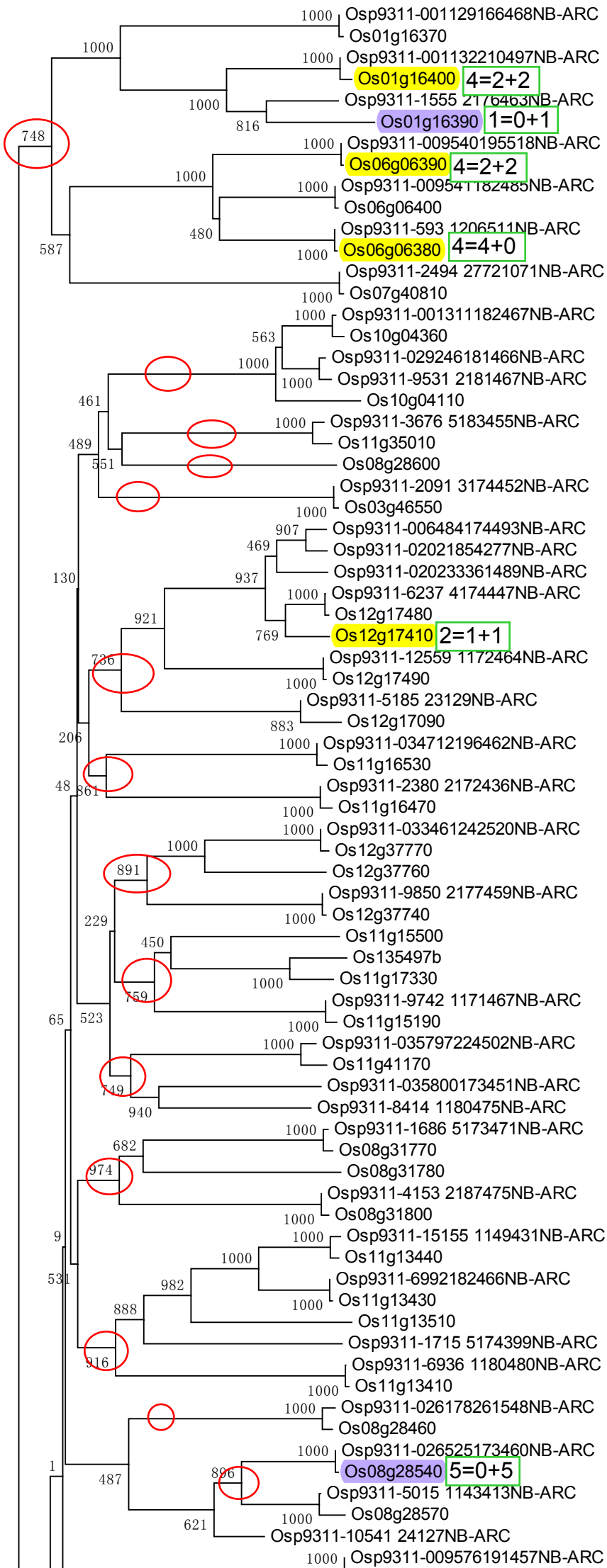
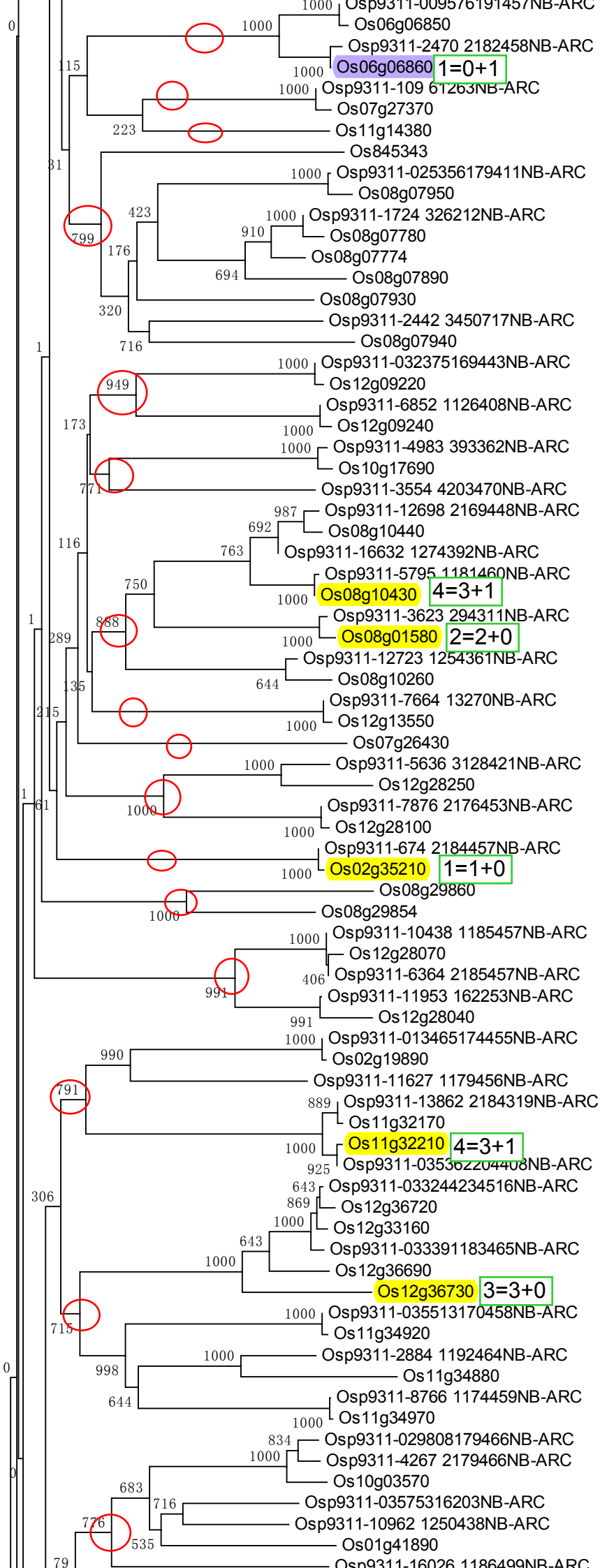


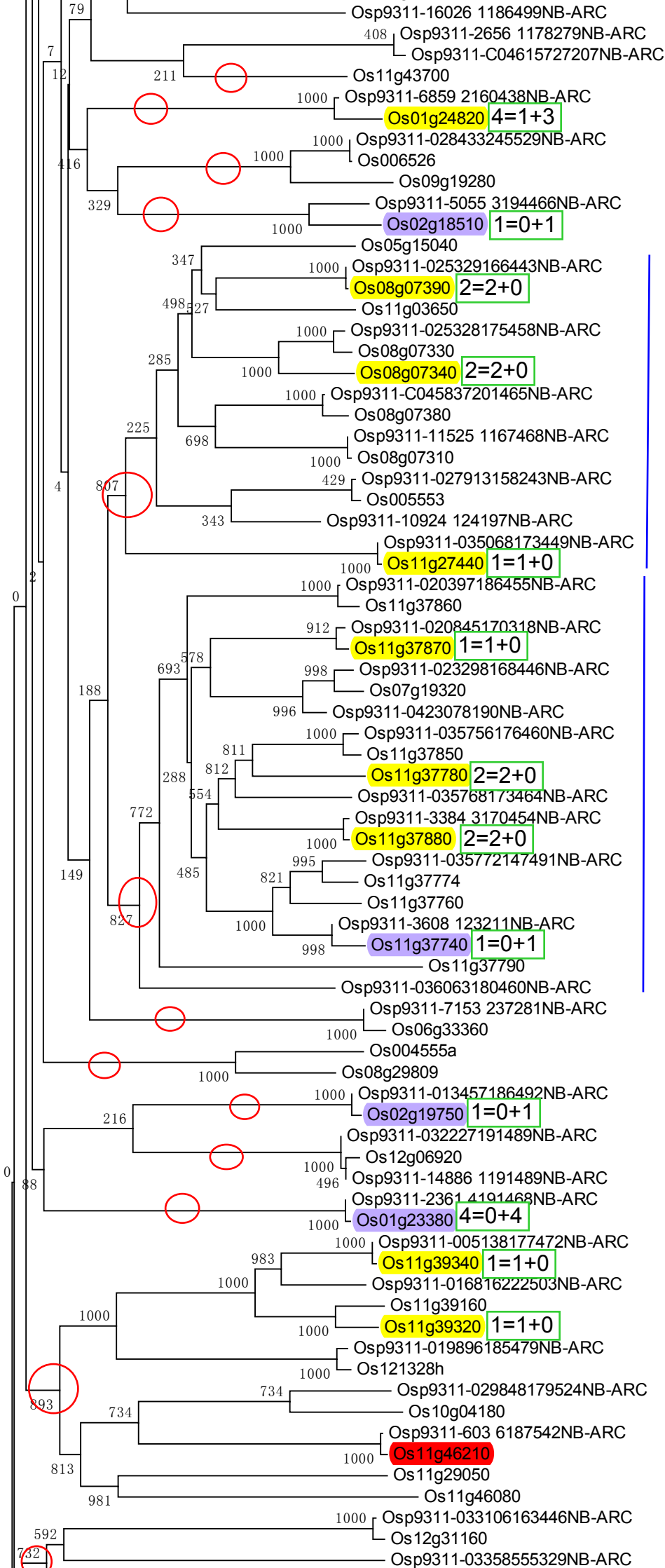
Figure S1. Phylogenetic tree of 937 *NBS-LRR* genes from two cultivars (Nipponbare and 9311 of *Oryza sativa*) based on NBS domains. The tree was determined by the bootstrap NJ method with p-distance model by MEGA v5.02. The stability of internal branches was assessed by bootstrap analysis with 1,000 replicates. Clades are defined as these branches with >70% bootstrap values and at the first layer from the root. A clade can have one or more branches that also have >70% bootstrap values. The total numbers of clades, the 96 single-copy and 115 multi-copy clades, were counted only for Nipponbare; 9311 unique clades (64) were excluded. A multi-copy clade has at least two or more genes from one genome. Clades 1-10 indicated with blue-colors correspond to those in Supplementary Table 9. Red circles denote single- or multi-copy clades. Yellow or purple shadows denote that the cloned genes in this branch are all identified as resistant in this study, and purple shadows denote that the cloned genes in this branch are all identified as susceptible. The numbers in the green square box at each locus denote the total number of cloned genes, the sum of resistant and moderately resistant genes, and the number of susceptible genes. The red shadows indicate that resistant blast *R*-gene(s) have been reported previously in those branches.



Clade 1 in Table S9



Clade 2 in Table S9

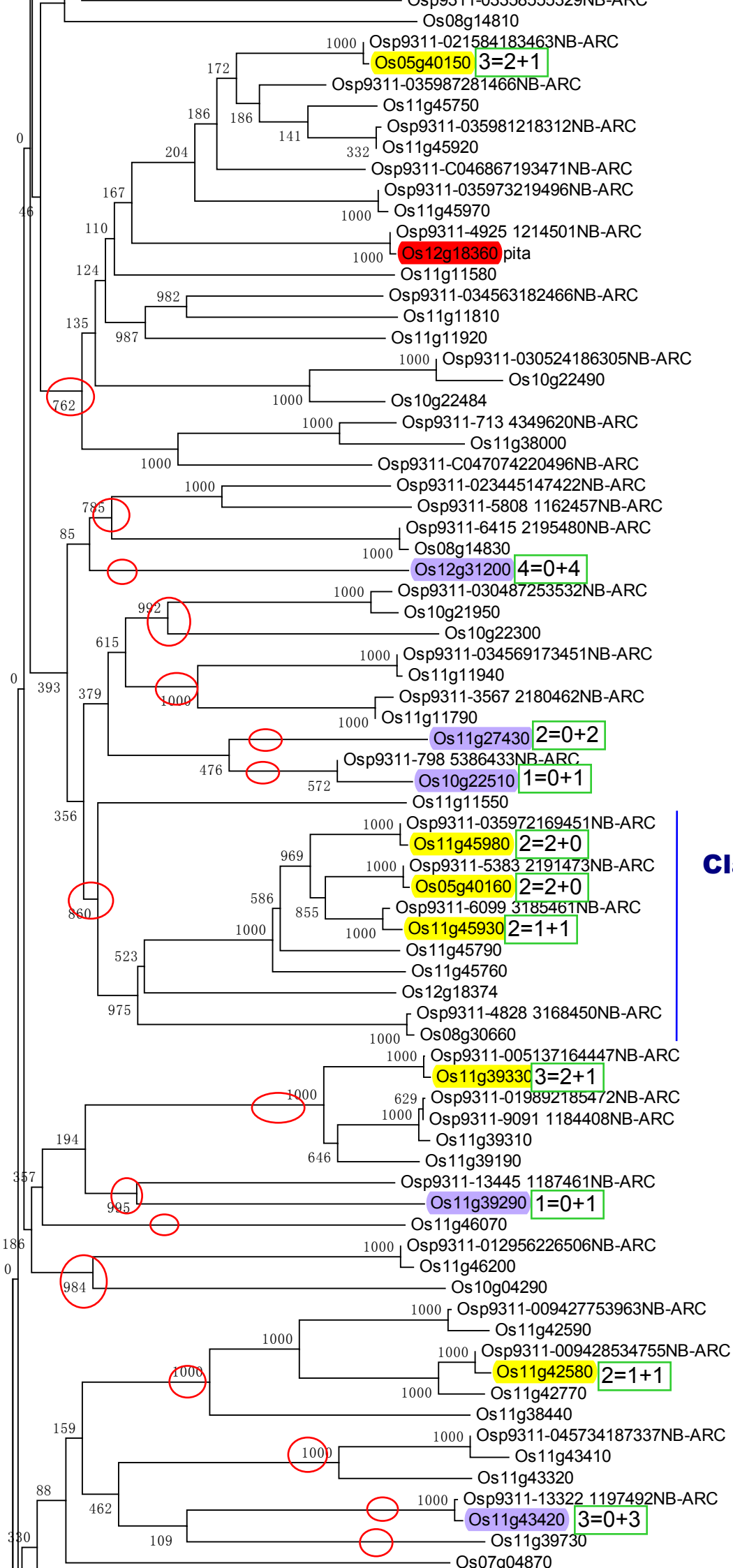


Clade 3 in Table S9

Clade 4 in Table S9

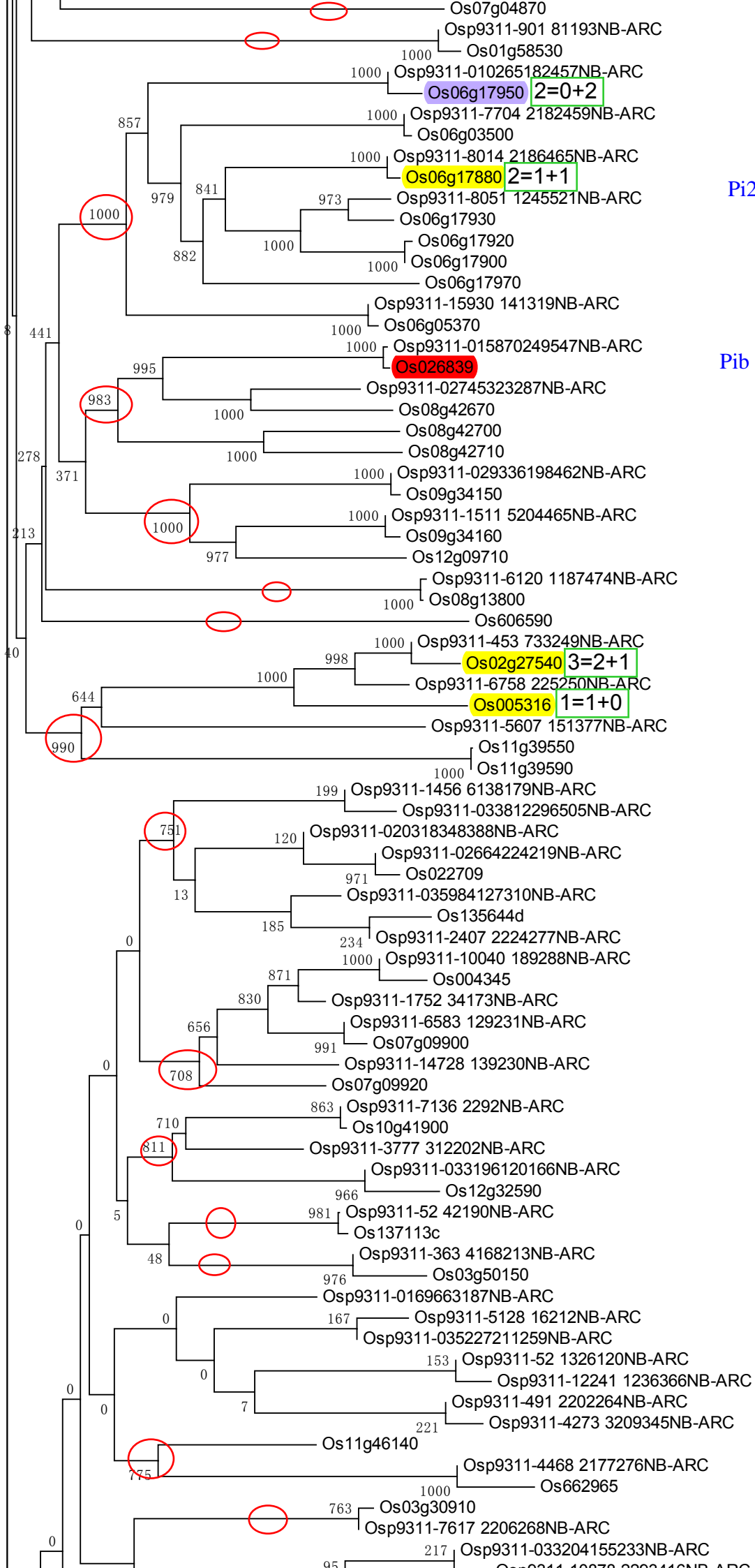
Pik, Pikm, Pikh loci (clade)

(3)



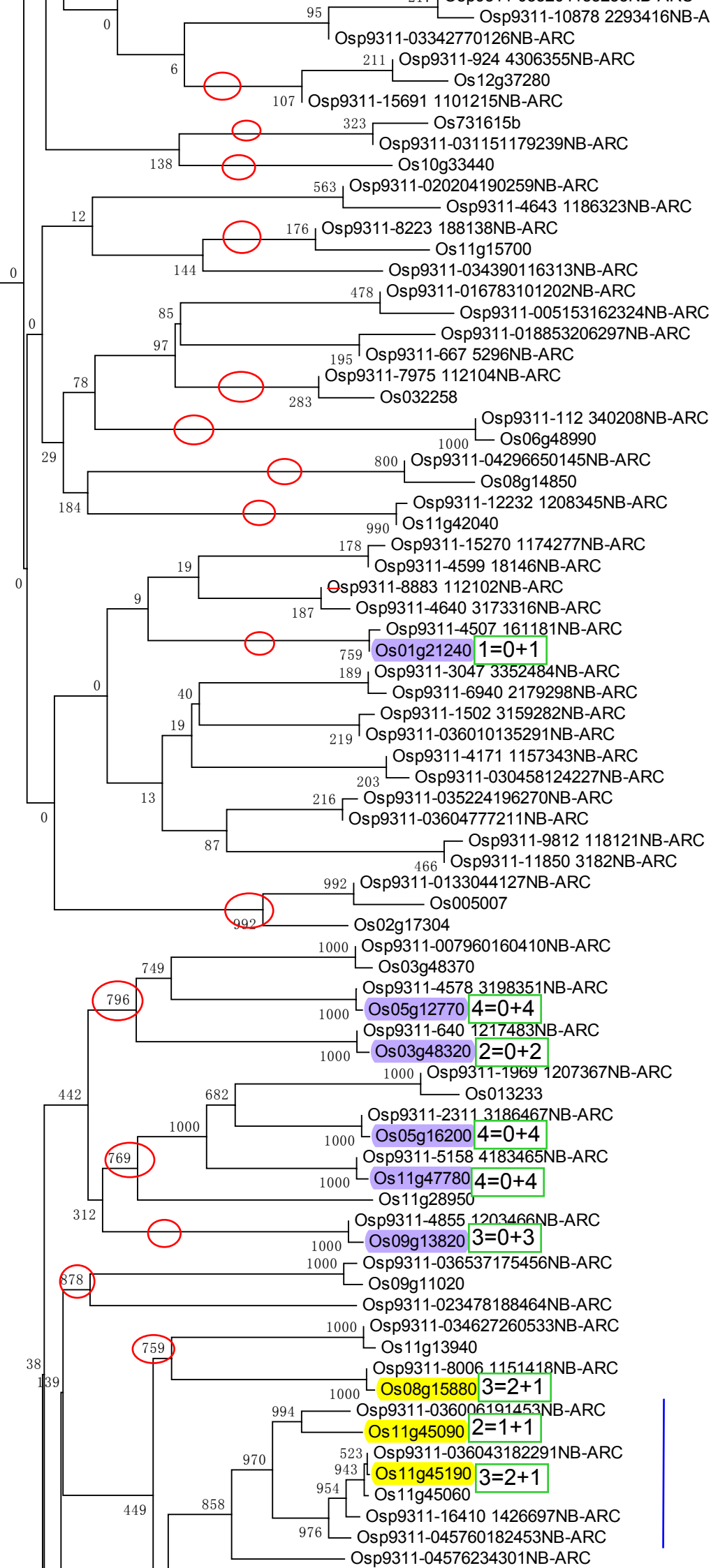
Pita locus
(1)

Clade 5 in Table S9



Pi2, Pi9, Piz-t, Pi50(t) loci (clade)
(4)

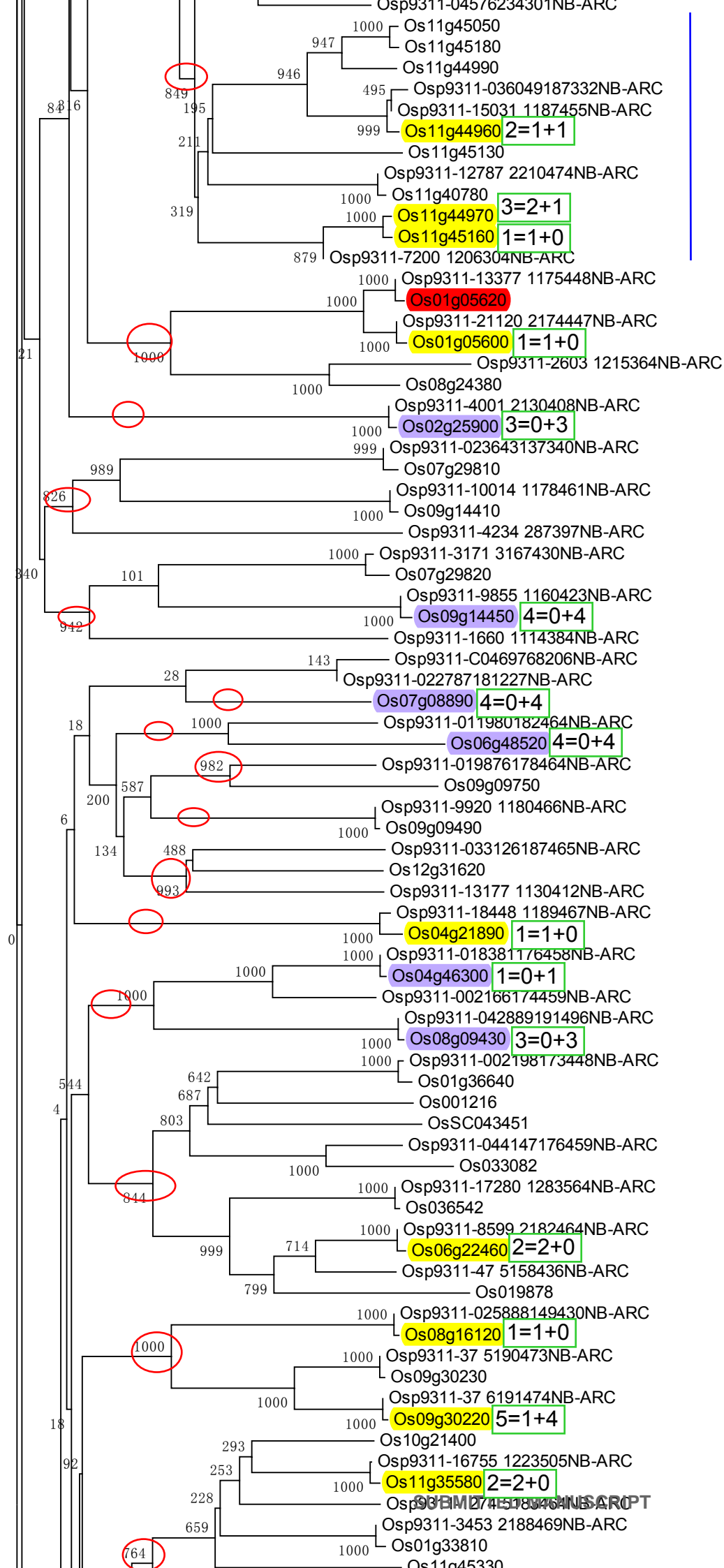
Pib locus (clade)
(1)



AC134922 locus

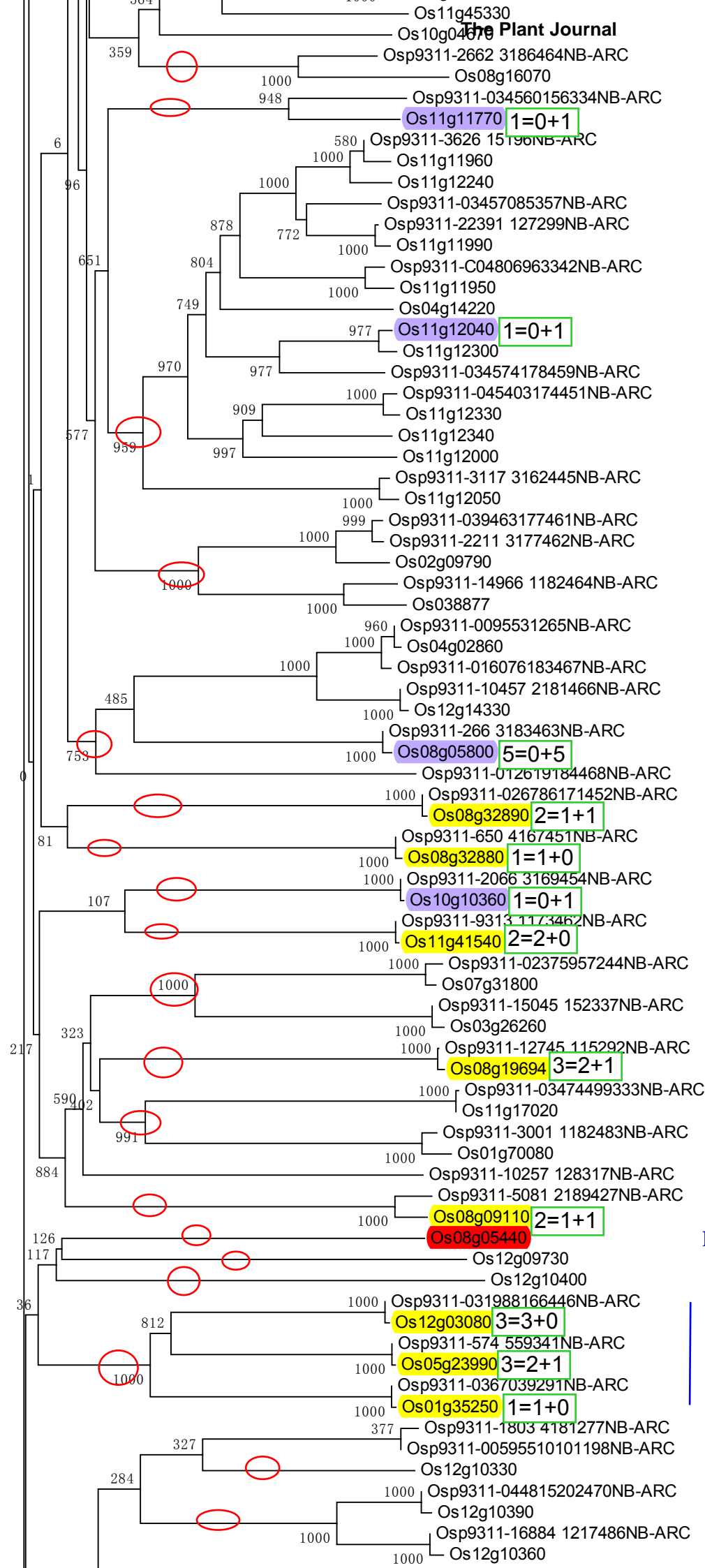
(6)

Clade 6 in Table S9



Pit locus (clade)
(1)

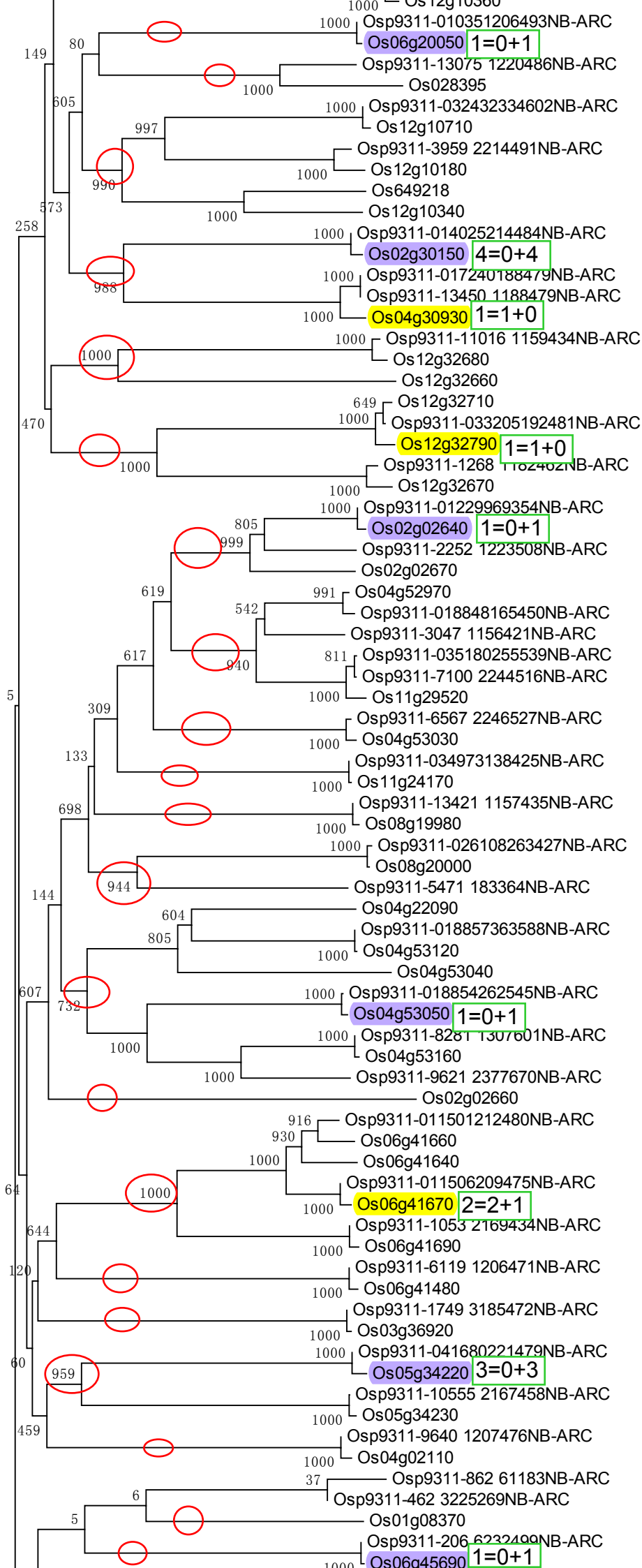
Pd3 locus (clade)
(1)

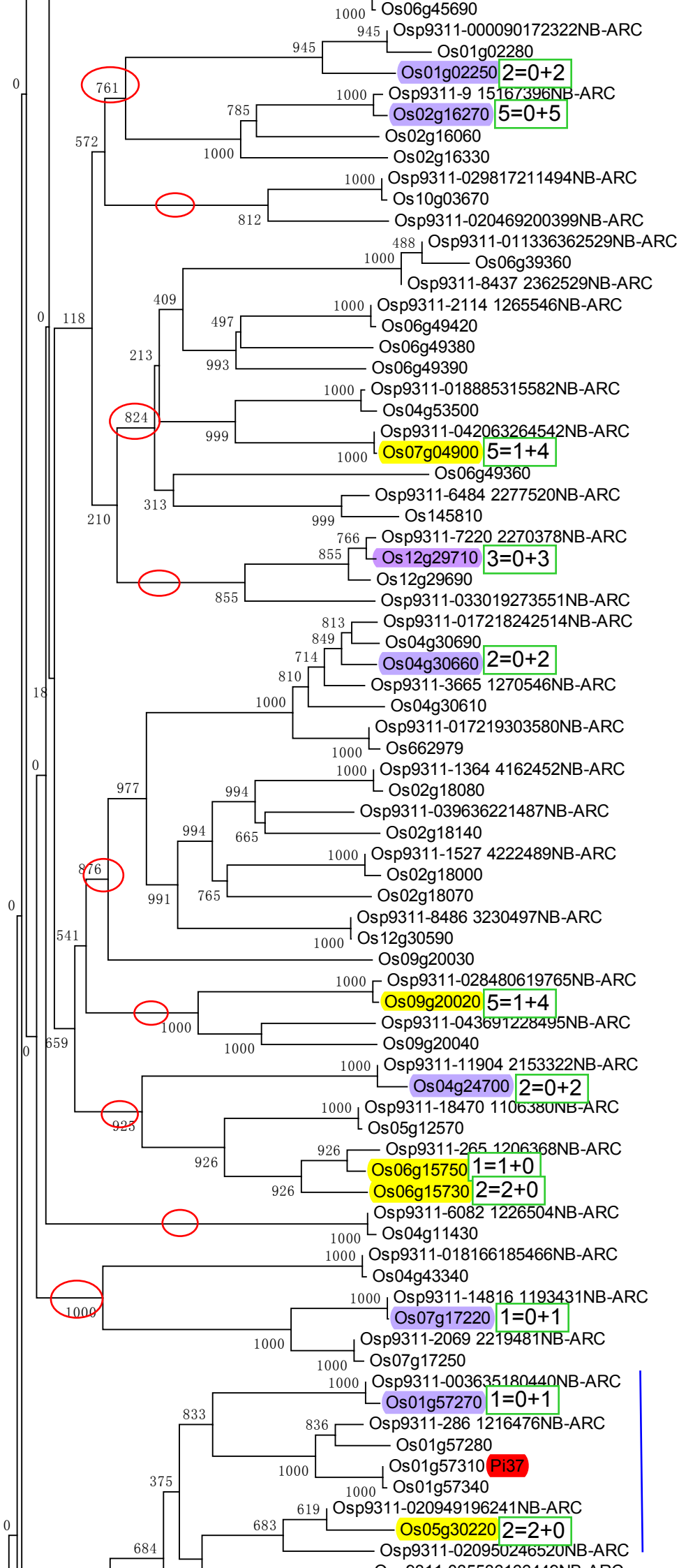


Pi36 locus (clade)
(1)

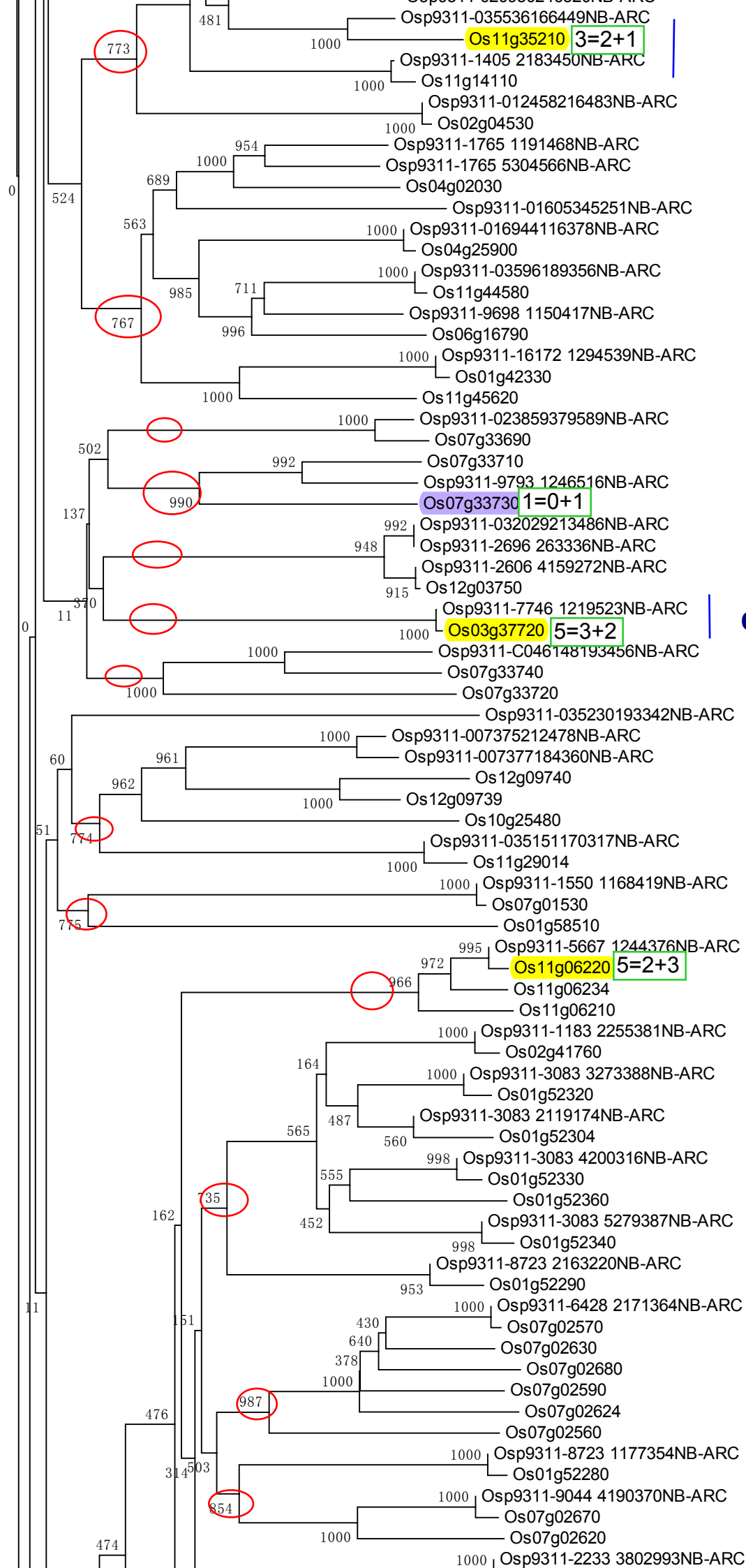
Rp3/Pc locus (4)

Clade 7 in Table S9

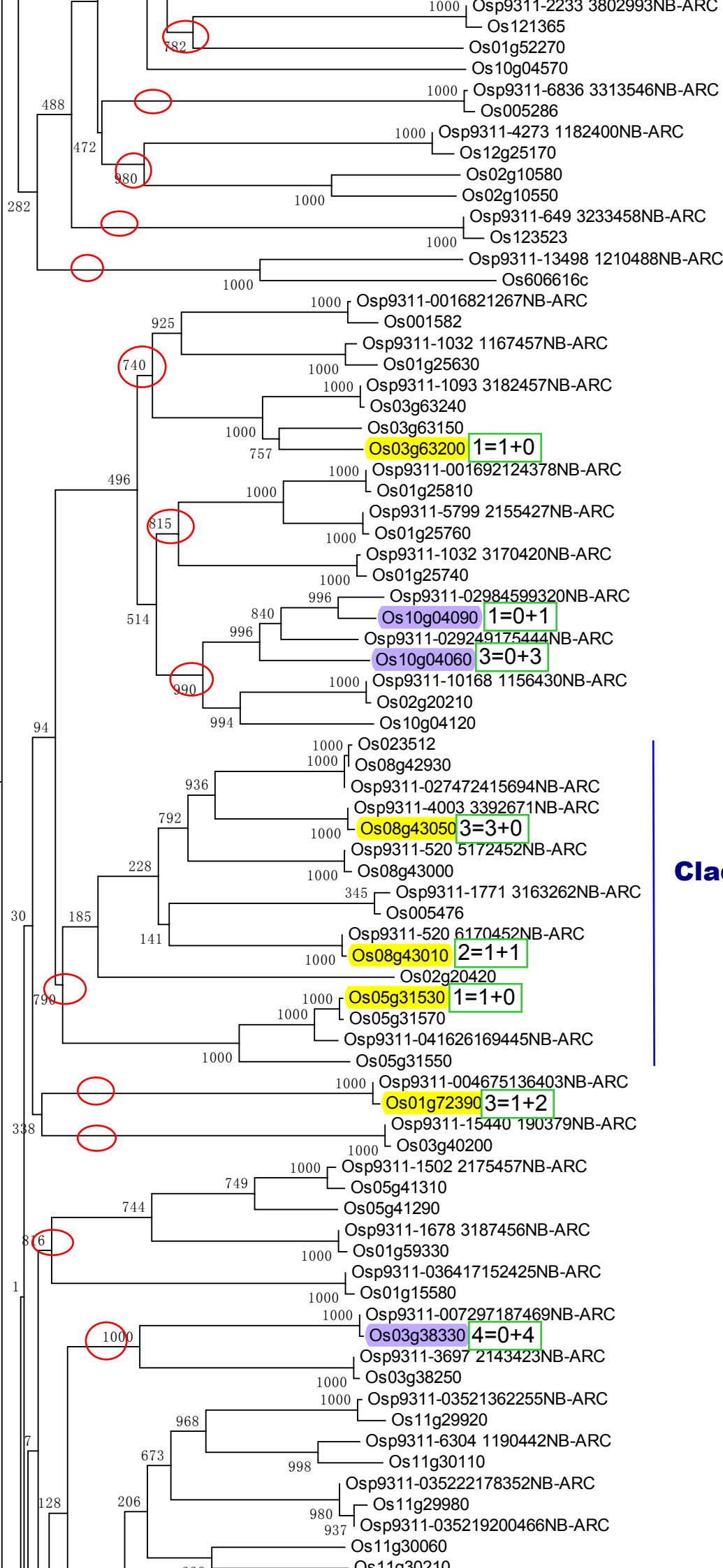




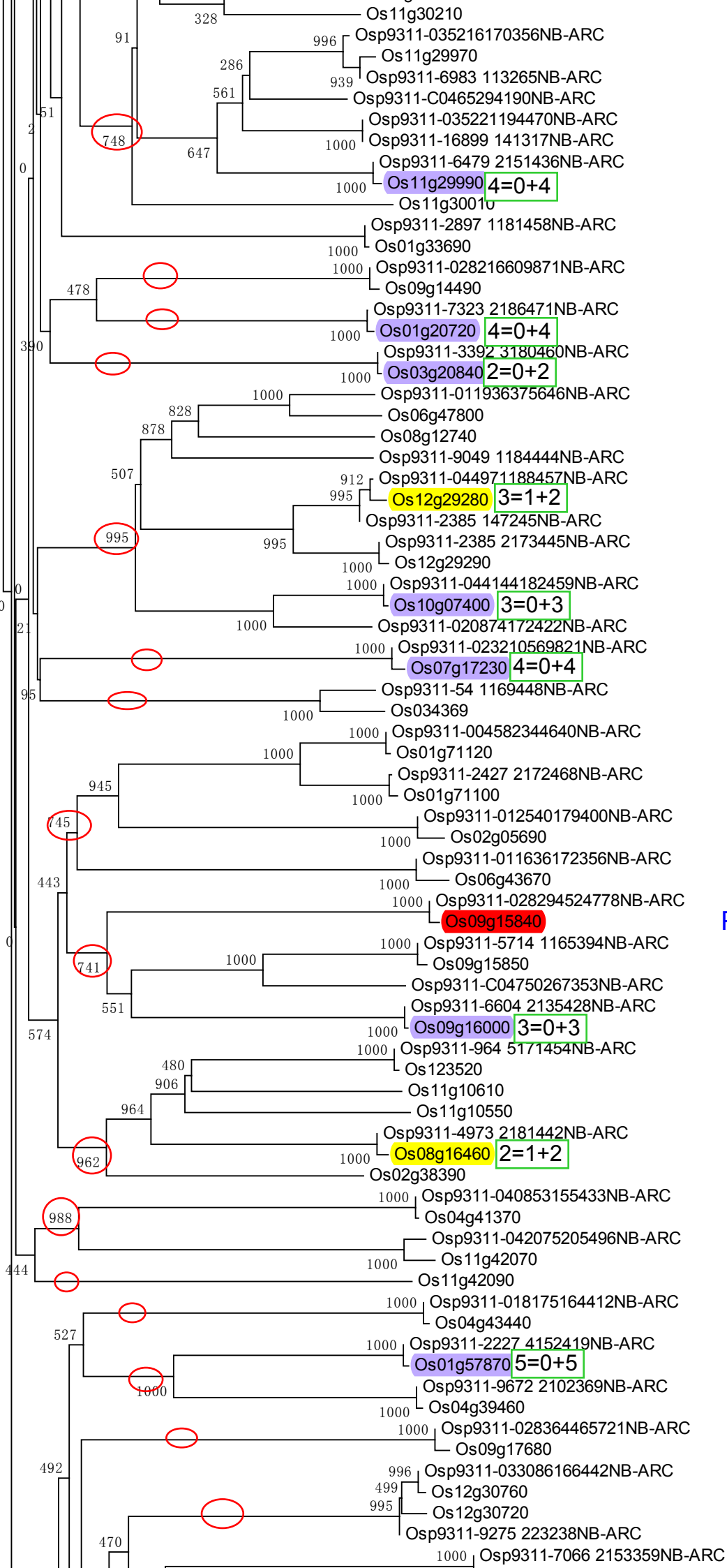
Rp1/Pi37 locus (4)
Clade 8 in Table S9



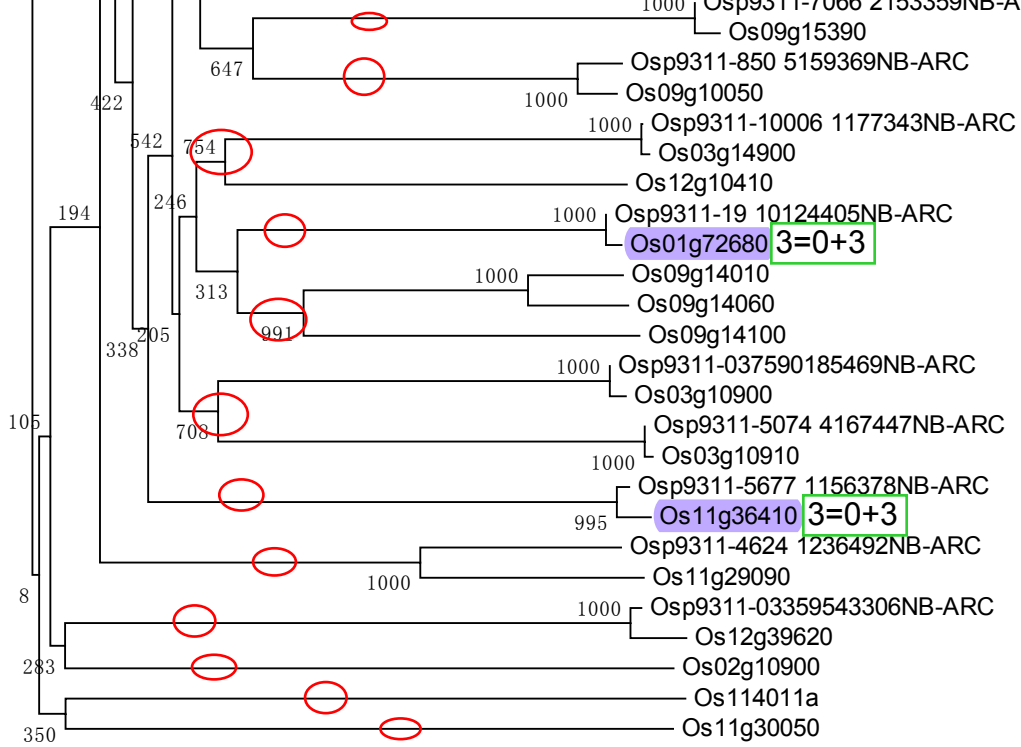
Clade 9 in Table S9



Clade 10 in Table S9

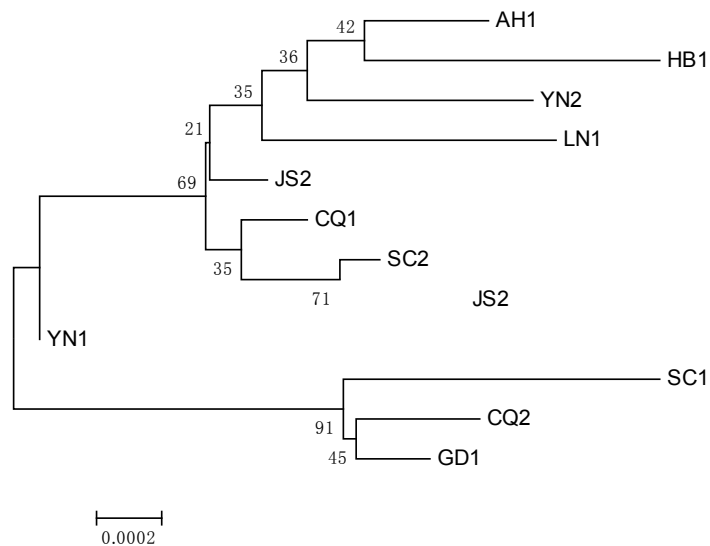


Pi5 locus
(1)



0.1

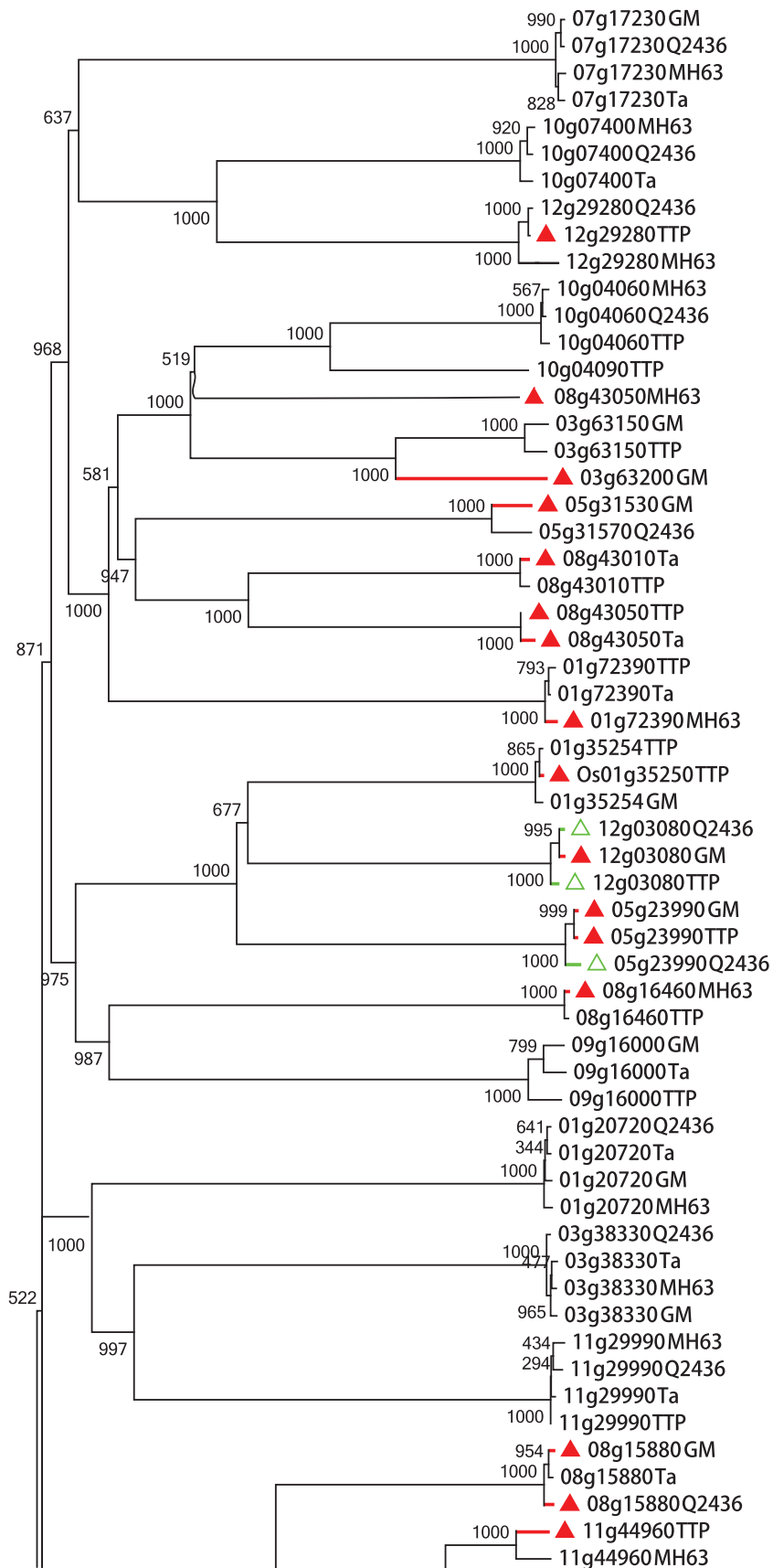
Figure S3. Phylogenetic tree of 12 rice blast strains constructed by nucleotide sequences from 11 loci, including six *Avr* genes (*Avr-pita*, *Avr-pia*, *Avr-pik*, *Avr-pii*, *Avr-pwl2* and *Avr-Ace-1*; Bohnert et al. 2004; Schneider et al. 2010; Yoshida et al. 2009; Zhou et al. 2007). The amino acid sequences were first aligned with the program MUSCLE using default options, and MEGA v5.0 was used subsequently to manually correct the alignments (Tamura et al. 2011). The resulting amino acid sequence alignments were then used to guide the alignments of the corresponding nucleotide coding sequences (CDSs). Based on the alignment results, phylogenetic trees were generated using the bootstrap Maximum Likelihood (ML) method with Kimura 2-parameter model by MEGA v5.0.2. The stability of internal nodes was assessed by bootstrap analysis with 1,000 replicates.

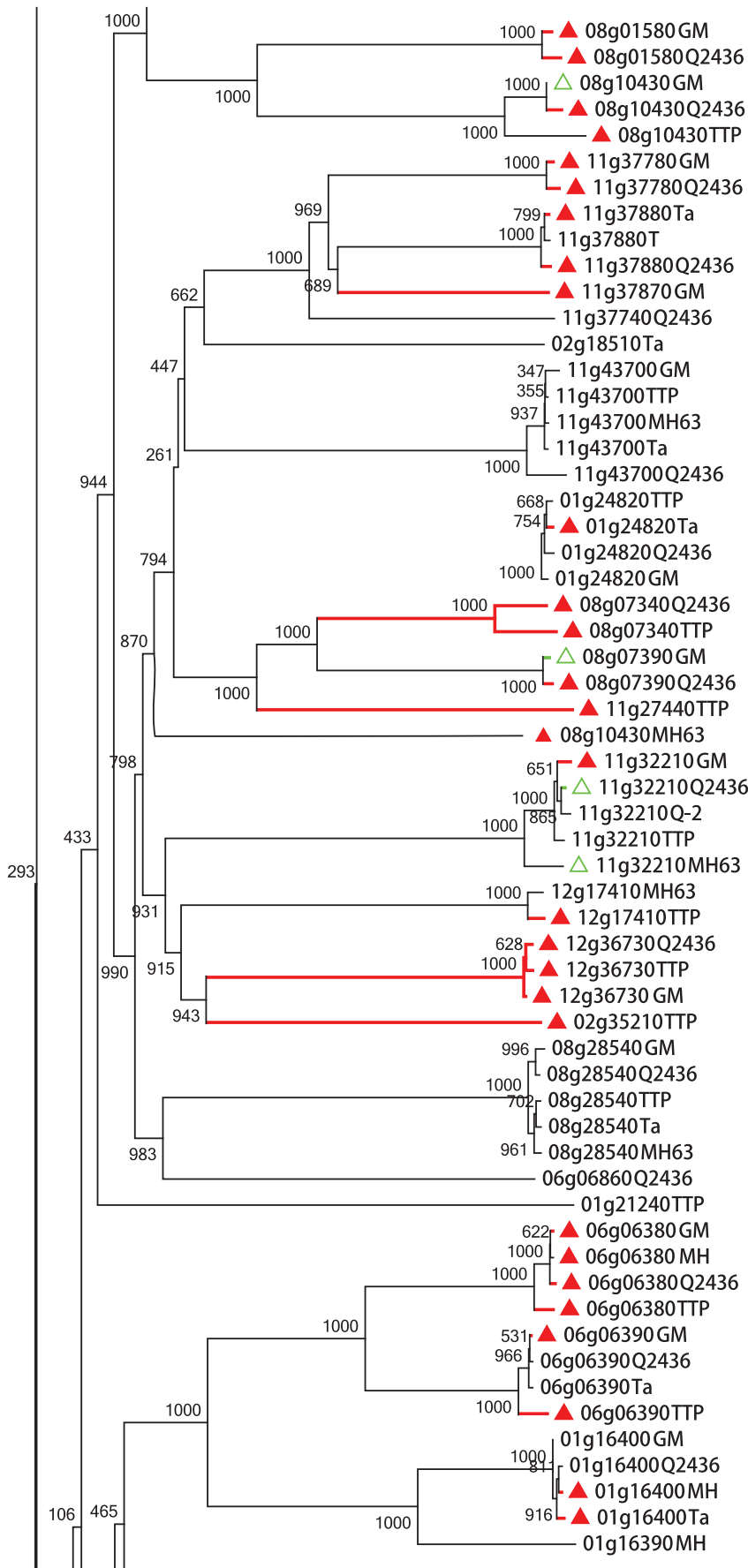


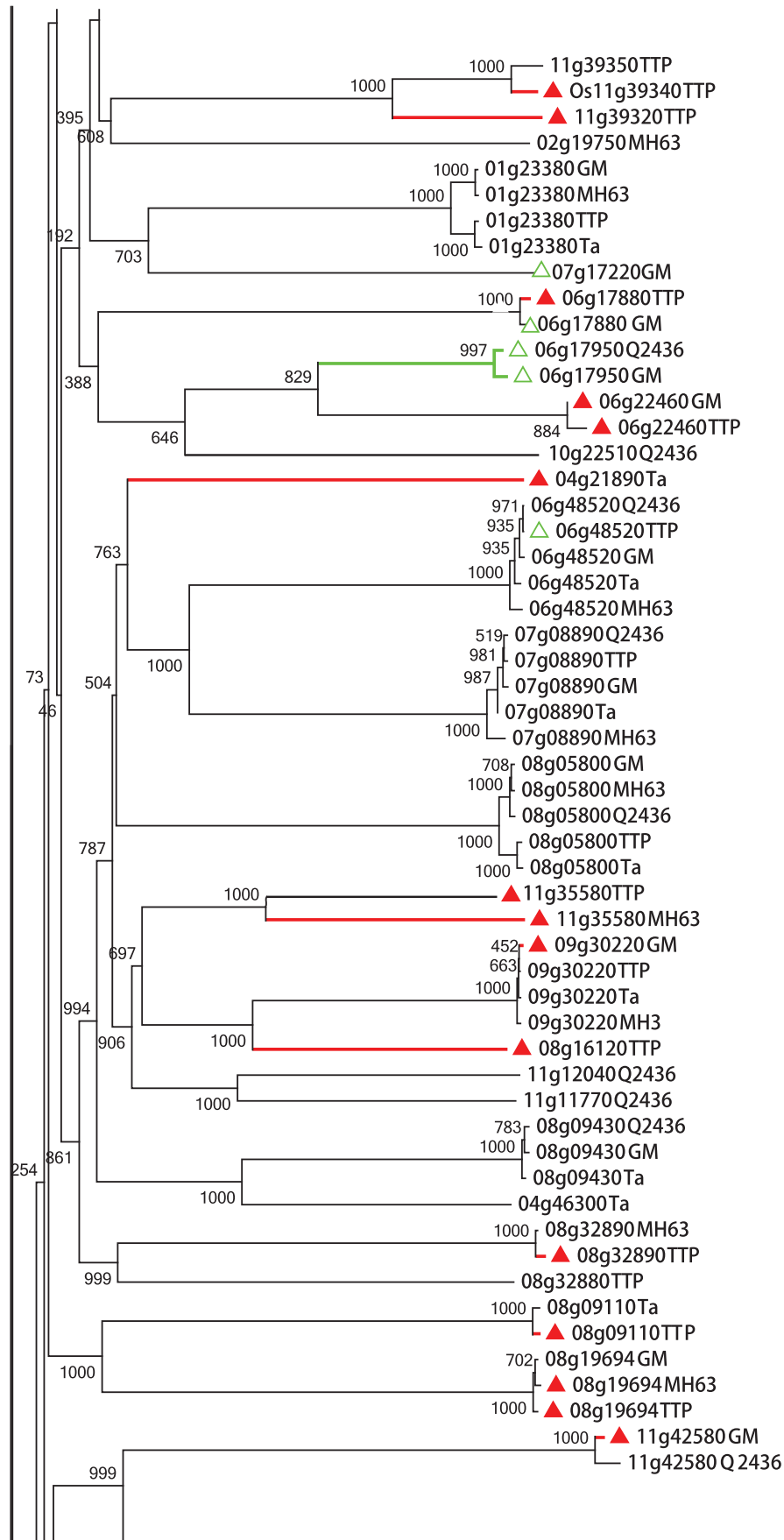
Reference

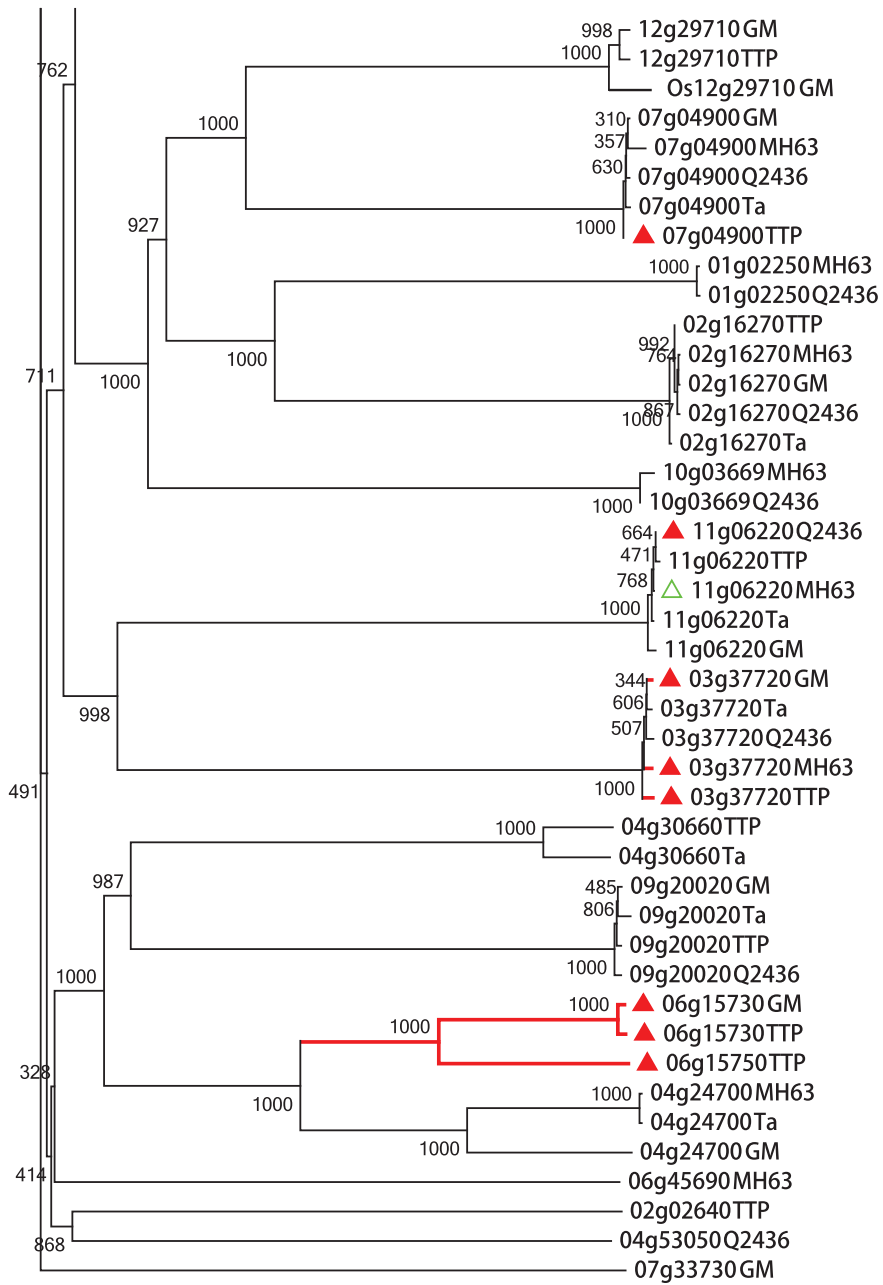
- Bohnert HU, Fudal I, Diou W, Tharreau D, Notteghem JL, et al. (2004) A putative polyketide synthase/peptide synthetase from *Magnaporthe grisea* signals pathogen attack to resistant rice. *Plant Cell* 16: 2499-2513.
- Schneider DRS, Saraiva AM, Azzoni AR, Miranda HRCAN, de Toledo MAS, et al. (2010) Overexpression and purification of PWL2D, a mutant of the effector protein PWL2 from *Magnaporthe grisea*. *Protein Expression and Purification* 74: 24-31
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, and Kumar S (2011) MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Mol Biol Evol* 28 (10): 2731-2739.
- Yoshida K, Saitoh H, Fujisawa S, Kanzaki H, Matsumura H, et al. (2009) Association genetics reveals three novel avirulence genes from the rice blast fungal pathogen *Magnaporthe oryzae*. *Plant Cell* 21: 1573-1591.
- Zhou E, Jia Y, Singh P, Correll JC, Lee FN (2007) Instability of the *Magnaporthe oryzae* avirulence gene *AVR-Pita* alters virulence. *Fungal Genet Biol* 44: 1024-1034

Figure S4. Phylogenetic trees of cloned NBS-LRR genes from five resistant rice cultivars (red, resistant lines; green, *M*-resistant lines; please see this figure in a separate PDF file). The amino acid sequences of these NBS-LRR genes were first aligned with the program MUSCLE using default options, and MEGA v5.0 was used subsequently to manually correct the alignments (Tamura et al. 2011). The resulting amino acid sequence alignments were then used to guide the alignments of the corresponding nucleotide coding sequences (CDSs). Based on the CDS alignment results, phylogenetic trees were constructed using the bootstrap NJ method with *p*-distance model by MEGA v5.02. The stability of internal nodes was assessed by bootstrap analysis with 1,000 replicates.









0.02

Figure S5. Phenotypes of control rice cultivars. The *R* represents that no evidence of infection was observed on the rice leaf; *MR* represents only brown specks with smaller than 1 mm in diameter but without sporulation on the leaf; *S* represents typical spindle-shaped blast lesions with at least 3 mm in diameter on the leaf



Table S1. List of rice cultivars used in this study.

Items	Rice cultivars (Abbreviation)(Genotype)	Phenotype to rice blast	Source
Gene donors (<i>R</i> -cultivars)	Tetep (TTP) (<i>Indica</i>)	High level of resistance	China National Rice Research Institute, Hangzhou, Zhejiang, China
	Gumei2 (GM2) (<i>Indica</i>)	High level of resistance	
	Minghui63 (MH63) (<i>Indica</i>)	Intermediate level of resistance	
	Tadukan (TDK) (<i>Indica</i>)	Intermediate level of resistance	
	Q2436 (Q) (<i>Indica</i>)	Intermediate level of resistance	Dr. Qinhua Pan at South China Agricultural University, Guangzhou, Guangdong, China
Transgenic recipients (<i>S</i> -cultivars)	Shin2 (SH) (<i>Japonica</i>)	High level of susceptibility	Dr. Cailin Wang at Jiangsu Academy of Agricultural Sciences, Nanjing, China
	TP309 (TP) (<i>Japonica</i>)	High level of susceptibility	

R, Resistance; *S*, Susceptibility. Phenotypes are based on both published observations and our screen of rice blast isolates (references and screening details in Table S8).

Table S2. List of the 155 primer pairs of these cloned genes

gene loci	primer name	primer sequence (5' to 3')	Restriction site (RS)
AP005316	AP005316-F	ACAGGCGCGCCAAGCTATTTTCGTGGGCGTCT	AscI
	AP005316-R	GAAGGCGCGCCATCCACAAGCGCGACCTAAT	
01g02250	01g02250-F	AAGGCGCGCCTTCATCATTTTGCATCCAC	AscI
	01g02250-R	AAGGCGCGCCTGAGATTGGTATGGACTTTG	
01g05600	01g05600-F	CCTGGTACCGGGCATGTTTCAGAGACTCGT	SalI KpnI
	01g05600-R	CTCGTTCGACGCTCAGGGCAACCAATTAAC	
01g16390	01g16390-F	AAGGCGCGCCGATTCTCTGAGCGGGTTCAT	AscI
	01g16390-R	ATGGCGCGCCTGGGCATCAGAACGGTTGTA	
01g16400	01g16400-F	AAGGCGCGCCCCGCTTGGTGTTCGATATTTA	AscI
	01g16400-R	AAGGCGCGCCAGGTGTCTCTCAGGCGTAT	
01g20720	01g20720-F	AAGGCGCGCCAGCACCTGCACGATGACTAC	AscI
	01g20720-R	AAGGCGCGCCCCGAACAACCCTCCTAATCA	
01g21240	01g21240-F	CAGGTCGACGTTTGAGACCGAAGGCAGAC	SalI XbaI
	01g21240-R	TCCTCTAGACTTGATGAAAAGATACGGGA	
01g23380	01g23380-F	AAGGCGCGCCGGGTGCCATTATGTCTCAGA	AscI
	01g23380-R	AAGGCGCGCCGACCCACCATCATTAGCAG	
01g24820	01g24820-F	AAGGCGCGCCAGGTCGGTGAATTTCTCGGT	AscI
	01g24820-R	AAGGCGCGCCGGAGGAGTTTGGCTAGTCA	
01g25740	01g25740-F	CGGGCGCGCCTGGGCAAGTTTCATGTCAAT	AscI
	01g25740-R	CGGGCGCGCCTTCTCTTATGGGCAGCAAT	
01g35250	01g35250-F	CAAGTCGACATGCGGACTGATGTGAGGTT	SalI
	01g35250-R	CCAGGTACCGCCGATTACAGCAGGATACTC	
01g57270	01g57270-F	TCTGGCGCGCCGCTGGTGCCTGGTTCATCTAT	AscI
	01g57270-R	GGAGGCGCGCCCCTTCTCCGTTCTCCCCTATT	
01g57870	01g57870-F	AAGGCGCGCCTGCCATCTTGTACGAGTTGC	AscI
	01g57870-R	AAGGCGCGCCTGCGACTTGAGGGACCTAGA	
01g72390	01g72390-F	TTGGCGCGCCACTGTGACCGGCCTTAGATT	AscI
	01g72390-R	TAGGCGCGCCGTAGGAAGCCGACGACATCA	
01g72680	01g72680-F	TTGGCGCGCCACAACCTAAATCACGCAACC	AscI
	01g72680-R	AAGGCGCGCCATTTCGGTGCAGACTTGTTCAG	
02g02640	02g02640-F	CGGGGTACCACCAGTAAACCAGACAAGTG	KpnI BamHI
	02g02640-R	CGCGGATCCCCTATGGACTATGGTATTCAG	
02g09790	02g09790-F	CTCGGTACCATAGAATTGAGCGCCCCGTA	KpnI BamHI
	02g09790-R	AGAGGATCCTTGGGTGTAATGCCAGAAA	
02g16270	02g16270-F	ATGGCGCGCCTCTGTAGCAAATATGGTGGC	AscI
	02g16270-R	ATGGCGCGCAAGCGTACCTGGAGATTAGC	
02g18510	02g18510-F	CGCGGATCCTCTTATGAAACGACCATCTCC	KpnI BamHI
	02g18510-R	CGGGGTACCACTCACCTTTACCTCACCT	
02g19750	02g19750-F	CCGGAATTCAGCACATGGGACGCCTAGA	EcoRI
	02g19750-R	CGGGAATTCTAGGTTTGAATTGCCATGCC	
02g25900	02g25900-F	TCGGCGCGCAATAGATTTCGAGCGTCATGG	AscI
	02g25900-R	TTGGCGCGCCCGCATATAGCAGGAACGTCA	
02g27540	02g27540-F	AAGGCGCGCCTTGAACGACTTACGACGCTA	AscI
	02g27540-R	AAGGCGCGCCGCGGTGTTTGTGAGTACTT	
02g30150	02g30150-F	AAGGCGCGCCTGTTAAACGAGAATGGCAT	AscI
	02g30150-R	AAGGCGCGCCACCTTCGGAAAATACTGCT	
03g20840	03g20840-F	AAGGCGCGCCTGCGTTTGTATCATGTTCA	AscI
	03g20840-R	AAGGCGCGCCTCAAAGTTCACCTCTACCAA	
03g37720	03g37720-F	GCAGAATTCGCCGATCCTTGTGTAGACTC	EcoRI
	03g37720-R	GGTGAATTCATCCATCCCAAGTAGCTC	
03g38330	03g38330-F	AAGGCGCGCCTGCCTCTTCGGTACTATCA	AscI

03g48320	03g38330-R 03g48320-F	AAGGCGCGCCTGGAGATTGGATGCAGTATT TTGGCGCGCCGGGCACATGCACATAGGACA	AscI	
03g50150	03g48320-R 03g50150-F	TTGGCGCGCCCGGGAAGACCAACGATGAAG ACGCGTCGACGCTCCTCCACTCTAACATC	XbaI	SaII
03g63200	03g50150-R 03g63200-F	ACGCGTCGACATTTCGTCTGTGGCAGTTGAG CGAGGCGCGCCATTCCATTGCAGCGTTATCG	AscI	
04g21890	03g63200-R 04g21890-F	TCTGGCGCGCCCTGGTGCATGGCTAGTCGTC AAGGGCGCGCCTAGTCTGATGCCTGTCTCCA	BamHI	
04g24700	04g21890-R 04g24700-F	TCAGGCGCGCCGGTTCGACAGGTAAGATAAGTC TCGGCGCGCCTGATGCTTGAACACGGAATA	AscI	
04g30660	04g24700-R 04g30660-F	ACGGCGCGCCCTAACGGGAGCACACACTAA ACGGCGCGCCGCTCAACCTGGCTATGGACG	AscI	
04g30930	04g30660-R 04g30930-F	CGGGCGCGCCTACACATTCCTAAAACCCGA AAGGCGCGCCATTTCATGCTGGTTTGGACT	AscI	
04g46300	04g30930-R 04g46300-F	AAGGCGCGCCCGTAAGCTGTGTTTCGTCGTC AAGGCGCGCCAGGCCAGGATGACTTACA	AscI	
04g53050	04g46300-R 04g53050-F	AAGGCGCGCCTCGACTGTCTGTGGCATGT AAGGCGCGCCACCTTACCCTCGGACTTT	AscI	
05g12770	04g53050-R 05g12770-F	AAGGCGCGCCCATGACATTTCGCTCGATTT AAGGCGCGCCTCTTTGAAGCACTGGCGATT	AscI	
05g16200	05g12770-R 05g16200-F	ATGGCGCGCCTTGGCAGGCTTAATTGGAC TAGGCGCGCCGACCTTCGACAATGGCTCCT	AscI	
05g23990	05g16200-R 05g23990-F	TGGGCGCGCCAATAGGCTCTCCGCTGTCAC CTGGAATCCGGCATAGTGGCATCGTTTGA	EcoRI	SaII
05g30220	05g23990-R 05g30220-F	GCGGTCGACTCTTCGACAGTCCAATCCTTC TCGGCGCGCCTGTAGAGGTGACGGGCTTTC	AscI	
05g31530	05g30220-R 05g31530-F	ACGGCGCGCCTGTCTGGATGCGTTTGTCTT TCGGCGCGCCGTATGCGTGGATCGGTCTAG	AscI	
05g31570	05g31530-R 05g31570-F	ACGGCGCGCCAAACTCGGATCATGCCATA AGAGGCGCGCCAATACTTCAAATGCGTGTGT	AscI	
05g34220	05g31570-R 05g34220-F	ATTGGCGCGCCTATGAGCATCTGAACCTACG AAGGCGCGCCCGGTTGGATCTAAGAATGGT	AscI	
05g40150	05g34220-R 05g40150-F	AAGGCGCGCCACTCGGGTTGTCCACTACTG AAGGCGCGCCTGCCAGATAATGTCAACCAA	AscI	
05g40160	05g40150-R 05g40160-F	AAGGCGCGCCAGACCTGCAACCTTCAACA TCGGCGCGCCGGGTCGGTCCACTTTTGTTT	AscI	
06g06380	05g40160-R 06g06380-F	ACGGCGCGCCTTGCCTGATGAGCGGTATCT CGCGGATCCTAAGTCACGCTTAAAGTCCC	KpnI	BamHI
06g06390	06g06380-R 06g06390-F	CGGGGTACCACTGGAGATGCTTTCTTCC ACGCGTCGACATTAGGGTCCGCAGGCTTTT	EcoRI	SaII
06g06860	06g06390-R 06g06860-F	CCGGAATTCAGCTCTTATCGCAGAGTCGC TATGGCGCGCCAGCCTTCGGATAAATTGATA	AscI	
06g15730	06g06860-R 06g06860-2R	AAAGGCGCGCCTGGATTTGTGGAGTACCTGG TATGGCGCGCCGCAAGAGGTTACAAGAGGGT	AscI	
06g15750	06g15730-F 06g15730-R	ACGGCGCGCCTCAGATGGATGGGCACTTAT TCGGCGCGCCGCTCAGCACAAATCTTCAAG	AscI	
06g17880	06g15750-F 06g17880-F	ACGGCTGCAGCGCATTACTCATCCTCTAAA CCGGAATTCATAAGCAGAATAGCATATCACTG	PstI	EcoRI
06g17950	06g17880-R 06g17950-F	CGGGGTACCTGCTGAACAAGGTGTAGAGG CCGCTCGAGCAAGGCGAAAGACAGATAAA	XhoI	KpnI
06g20050	06g17950-R 06g20050-F	TTGGCGCGCCGATGCGAAAGAAGCCCGATAC TTGGCGCGCCTGGTTAAGGACCTGCACTCC	AscI	
06g22460	06g20050-R 06g22460-F	AAGGCGCGCCTCTCGATGTTCTAGCTTAA AAGGCGCGCCTTGTTAGGAAGTTGCGAATC	AscI	
		TCGGCGCGCCTTGGGACGAAGGGAGTACAT	AscI	

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	06g22460-R	ACGGCGCGCCTGTGGGGTGAACGACAAGTG		
06g41670	06g41670-F	AAAGGCGCGCCTGGGTTGCCTGTTGACTGAT	AscI	
	06g41670-R	AAAGGCGCGCCGATTTATGCCGCTGTATTGC		
06g45690	06g45690-F	CGGGGTACCTTTTCGATCTATTCCGGGTAC	SalI	KpnI
	06g45690-R	ACGCGTCGACGTGACTCGGCTGTTTCTGCT		
06g48520	06g48520-F	AAGGCGCGCCTCAGCCAAATCGTACACCAT	AscI	
	06g48520-R	AAGGCGCGCCAAAGGTACAGCAAGCCAGAA		
07g04900	07g04900-F	AAGGCGCGCCTGGCATTAGCACATTAGA	AscI	
	07g04900-R	AAGGCGCGCCTGCTTACGAACCTACCCAAT		
07g08890	07g08890-F	ATGGCGCGCCTTACCGTTGCATTGGCTTAC	AscI	
	07g08890-R	AAGGCGCGCCTTCCATTGTTTCGCCCTAC		
07g17220	07g17220-F	TTCGAGCTCGGTACCCGTTGAAGCTTTGTGG	KpnI	
	07g17220-R	GGATCCCCGGGTACCTAATCGGCTGGTGGCATA		
07g17230	07g17230-F	AAGGCGCGCCCCGATGGTTAGTGGGTCTTC	AscI	
	07g17230-R	AAGGCGCGCCATGAGCGTCCGTAATAGTGG		
07g27370	07g27370-F	CGCGGATCCATTGCTCCATTGTCAGAAGA	BamHI	
	07g27370-R	CGCGGATCCCCATGAGCTACTGATTGTT		
07g33730	07g33730-F	AAGGCGCGCCAACGCCATTTAGGTGATCTC	AscI	
	07g33730-R	AAGGCGCGCCATAAAGTCTCGCTGTCAACG		
08g01580	08g01580-F	ACGGCGCGCCTGGATGGGCGATATGATGTC	AscI	
	08g01580-R	TCGGCGCGCCCGGATTGGTTTGAGCAAGTT		
08g05800	08g05800-F	AAGGCGCGCCATGGATCACTTCACGAACCTA	AscI	
	08g05800-R	AAGGCGCGCCTTTGGTTGGTTCAGTCATAC		
08g07340	08g07340-F	AAGGCGCGCCAGAACCAGGAGGAGATGAAT	AscI	
	08g07340-R	TTGGCGCGCCTCCGATTGTGGTTCAGTAGTT		
08g07390	08g07390-F	TCGGCGCGCCACAAATCAACCTGGCTACA	AscI	
	08g07390-R	ACGGCGCGCCTCCGACGATGACAACCTCTA		
08g07774	08g07774-F	CATGGCGCGCCCAACCAATGGCAACAAATC	AscI	
	08g07774-R	TAAGGCGCGCCGTGAGAATTTGGCAGCTTGA		
08g09110	08g09110-F	ACGCGTCGACCAGTACCCCATGTATTACCA	EcoRI	SalI
	08g09110-R	CCGGAATTCGTACCATATTCTATTTCGTCCC		
08g09430	08g09430-F	AAGGCGCGCCTAGCTGGCAAGGATGTGACA	AscI	
	08g09430-R	AAGGCGCGCCGATAGCGGCATGATAGTGT		
08g10430	08g10430-F	GTGGCGCGCCTTAGTTCACATGCACGTACAAGA	AscI	
	08g10430-R	GAGGCGCGCCATCACACATTACTACCGCCTAT		
08g14830	08g14830-F	ACGCGTCGACGGATATGATTCTGGACGCTC	EcoRI	SalI
	08g14830-R	CCGGAATTCACGCTAGTTGCTACCCCTTA		
08g15880	08g15880-F	ACGCGTCGACAACCCTGCTCCTCAACCTAT	EcoRI	SalI
	08g15880-R	CCGGAATTCCTAAGCACCTTATTCAAAC		
08g16070	08g16070-F	CTCGGTACCAGCGGACTTGCTACGTTCTA	KpnI	XbaI
	08g16070-R	GACTCTAGAGGATCTTTCAAGGAGCCATA		
08g16120	08g16120-F	CCGGAATTCACGGTGTCTACGGATACTGA	XbaI	EcoRI
	08g16120-R	TGCTCTAGATCAAAGGAACTTCATAGGATAG		
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	08g16460-R	CCGCTCGAGGTGGCATCAGTTGATAATAGTG		
08g19694	08g19694-F	ACGCGTCGACTGCCTACCATACTAATCCA	EcoRI	SalI
	08g19694-R	CCGGAATTCGTTCCGCTAATCCCTCTGTC		
08g28540	08g28540-F	AAGGCGCGCCATGTCCCTGTATATGATTCG	AscI	
	08g28540-R	AAGGCGCGCCGTGCAATCGCTACAATGGAG		
08g32880	08g32880-F	TGCTCTAGAGTTAGGCATAAGACATAGGAAT	XbaI	SalI
	08g32880-R	ACGCGTCGACAGTAAGCACTCACAGCACAG		
08g32890	08g32890-F	CCGGAATTCAAACAGCCAAGATAAATGACA	EcoRI	SalI
	08g32890-R	ACGCGTCGACCTAATAAACACTCGCACAGG		
08g43010	08g43010-F	ACGGCGCGCCTGCGTCGCTTGTCTGTAGG	AscI	
	08g43010-R	TCGGCGCGCCGCGAGAAACCCCTCCTAGT		

08g43050	08g43050-F 08g43050-R	CGTGGCGCGCCTGCCAGATACAGAATTACGA TTAGGCGCGCCGAAGCAACAGGGAAGGTATG	AscI	
09g13820	09g13820-F 09g13820-R	AAGGCGCGCCCCCTTGCTAGACTCAGACTG AAGGCGCGCCTATCTATGGGCAACTGCTGT	AscI	
09g14450	09g14450-F 09g14450-R	AAGGCGCGCCAGGGGTGATCTAAATTCCAA AAGGCGCGCCTTCTCCAACCATGTATGAT	AscI	
09g16000	09g16000-F 09g16000-R	AAGGCGCGCCGAGTGGTCGCTACATGAAGA AAGGCGCGCCAAGCTGAGGAGGATTATGTT	AscI	
09g20020	09g20020-F 09g20020-R	AATGGCGCGCCTTAGTGGGCTCTTACGGTCT AAAGGCGCGCCCCGCTTCTATCCACTCGTTCT	AscI	
09g30220	09g30220-F 09g30220-R	CCAGGCGCGCCCAGGTTGAGGTACGTCGATT AACGCGCGCCCCGATTGGGTGTATAGTTCC	AscI	
10g03669	10g03669-F 10g03669-R	AAGGCGCGCCCCGTGTGCTTAATGGGTTGAT AAGGCGCGCCCCCTCGTCTTATTTGCGTCTG	AscI	
10g04060	10g04060-F 10g04060-R	AAGGCGCGCCCATTTTCGTCTGCCGTTCAAC ATGGCGCGCCCCGTGTCAGAAGAAGCGTA	AscI	
10g04090	10g04090-F 10g04090-R	AAGGCGCGCCGAAAACCAAGCTCATCAA AAGGCGCGCCTTCAAGTGTGGCAAGCTAGT	AscI	
10g07400	10g07400-F 10g07400-R	ATGGCGCGCCAACAATGCCTCGACCAACT AGGGCGCGCCACCGTAGGCCAATTCTCTTC	AscI	
10g10360	10g10360-F 10g10360-R	CGGGGTACCATAAACTCGTCCTGTCTGGT CCGGAATTCATAGGGCTTACTTAGGGTC	EcoRI	KpnI
10g22510	10g22510-F 10g22510-R	AAGGCGCGCCTTCTACGTTGGTGTCTTGA AAGGCGCGCCGCTGACGTTCTGTGGTAAGT	AscI	
11g03650	11g03650-F 11g03650-R	CCGCTCGAGAAACAGGAAGGGATGAACAA CCGGAATTCAAATATGCCACAGCTAGTGC	XhoI	EcoRI
11g06220	11g06220-F 11g06220-R	TCGGCGCGCCGACAAACCGGAGAAATCAAT ACGGCGCGCCGATGGAGGAAGTAGACGGCA	AscI	
11g11770	11g11770-F 11g11770-R	AAGGCGCGCCACCATTGTTCCAGGACTTAT AAGGCGCGCCTGCCTAGACTTGTATGATGA	AscI	
11g11960	11g11960-F 11g11960-R	AATGGCGCGCCGGTCAAGTCGTCGCTGTCT AACGGCGCGCCTTCGTGAATTTTCGCTTGT	AscI	
11g12040	11g12040-F 11g12040-R	ACGGCGCGCCAGGGATCAAGTGGGCTATTC TGCGGCGCGCCAGATTCGCCTGGTAACTCAC	AscI	
11g27430	11g27430-F 11g27430-R	TTGGCGCGCCCTAACTGATGGATGCGTGAA AAGGCGCGCCAGTTTGCATGTGCTGAGAGG	AscI	
11g27440	11g27440-F 11g27440-R	CGGGGTACCAGTCTCCATCCCCGAAACTT CCGCTCGAGTATTTTCAGAAAATAGCAGCACCTT	XhoI	KpnI
11g29990	11g29990-F 11g29990-R	AAGGCGCGCCATCCTCTGGTTCATCATCT AAGGCGCGCCATCTCTCATCGGCCTAACTA	AscI	
11g32210	11g32210-F 11g32210-R	TAAGGCGCGCCCTCTTGTACCTCGGCGGATG TAAGGCGCGCCGCTTTCAGGCTTGCCAACG	AscI	
11g35210	11g35210-F 11g35210-R	TCGGCGCGCCCCTTATGCGTGGGATTAGAA ACGGCGCGCCCACTTGAAGCGTCCAGGGTA	AscI	
11g35580	11g35580-F 11g35580-R	AGAGTCGACGACGTGGCTTACAAACAATG CGTGGTACCTGTGATGGGCTCTAATATGC	SalI	KpnI
11g36410	11g36410-F 11g36410-R	TCGGCGCGCCGACATTGACGTGGCATTAGA ACGGCGCGCCTAAGGATACATAGCCGAAGG	AscI	
11g37740	11g37740-F 11g37740-R	AATGGCGCGCCGAAGAGCCGTGCATGATTAG AATGGCGCGCCTTCTCCTGATGCCGCTGTT	AscI	
	11g37740-2F 11g37740-2R	AATGGCGCGCCGCGTCACATGGCAGTCTAAG AAAGGCGCGCCCTCGTCGTCACCATTTCTCGT	AscI	
11g37780	11g37780-F 11g37780-R	CTAGTCTAGACTGGGACAAGGAATAATACA ACGCGTCGACAACGGATAACAAGAACGAAT	XbaI	SalI
11g37870	11g37870-F	CCGGAATTCCTGAGTGAGTGAGAAATGCTGGAG	PstI	EcoRI

	11g37870-R	ACGGCTGCAGAGGAAGGGGACGGTGGGTGT		
11g37880	11g37880-F	CCGGAATTTCCCATGACCGCTACCTCCAAG	EcoRI	SalI
	11g37880-R	ACGCGTCGACGGTAATGCAGATTTTCCCAACT		
11g39290	11g39290-F	CTAGTCTAGATAGGATGTCGTATTGGGTATT	XbaI	SalI
	11g39290-R	ACGCGTCGACACGACTTATTGACTTGCTG		
11g39320	11g39320-F	CCGGAATTCAGCCAACCTTCGTGTCTATC	XhoI	EcoRI
	11g39320-R	CCGCTCGAGTGAATCCTTCTACAGGCAAT		
11g39330	11g39330-F	AAGGCGCGCCTCCGTGTGGTGAGAGATGCT	AscI	
	11g39330-R	AAGGCGCGCCATGTTGCCAAAGGGAGAGGT		
11g39340	11g39340-F	GTGGGCGCGCCATCCTCAGGTATGCGACAAT	AscI	
	11g39340-R	CTTGGCGCGCCGGCTAAATGGTGGTGACAGT		
11g39730	11g39730-F	AAGGCGCGCCAATCTTCAGCTTCCCTTGA	AscI	
	11g39730-R	AAGGCGCGCCATATCGCATGGACAGCTTAG		
11g41540	11g41540-F	CGGGGTACCTTCTTGTGCGGAAACTTGTGA	KpnI	BamHI
	11g41540-R	CGCGGATCCCTCCCTTAAATAAAAATCCAGATC		
11g42580	11g42580-F	AAGGCGCGCCCTAGCTTGATCCGGCCAGAC	AscI	
	11g42580-R	AAGGCGCGCCTAATTCATGGAGCAGGCGAT		
11g43420	11g43420-F	AATGGCGCGCCTTGCTCCCTGGATTGAAC	AscI	
	11g43420-R	TTGGCGCGCCGGACACTACTAGCCGTTGGA		
11g43700	11g43700-F	AAGGCGCGCCTACCCTTCCACCTTAGTTCT	AscI	
	11g43700-R	AAGGCGCGCCTTCATCTAGTGTGCAGGCAT		
11g44960	11g44960-F	TTGGCGCGCCAGTCTTTCTTCTCACGCACCA	AscI	
	11g44960-R	TTGGCGCGCCAAAGTGCCTGCACTGCCCAAAT		
11g44970	11g44970-F	TCGGCGCGCCTTGCGATGCATTTGTGATTC	AscI	
	11g44970-R	ACGGCGCGCCTTCATGGCTTCATAACAAGGT		
11g45090	11g45090-F	CAAGGCGCGCCCCTGGGTTGTGGAGCATAG	AscI	
	11g45090-R	CCAGGCGCGCCCAGAGGAGGGGTTAGGGCTA		
11g45160	11g45160-F	TCGGCGCGCCGAACGGTGGCTTCTGGAATG	AscI	
	11g45160-R	ACGGCGCGCCGGCGAGGTTGATGGTGGAGA		
11g45190	11g45190-F	TTGGCGCGCCCTCGGAAGAGATGGAACAGTTG	AscI	
	11g45190-R	TTGGCGCGCCCGGAGTTACCTACACACCTACA		
11g45930	11g45930-F	ACGGCGCGCCCGCACTAGCACCATCCTGAA	AscI	
	11g45930-R	TCGGCGCGCCACGCCACCGATTGAACTTA		
11g45980	11g45980-F	AAGGCGCGCCGCTTCTTGCGGACTACTGTT	AscI	
	11g45980-R	TTGGCGCGCCGTGTTGCCCTATTGATTTGT		
11g47780	11g47780-F	AAGGCGCGCCTTAACCTGCATACCACTCGT	AscI	
	11g47780-R	AAGGCGCGCCACGGGATAGGTGATTTCGACA		
12g03080	12g03080-F	TATGGCGCGCCAGAAACAGCAACGGGAGTG	AscI	
	12g03080-R	TATGGCGCGCCTGAGACAAAGGAGTGGCAGG		
12g17410	12g17410-F	AAGGCGCGCCTTGATTCCCACTAAAACGCA	AscI	
	12g17410-R	AAGGCGCGCCATTGGGTGGTGGACTAAGCA		
12g29280	12g29280-F	TATGGCGCGCCCCAACCCAGCACCTATTCAA	AscI	
	12g29280-R	AAAGGCGCGCCATCTCGTGCGGTCGTGTTAT		
12g29710	12g29710-F	ACGGCGCGCCCCATCATCTAGTTATGCTAA	AscI	
	12g29710-R	TCGGCGCGCCAGGGCTCTTACAGTAGGTTG		
12g31200	12g31200-F	CCGGAATTCGGTTTGAAGCCGACTCGAT	EcoRI	
	12g31200-R	CCGGAATTCGTCTCAAGGAAGCGCATCTC		
12g32790	12g32790-F	ACGGCGCGCCCTTGATTGTGTCGTCGAGTCT	AscI	
	12g32790-R	GATGGCGCGCCGGGCTGTATATCGACCAAAC		
12g36730	12g36730-F	ACGGCGCGCCGTTTGAAGCCGACTCGAT	AscI	
	12g36730-R	TCGGCGCGCCGGTGGCACAGACTCCTAATA		

Table S3. List of the cloned genes and their donors. In the cloned 332 NBS-LRR genes, all have their own promoters and terminators except for 20 genes (6%) which are marked with CDS. Those genes have the rice promoter and terminator of *Pi9*.

No.	Loci	Donor	Gene/CDS length (bp)	No.	Loci	Donor	Gene/CDS length (bp)	
1	01g02250	Q2436	5957	47	02g18510	TDK	6327	
2	01g02250	MH63	5957	48	02g19750	MH63	6200	
3	01g05600	Q2436	5945	49	02g25900	MH63	6414	
4	01g05600	TTP	5945	50	02g25900	TTP	6414	
5	01g16390	MH63	7585	51	02g25900	Q2436	6414	
6	01g16400	GM2	6400	52	02g27540	TTP	6452	
7	01g16400	MH63	6400	53	02g27540	Q2436	6452	
8	01g16400	Q2436	6400	54	02g27540	GM2	6452	
9	01g16400	TDK	6400	55	02g30150	GM2	6004	
10	01g20720	Q2436	6830	56	02g30150	TDK	6004	
11	01g20720	TDK	6830	57	02g30150	Q2436	6004	
12	01g20720	GM2	6830	58	02g30150	TTP	6004	
13	01g20720	MH63	6830	59	03g20840	TTP	7644	
14	01g21240	TTP	7060	60	03g20840	Q2436	7644	
15	01g23380	TDK	1780	CDS	61	03g37720	TTP	6100
16	01g23380	MH63	1780	CDS	62	03g37720	GM2	6100
17	01g23380	GM2	1780	CDS	63	03g37720	Q2436	6100
18	01g23380	TTP	1780	CDS	64	03g37720	MH63	6100
19	01g24820	GM2	6000	65	03g37720	TDK	6100	
20	01g24820	MH63	6000	66	03g38330	GM2	5241	
21	01g24820	TTP	6000	67	03g38330	MH63	5241	
22	01g24820	TDK	6000	68	03g38330	Q2436	5241	
23	01g24820	Q2436	6000	69	03g38330	TTP	5241	
24	01g25740	TTP	5662	70	03g38330	TDK	5241	
25	01g35250	TTP	3500	CDS	71	03g48320	Q2436	7000
26	01g35250	GM2	3500	CDS	72	03g48320	GM2	7000
27	01g57270	GM2	8002	73	03g48320	MH63	7000	
28	01g57340	MH63	3899	CDS	74	03g50150	MH63	5624
29	01g57340	TTP	3899	CDS	75	03g50150	TTP	5624
30	01g57870	GM2	6000	76	03g63200	TTP	7284	
31	01g57870	TDK	6000	77	03g63200	GM2	7284	
32	01g57870	TTP	6000	78	04g21890	TDK	5300	
33	01g57870	Q2436	6000	79	04g24700	GM2	7776	
34	01g57870	MH63	6000	80	04g24700	TDK	7776	
35	01g72390	TTP	5100	81	04g24700	MH63	7776	
36	01g72390	MH63	5100	82	04g30660	TTP	4298	
37	01g72390	TDK	5100	83	04g30660	TDK	4298	
38	01g72680	TDK	5384	84	04g30930	TTP	6700	
39	01g72680	Q2436	5384	85	04g46300	TDK	6100	
40	02g02640	TTP	8812	86	04g53050	Q2436	7300	
41	02g09790	TTP	5076	87	05g12770	TTP	6800	
42	02g16270	GM2	4500	88	05g12770	TDK	6800	
43	02g16270	Q2436	4500	89	05g12770	Q2436	6800	
44	02g16270	MH63	4500	90	05g12770	GM2	6800	
45	02g16270	TDK	4500	91	05g16200	GM2	6500	
46	02g16270	TTP	4500	92	05g16200	Q2436	6500	

No.	Loci	Donor	Gene/CDS length (bp)	No.	Loci	Donor	Gene/CDS length (bp)
93	05g16200	MH63	6500	142	07g08890	Q2436	5917
94	05g23990	GM2	5700	143	07g08890	MH63	5917
95	05g23990	TTP	5700	144	07g08890	TDK	5917
96	05g23990	Q2436	5700	145	07g08890	TTP	5917
97	05g30220	TTP	7937	146	07g17220	GM2	6000
98	05g30220	GM2	7637	147	07g17230	Q2436	6626
99	05g31530	GM2	10827	148	07g17230	TDK	6626
100	05g31570	Q2436	8200	149	07g17230	GM2	6626
101	05g34220	Q2436	7600	150	07g17230	MH63	6626
102	05g34220	GM2	7600	151	07g27370	GM2	5705
103	05g34220	MH63	7600	152	07g27370	TTP	5705
104	05g40150	TDK	7334	153	07g27370	MH63	5705
105	05g40150	TTP	7334	154	07g33730	GM2	7005
106	05g40150	Q2436	7334	155	08g01580	TTP	6733
107	05g40160	Q2436	6263	156	08g01580	GM2	6733
108	05g40160	TTP	6263	157	08g01580	Q2436	6733
109	06g06380	TTP	7491	158	08g05800	MH63	6438
110	06g06380	TDK	7491	159	08g05800	TTP	6438
111	06g06380	GM2	7491	160	08g05800	GM2	6438
112	06g06380	Q2436	7491	161	08g05800	TDK	6438
113	06g06390	TDK	6078	162	08g05800	Q2436	6438
114	06g06390	Q2436	6078	163	08g07340	TTP	5753
115	06g06390	GM2	6078	164	08g07340	Q2436	5753
116	06g06390	TTP	6078	165	08g07390	Q2436	8594
117	06g06860	Q2436	6999	166	08g07390	GM2	8594
118	06g15730	TTP	6067	167	08g07774	Q2436	7091
119	06g15730	GM2	6067	168	08g09110	TTP	6917
120	06g15750	TTP	6432	169	08g09110	TDK	6917
121	06g17880	TTP	6676	170	08g09430	TDK	5240
122	06g17880	MH63	6676	171	08g09430	GM2	5240
123	06g17950	Q2436	6200	172	08g09430	MH63	5240
124	06g17950	GM2	6200	173	08g09430	Q2436	5240
125	06g20050	GM2	6646	174	08g10430	TTP	7000
126	06g22460	TTP	5229	175	08g10430	GM2	7000
127	06g22460	GM2	5229	176	08g10430	TDK	7000
128	06g41670	Q2436	5468	177	08g10430	MH63	7000
129	06g41670	TTP	5468	178	08g10430	Q2436	7000
130	06g45690	MH63	6203	179	08g14830	TTP	5610
131	06g48520	GM2	4442	180	08g14830	MH63	5610
132	06g48520	MH63	4442	181	08g15880	TDK	7437
133	06g48520	TTP	4442	182	08g15880	Q2436	7437
134	06g48520	Q2436	4442	183	08g15880	GM2	7437
135	06g48520	TDK	4442	184	08g16070	MH63	6153
136	07g04900	TTP	6269	185	08g16120	TTP	6698
137	07g04900	GM2	6269	186	08g16460	TTP	6097
138	07g04900	MH63	6269	187	08g16460	MH63	6097
139	07g04900	Q2436	6269	188	08g19694	TTP	5880
140	07g04900	TDK	6269	189	08g19694	MH63	5880
141	07g08890	GM2	5917	190	08g19694	GM2	5880

No.	Loci	Donor	Gene/CDS length (bp)	No.	Loci	Donor	Gene/CDS length (bp)
191	08g28540	GM2	5572	240	11g06220	Q2436	3623 CDS
192	08g28540	TTP	5572	241	11g06220	GM2	3623 CDS
193	08g28540	MH63	5572	242	11g11770	Q2436	3405 CDS
194	08g28540	Q2436	5572	243	11g11960	Q2436	5817
195	08g28540	TDK	5572	244	11g12040	Q2436	6200
196	08g32880	TTP	5392	245	11g27430	GM2	8000
197	08g32890	TTP	6253	246	11g27430	TDK	8000
198	08g32890	MH63	6253	247	11g27440	TTP	6519
199	08g43010	TTP	6958	248	11g29990	MH63	5768
200	08g43010	TDK	6958	249	11g29990	TTP	5768
201	08g43050	TTP	7000	250	11g29990	Q2436	5768
202	08g43050	TDK	7000	251	11g29990	TDK	5768
203	08g43050	MH63	7000	252	11g32210	TTP	9300
204	09g13820	GM2	6701	253	11g32210	GM2	9300
205	09g13820	TTP	6701	254	11g32210	MH63	9300
206	09g13820	TDK	6701	255	11g32210	Q2436	9300
207	09g14450	MH63	5064	256	11g35210	GM2	6523
208	09g14450	GM2	5064	257	11g35210	TTP	6523
209	09g14450	Q2436	5064	258	11g35210	Q2436	6523
210	09g14450	TDK	5064	259	11g35580	MH63	6240
211	09g16000	TTP	5507	260	11g35580	TTP	6240
212	09g16000	GM2	5507	261	11g36410	GM2	5837
213	09g16000	TDK	5507	262	11g36410	MH63	5837
214	09g20020	TTP	5913	263	11g36410	TDK	5837
215	09g20020	GM2	5913	264	11g37740	Q2436	5927
216	09g20020	Q2436	5913	265	11g37780	Q2436	6387
217	09g20020	TDK	5913	266	11g37780	GM2	6387
218	09g30220	TTP	5565	267	11g37870	GM2	5874
219	09g30220	TDK	5565	268	11g37880	TTP	6151
220	09g30220	MH63	5565	269	11g37880	TDK	6151
221	09g30220	GM2	5565	270	11g37880	Q2436	6151
222	10g03369	Q2436	6835	271	11g39290	TTP	5601
223	10g03369	MH63	6835	272	11g39320	TTP	6237
224	10g04060	MH63	8200	273	11g39330	TTP	4848
225	10g04060	TTP	8200	274	11g39330	MH63	4848
226	10g04060	Q2436	8200	275	11g39330	TDK	4848
227	10g04090	TTP	8072	276	11g39340	TTP	7418
228	10g07400	Q2436	7064	277	11g39730	MH63	2921 CDS
229	10g07400	MH63	7064	278	11g39730	TDK	2921 CDS
230	10g07400	TDK	7064	279	11g39730	Q2436	2921 CDS
231	10g10360	TTP	5860	280	11g39730	TTP	2921 CDS
232	10g22510	TTP	5786	281	11g41540	TTP	5066
233	10g22510	MH63	5786	282	11g41540	TDK	5066
234	10g22510	Q2436	5786	283	11g42580	Q2436	4438
235	11g03650	TTP	7138	284	11g42580	GM2	4438
236	11g03650	TDK	7138	285	11g43420	MH63	6400
237	11g06220	TDK	3623 CDS	286	11g43420	TTP	6400
238	11g06220	TTP	3623 CDS	287	11g43420	TDK	6400
239	11g06220	MH63	3623 CDS	288	11g43700	MH63	5823

No.	Loci	Donor	Gene/CDS length (bp)	
289	11g43700	TTP	5823	
290	11g43700	Q2436	5823	
291	11g43700	TDK	5823	
292	11g44960	TTP	5200	
293	11g44970	TTP	5288	
294	11g44970	Q2436	5288	
295	11g44970	GM2	5288	
296	11g45090	TTP	5600	
297	11g45160	TTP	4869	
298	11g45190	TTP	5564	
299	11g45190	MH63	5564	
300	11g45930	TTP	6047	
301	11g45930	Q2436	6047	
302	11g45980	TTP	6727	
303	11g45980	Q2436	6727	
304	11g47780	Q2436	4824	
305	11g47780	MH63	4824	
306	11g47780	GM2	4824	
307	11g47780	TDK	4824	
308	12g03080	TTP	9970	
309	12g03080	GM2	9970	
310	12g03080	Q2436	9970	
311	12g17410	TTP	7409	
312	12g17410	MH63	7409	
313	12g29710	GM2	6874	
314	12g29710	TTP	6874	
315	12g29280	TTP	6800	
316	12g29280	GM2	6800	
317	12g29280	Q2436	6800	
318	12g29280	MH63	6800	
319	12g29280	TDK	6800	
320	12g31200	TTP	3800	CDS
321	12g31200	GM2	3800	CDS
322	12g32790	Q2436	5496	
323	12g32790	TDK	5496	
324	12g32790	MH63	5496	
325	12g32790	TTP	5496	
326	12g32790	GM2	5496	
327	12g36730	TTP	6488	
328	12g36730	Q2436	6488	
329	12g36730	GM2	6488	
330	Ap005316	GM2	7500	
331	Ap005316	TTP	7500	
332	Ap005316	Q2436	7500	

Table S4. Locations of the collected isolates of *M.oryzae* used in this study. These isolates were maintained at Nanjing University, Nanjing, China.

Isolates	Collected locations	Collected years
YN1	Dali, Yunnan Province at the far southwest of China.	2008
YN2	Yuxi, Yunnan Province at the far southwest of China	2008
SC1	Ya'an, Sichuan Province at west of China	2009
SC2	Mianyang, Sichuan Province at west of China	2009
CQ1	Beibei, Chongqing city at southwest of China	2009
CQ2	Wuqi, Chongqing city at southwest of China	2009
HB1	Wuhan, Hubei Province at central part of China	2008
AH1	Liu'an, Anhui Province at central part of China	2009
JS1	Nanjing, Jiangsu Province at east of China	2008
JS2	Nantong, Jiangsu Province at east of China	2008
GD1	Guangzhou, Guangdong Province at south of China	2009
LN1	Dandong, Liaoning Province at north of China	2009

08g01580	GM2	SH	S	S	S	S	R	S	S	S	R	S	S	ND	S	ND	ND	ND	ND	ND	ND	ND	ND
08g01580	GM2	TP	R	R	S	ND	S	R	S	S	R	ND	ND	R	ND	ND	ND	R	ND	S	ND	R	ND
08g01580	Q2436	TP	S	S	S	R	ND	ND	S	S	R	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g07340	Q2436	SH	R	S	S	S	R	R	S	S	S	ND	ND	R	ND	ND	ND	S	ND	R	ND	S	ND
08g07340	TTP	TP	S	S	S	S	ND	ND	S	S	R	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g07390	Q2436	SH	R	S	S	S	S	S	S	R	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g07390	Q2436	TP	ND	S	S	ND	ND	R	S	S	R	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g09110	TTP	TP	R	S	S	R	ND	ND	S	S	R	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g10430	TTP	SH	S	S	S	ND	S	R	S	ND	ND	S	S	R	R	R	S	S	S	S	ND	ND	ND
08g10430	MH63	TP	ND	R	S	S	ND	ND	S	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g10430	Q2436	TP	R	S	S	S	ND	S	S	S	R	ND	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND
08g15880	Q2436	SH	R	S	R	S	R	S	S	S	S	ND	ND	R	ND	ND	ND	S	ND	R	ND	R	ND
08g15880	GM2	SH	R	S	S	S	R	S	S	S	S	ND	ND	R	ND	ND	ND	ND	ND	R	R	ND	R
08g15880	Q2436	TP	S	S	S	S	S	R	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g15880	GM2	TP	R	S	S	R	R	R	S	S	R	S	S	S	R	ND	ND	ND	ND	R	S	ND	R
08g16120	TTP	SH	ND	S	R	S	ND	ND	S	S	ND	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g16460	MH63	SH	R	S	S	R	ND	ND	R	S	S	R	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g19690	TTP	SH	ND	S	S	S	ND	ND	R	R	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g19690	MH63	SH	ND	S	R	S	ND	ND	S	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g32890	TTP	SH	S	S	S	S	ND	ND	S	R	R	R	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g43010	TDK	SH	S	S	S	R	R	R	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
08g43050	TDK	SH	S	S	S	S	S	S	ND	S	ND	ND	ND	S	ND	ND	ND	ND	ND	R	R	ND	S
08g43050	TTP	SH	R	S	S	S	S	ND	S	S	ND	ND	ND	S	ND	ND	ND	ND	ND	R	R	ND	S
08g43050	MH63	SH	S	S	S	S	R	ND	S	S	ND	ND	ND	S	ND	ND	ND	ND	ND	R	R	ND	S
08g43050	TTP	TP	R	S	S	S	S	S	ND	S	ND	ND	ND	S	ND	ND	ND	ND	ND	R	R	ND	S
09g30220	GM2	TP	S	S	S	S	S	S	R	R	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
11g06220	Q2436	TP	S	S	R	ND	ND	R	R	R	R	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
11g27440	TTP	SH	S	S	ND	S	S	R	S	S	ND	S	S	R	S	R	S	S	S	S	ND	ND	ND
11g32210	GM2	SH	S	S	R	ND	ND	R	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
11g35210*	TTP	SH	R	S	S	S	R	ND	S	R	R	S	ND	ND	S	ND	ND	ND	ND	ND	ND	ND	ND
11g35580	MH63	SH	ND	S	S	S	ND	S	R	S	R	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
11g35580	TTP	SH	S	S	S	S	S	S	S	S	S	ND	ND	S	ND	ND	ND	ND	ND	R	R	ND	S

11g35580	TTP	TP	R	S	S	ND	ND	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g37780	Q2436	SH	S	S	S	R	R	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g37780	GM2	SH	R	S	R	R	S	S	S	S	S	S	S	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	
11g37780	Q2436	TP	S	S	S	S	R	R	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g37780	GM2	TP	ND	S	S	S	S	R	ND	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g37870	GM2	TP	S	S	S	S	R	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g37880	TDK	SH	ND	S	R	S	ND	S	R	R	ND	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g37880	Q2436	SH	R	S	S	R	R	S	S	S	S	S	S	ND	S	ND	ND	ND	ND	ND	R	S	ND	S
11g37880	Q2436	TP	ND	S	S	ND	S	R	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g39320	TTP	SH	ND	S	R	S	ND	ND	R	R	S	S	R	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g39330	MH63	TP	ND	S	S	S	ND	ND	R	S	S	S	R	S	R	ND	ND	ND	ND	ND	ND	R	ND	
11g39340	TTP	TP	S	S	S	S	ND	S	S	S	R	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g41540	TTP	SH	S	S	S	S	S	S	S	S	ND	S	S	S	R	R	S	S	S	S	ND	ND	ND	
11g41540	TDK	SH	ND	S	R	S	ND	ND	R	S	S	S	R	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g42580	GM2	TP	R	S	R	ND	ND	S	S	S	S	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g44960	TTP	SH	S	S	S	S	R	S	S	S	S	S	S	S	ND	ND	ND	ND	ND	R	R	ND	S	
11g44960	TTP	TP	S	R	S	S	S	R	S	S	R	S	S	S	S	ND	ND	ND	ND	R	S	ND	R	
11g44970*	Q2436	SH	S	S	R	S	S	S	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g44970*	GM2	SH	S	S	S	S	ND	R	S	S	R	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g45090*	TTP	SH	S	S	R	ND	ND	R	S	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g45160*	TTP	TP	S	S	S	S	ND	ND	S	S	R	ND	S	S	R	ND	ND	ND	ND	ND	ND	ND	ND	
11g45190	TTP	TP	R	S	R	S	R	S	S	S	S	S	S	S	S	ND	ND	ND	ND	R	R	ND	S	
11g45190	MH63	TP	S	R	R	R	R	R	S	S	R	S	S	R	S	ND	ND	ND	ND	R	S	R	R	
11g45930	Q2436	TP	S	S	S	S	S	R	S	S	S	S	S	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	
11g45980	TTP	SH	S	R	S	S	R	S	ND	ND	ND	ND	ND	R	ND	ND	ND	S	ND	R	ND	S	ND	
11g45980	Q2436	SH	S	S	S	R	S	S	S	S	R	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
11g45980	TTP	TP	S	S	S	S	R	S	S	ND	ND	ND	ND	S	ND	ND	ND	S	ND	S	ND	S	ND	
11g45980	Q2436	TP	ND	S	S	S	S	S	R	S	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
12g03080	GM2	SH	S	R	R	R	ND	S	R	R	R	ND	R	S	S	ND	ND	ND	ND	ND	ND	ND	ND	
12g03080	GM2	TP	S	S	S	S	ND	ND	S	S	R	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
12g17410	TTP	TP	R	S	S	ND	ND	R	S	S	R	ND	S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	
12g29170	GM2	SH	S	S	S	ND	R	S	S	ND	S	ND	S	S	ND	ND	ND	ND	ND	R	S	ND	S	

11g32210	MH63	TP	S	S	S	S	S	S	S	S	M	ND	ND
11g32210	Q2436	SH	S	M	S	S	S	S	S	S	S	ND	S
06g15730	GM	TP	M	S	S	S	S	S	S	S	S	S	ND
11g39330	TDK	TP	S	S	ND	S	R	S	S	ND	ND	ND	S
07g17220	GM	TP	S	S	M	S	S	S	S	S	S	ND	ND
AC-MH-12	MH63	TP	S	S	S	S	S	S	S	S	ND	ND	M
03g37720	TTP	SH	S	S	S	M	S	S	S	S	ND	ND	M
AC-GM-3	GM-3	SH	S	S	S	ND	ND	M	S	S	S	S	S
06g48520	TTP	TP	S	S	ND	S	S	S	M	S	ND	S	S
05g23990	Q2436	TP	S	S	S	S	ND	M	ND	ND	S	S	S
11g32210	Q2436	TP	S	ND	S	ND	S	S	ND	S	M	ND	S
12g03080	TTP	TP	S	S	S	S	S	M	ND	S	S	ND	S
12g03080	Q2436	TP	S	S	S	ND	ND	S	S	S	M	ND	S
08g10430	Q2436	SH	S	S	S	S	ND	S	S	S	M	ND	S
08g10430	GM	TP	S	S	ND	S	S	ND	S	S	M	S	S
06g17950	Q2436	TP	S	S	M	S	S	S	S	ND	ND	S	S
Ap005316	GM	TP	S	M	S	S	S	S	S	ND	S	S	ND
Ap005316	Q2436	SH	S	M	S	S	S	S	S	S	ND	S	ND
08g07390	GM	SH	M	S	ND	S	S	S	ND	S	S	S	S
08g07390	GM	TP	S	S	S	ND	S	S	ND	S	M	ND	S
06g06380	Q2436	TP	M	ND	S	S	S	S	ND	S	S	S	ND
08g43050	TDK	TP	S	S	S	S	ND	S	S	S	M	S	ND
11g35210	Q2436	TP	S	S	ND	S	ND	S	S	M	S	ND	S
6g17950	GM	SH	M	ND	S	S	S	ND	S	S	S	ND	S
6g17950	GM	TP	S	M	ND	S	S	S	ND	S	S	S	S
05g30220	GM	SH	ND	S	S	S	M	S	S	S	S	ND	S

R, Resistance; S, Susceptibility; ND, Not determined; M, Moderate resistance

* The names of 11 R-lines reported recently are Os11g35210-TTP-SH, Os05g30220-TTP-SH, Os05g30220-GM-TP, Os05g23990-TTP-SH, Os05g23990-TTP-TP, Os05g23990-Q2436-SH, Os05g23990-GM-SH, Os11g44970-Q2436-SH, Os11g44970-GM-SH, Os11g45160-TTP-TP and Os11g45090-TTP-SH, which correspond to OspTetep-Rp1F, OspTetep-Rp1G, OspGM-Rp1G, OspTetep-Rp3B-SH, OspTetep-Rp3B-TP, OspQ2436-Rp3B-SH, OspGM-Rp3B-SH, OspQ2436-AC-C-SH, OspGM-AC-C-SH, OspTTP-1-AC-C-TP, and OspTTP-2-AC-C-SH, respectively in Yang et al. 2013.

Table S6. Phenotypic results of transgenic rice lines inoculated by two *Xanthomonas oryzae* pv. *Oryzae* (*Xoo*) races, one Philippine strain (PXO61) and one Chinese strain (ZJ173), provided by Jiangsu Academy of Agricultural Sciences, China. All of the 11 screened transgenic lines in this table are of the 15 broadly effective *R*-lines (Table S11). Three to five uppermost fully expanded leaves of each plant and at least five plants (replicates) for each transgenic line were inoculated for each *Xoo* strain using the leaf clipping method (Chen et al., 2002) at three-week-old seedlings. The phenotype of disease was scored by measuring percent lesion area (lesion length/leaf length% \pm standard deviation) 14 days after inoculation (Sun et al., 2004 and Huang et al. 2008). To ensure the reliability of the screening experiment, a resistant rice control (DV85) to *Xoo* races was employed. The screened results showed that the lesion areas of the screened transgenic lines did not have a significant difference ($P > 0.24$) compared to their transgenic recipients, SH or TP. In particular, the size of lesions on transgenic and paired-recipient lines did not differ ($P > 0.05$, ranging from 0.24 to 0.56 by *t*-test) when infected with PXO61 or ZJ173.

	Gene ID	Transgenic Donors	Transgenic Recipients	Phenotype about lesion areas (%) identified by <i>Xoo</i> races	
				PX061	ZJ173
Controls of recipients			SH	33.6 \pm 2.2	37.5 \pm 4.6
			TP	32.4 \pm 4.2	34.1 \pm 4.1
Controls of Donors		TTP		27.4 \pm 3.3	34.1 \pm 4.9
		GM2		22.7 \pm 1.8	31.1 \pm 3.2
		Q2436		29.4 \pm 3.8	26.2 \pm 3.9
		MH63		15.6 \pm 2.3	32.1 \pm 3.8
Resistant control (DV85)				8.1 \pm 0.7	6.9 \pm 0.9
Transgenic lines	Os12g36730	TTP	SH	34.8 \pm 3.7	42.3 \pm 3.5
	Os06g15750	TTP	SH	31.3 \pm 3.6	34.6 \pm 1.2
	Os06g06380	TTP	SH	29.9 \pm 3.2	35.6 \pm 5.8
	Os06g06390	TTP	SH	35.6 \pm 4.3	39.9 \pm 4.6
	Os08g15880	Q2436	SH	33.1 \pm 3.9	38.2 \pm 3.6
	Os08g07340	Q2436	SH	33.7 \pm 3.3	36.3 \pm 4.2
	Os11g45190	MH63	TP	34.9 \pm 1.8	33.7 \pm 3.2
	Os08g15880	GM2	TP	33.7 \pm 3.6	37.1 \pm 4.6
	Os08g01580	GM2	TP	31.9 \pm 3.7	36.4 \pm 2.1
	Os11g06220	Q2436	TP	36.6 \pm 3.1	30.7 \pm 3.6
	Ap005316	Q2436	TP	30.1 \pm 4.2	33.1 \pm 3.5

1. Chen H, Wang S, Zhang Q. (2002) New gene for bacterial blight resistance in rice located on chromosome 12 identified from Minghui 63, an elite restorer line. *Phytopathology* 92: 750-754.
2. Sun X, Cao Y, Yang Z, Xu C, Li X, Wang S, Zhang Q. (2004) Xa26, a gene conferring resistance to *Xanthomonas oryzae* pv. *Oryzae* in rice, encodes an LRR receptor kinase-like protein. *Plant J* 37: 517-527.
3. Huang J-N, Wang C-C, Hu H-T, Ma B-J, Yan C-Q, Yang L. (2008) Primary identification of a new resistance gene to bacterial blight from *oryza meyeriana*. *Chinese J Rice Sci* 22: 33-37

Table S7. Evaluation of rice panicle blast resistance in an experimental paddy field at Nanjing University Xianlin Campus, China. 4×8 plants were planted for each rice line. The blast spores, purchased from Jiangsu Academy of Agricultural Science, Nanjing, China, were injected into the leaf sheaths of emerging panicles. The proportions of diseased grains per panicle were examined three weeks after inoculation based on 11 classes from 0 (no diseased grain) to 10 (100% diseased grain) according to the description of Asaga (1981). The phenotypes for leaf blast resistance were from Table S5.

Gene ID Corresponding to Nipponbare genome	Transgenic Donor	Transgenic Recipients	Phenotypes of panicle blast test in the natural field		Phenotypes of leaf blast test (Resistance blast strains)
			Percentage diseased grains	Phenotypes	
Os06g15750	TTP	SH2	11.7±4.9%	R	R (CQ1, HB1, SC2, CQ2, YN1, AH1, JS1, YN2, YN4, B3, 21, 32, YN3, SC3)
Os12g36730	TTP	SH2	7.3±4.2%	R	R (CQ1, HB1, LN1, SC2, CQ2, YN1, AH1, JS1, JS2, GD1, SC1, YN2, YN4, B3, 21, 32, YN3, SC3)
Os08g01580	GM	TP309	9.4±6.4%	R	R (CQ1, HB1, YN1, JS2, YN2, 32, 33)
Os08g15880	Q2436	SH2	12.6±5.5%	R	R (CQ1, LN1, CQ2, YN2, SC3, 33)
Os11g35210	TTP	SH2	10.7±6.3%	R	R (CQ1, CQ2, JS1, JS2)
Os11g32210	MH63	TP309	11.7±3.2%	R	M (JS2)
Os08g19694	TTP	SH2	31.7±7.6%	M	R (AH1, JS1)
Os11g45090	TTP	TP309	28.6±6.9%	M	R (JS2, YN4)
Os11g45930	Q2436	TP309	74.3±8.2%	S	R (YN1)
Os03g63200	GM	SH2	78.6±3.7%	S	S
Os02g27540	TTP	SH2	83.4±3.9%	S	S
Os01g16390	MH63	TP309	82.1±4.1%	S	S
Os02g18510	TDK	TP309	77.3±6.8%	S	S
Os02g19750	MH63	SH2	79.1±4.2%	S	S
Os11g27430	GM	SH2	75.6±8.8%	S	S
Os03g50150	TTP	SH2	82.9±2.6%	S	S
Os01g21240	TTP	SH2	76.4±6.4%	S	S
Os05g12770	TTP	SH2	78.7±6.9%	S	S
TTP (control)			4.1±2.4%	R	R
GM (control)			5.9±3.6%	R	R
SH2 (control)			83.1±3.7%	S	S
TP309(control)			84.9±4.2%	S	S

R,Resistance; S, Susceptibility; M, moderate resistance

Reference

Asaga K. (1981) A procedure for evaluating field resistance to blast in rice varieties. J Cent Agri Stn 35:51-138

Table S8. Phenotypes of five resistant and two highly susceptible rice cultivars screened by 21 isolates.

Rice cultivars Isolates	TTP (Donor)	GM2 (Donor)	Q2436 (Donor)	MH63 (Donor)	TDK (Donor)	Shin2 (Recipient)	TP309 (Recipient)
CQ1	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
HB1	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>MR</i>	<i>S</i>	<i>S</i>
LN1	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
SC2	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
CQ2	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
YN1	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
AH1	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
JS1	<i>R</i>	<i>R</i>	<i>R</i>	<i>MR</i>	<i>R</i>	<i>S</i>	<i>S</i>
JS2	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
GD1	<i>R</i>	<i>R</i>	<i>MR</i>	<i>R</i>	<i>MR</i>	<i>S</i>	<i>S</i>
SC1	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
YN2	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>MR</i>	<i>S</i>	<i>S</i>
YN4	<i>R</i>	<i>R</i>	<i>MR</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
B3	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>MR</i>	<i>S</i>	<i>S</i>
21	<i>R</i>	<i>R</i>	<i>R</i>	<i>MR</i>	<i>R</i>	<i>S</i>	<i>S</i>
32	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
YN3	<i>R</i>	<i>R</i>	<i>R</i>	<i>MR</i>	<i>MR</i>	<i>S</i>	<i>S</i>
SC3	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
12-4-2	<i>R</i>	<i>R</i>	<i>MR</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
33	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>
JS3	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>

The *R* indicates that no evidence of infection was observed on the rice leave; *MR* indicates only brown specks with smaller than 1 mm in diameter but without sporulation on the leave; *S* represents typical spindle-shaped blast lesions with at least 3 mm in diameter on the leave (Fig. S5)

TTP and GM2 are well known resistant lines to rice blast disease. In fact, TTP was identified as a blast *R*-resource 50 years ago by IRRI (Ou and Jennings 1969). Many previous studies have also reported that these two rice cultivars are resistant to most of the pathogenic races of the blast fungus *Magnaporthe grisea* (Barman et al. 2004; Peng et al. 1995; Padmanabhan et al. 1974; Wu et al. 2005). These two plant lines were widely used in breeding program at IRRI and China, for developing high-yielding blast-resistant cultivars due to their durable resistance to broad spectrum disease (Ou 1980; Wu et al. 2007). In addition, a long-term nationwide evaluation of blast resistance of 38,000 rice accessions by 33 Chinese rice research groups showed that TTP and GM2 are highly resistant to rice blast strains in China, whereas Tadukan and MH63 had medium levels of resistance to these pathogens (Peng et al. 1996). These results are consistent with our phenotyping results screened by 21 isolates.

Reference

- Barman SR, Gowda M, Venu RC, Chattoo BB. (2004) Identification of a major blast resistance gene in the rice cultivar ‘Tetep’. *Plant Breeding* 123:300–302
- Padmanabhan SY, Mathur SC, Misra RK. (1974) Breeding for blast resistance in India: genetics of blast resistance. *Indian J Genet Plant Breed.* A34, 424–429.
- Peng SQ, Huang FY, Sun GC, Liu EM, Sun YJ, Ai RX, Zhao JX, Bai SZ, Xiao FH (1996) Studies on durable resistance to blast disease in different latitudes for rice (in Chinese with English summary). *Sci Agric Sin* 29:52–58
- Ou SH. (1980) Pathogen variability and host resistance in rice blast disease. *Annu Rev Phytopathol* 18: 167-187
- Ou SH and Jennings PR (1969) Progress in the development of disease-resistant rice. *Annu Rev Phytopathol* 7:383-410
- Wu J, Liu X, Dai L, Wang G. (2007) Advances on the identification 38 characterization of broad-spectrum blast resistance genes in rice (in Chinese with English summary). *Chinese Bulletin of Life Sciences* 19: 233-
- Wu JL, Fan YY, Li DB, Zheng KL, Leung H, Zhuang JY. (2005) Genetic control of rice blast resistance in the durably resistant cultivar Gumei 2 against multiple isolates. *Theor Appl Genet* 111:50-56

Table S9. Ten clades identified from the cloned 332 candidate genes which contain significantly more blast *R*-genes relative to that expected based from a random distribution among clades ($P < 0.05$).

In our study, 98 blast *R*-genes, out of 332 cloned genes from 95 selected clades in Supplementary Fig. 1, were identified. In these 95 clades, 25 have five or more cloned genes; we considered this number the minimum necessary for testing whether a clade contains more functional *R*-genes than expected. We randomly assigned a *R* phenotype to 98 genes in the 95 clades and calculated the ‘*R*-gene’ number in each of the 25 clades. This process was repeated 10,000 times to determine a null distribution of ‘*R*-genes’ per clade. When the number of observed *R*-genes (identified *R*-genes) and expected *R*-genes (‘*R*-genes’ by random simulation) were compared for each of 25 clades, 10 clades were identified as significantly different from the null expectation ($P < 0.05$). These clades contain 61 out of 98 identified *R*-genes (62%), suggesting an uneven distribution of blast *R*-genes on the tree of Supplementary Fig. 1 (the clade number in the first column is corresponding to the marked 10 clades in Fig. S1).

Clades in Supplementary Fig. 1	Numbers of Genes	Observed <i>R</i> -genes	Expected		<i>P</i> value
			<i>R</i> -genes	Numbers out of the 10,000 iterations	
1	13	7	0	123	=0.04
			1	647	
			2	1555	
			3	2362	
			4	2333	
			5	1687	
			6	886	
			7	304	
			8	84	
			9	16	
			10	3	
			11	0	
			12	0	
			13	0	
2	8	7	0	553	0.001
			1	1937	
			2	2956	
			3	2590	
			4	1387	
			5	444	
			6	119	
			7	13	
			8	1	
3	7	5	0	730	0.032
			1	2424	
			2	3239	
			3	2272	
			4	1018	
			5	274	
			6	36	
			7	7	
4	7	5	0	730	0.032
			1	2424	
			2	3239	
			3	2272	
			4	1018	
			5	274	
			6	36	
			7	7	
5	6	5	0	1149	0.014
			1	2992	
			2	3232	
			3	1883	
			4	609	
			5	124	
			6	11	
6	22	10	0	0	
			1	41	
			2	212	
			3	599	
			4	1168	

			5	1681	
			6	1909	
			7	1763	
			8	1297	
			9	743	
			10	378	0.05
			11	143	
			12	57	
			13	5	
			14	4	
			15	0	
			16	0	
			17	0	
			18	0	
			19	0	
			20	0	
			21	0	
			22	0	
7	8	7	0	553	
			1	1937	
			2	2956	
			3	2590	
			4	1387	
			5	444	
			6	119	
			7	13	0.001
			8	1	
8	8	6	0	553	
			1	1937	
			2	2956	
			3	2590	
			4	1387	
			5	444	
			6	119	0.011
			7	13	
			8	1	
9	5	4	0	1626	
			1	3552	
			2	3172	
			3	1316	
			4	310	0.033
			5	24	
10	7	5	0	730	
			1	2424	
			2	3239	
			3	2272	
			4	1018	
			5	274	0.032
			6	36	
			7	7	

Table S10. Eight *R*-genes identified from 110 transgenic lines screened independently by one blast isolate at Dr. Pan's lab at South China Agricultural University (50 and 60 lines screened by CHL346 and EL0917, respectively).

Gene ID	Transgenic Donor	Transgenic Recipients	Phenotype	
			Screening by only one blast strain in Pan's lab (Strain)	Screening by 12 blast strain in Tian's lab (Strains)
06g15750	TTP	Shin2	<i>R</i> (CHL346)	<i>R</i> (CQ1, HB1, SC2, CQ2, YN1, AH1, JS1, YN2)
11g44960	TTP	TP309	<i>R</i> (CHL346)	<i>R</i> (HB1, YN1, JS2)
05g40150	Q2436	TP309	<i>R</i> (CHL346)	<i>R</i> (CQ1, CQ2, YN1)
11g35580	TTP	TP309	<i>R</i> (EL0917)	<i>R</i> (CQ1)
12g36730	TTP	Shin2	<i>R</i> (EL0917)	<i>R</i> (CQ1, HB1, LN1, SC2, CQ2, YN1, AH1, JS1, JS2, GD1, SC1, YN2)
06g06380	TTP	Shin2	<i>R</i> (EL0917)	<i>R</i> (HB1, LN1, SC2, CQ2, YN1, JS1, SC1, YN2)
08g10430	MH63	Shin2	<i>R</i> (EL0917)	<i>S</i>
08g16460	TTP	Shin2	<i>R</i> (EL0917)	<i>S</i>

R, Resistance; *S*, Susceptibility

Table S11. Patterns of broadly effective *R*-genes.

Gene ID	Clade number in Supplementary Table 9	Copy number in the same locus of Fig.S1	Divergence with the least divergent paralog	Transgenic Donor	Transgenic Recipients	Strains resistant to out of 12
06g06380	1	1	0.22	TTP	SH	8
06g06390		1	0.34	TTP	SH	6
06g15750	/	1	0.19	TTP	SH	8
08g01580	2	1	0.36	GM2	TP	5
08g07340	3	1	0.15	Q2436	SH	5
08g15880	Next to 6	1	0.46	Q2436	SH	6
				GM2	SH	6
				GM2	TP	8
11g44960	6	2	0.06	TTP	TP	5
11g45190		2-3	0.01	TTP	TP	5
11g45190				MH63	TP	10
12g03080	7	1	0.41	GM2	SH	7
12g32790	/	2	0.01	GM2	TP	5
12g36730	/	1	0.05	TTP	SH	12
Ap005316	/	1	0.13	TTP	TP	5
11g06220	/	2	0.03	Q2436	TP	8

Sixteen *R*-lines (15 *R*-genes and 14 loci from 11 clades) were capable of recognizing five or more isolates. Eight out of these broadly effective *R*-genes are in the clades of Table S9 that contain significantly more blast *R*-genes than expected if functional *R*-genes were randomly distributed among clades. Loci with only a single copy in the genome are denoted as single copy loci; ten of the broadly resistant *R*-genes are identified as single copy loci.

Table S12. Co-segregation analysis of the 15 broadly effective *R*-genes during infection of isolates.

Gene ID Corresponding to Nipponbare genome	Transgenic Donor	Transgenic Recipients	C Q1	H B1	LN1	S C2	C Q2	Y N1	A H1	JS 1	JS2	GD 1	SC 1	Y N2	Total	Cosegregation of resistance (No.-R/N o.-S)
06g06380	TTP	SH	<i>N</i> <i>D</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>R</i>	<i>ND</i>	<i>S</i>	<i>R</i>	<i>R</i>		
				22	31	$\frac{2}{5}$	29	33		31			24	24	219	3.13
				4	7	$\frac{9}{9}$	9	13		13			6	9	70	
06g06390	TTP	SH	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>R</i>	<i>ND</i>	<i>R</i>	<i>R</i>		
			29	31	21						28		33	31	173	3.09
			7	15	8						4		10	12	56	
06g15750	TTP	SH	<i>R</i>	<i>R</i>	<i>S</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>ND</i>	<i>S</i>	<i>S</i>	<i>R</i>		
			14	36		$\frac{3}{1}$	27	33	29	36				33	239	2.78
			3	12		$\frac{1}{5}$	12	10	11	9				14	86	
08g01580	GM2	TP	<i>R</i>	<i>R</i>	<i>S</i>	<i>N</i> <i>D</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>R</i>	<i>ND</i>	<i>ND</i>	<i>R</i>		
			44	26				35			28			24	157	3.57
			7	5				11			14			7	44	
08g15880	Q243 6	SH	<i>R</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>R(S</i> <i>C3)</i>	<i>R(3</i> <i>3)</i>	<i>R</i>		
			22		34		35					26	29	27	173	3.39
			5		12		7					7	9	11	51	
08g15880	GM2	SH	<i>R</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>R(12-4-2)</i>	<i>R(S</i> <i>C3)</i>	<i>R(J</i> <i>S3)</i>	<i>R</i>		
			38				28				25	28	31	29	179	3.25
			7				11				5	9	10	13	55	
08g15880	GM2	TP	<i>R</i>	<i>S</i>	<i>R(Y</i> <i>N4)</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>R</i>	<i>R(S</i> <i>C3)</i>	<i>R(J</i> <i>S3)</i>	<i>S</i>		
			25		29	$\frac{2}{3}$	29	33			24	21	24		208	2.85
			11		10	$\frac{8}{8}$	9	10			9	7	9		73	
11g06220	Q243 6	TP	<i>S</i>	<i>S</i>	<i>R</i>	<i>N</i> <i>D</i>	<i>N</i> <i>D</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>ND</i>	<i>S</i>	<i>N</i> <i>D</i>		
					27			31	35	26	24				143	2.86
					8			12	11	8	11				50	
11g44960	TTP	TP	<i>S</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>R</i>	<i>R(S</i> <i>C3)</i>	<i>R(J</i> <i>S3)</i>	<i>S</i>		
				25				29			24	36	31		145	3.30
				7				6			10	11	10		44	
11g45190	TTP	TP	<i>R</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>R</i>	<i>S</i>	<i>S</i>	<i>S</i>	<i>R(12-4-2)</i>	<i>R(S</i> <i>C3)</i>	<i>S</i>	<i>S</i>		
			31		28		28				22	32			141	3.13
			9		10		9				5	12			45	
11g45190	MH63	TP	<i>S</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>R</i>	<i>S</i>	<i>R(33)</i>	<i>R</i>	<i>R(S</i> <i>C3)</i>	<i>R(J</i> <i>S3)</i>	<i>R</i>		

