TGTTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGTTGCATTCCAATGGT
S3_1273_ TGTTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGTTGCATTCCAATGGT

Pei' ai64S_2378_ TTTTATGGTGTTCGACCGTCCAGGAAGCTGCTTGGCAATCGCCGACCAGCTGTTC
S1_2320_ TTTTATGGTGTTCGACCGTCCAGGAAGCTGCTTGGCAATCGCCGACCAGCTGTTC
S2_1701_ TTTTATGGTGTTCGACCGTCCAGGAAGCTGCTTGGCAATCGCCGACCAGCTGTTC
S3_1273_ TTTTATGGTGTTCGACCGTCCAGGAAGCTGCTTGGCAATCGCCGACCAGCTGTTC

Pei' ai64S_2378_ CATAAGTTGGTGTGCTTCGATCAGCATCCTGCCTCTTCTTGTCCAGATGTCTTTCT
S1_2320_ CATAAGTTGGTGTGCTTCGATCAGCATCCTGCCTCTTCTTGTCCAGATGTCTTTCT
S2_1701_ CATAAGTTGGTGTGCTTCGATCAGCATCCTGCCTCTTCTTGTCCAGATGTCTTTCT
S3_1273_ CATAAGTTGGTGTGCTTCGATCAGCATCCTGCCTCTTCTTGTCCAGATGTCTTTCT

Pei' ai64S_2378_ GCAGTGTAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA
S1_2320_ GCAGTGTAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA
S2_1701_ GCAGTGTAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA
S3_1273_ GCAGTGTAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA

Pei' ai64S_2378_ AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTTAGATTGTATCCATT
S1_2320_ AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTTAGATTGTATCCATT
S2_1701_ AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTTAGATTGTATCCATT
S3_1273_ AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTTAGATTGTATCCATT

Pei' ai64S_2378_ AAGAAAAGGAACCCACGGATTCCACTTTAATGGTTTTTAATTTGAGCACATTTATTGA
S1_2320_ AAGAAAAGGAACCCACGGATTCCACTTTAATGGTTTTTAATTTGAGCACATTTATTGA
S2_1701_ AAGAAAAGGAACCCACGGATTCCACTTTAATGGTTTTTAATTTGAGCACATTTATTGA
S3_1273_ AAGAAAAGGAACCCACGGATTCCACTTTAATGGTTTTTAATTTGAGCACATTTATTGA

Pei' ai64S_2378_ GAAATAAAAGCATATATACATAGATATGATAATTAACATATAACCATTTTGTACAGGGTG
S1_2320_ GAAATAAAAGCATATATACATAGATATGATAATTAACATATAACCATTTTGTACAGGGTG
S2_1701_ GAAATAAAAGCATATATACATAGATATGATAATTAACATATAACCATTTTGTACAGGGTG
S3_1273_ GAAATAAAAGCATATATACATAGATATGATAATTAACATATAACCATTTTGTACAGGGTG

Pei' ai64S_2378_ CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA
S1_2320_ CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA
S2_1701_ CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA
S3_1273_ CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA

Pei' ai64S_2378_ AATGTAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGTCATACACATTTTGG
S1_2320_ AATGTAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGTCATACACATTTTGG
S2_1701_ AATGTAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGTCATACACATTTTGG
S3_1273_ AATGTAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGTCATACACATTTTGG

Pei' ai64S_2378_ ACTAATAAGTGTCTAAAACATTGAGCTTAATTTGCATATACAACAATGATTA AAAACACA
S1_2320_ ACTAATAAGTGTCTAAAACATTGAGCTTAATTTGCATATACAACAATGATTA AAAACACA
S2_1701_ ACTAATAAGTGTCTAAAACATTGAGCTTAATTTGCATATACAACAATGATTA AAAACACA
S3_1273_ ACTAATA-----

Pei' ai64S_2378_ AATAAACTTGGTGGACTACTGTCCAGAGTAGTTTTTTCCTAGGACTACAAATAATGTGTG
S1_2320_ AATAAACTTGGTGGACTACTGTCCAGAGTAGTTTTTTCCTAGGACTACAAATAATGTGTG
S2_1701_ AATAAACTTGGTGGACTACTGTCCAGAGTAGTTTTTTCCTAGGACTACAAATAATGTGTG
S3_1273_ -----

Pei' ai64S_2378_ GGATCCATTAATGGCCCTAGCGAAGAAATTCCTACATTTATTA ACTAGAATAAAAGACAT
S1_2320_ GGATCCATTAATGGCCCTAGCGAAGAAATTCCTACATTTATTA ACTAGAATAAAAGACAT
S2_1701_ GGATCCATTAATGGCCCTAGCGAAGAAATTCCTACATTTATTA ACTAGAATAAAAGACAT
S3_1273_ -----

Pei' ai64S_2378_ GCAACATGACTAACTAATTACTCAAATAATCGGCTCCCGTTTAAATGTTGAATATTATGAA
S1_2320_ GCAACATGACTAACTAATTACTCAAATAATCGGCTCCCGTTTAAATGTTGAATATTATGAA
S2_1701_ GCAACATGACTAACTAATTACTCAAATAATCGGCTCCCGTTTAAATGTTGAATATTATGAA
S3_1273_ -----

Pei' ai64S_2378_ ATTTGTACCATTTTCACGTAAATCTGAAAATAAACTCCACCTCTAAAATTGCACAGAGAA
S1_2320_ ATTTGTACCATTTTCACGTAAATCTGAAAATAAACTCCACCTCTAAAATTGCACAGAGAA
S2_1701_ ATTTGTACCATTTTCACGTAAATCTGAAAATAAACTCCACCTCTAAAATTGCACAGAGAA
S3_1273_ -----

Pei' ai64S_2378_ AGAACTAGGATCCCTTAGATATACACATATAACCGAAGGAATATAGCAAGATACAGACCT
S1_2320_ AGAACTAGGATCCCTTAGATATACACATATAACCGAAGGAATATAGCAAGATACAGACCT
S2_1701_ AGAACTAGGATCCCTTAGATATACACATATAACCGAAGGAATATAGCAAGATACAGACCT
S3_1273_ -----

Pei' ai64S_2378_ TGATGTCCGGTGCAGATGGTTGGTCCATCTCTCGGGCACTGCTTCCCAACCCGACCTG
S1_2320_ TGATGTCCGGTGCAGATGGTTGGTCCATCTCTCGGGCACTGCTTCCCAACCCGACCTG
S2_1701_ TGATGTCCGGTGCAGATGGTTGGTCCATCTCTCGGGCACTGCTTCCCAACCCGACCTG
S3_1273_ -----

Pei' ai64S_2378_ GGAGGCTCTTTGCAATCTCTGCCACTTGGCATCTCCATGGTGTCTCACCATCTGCCTAA
S1_2320_ GGAGGCTCTTTGCA-TCTCTGCCACTTGGCATCTCCATGGTGTCTCACCATCTGCCTAA
S2_1701_ GGAGGCTCTTTGC-----
S3_1273_ -----

Pei' ai64S_2378_ GAACTCTATAATCAAAGAACAACAATAGTTCAAGATCTCATCACAAGAATGAAGAGA
S1_2320_ GAACTCTATAATCAAAGAACAACAATAGTTCAAGATCTCATCACAAGAATGAAGAGA
S2_1701_ -----
S3_1273_ -----

Pei' ai64S_2378_ TGCCAAGAAACAAGAATTAATACTGATTAGAAGTAGACAGATCTCTCACTTACTCATCC
S1_2320_ TGCCAAGAAACAAGAATTAATACTGATTAGAAGTAGACAGATCTCTCACTTACTCATCC
S2_1701_ -----
S3_1273_ -----

Pei' ai64S_2378_ TCTTCCCTTGCCACCCTCCTTTGACCAACCCTGGGTTGTCGTTGCTACCTGCAGCTTGC
S1_2320_ TCTTCCCTTGCCACCCTCCTTTGACCAACCCTGGGTTGTCGTTGCTACCTGCAGCTTGC
S2_1701_ -----
S3_1273_ -----

Pei' ai64S_2378_ GTCTGCTGTTGTTGAGGCACCATCGTAGCACCTACTGAAAGGCAACAACCGAGTTGTAA
S1_2320_ GTCTGCTGTTGTTGAGGCACCATCGTAGCACCTACTGAAAGGCAACAACCGAGTTGTAA

S2_1701_ -----
S3_1273_ -----

Pei'ai64S_2378_ CTAGCGGTTGTCAGGCCCTCCTTTGGCATTAGAGAGCTTGACGTAGCCATGCCTATGCTA
S1_2320_ CTAGCGGTTGTCAGGCCCTCCTTTGGCATTAGAGAGCTTGACGTAGCCATGCCTATGCTA
S2_1701_ -----
S3_1273_ -----

Pei'ai64S_2378_ GAAACAGGGCACCCCTAAGTCGGGGACCCCCACGGTGATTGGAGCACCACGAGTGTTCGTG
S1_2320_ GAAACAGGGCACCCCTAAGTCGGGGACCCCCACGGTGATTGGAGCACCACGAGTGTTCGTG
S2_1701_ -----
S3_1273_ -----

Pei'ai64S_2378_ TGGCAAGTACCACCATGGCTAGAGCTCGGAAGGTGCCAATCCGACACCCCGTCGGCCACC
S1_2320_ TGGCAAGTACCACCATGGCTAGAGCTCGGAAGGTGCCAATCCGACACCCCGTCGGCCACC
S2_1701_ -----
S3_1273_ -----

Pei'ai64S_2378_ TTCACTAACTCCTGGTTGAGGAAGGAGTTACCTGCAGCCGCCATGATTCACCTTCCAAGG
S1_2320_ TTCACTAACTCCTGGTTGAGGAAGGAGTTACCTGCAGCCGCCATGATTCACCTTCCAAGG
S2_1701_ -----
S3_1273_ -----

Pei'ai64S_2378_ AAAGAAGCAACGAAAGAATTGCCGAGGATTGGGGAGGCAAATCGACCTCGATATGGAGG
S1_2320_ AAAGAAGCAACGAAAGAATTGCCGAGGATTGGGGAGGCAAATCGACCTCGATATGGAGG
S2_1701_ -----
S3_1273_ -----

Pei'ai64S_2378_ AAATTGAGAAGGGGATTGTCTAGTGTGGAGATGGGTCA
S1_2320_ AAATTGAGAAGGGGATTGTCTAGTGTGGAGATGGG---
S2_1701_ -----
S3_1273_ -----

Note: there is no difference in LOC_Os07g12130 between Pei'ai64S and two sterile plants except a single base deletion for S1.

Supplementary Data 3 Multiple DNA sequence alignment for LOC_Os07g12130 in Pei'ai64S, 9311, and Nipponbare

Sequence 1: Pei'ai64S 2378 bp
Sequence 2: Nipponbare 2377 bp
Sequence 3: 9311 2386 bp

CLUSTAL W (1.81) multiple sequence alignment

Nipponbare -ACACGC-AGGTGAGAGTTCAACTTCATTGGAGAAAGAAAACTAAGAGATGATAATCAT
9311 -ACACGC-AGGTGAGAGTTCAACTTCATTGGAGAAAGAAAACTAAGAGATGATAATCAT
Pei'ai64S TACACGCCAGGTTAGAGTTCAACTTCATTGGAGAAAGAAAACTAAGAGATGATAATCAT
***** ** *****

Nipponbare AATTGTTATTATTAATGGGTGATGGTTTGAAGTACTGTGAACAAGCCTCAGTTGATCC
9311 AATTGTTATTATTAATGGGTGATGGTTTGAAGTACTGTGAACAAGCCTCAGTTGATCC
Pei'ai64S AATTGTTATTATTAATGGGTGATGGTTTGAAGTACTGTGAACAAGCATCAGTTGATCC
***** *****

Nipponbare ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
9311 ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
Pei'ai64S ACCTGGCCAGGTCAAGAATACCCTCATCCTCAGATGGCATCATAAACTGGTTGGACGCCA
***** *****

Nipponbare TTTGGACGACGTCATTGTATCCATGCCATTGGCGTGCCACCAGTGGCGACGCTACTTG
9311 TTTGGACGACGTCATTGTATCCATGCCATTGGCGTGCCACCAGCGGCGACGCTACTTG
Pei'ai64S TTTGGACGACGTCATTGTATCCATGCCATTGGCGTGCCACCAGCGGCGACGCTACTTG
***** *****

Nipponbare GGCCTGCCTCCTCGCCATAGTGGCCGCCGTTCCGGTTGGACAACCTGGTGATTGAACTCCA
9311 GGCCTGCCTCCTCGCCATAGTGGCCGCCGTTCCGGTTGGACAACCTGGTGATCGAACTCCA
Pei'ai64S GGCCTGCCTCCTCACCATAGTGGCCGCCGTTCCGGTTGGACAACCTGGTGATCGAACTCCA
***** *****

Nipponbare CAGTGCCATCCGTGTGGCTCCCGCAAATGACGACAGCGGGTAGTACAGGCTTAGTTGCC
9311 CAGTGCCATCCGTGTGGCTCCCGCAAATGACGACAGCGGGTAGTACAGGCTTAGTTGCC
Pei'ai64S CAGTGCCATCCGTGTGGCTCCCGCAAATGATGACGACAGCGGGTAGTACAGGCTTAGTTGCC
***** *****

Nipponbare GAGTATCCTGCAGTCTCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTGCTGGTA
9311 GAGTATCCTGCAGTCTCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTGCTGGTA
Pei'ai64S GAGTATCCTGCAGTCTCTGGTACTGATCCCATGTGGCTGCACCGGTGCTGGTACTGGTA
***** *****

Nipponbare GCGGCCATAATACAGGTTGCCCCCTGCATCGAGCTGTAGACAGTATCCACTAGTGTGA
9311 GCGGCCATAATACAGGTTGCCCCCTGCATCGAGCTGTAGACAGTATCCACTGGTGTGA
Pei' ai64S GCGGCCATAATACAGGTTGCCCCCTGCATCGAGCTGTAGACAGTATCCACTGGTGTGA

Nipponbare GGTGTGATACCTCCGGTGCATGTTGAACAAGTCCATGGTCTCTGGCTGCGGTGGGTGG
9311 GGTGTGATACCTCCGGTGCATGTTGAACAAGTCCATGGTCTCTGGCTGCGGTGGGTGG
Pei' ai64S GGTGTGATACCTCCGGTGCATGTTGAACAAATCCATGGTCTCTGGCTGCGGTGGGTGG

Nipponbare GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG
9311 GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG
Pei' ai64S GTATGGCCTGGTTGAGTAGATCAAGGAACATTACCAATCCTGGTGGTGTGGAGGTGCCTG

Nipponbare GCTCCTGCACAACGGGTAGAGTTGGACTTGCACCTATCACCCACTATTGCCATACCTGC
9311 GCTCCTGCACAATGGGTAGAGTTGGACTTGCACCTATCACCCACTATTGCCATACCTGC
Pei' ai64S GCTCCTGCACAACGGGTAGAGTTGGACTTGCATCTATCACCCACTATTGCCATACCTGC

Nipponbare TGATGTCAAATGGTGC GGGCG-----GTGGCGGTACAGTTTACTGGGAAGCATGT
9311 TGATGTCAAATGGTGC GGGCGGGCGGGCGGGCGGTGGCGGTACAGTTTACTGGGAAGCATGT
Pei' ai64S TGATGTCAAATGGTGC GGGCGGGCGGGCGGGCGGTGGCGGTACAGTTTACTGGGAAGCATGT

Nipponbare GCTGGCAGCTACGGATGTAATTTCAAGGAGGAAGGCTGCCCTGGCACAGTTTGTCTCGC
9311 GTTGGCAGCTACGGATGTAATTTCAAGGAGGAAGGCTGCCCGGCACAGTTTGTCTCGC
Pei' ai64S GCTGGCAGCTACGGATGTAATTTCAAGGAGGAAGGCTGCCCGGCACAGTTTGTCTCGC
* *****

Nipponbare TGT TTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGGTTCGATTCCAATGGT
9311 TGT TTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGGTTCGATTCCAATGGT
Pei' ai64S TGT TTTTCTTTCTCAGTCGCGCTTTGAGTTCAGGCTTCGCTTGGTTCGATTCCAATGGT

Nipponbare TTTTATGGTGTCTCCGACCGTCCAGGAAGCTGCTTGGCAATCGCCGACCAGCTGTTC
9311 TTTTACGGTGTCTCCGACCGTCCAGGAAGCGCTTGGCAATCGCCGACCAGCTGTTC
Pei' ai64S TTTTATGGTGTCTCCGACCGTCCAGGAAGCTGCTTGGCAATCGCCGACCAGCTGTTC

Nipponbare CATAAGTTGGTGTGCTTCGATCAGCATCCTGTCTTCTTCTGTCCAGATGTCTTCT
9311 CATAAGTTGGTGTGCTTCGATCAGCATCCTGTCTTCTTCTTCTGTCCAGATGTCTTCT
Pei' ai64S CATAAGTTGGTGTGCTTCGATCAGCATCCTGTCTTCTTCTTCTGTCCAGATGTCTTCT

Nipponbare GCAGTGTAAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA
9311 GCAGTGTAAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA
Pei' ai64S GCAGTGTAAATCGCATTGCAATTTATTAATTTGGAAGCATCCATATGATCAACAGCATA

Nipponbare AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTAGATTGTATCCATT
9311 AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTAGATTGTATCCATT
Pei' ai64S AGGCTATTAAGGTCAATGTACCATTAAGAAAATCAGTGAATTTAGATTGTATCCATT

Nipponbare AAGAAAAAGGAATCCACGGATTCCACTTAAATGGTTTTAATTTGAGCACATTTATTGA
9311 AAGAAAAAGGAATCCACGGATTCCACTTAAATGGTTTTAATTTGAGCACATTTATTGA
Pei' ai64S AAGAAAAAGGAATCCACGGATTCCACTTAAATGGTTTTAATTTGAGCACATTTATTGA

Nipponbare GAAATAAAGCATATATACATAGATATGATAATTAACATATACCATTTTGTACAGGGTG
9311 GAAATAAAGCATATATACATAGATATGATAATTAACATATACCATTTTGTACAGGGTG
Pei' ai64S GAAATAAAGCATATATACATAGATATGATAATTAACATATACCATTTTGTACAGGGTG

Nipponbare CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA
9311 CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA
Pei' ai64S CCACCAAATAATGTTAGTGATTACTCTAGTGACAAATAAAGAAGATATTGTACCTAGTAA

Nipponbare AATGTAAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGCATACACATTTTGG
9311 AATGTAAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGCATACACATTTTGG
Pei' ai64S AATGTAAAGCAATATATAAAAACATAGGATTGGGACTGATAAGTGCATACACATTTTGG

Nipponbare ACTAATAAGTGCTAAAACATTGAGCTTAATTTGCATATACAACAATGATTA AAAACACA
9311 ACTAATAAGTGCTAAAACATTGAGCTTAATTTGCATATACAACAATGATTA AAAACACA
Pei' ai64S ACTAATAAGTGCTAAAACATTGAGCTTAATTTGCATATACAACAATGATTA AAAACACA

Nipponbare AATAAACTTGGTGGACTACTGTCCAGAGTAGTCTTTCCTAGGACTACAATAATGTGTG
9311 AATAAACTTGGTGGACTACTGTCCAGAGTAGTCTTTCCTAGGACTACAATAATGTGTG
Pei' ai64S AATAAACTTGGTGGACTACTGTCCAGAGTAGTCTTTCCTAGGACTACAATAATGTGTG
***** *****

Nipponbare GGATCCATTAATGGCCCTAGCGAAGAAATTCCTACATTTATTA ACTAGAATAAAAGACAT
9311 GGATCCATTAATGGCCCTAGCGAAGAAATTCCTACATTTATTA ACTAGAATAAAAGACAT
Pei' ai64S GGATCCATTAATGGCCCTAGCGAAGAAATTCCTACATTTATTA ACTAGAATAAAAGACAT

Nipponbare GCAACATGACTAACTAATTACTCAAATAATCGGCTCCCGTTAATGTTGAATATTATGAA
9311 GCAACATGACTAACTAATTACTCAAATAATCGGCTCCCGTTAATGTTGAATATTATGAA
Pei' ai64S GCAACATGACTAACTAATTACTCAAATAATCGGCTCCCGTTAATGTTGAATATTATGAA

Nipponbare ATCTGTACCATTTTCACGTAATCTGAAAATAAACTCCACCTCTAAAATTGCACAGAGAA
9311 ATTTGTACCATTTTCACGTAATCTGAAAATAAACTCCACCTCTAAAATTGCACAGAGAA
Pei' ai64S ATTTGTACCATTTTCACGTAATCTGAAAATAAACTCCACCTCTAAAATTGCACAGAGAA

** *****

Nipponbare AGAACTAGGATCCCTTAGATCTACACATATAACCGAAGGAATATAGCAAGATACAGACCT
9311 AGAACTAGGATCCCTTAGATCTACACATATAACCGAAGGAATATAGCAAGATACAGACCT
Pei' ai64S AGAACTAGGATCCCTTAGATATAACCGAAGGAATATAGCAAGATACAGACCT

Nipponbare TGATGTCGGGTGCAGATGGTTGGTCCATCTCTCGCGGCACTGCTTCCCAACCCGACCTG
9311 TGATGTCGGGTGCAGATGGTTGGTCCATCTCTCGCGGCACTGCTTCCCAACCCGACCTG
Pei' ai64S TGATGTCGGGTGCAGATGGTTGGTCCATCTCTCGCGGCACTGCTTCCCAACCCGACCTG

Nipponbare GGAGGCTCTTTGCAATCTCTGCCCACTTGGATCTCCATGGTGTCTCACCATTGCTTAA
9311 GGAGGCTCTTTGCAATCTCTGCCCACTTGGATCTCCATGGTGTCTCACCATTGCTTCA
Pei' ai64S GGAGGCTCTTTGCAATCTCTGCCCACTTGGATCTCCATGGTGTCTCACCATTGCTTAA

Nipponbare GAACTCTATAATCAAAGAACAACAATAGTTCAAGATCTCATCACAAGATTGAAGAGA
9311 GAACTCTATAATCAAAGAACAACAATAGTTCAAGATCTCATCACAAGATTGAAGATA
Pei' ai64S GAACTCTATAATCAAAGAACAACAATAGTTCAAGATCTCATCACAAGATTGAAGAGA

Nipponbare TGCCAAGAAACAAGAATTAATACTGATTAGAAGTAGACAGATCTGCACTTACTCATCC
9311 TGCCAAGAAACAAGAATTAATACTGATTAGAAGTAGACAGATCTATCACTTACTCATCC
Pei' ai64S TGCCAAGAAACAAGAATTAATACTGATTAGAAGTAGACAGATCTGCACTTACTCATCC

Nipponbare TCTTCCCTTGTCACCCTCCTTTGACCAACCCTGGGTTGTCGTTGCTACCTGCAGCTTGC
9311 TCTTCCCTTGTCACCCTCCTTTGACCAACCCTGGGTTGTCGTTGCTACCTGCAGCTTGC
Pei' ai64S TCTTCCCTTGTCACCCTCCTTTGACCAACCCTGGGTTGTCGTTGCTACCTGCAGCTTGC

Nipponbare GTCTGCTGTTGTTGAGGCACCATCGTAGCACCTACTGGAAAGGCAACAACCGAGTTGTAA
9311 GTCTGCTGTTGTTGAGGCACCATCGTAGCACCTACTGGAAAGGCAACAACCGAGTTGTAA

```

Pei' ai64S      GTCTGCTGTTGTTGAGGCACCATCGTAGCACCTACTGGAAAGGCAACAACCGAGTTGTAA
*****

Nipponbare     CTAGCGGTTGTCAGGCCCTCCTTTGGCATTAGAGAGCTTGACGTAGCCATGCCTATGCTA
9311           CTAGCGGTTGTCAGGCCCTCCTTTGGCATTAGAGAGCTTGACGTAGCCATGCCTATGCTA
Pei' ai64S     CTAGCGGTTGTCAGGCCCTCCTTTGGCATTAGAGAGCTTGACGTAGCCATGCCTATGCTA
*****

Nipponbare     GAAACAGGGCACCTAAGTCGGGGACCCACGGTGATTGGAGCACCACGAGTGTTCGTG
9311           GAAACAGGGCACCTAAGTCGGGGACCCACGGTGATTGGAGCACCACGAGTGTTCGTG
Pei' ai64S     GAAACAGGGCACCTAAGTCGGGGACCCACGGTGATTGGAGCACCACGAGTGTTCGTG
*****

Nipponbare     TGGCAAGTACCACCATGGCTAGAGCTCGGAAGGTGCCAATCCGACACCCCGTCGGCCACC
9311           TGGCAAGTACCACCATGGCTAGAGCTCGGAAGGTGCCAATCCGACACCCCGTCGGCCACC
Pei' ai64S     TGGCAAGTACCACCATGGCTAGAGCTCGGAAGGTGCCAATCCGACACCCCGTCGGCCACC
*****

Nipponbare     TTCCTAACTCCTGGTTGAGGAAGGAGTTACCTGCAGCCGCATGATTCACCTTCCAAGG
9311           TTCCTAACTCCTGGTTGAGGAAGGAGTTACCTGCAGCCGCATGATTCACCTTCCAAGG
Pei' ai64S     TTCCTAACTCCTGGTTGAGGAAGGAGTTACCTGCAGCCGCATGATTCACCTTCCAAGG
*****

Nipponbare     AAAGAAGCAACGAAAGAATTGCCGAGGATTGGGGAGGCAAATCGACCTCAATATGGAGG
9311           AAAGAAGCAACGAAAGAATTGCCGAGGATTGGGGAGGCAAATCGACCTCGATATGGAGG
Pei' ai64S     AAAGAAGCAACGAAAGAATTGCCGAGGATTGGGGAGGCAAATCGACCTCGATATGGAGG
*****

Nipponbare     AAATTGAGAAGGGGATTGTCTAGTGTGGAGATGGGGACTCAAGTCCC
9311           AAATTGAGAAGGGGATTGTCTAGTGTGGAGATGGGGACTCAAGTCCC
Pei' ai64S     AAATTGAGAAGGGGATTGTCTAGTGTGGAGATGGG---TCA-----
*****

```

Note: 29 differences of single nucleotide polymorphisms were detected among Pei'ai64S, 9311 and Nipponbare.

Supplementary Data 4 Multiple DNA sequence alignment for LOC_Os07g12240 in Pei'ai64S, 9311, and Nipponbare

Sequence 1: Nipponbare 564 bp
Sequence 2: 9311 564 bp
Sequence 3: Pei'ai64S 822 bp

CLUSTAL W (1.81) multiple sequence alignment

```
Nipponbare -----  
Pei'ai64S  GGATCTATGTCAGCTATATATACAGGCTATTTGCATGTAAGTTGAGATGTTCTTTGAGT  
9311 -----
```

```
Nipponbare -----  
Pei'ai64S  AAGCACTTCAATAAGGTACTGGATTTCAATTGCTGTTCAATTTGCTGCATTTCACACAA  
9311 -----
```

```
Nipponbare -----ATGGATCACAACATCCTAATCCACTGGTGCATCCCT  
Pei'ai64S  AGATATATAGTGGTGATGATGATGGATCACAACATCCTAATCCACTGGTGCATCCCT  
9311 -----ATGGATCACAACATCCTAATCCACTGGTGCATCCCT  
*****
```

```
Nipponbare  CATGATGTTGGTACTGGGACCATTGATCATAGATGTGATTCGGTAAGTAATAAGATTGG  
Pei'ai64S  CATGATGTTGGTACTGGGACCATTGATCATAGATGTGATTCGGTAAGTAATAAGATTGG  
9311  CATGATGTTGGTACTGGGACCATTGATCATAGATGTGATTCGGTAAGTAAGAAAGATTGG  
*****
```

```
Nipponbare  AAGGTTATTTAGCGCAATTGCAAGGTTCTTAGCGCATGACGATAGTGTATCAACTCTAT  
Pei'ai64S  AAGGTTATTTAGCGCAATTGCAAGGTTCTTAGCGCATGACGATAGTGTATCAACTCTAT  
9311  AAGGTTATTTAGCGCAATTGCAAGGTTCTTAGCGCATGACGATAGTGTATCAACTCTAT  
*****
```

```
Nipponbare  GGTCGTGGACAACGACCTCCTCCTTCTTCGCAGTTGCTTGAGGAGGGGTGCATGCTT  
Pei'ai64S  GGTCGTGGACAACGACCTCCTCCTTCTTCGCAGTTGCTTGAGGAGGGGTGCATGCTT  
9311  GATCGTGGACAACGACCTCCACCTTCTTACAGTTGCTTGAGGAGGGGTGCATGCTG  
* *****
```

```
Nipponbare  TGATGCAATGACTGTCACAACGAGGTTAGGCCTCAGGTGGCAAAGGAGTGGGAGGCCGC  
Pei'ai64S  TGATGCAATGACTGTCACAACGAGGTTAGGCCTCAGGTGGCAAAGGAGTGGGAGGCCGC  
9311  TGATGCAATGGCTGTACAACGAGGTTAGGCCTCAGGTGGCGAAGGAGTGGGAGGCTGC  
*****
```

```
Nipponbare  CATGGAGTGCCAAGGGTGTGACATCCCTATGGATGCTACCGTGGATGAGCTGTTGGATAG
```

Pei' ai64S	CATGGAGTGCCAAGGGTGTGACATCCCTATGGATGCTACCGTGGATGAGCTGTTGGATAG
9311	CATGGAGTGCCAAGGGTGTGACATCCCTATGGATGCTACTGTGGATGAGCTGTTGGATAG

Nipponbare	GAAGATGGCGAGCGAGGGTGAAGCTTAAGGATGCCTTTTATGTGTTTCGATCGCAATGAGGA
Pei' ai64S	GAAGATGGCGAGCGAGGGTGAAGCTTAAGGATGCCTTTTATGTGTTTCGATCGCAATGAGGA
9311	GAAGATGGCGAGCGAGGATGAGCTTAAGGATGCCTTCTATGTGTTTCGATCGCAATGAGGA

Nipponbare	TGGCTTCATATGTGCCTCGGAACGTGGAGCGTGATGAGGAGGCTAGGGTTCAAAGAAGG
Pei' ai64S	TGGCTTCATATGTGCCTCGGAACGTGGAGCGTGATGAGGAGGCTAGGGTTCAAAGAAGG
9311	TGGCTTCATATGCGCCTCGGAACCTGGAGCGTGATGAGGAGGCTAGGGTTCAAAGAAGG

Nipponbare	GCAAAGGTATGAGGACTGTATGAGGATGATCCACACCTTCGATGAGGACAGAGATGGGAG
Pei' ai64S	GCAAAGGTATGAGGACTGTATGAGGATGATCCACACCTTCGATGAGGACAGAGATGGGAG
9311	GCAAAGATATGAGGACTGTATGAGGATGATCCACACCTTCGATGAGGACAGAGATGGGAG

Nipponbare	GATCAGCTACTTAGAATTTAGAAGGATGATGGAAGATGCAGTATAG-----
Pei' ai64S	GATCAGCTACTTAGAATTTAGAAGGATGATGGAAGATGCAGTATAGTTATTAGCTAATCT
9311	GATCAGCTACTTAGAATTTAGAAGGATGATGGAAGATGCAGTATAG-----

Nipponbare	-----
Pei' ai64S	TCCTCATTGAACCTTAATTGTCTTTCCATATTGTGGTAACATTAGTAACTTTGGAATGT
9311	-----
Nipponbare	-----
Pei' ai64S	GATGTTACATTAGACATTCTTGAATAACATGTTGGTTGTGA
9311	-----

Note: the LOC_Os07g12240 sequence of Peiai 64S is identical to that of Nipponbare. However, there are 13 single nucleotide polymorphisms between Pei'ai64S and 9311.