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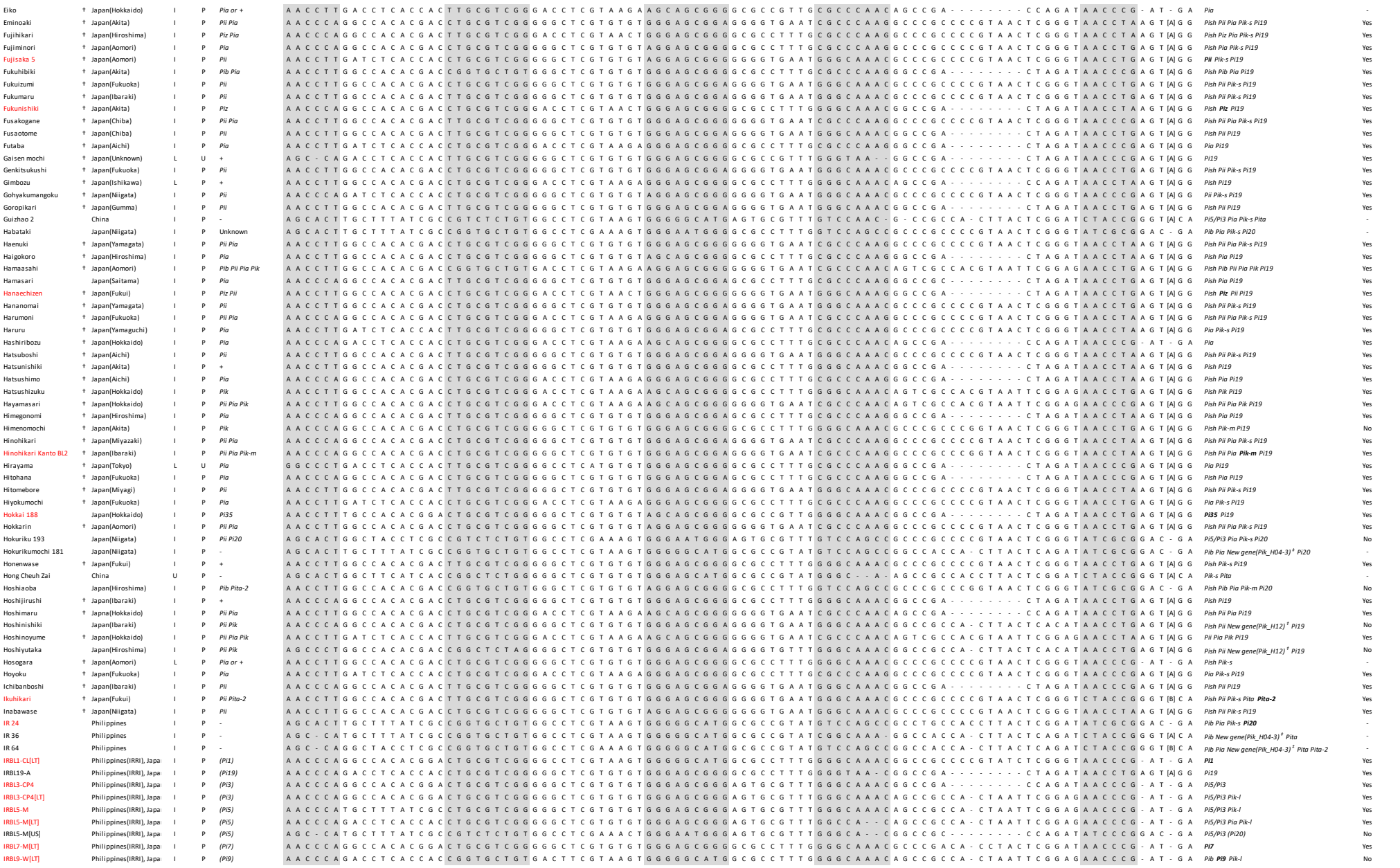
Supplemental Table 1. List of the varieties used in this study and genotypes obtained by using the 96 SNP genotyping assays, BRA1

Cultivar name (listed alphabetically)		Origin	Cultivar type[a]	Habitat[b]	A) Genotype estimate in public databases	*Pit*	*Pish*	*Pib*	*Piz*	*Pi13*	*Pii*	*Pia*	*Pik*	*Pita*	*Pita-2*	B) Estimated allele[f]	Concordance between A) and B)
No.[d]						1 2 3 4 5 6	7 8 9 10 11 12 13 14 15 16 17	18 19 20 21 22 23 24 25 26	27 28 29 30 31 32 33 34 35 36 37 38	39 40 41 42 43 44 45 46 47	48 49 50 51 52 53 54 55 56	57 58 59 60 61 62 63 64	65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84	85 86 87 88 89 90	91 92 93 94 95 96		
No.[c]						1 2 3 4 5 6	1 2 3 4 5 6 7 8 9 10 11	1 2 3 4 5 6 7 8 9	1 2 3 4 5 6 7 8 9 10 11 12	1 2 3 4 5 6 7 8 9	1 2 3 4 5 6 7 8 9	1 2 3 4 5 6 7 8	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	1 2 3 4 5 6	1 2 3 4 5 6		
Assay name						FA4467 FA4453 FA4455 FA4461 FA4482 FA4483	FA4649 FA4645 FA4644 FA4636 FA4627 FA4650 FA4651 FA4652 FA4654 FA4665 FA4667	FA4424 FA4422 FA4416 FA4408 FA4407 FA4404 FA4401 FA4439 FA4446	FA5376 FA4676 FA4678 FA4679 FA4680 FA5378 FA4697 FA4698 FA4683 FA4702 FA4703 FA4704	FA5269 FA5270 FA5271 FA5280 FA5294 FA5283 FA5288 FA5292 FA5293	FA4515 FA4505 FA4494 FA4495 FA4501 FA4526 FA4527 FA4533 FA4536	FA4608 FA4605 FA4598 FA4615 FA4617 FA4620 FA4624 FA4625	FA4742 FA4740 FA4737 FA4735 FA4734 FA4732 FA4710 FA4712 FA5375 FA4717 FA4718 FA4721 FA4723 FA4726 FA4729 FA4750 FA4751 FA4752 FA4753 FA4758	FA4541 FA4544 FA4546 FA4553 FA4556 FA4569	FA4580 FA4571 FA4572 FA5655[e] FA4585 FA4588		
AC 540		India	U	P	-	G G C C C T	G G C T T C A T C A C	C G T C T C T G T	G G C C T C G T A A G T	G G G G G C A T G	G G G G T G T T T	G G G C A A C C	G G C C G A - - - - - - - - C T A G A T	A T A C C G	G G T [A] G G	*Pii Pi19*	-
Aichiasahi	†	Japan(Aichi)	I	P	*Pia*	A A C C C A	G A T C T C A C C A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C T G	A G T [A] G G	***Pia*** *Pi19*	Yes
Aichinokaori	†	Japan(Aichi)	I	P	*Pii Pia*	A A C C C A	G G C C A C A C G A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C C G	A G T [A] G G	*Pish Pii Pia Pi19*	Yes
Aichinokaori SBL	†	Japan(Aichi)	I	P	*Pii Pia*	A A C C C A	G G C C A C A C G A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C C G	A G T [A] G G	*Pish Pii Pia Pi19*	Yes
Aikoku	†	Japan(Fukui)	L	P	+	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C T A	A G T [A] G G	*Pish Pik-s Pi19*	Yes
Akage	†	Japan(Akita)	L	P	*Pia or +*	A A C C T T	G A C C T C A C C A C	T T G C G T C G G	G A C C T C G T A A G A	A G C A G C G G G	G C G C C G T T G	C G C C C A A C	A G C C G A - - - - - - - - C C A G A T	A A C C C G	- A T - G A	*Pia*	-
Akamai_Kanto	†	Japan(Kanto)	L	U	-	A G C A C T	G G C T T C A T C A C	C G G C G T T G T	G G G C T C G T G T G T	G G G A G C G G G	G C G C C G T A T	G T C C - - C C	G G C C G C - - - - - - - - C C A G A T	C T A C C G	G G T [A] C A	*Pia Pita*	-
Akamai_Kochi	†	Japan(Kochi)	L	P	-	A G C A C T	G G C T T C A T C A C	C G G C G T T G T	G G G C T C G T G T G T	G G G A G C G G G	G C G C C G T A T	G T C C - - C C	G G C C G C - - - - - - - - C C A G A T	C T A C C G	G G T [A] C A	*Pia Pita*	-
Akanezora	†	Japan(Aichi)	I	P	+	A A C C C A	G G C C A C A C G A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G C G C C T T T G	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C T A	A G T [A] G G	*Pish Pik-s Pi19*	Yes
Akenohoshi	†	Japan(Hiroshima)	I	P	*Pik*	A A C C C A	G A T C T C A C C A C	C G G C T C T A G	G G G C T C G T G T G T	G G G A G C G G A	G C G C C T T T G	G G G C A A A C	G C C C G C C A - C T T A C T C A C A T	A A C C C G	A G T [A] G G	*New gene(Pik_H12)*[‡] *Pi19*	No
Akibare	†	Japan(Aichi)	I	P	*Pia*	A A C C T T	G G C C A C A C G A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C C G	A G T [A] G G	*Pish Pia Pik-s Pi19*	Yes
Akichikara	†	Japan(Niigata)	I	P	*Pia*	A A C C T T	G G C C A C A C G A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T A	A G T [A] G G	*Pish Pia Pik-s Pi19*	Yes
Akidawara	†	Japan(Ibaraki)	I	P	*Pii*	A A C C C A	G G C C A C A C G A C	C G G C T C T A G	G G G C T C G T G T G T	G G G A G C G G A	G G G G T G A A T	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pii Pik-s Pi19*	Yes
Akihikari	†	Japan(Aomori)	I	P	*Pia*	A A C C T T	G G C C A C A C G A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pia Pik-s Pi19*	Yes
Akiho	†	Japan(Hokkaido)	I	P	*Pii Pia Pik*	A A C C T T	G G C C A C A C G A C	C T G C G T C G G	G A C C T C G T A A G A	A G C A G C G G G	G G G G T G A A T	C G C C C A A C	A G T C G C C A C G T A A T T C G G A G	A A C C T G	A G T [A] G G	*Pish Pii Pia Pik Pi19*	Yes
Akimatsuri	†	Japan(Yamaguchi)	I	P	*Pii Pita-2*	A A C C C A	G G C C A C A C G A C	T T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	C T A C C G	G G T [B] C A	*Pish Pii Pia Pita Pita-2*	No
Akisayaka	†	Japan(Fukuoka)	I	P	*Pii*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G G G G T G A A T	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C C G	A G T [A] G G	*Pish Pii Pik-s Pi19*	Yes
Akita 63		Japan(Akita)	I	P	*Pik Pita-2*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	A G G A G C G G G	G C G C C T T T G	C G C C C A A C	G C C C G C C C G G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pia Pik-m Pi19*	No
Akitakomachi	†	Japan(Akita)	I	P	*Pii Pia*	A A C C T T	G G C C A C A C G A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T A	A G T [A] G G	*Pish Pii Pia Pik-s Pi19*	Yes
Anjana Dhan		Nepal	L	P	-	A A C C C A	G G C C T C A C C G C	C G G C T C T A G	G G G C T C G T G T G T	G G G A G T G G G	G C G G C G T A -	G G G C - - A -	G G C T G C - - - - - - - - C T A G A T	A T A C C G	G G T [A] G G	*Pi13 Pi19*	-
Aoinokaze	†	Japan(Aichi)	I	P	+	A A C C C A	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G C G C C T T T G	G G G C A A A C	G G C C G A - - - - - - - - C T A G A T	A A C C T A	A G T [A] G G	*Pish Pi19*	Yes
Aokei IL2		Japan(Aomori)	I	P	*Pi35 Pii Pia*	A A C C T T	T G C C A C A C G G A	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pi35 Pii Pia Pik-s Pi19*	Yes
ARC 11094		India	L	P	-	A G C - C A	T G C C T C A C C G C	C G G C T C T A G	G G G C T C G T G T G T	G G G A A T G G G	G C G G C G T A T	G G G C A A A -	G G C T G C - - - - - - - - C T A G A T	A T C C C G	G G T [A] G G	*Pi19*	-
ARC 5955		India	L	P	-	A G C - C A	T G C C T C A C C G C	C T G C G T C G T	G G G C T C G T G T G T	G G G A G T G T G	G C G G C G T A T	G G G C A A A -	G C C C G A C A - C C T A C T C G G A T	A T A C C G	A G T [A] G G	*Pi7 Pi19*	-
ARC 7047		India	L	P	-	A G C - C A	T G C C T C A C C G C	C G G C T C T G T	G G G C T C G T G T G T	G G G A G T G T G	G C G G C G T A T	G G G C A A A -	G G C C G C - - - - - - - - C T A G A T	A T A C C G	G G T [A] G G	*Pi19*	-
ARC 7098		India	L	P	-	A G C - C A	T G C C T C A C C G C	C T G C G T C G T	G G G C T C G T G T G T	G G G A A T G G G	A G T G C G T T T	G G C C - - A G	G G C T G C - - - - - - - - C T A G A T	A T A C C G	A G T [A] G G	*Pi5/Pi3 Pia Pi19*	-
ARC 7291		India	L	P	-	A G C - C A	T G C C T C A C C G C	C G G C T C T A G	G G G C T C G T G T G T	G G G A A T G G G	G C G G C G T A T	G G G C A A A -	G C C C G A C A - C C T A C T C G G A T	A T A C C G	G G T [A] G G	*Pi7 Pi19*	-
Asahi	†	Japan(Unknown)	L	P	*Pia or +*	A A C C C A	G A T C T C A C C A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C C G	A G T [A] G G	*Pia Pi19*	-
Asahinoyume	†	Japan(Aichi)	I	P	*Pii Pia*	A A C C C A	G G C C A C A C G A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C C G	A G T [A] G G	*Pish Pii Pia Pik-s Pi19*	Yes
Asanohikari	†	Japan(Aichi)	I	P	*Pii Pia*	A A C C C A	G G C C A C A C G A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G G G G T G A A T	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C T G	A G T [A] G G	*Pish Pii Pia Pi19*	Yes
Asominori	†	Japan(Fukuoka)	I	P	*Pia*	A A C C T T	G A T C T C A C C A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C T G	A G T [A] G G	*Pia Pi19*	Yes
Asu		Bhutan	L	P	-	A G T C C A	G G C T T C A T C A C	C G G C T C C A T	G G C C T C A T G T G T	G G G A A T G G G	G C G G C G T A T	- G G C A A A -	G G C C G A - - - - - - - - C C A G A T	A - C C C G	A G T [A] G G	*Pit Pi19*	-
Badari Dhan		Nepal	L	P	-	A G C - C A	G G C C A T A T C A C	C G G C G T C G G	- G C - - C G - - - - -	G G G A G T G G G	A G T G C G T T T	G G G C A A - C	G G C C G C - - - - - - - - C T A G A T	A T A C C G	G G T [A] G G	*Pi13 Pi5/Pi3 Pi19*	-
Basilanon		Philippines	L	P	-	G G C C C T	G G C T T C A T C A C	C G G C G T C G G	G G C C T C G T A A G T	G G G G G C A T G	A G T G C G T T T	G T C C - - C C	G G C C G C - - - - - - - - C T A G A T	A T C C C G	A G T [A] G G	*Pi5/Pi3 Pia Pi19*	-
Bei Khe		Cambodia	L	P	-	A G C A C T	G G C T T C A T C A C	C G G C G C T G G	G A C C T T G - - T G T	G G G A A T G G G	G C G C C G T A T	G T C C A G C C	G G C C A C C A - C T T A C T C A G A T	A T C C C G	G G T [A] G A	*Pia New gene(Pik_H04-3)*[‡] *Pi19*	-
Bekoaoba		Japan(Akita)	I	P	*(Pita) Pita-2*	A A C C T T	G G C T T T A T C G C	C T G C G T C G G	G A C C T C G T A A G A	G A G A G C G G G	G C G C C T T T G	C G C C C A A G	G C C C G C C A C C T T A C T C G G A T	C T A C C G	G G T [B] C A	*Pia Pik-s Pita Pita-2*	No
Bekogenki		Japan(Akita)	I	P	*Pib Pia*	A A C C T T	G G C C A C A C G A C	C G G T G C T G T	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	G T C C A G C C	G C C C G C C A C C T T A C T C G G A T	A A C C C G	A G T [A] G G	*Pish Pib Pia Pik-s Pi19*	Yes
Bekogonomi		Japan(Akita)	I	P	*Pib Pik*	G G C C C T	G G C C A C A C G A C	C G G T G C T G T	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	A G T C G C G A C G T A A T T C G G A G	A A C C T A	A G T [A] G G	*Pish Pib Pia Pik Pi19*	No
Bingala		Myanmar(Burma)	L	P	-	A G C A C T	G A C C T C A C C A C	C G T C T C T A G	G G C C T C G T A T G T	G G G A A T A G G	G C G C C T T T T	G T C C A G C C	G G C C G C - - - - - - - - C T A G A T	C T A C C G	G G T [A] C A	*Pia Pita*	-
BL1		Japan(Unknown)	I	P	*Pib*	A A C C T T	G G C C A C A C G A C	C G G T G C T G T	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	G G G C A A A C	G G C C G C - - - - - - - - C T A G A T	A A C C T G	A G T [A] G G	*Pish* ***Pib*** *Pi19*	Yes
Bleiyo		Thailand	L	P	-	A G C - C A	T G C C A T A T C A C	C G G C G T T A G	G G C C T C G T A T G T	G G G G G C A T G	G C G C C T T T T	G G G C A A A -	G G C C A C C A - C T T A C T C A G A T	A T C G C G	G A C - G A	*New gene(Pik_H04-3)*[‡] *Pi20*	-
Bozu	†	Japan(Hokkaido)	I	P	*Pia*	A A C C T T	G A C C T C A C C A C	T T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	C G C C C A A C	A G C C G A - - - - - - - - C C A G A T	A A C C C G	- A T - G A	***Pia***	Yes
Bozu 6	†	Japan(Hokkaido)	I	P	*Pia or +*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G A C C T C G T A A G A	A G C A G C G G G	G C G C C G T T G	G G G C A A A C	A G C C G A - - - - - - - - C C A G A T	A A C C C G	- A T - G A	*Pish*	-
Calotoc		Philippines	L	P	-	A G C C C T	G A C C T C A C C A C	C G G C G T C G G	G G C C T C G T A A G T	G G G G G C A T G	G C G C C T T T T	G T C C - - C C	G C C C G C - - - - - - A C C C A G A T	A T C C C G	A G T [A] G G	*Pia Pi19*	-
Chin Galay		Myanmar(Burma)	L	P	-	G G C C C T	G G C T T C A T C A C	C G T C T C T G T	G A C C T C G T A A G T	G G G A A T G G G	A G T G C G T T T	G G G C A A C -	G G C C G C - - - - - - - - C T A G A T	A T A C C G	G G T [A] G G	*Pi5/Pi3 Pi19*	-
Chiyohonami	†	Japan(Miyagi)	I	P	*Pia*	A A C C T T	G A T C T C A C C A C	C T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pia Pik-s Pi19*	Yes
Chiyonishiki	†	Japan(Aichi)	I	P	*Pia*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pia Pik-s Pi19*	Yes
Chubu 22		Japan(Aichi)	I	P	+	A A C C C A	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pik-s Pi19*	Yes
Chubu 32		Japan(Aichi)	I	P	*Pia*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pia Pik-s Pi19*	Yes
Chugoku 117		Japan(Hiroshima)	I	P	-	G G C C C T	G G C C A C A C G A C	C G G C T C T A G	G A C C T C G T A A G A	G A G A G C G G G	G C G C C T T T G	G G G C A A C -	G G C C G C - - - - - - - - C T A G A T	A A C C T G	A G T [A] G G	*Pish Pi19*	-
Chujo 2	†	Japan(Aichi)	I	P	-	A A C C C A	G A T C T C A C C A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C C G	A G T [A] G G	*Pia Pik-s Pi19*	-
Chukyoasahi	†	Japan(Aichi)	I	P	*Pia*	A A C C C A	G A T C T C A C C A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C T G	A G T [A] G G	*Pia Pi19*	Yes
Co 13		India	L	P	-	A G C - C A	G G C T T C A T C A C	C G G C T C T G G	G A C C T C G T A A C T	G G G A A T A G G	G C G C C G T A T	- G G C A A A -	G G C C G A - - - - - - - - C C A G A T	A T C C C G	G G T [A] G G	*Piz Pi19*	-
Daichinokaze	†	Japan(Aichi)	I	P	*Pii Pia*	A A C C C A	G G C C A C A C G A C	T T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G G C C G A - - - - - - - - C T A G A T	A A C C C G	A G T [A] G G	*Pish Pii Pia Pi19*	Yes
Davao 1		Philippines	L	P	-	A G C A C T	G G C T T C A T C A C	C G T C T C T G G	G G C C T C G T A A G T	G G G G G C A T G	G C G C C G T A T	G T C C - - C C	G C C T G C C A C C T T A C T C G G A T	C T A C C G	G G T [A] C A	*Pia Pik-s Pita*	-
Deejiaohualuo		China	U	P	-	G G C C C T	G G C T T C A T C A C	C G G C G T T G G	G G C C T C G T A A G T	G G G G G C A T G	G C G C C G T A T	G T C C - - C C	A G C C G C C A C C T T A C T C G G A T	A T A C C G	G G T [A] G G	*Pia Pik-s Pi19*	-
Deng Pao Zhai		China	I	P	-	A G T C C A	G G C T T C A T C A C	C G G C T C T G G	G G G C T C G T G T G T	G G G A G C G G G	G C G C C G T A T	G T C C A G C C	G G C C G C - - - - - - - - C C A G A T	C T A C C G	G G T [A] C A	***Pit*** *Pia Pita*	-
Dianyu 1		China	I	P	-	G G C C C T	G G C C A C A C G A C	C T G C G T C G G	G A C C T C G T A A G A	G G G A G C G G G	G C G C C T T T G	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C C G	A G T [A] G G	*Pish Pik-s Pi19*	-
Domannaka	†	Japan(Yamagata)	I	P	*Pii Pia*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G G	G G G G T G A A T	C G C C C A A G	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pii Pia Pik-s Pi19*	Yes
Dontokoi	†	Japan(Niigata)	I	P	*Pii*	A A C C T T	G G C C A C A C G A C	T T G C G T C G G	G G G C T C G T G T G T	G G G A G C G G A	G G G G T G A A T	G G G C A A A C	G C C C G C C C C G T A A C T C G G G T	A A C C T G	A G T [A] G G	*Pish Pii Pik-s Pi19*	Yes

(Continued)



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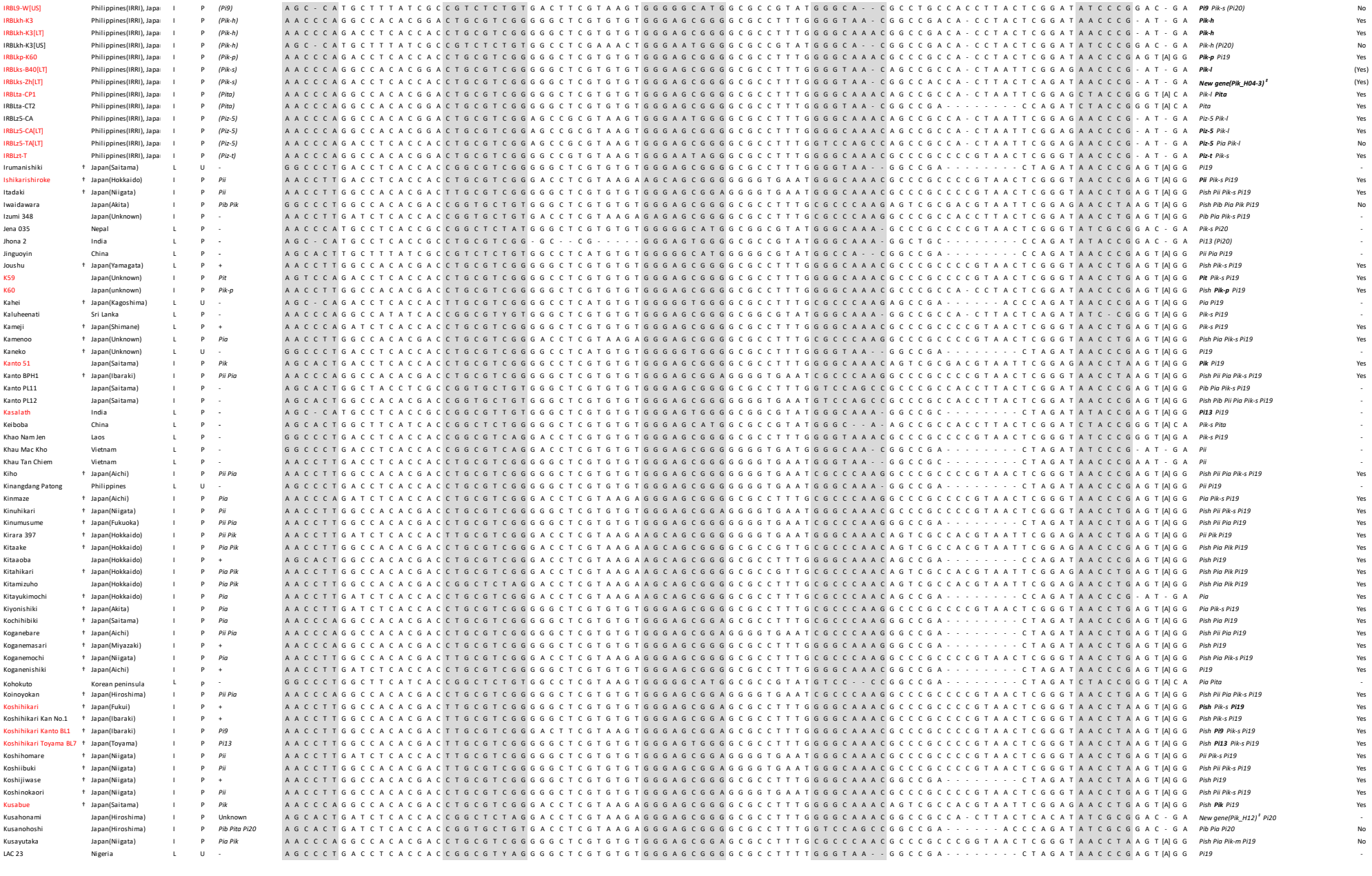

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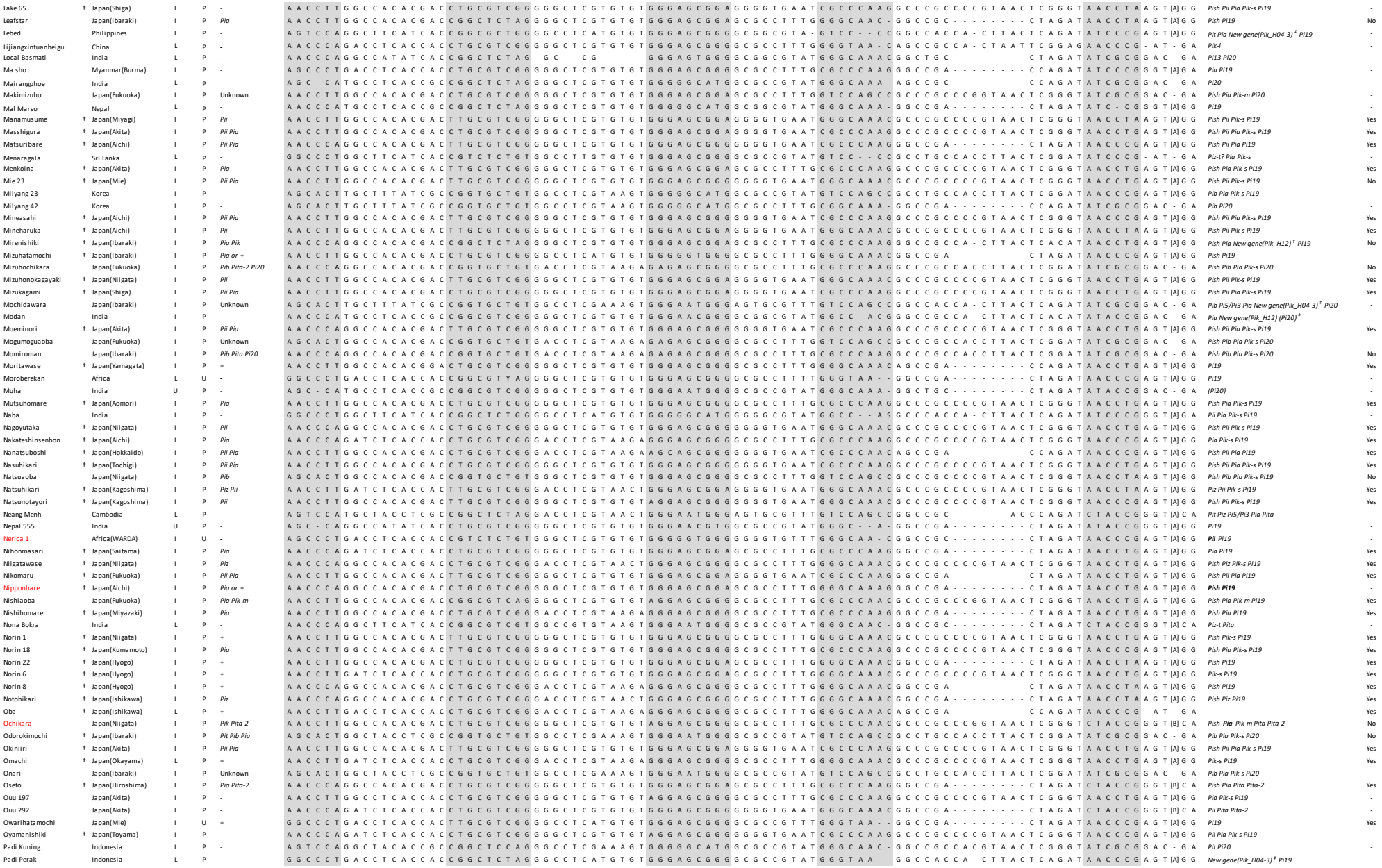

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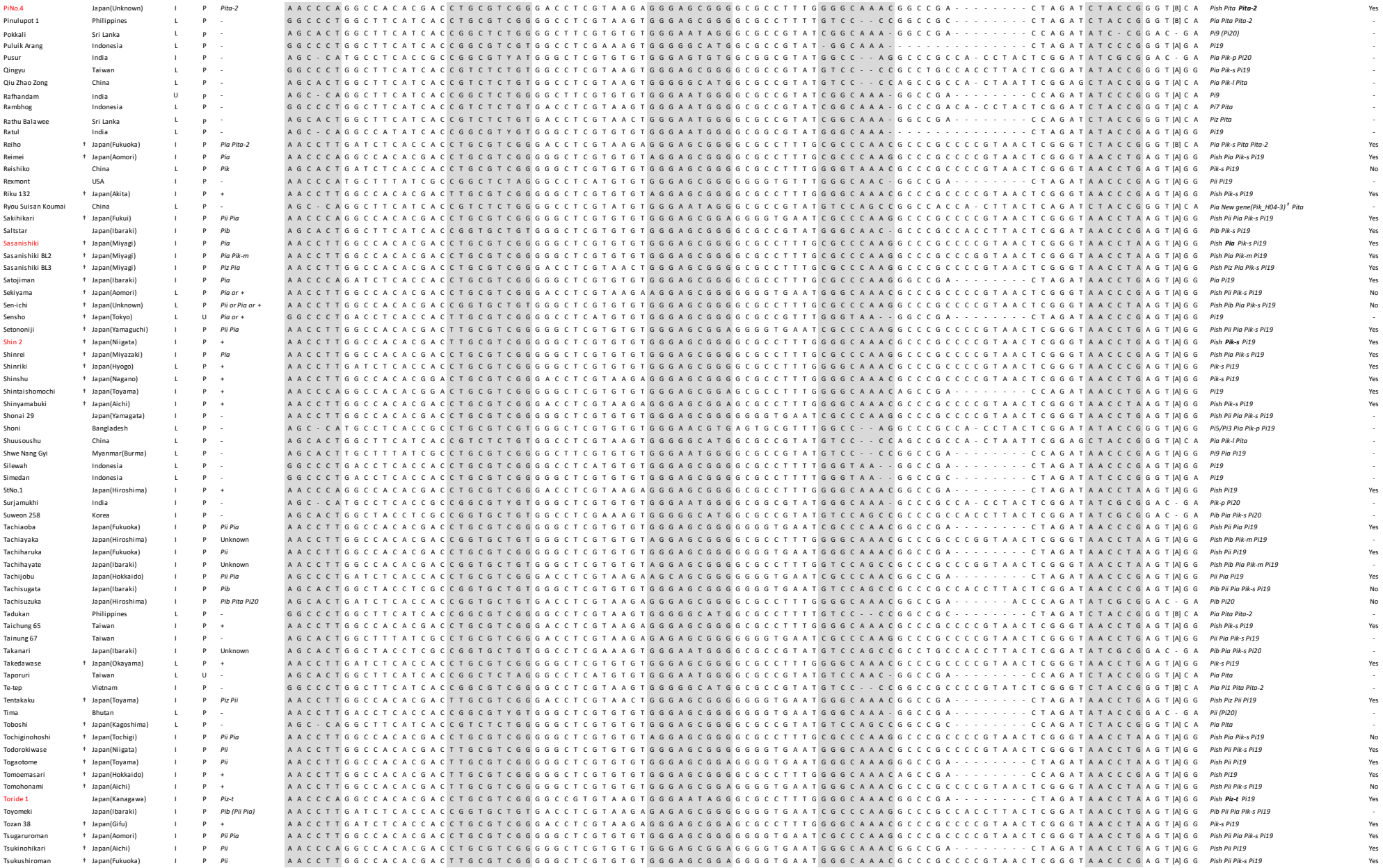

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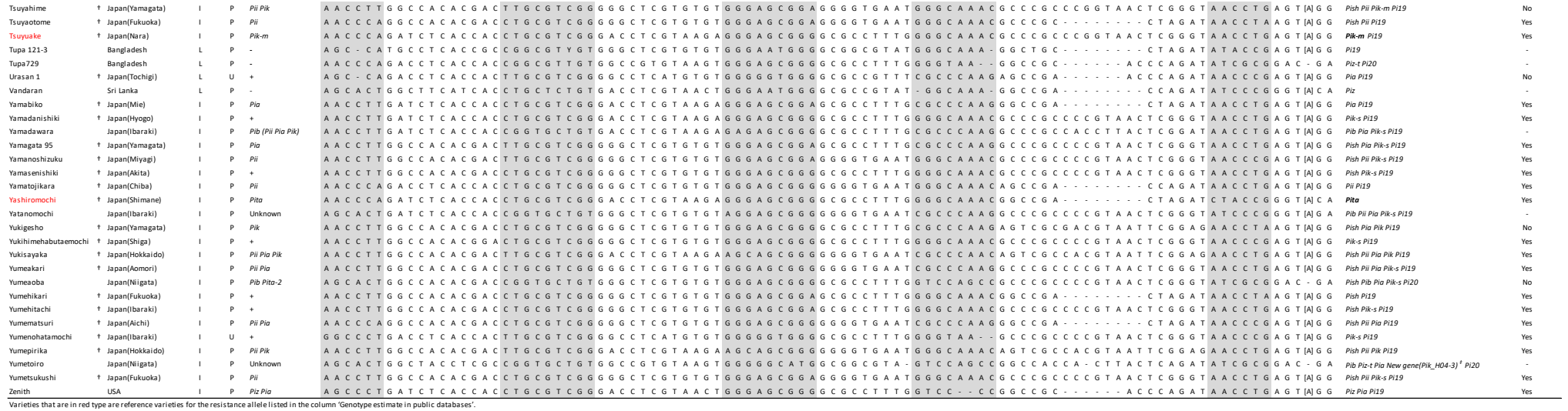

Tsuyahime	†	Japan(Yamagata)	I	P	*Pii Pik*	*Pish Pii Pik-m Pi19*	No
Tsuyaotome	†	Japan(Fukuoka)	I	P	*Pii*	*Pish Pii Pi19*	Yes
Tsuyuake	†	Japan(Nara)	I	P	*Pik-m*	***Pik-m*** *Pi19*	Yes
Tupa 121-3		Bangladesh	L	P	-	*Pi19*	-
Tupa729		Bangladesh	L	P	-	*Piz-t Pi20*	-
Urasan 1	†	Japan(Tochigi)	L	U	+	*Pia Pi19*	No
Vandaran		Sri Lanka	L	P	-	*Piz*	-
Yamabiko	†	Japan(Mie)	I	P	*Pia*	*Pia Pi19*	Yes
Yamadanishiki	†	Japan(Hyogo)	I	P	+	*Pik-s Pi19*	Yes
Yamadawara		Japan(Ibaraki)	I	P	*Pib (Pii Pia Pik)*	*Pib Pia Pik-s Pi19*	-
Yamagata 95	†	Japan(Yamagata)	I	P	*Pia*	*Pish Pia Pik-s Pi19*	Yes
Yamanoshizuku	†	Japan(Miyagi)	I	P	*Pii*	*Pish Pii Pik-s Pi19*	Yes
Yamasenishiki	†	Japan(Akita)	I	P	+	*Pish Pik-s Pi19*	Yes
Yamatojikara	†	Japan(Chiba)	I	P	*Pii*	*Pii Pi19*	Yes
Yashiromochi	†	Japan(Shimane)	I	P	*Pita*	***Pita***	Yes
Yatanomochi		Japan(Ibaraki)	I	P	Unknown	*Pib Pii Pia Pik-s Pi19*	-
Yukigesho	†	Japan(Yamagata)	I	P	*Pik*	*Pish Pia Pik Pi19*	No
Yukihimehabutaemochi	†	Japan(Shiga)	I	P	+	*Pik-s Pi19*	Yes
Yukisayaka	†	Japan(Hokkaido)	I	P	*Pii Pia Pik*	*Pish Pii Pia Pik Pi19*	Yes
Yumeakari	†	Japan(Aomori)	I	P	*Pii Pia*	*Pish Pii Pia Pik-s Pi19*	Yes
Yumeaoba		Japan(Niigata)	I	P	*Pib Pita-2*	*Pish Pib Pia Pik-s Pi20*	No
Yumehikari	†	Japan(Fukuoka)	I	P	+	*Pish Pi19*	Yes
Yumehitachi	†	Japan(Ibaraki)	I	P	+	*Pish Pik-s Pi19*	Yes
Yumematsuri	†	Japan(Aichi)	I	P	*Pii Pia*	*Pish Pii Pia Pi19*	Yes
Yumenohatamochi	†	Japan(Ibaraki)	I	U	+	*Pik-s Pi19*	Yes
Yumepirika	†	Japan(Hokkaido)	I	P	*Pii Pik*	*Pish Pii Pik Pi19*	Yes
Yumetoiro		Japan(Niigata)	I	P	Unknown	*Pish Piz-t Pia New gene(Pik_H04-3)* [d] *Pi20*	-
Yumetsukushi	†	Japan(Fukuoka)	I	P	*Pii*	*Pish Pii Pik-s Pi19*	Yes
Zenith		USA	I	P	*Piz Pia*	*Piz Pia Pi19*	Yes

Varieties that are in red type are reference varieties for the resistance allele listed in the column 'Genotype estimate in public databases'.

Varieties marked with a dagger (†) are *japonica* varieties that were used to calculate rate of concordance of the genotypes for blast resistance between the present study and publicly available data. Three alleles (*Pish* , *Pik-s* , *Pi19*), which were not in the publicly available data, were excluded from calculation.

[a] L, Landrace; I, Improved cultivar; U, Unknown

[b] P, Paddy rice; U, Upland rice

[c] Serial number in each locus

[d] Serial number in BRA1

[e] [A] indicates allele type "AAAAACCAG" and [B] indicates "TG".

[f] Resistance alleles in bold type are the target alleles in the reference variety (Table 3). *Pik-l* is an allele from 'Lijiangxintuanheigu' (Singh *et al.* 2015). Resistance alleles marked with a double dagger (‡) were discriminated from the known resistance alleles based on inoculation tests using additional isolates for the *Pik* locus (Supplemental Table 5).

Supplemental Table 2. Estimation of race-specific resistance alleles in two CSSLs, SL519 and SL521, which carry the *Piz* locus from 'Nona Bokra'

	Pyricularia oryzae				
		Piz-5 differential	*Piz-t* differential	*Piz* differential	
Race	437.1	477.1	003.0	037.1	Resistance genotype
Isolate name	IW81-04	Ai74-134	Ken54-04	24-22-1-1	
MAFF number[a]	MAFF101532	MAFF101533	MAFF101507	MAFF101519	
Variety	+ [b]	*AvrPiz5*	*AvrPizt*	*AvrPiz5 AvrPizt*	
IRBLz5-CA	S (4)[c]	R (1)	Undecidable (2)	R (0)	*Piz-5* (reference)
IRBLzt-T-19F	S (4)	S (5)	R (0)	R (0)	*Piz-t* (reference)
LTH	S (4)	S (4)	S (4)	S (5)	+ (reference) [b]
SL519	S (3)	S (5)	R (0)	R (0)	***Piz-t***
SL521	S (4)	S (4)	R (0)	R (0)	***Piz-t***

[a] Accession numbers at the Genetic Resources Center, National Agriculture and Food Research Organization, Japan (https://www.gene.affrc.go.jp/).

[b] Plus signs indicate absence of resistance alleles or avilurent genes.

[c] Numbers in parentheses indicate *Pyricularia oryzae* the disease score: 0 to 2 are resistant (R), 3 to 5 are susceptible (S) responses.

Supplemental Table 3. Primers used for direct sequencing of the *Pita-2* gene

Primer pair name/ Primer name	Forward primer sequences (5' to 3')	Reverse primer sequences (5' to 3')	Range covered by the amplicon	Objective
AoL1135_AOL1136	GATTTGGTATGGGAGGAGCA	TAAACCTGGCCCAAGACAAG	Exon 1 (5'UTR) and Exon 2 (5'UTR)	Acquisition of amplicon and cycle sequencing
AoL1137_AOL1138	TTGCTTGCCTCAGTAGACGA	TGCTTCTTGAAAAGGGGAGA	Exon 2 (5'UTR) and Exon 3 (5'UTR, CDS)	Acquisition of amplicon and cycle sequencing
AoL1139_AOL1140	AACCGACTCCCTCTTGGAAT	ATTTGTCGGCCACATCTTTC	Exon 4 (CDS)	Acquisition of amplicon and cycle sequencing
AoL1141_AOL1142	GTCCGCTGTTCCTGCTCTAC	GCTCTGCCATACAGGACCAT	Exon 4 (CDS)	Acquisition of amplicon and cycle sequencing
AoL1143_AOL1144	GCAACTTACAGGCATGCAGA	TGCTGCGAATGTAGAGGTTG	Exon 4 (CDS)	Acquisition of amplicon and cycle sequencing
AoL1145_AOL1179	TGCCACGATCATATTGAGGA	AACGTGGGTGTATGTGTCACA	Exon 4 (CDS) and Exon 5 (CDS, 3'UTR)	Acquisition of amplicon and cycle sequencing
AOL1188	ATCTGGCAGGTGTAGATCTGG		Exon 4 (CDS)	Cycle sequencing for the AoL1143_AOL1144 amplicon
AOL1196		GGAGTAGGGACTACACAGATG	Exon 4 (CDS)	Cycle sequencing for the AoL1143_AOL1144 amplicon
AOL1352	CATCTGTGTAGTCCCTACTCC		Exon 4 (CDS) and Exon 5 (CDS, 3'UTR)	Cycle sequencing for the AoL1145_AOL1179 amplicon
AOL1170	TGCAGGTGCTAAGAGAAGCA		Exon 5 (CDS, 3'UTR)	Cycle sequencing for the AoL1145_AOL1179 amplicon
AOL1195		TCAAGAGATACAACACGCGTTG	Exon 4 (CDS) and Exon 5 (CDS, 3'UTR)	Cycle sequencing for the AoL1145_AOL1179 amplicon
AOL1180		CTTCCTCGCCCAAAAACATA	Exon 4 (CDS) and Exon 5 (CDS, 3'UTR)	Cycle sequencing for the AoL1145_AOL1179 amplicon

UTR, untranslated region; CDS, coding sequence.

Supplemental Table 4. SNP haplotypes at ten loci and their genotypes for blast resistance

Chromosome number (Chr.)[a]

Locus	Chr. 1: No. 1, IRGSP-1.0 2680046, Assay name FA44467	No. 2, 2681202, FA44453	2682019	No. 3, 2682651, FA44455	No. 4, 2683065, FA44461	2684988	No. 5, 2688550, FA44482	No. 6, 2688828, FA44483	Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]	No. of varieties	(%)	Representative varieties[d]
Pit	A	G	*Pit* CDS_US	T	C	*Pit* CDS_DS	C	A	AGTCCA	T	Pit_H01	*Pit*	6	(1.6)	**K59**, **Deng Pao Zhai**, Asu
	A	A		C	C		C	A	AACCCA	C	Pit_H02	-	98	(26.6)	Nipponbare, Momiroman, Hamasari
	A	A		C	C		T	T	AACCTT	C	Pit_H03	-	156	(42.3)	Koshihikari, Fukuhibiki, Leafstar
	A	G		C	A		C	T	AGCACT	C	Pit_H04	-	43	(11.7)	Hokuriku 193, Takanari, Kusahonami
	G	G		C	C		C	T	GGCCCT	C	Pit_H05	-	29	(7.9)	Sensho, Owarihatamochi, Iwaidawara
	A	G		C	C		C	T	AGCCCT	C	Pit_H06	-	8	(2.2)	Hoshiyutaka, Tachijobu, Zenith
	A	G		C	-		C	A	AGC-CA	C	Pit_H07	-	29	(7.9)	Kahei, IR 64, Kasalath

Locus	Chr. 1: No. 1, IRGSP-1.0 32985740, Assay name FA4649	No. 2, 33074934, FA4645	No. 3, 33075459, FA4644	No. 4, 33080208, FA4636	No. 5, 33101529, FA4627	33141127	33144999	No. 6, 33146248, FA4650	No. 7, 33146996, FA4651	No. 8, 33148998, FA4652	No. 9, 33151594, FA4654	No. 10, 33174003, FA4665	No. 11, 33174848, FA4667	Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]		No. of varieties	(%)	Representative varieties[d]
Pish	G	G	C	C	A	*Pish* CDS_US	*Pish* CDS_DS	C	A	C	G	A	C	GGCCACACGAC	GGC	Pish_H01	*Pish*		178	(48.2)	**Nipponbare, Koshihikari**, Fukuhibiki
	T	G	C	C	A			C	A	C	G	G	A	TGCCACACGGA	TGA	Pish_H02	*Pi35*		2	(0.5)	**Hokkai 188**, Aokei IL2
	G	A	T	C	T			C	A	C	C	A	C	GATCTCACCAC	GCC	Pish_H03	-		47	(12.7)	Kimmaze, Kuhonami, Kirara 397
	G	A	C	C	T			C	A	C	C	A	C	GACCTCACCAC	GCC	Pish_H04	-	*	41	(11.1)	Sensho, Owarihatamochi, Kahei
	G	G	C	C	A			C	A	C	G	G	A	GGCCACACGGA	GGA	Pish_H05	-		15	(4.1)	Yukihimehabutaemochi, Shintaishomochi, Shinshu
	T	G	C	T	T			T	A	T	C	G	C	TGCTTTATCGC	TCC	Pish_H06	-		15	(4.1)	Mochidawara, IR 24, Habataki
	G	G	C	T	A			C	C	T	C	G	C	GGCTACCTCGC	GCC	Pish_H07	-	*	9	(2.4)	IR 64, Hokuriku 193, Takanari
	G	G	C	T	T			C	A	T	C	A	C	GGCTTCATCAC	GCC	Pish_H08	-	*	34	(9.2)	Tadukan, Davao 1, Taporuri, Basilanon, Bei Khe, Naba
	T	G	C	C	T			C	A	C	C	G	C	TGCCTCACCGC	TCC	Pish_H09	-	*	16	(4.3)	Pusur, Tupa 121-3, Kasalath, Modan
	G	G	C	T	T			T	A	T	C	G	C	GGCTTTATCGC	GCC	Pish_H10	-		2	(0.5)	Bekoaoba, Tainung 67
	G	G	C	C	A			T	A	T	C	A	C	GGCCATATCAC	GCC	Pish_H11	-		5	(1.4)	Badari Dhan, Kaluheenati, Local Basmati
	G	G	C	C	T			C	A	C	C	A	C	GGCCTCACCAC	GCC	Pish_H12	-		1	(0.3)	Ouu 197
	G	G	C	C	T			C	A	C	C	G	C	GGCCTCACCGC	GCC	Pish_H13	-		1	(0.3)	Anjana Dhan
	G	G	C	T	A			C	A	C	C	G	C	GGCTACACCGC	GCC	Pish_H14	-		1	(0.3)	Padi Kuning
	T	G	C	C	A			T	A	T	C	A	C	TGCCATATCAC	TCC	Pish_H15	-	*	1	(0.3)	Bleiyo
	T	G	C	T	A			C	C	T	C	G	C	TGCTACCTCGC	TCC	Pish_H16	-		1	(0.3)	Neang Menh

(Continued)

Locus	Assay name / No. / IRGSP-1.0 (Chr. 2)	FA4424 / 1 / 35089605	FA4422 / 2 / 35090234	FA4416 / 3 / 35092033	FA4408 / 4 / 35095702	FA4407 / 5 / 35095970	FA4404 / 6 / 35097776	35108842	FA4401 / 7 / 35111607	35115834	FA4439 / 8 / 35133756	FA4446 / 9 / 35138569	Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]		No. of varieties	(%)	Representative varieties[d]
Pib		C	G	G	T	G	C	*Pib* CDS_US	T	*Pib* CDS_DS	G	T	CGGTGCTGT	T	Pib_H01	*Pib*		39	(10.6)	**BL 1**, Fukuhibiki, Momiroman
		C	T	G	C	G	T		C		G	G	CTGCGTCGG	C	Pib_H02	-		175	(47.4)	Nipponbare, Fujisaka 5, Hinohikari
		T	T	G	C	G	T		C		G	G	TTGCGTCGG	C	Pib_H03	-		73	(19.8)	Koshihikari, Hamasari, Sensho
		C	G	G	C	T	C		T		A	G	CGGCTCTAG	C	Pib_H04	-		18	(4.9)	Kusahonami, Leafstar, Hoshiyutaka
		C	G	T	C	T	C		T		G	T	CGTCTCTGT	C	Pib_H05	-		15	(4.1)	Hokuriku 193, Guizhao 2, Nerica 1
		C	G	G	C	G	T		C		G	G	CGGCGTCGG	C	Pib_H06	-	*	8	(2.2)	Tadukan, Te-tep, Muha, Basilanon
		C	G	G	C	G	T		C		A	G	CGGCGTCAG	C	Pib_H07	-	*	3	(0.8)	Nishiaoba, Khao Nam Jen, Khau Mac Kho
		C	G	G	C	G	T		T		G	T	CGGCGTTGT	C	Pib_H08	-	*	4	(1.1)	Kasalath, Akamai_Kanto, Akamai_Kochi
		C	G	T	C	T	C		T		G	G	CGTCTCTGG	C	Pib_H09	-	*	3	(0.8)	Toboshi, Davao 1, Ryou Suisan Koumai
		C	G	G	C	T	C		T		G	G	CGGCTCTGG	C	Pib_H10	-	*	7	(1.9)	Deng Pao Zhai, Naba, Keiboba
		C	G	G	C	G	T		Y		G	T	CGGCGTYGT	C	Pib_H11	-	*	5	(1.4)	Tupa 121-3, Kaluheenati, Ratul
		C	T	G	C	G	T		C		G	T	CTGCGTCGT	C	Pib_H12	-		3	(0.8)	ARC 5955, ARC 7098, Shoni
		C	G	G	C	G	T		C		G	T	CGGCGTCGT	C	Pib_H13	-	*	2	(0.5)	Nona Bokra, Puluik Arang
		C	G	G	C	G	C		T		G	G	CGGCGCTGG	C	Pib_H14	-	*	2	(0.5)	Bei Khe, Lebed
		C	G	G	C	G	T		Y		A	G	CGGCGTYAG	C	Pib_H15	-	*	2	(0.5)	LAC 23, Moroberekan
		C	G	G	C	T	C		T		G	T	CGGCTCTGT	C	Pib_H16	-		2	(0.5)	ARC 7047, Kohokuto
		C	G	G	C	G	T		T		G	G	CGGCGTTGG	C	Pib_H17	-		1	(0.3)	Deejiaohualuo
		C	G	G	C	G	T		T		A	G	CGGCGTTAG	C	Pib_H18	-	*	1	(0.3)	Bleiyo
		C	G	G	C	T	C		C		A	G	CGGCTCCAG	C	Pib_H19	-		1	(0.3)	Padi Kuning
		C	G	G	C	G	T		Y		A	T	CGGCGTYAT	C	Pib_H20	-		1	(0.3)	Pusur
		C	T	G	C	T	C		T		G	T	CTGCTCTGT	C	Pib_H21	-		1	(0.3)	Vandaran
		C	G	G	C	T	C		C		A	T	CGGCTCCAT	C	Pib_H22	-		1	(0.3)	Asu
		C	G	T	C	T	C		T		A	G	CGTCTCTAG	C	Pib_H23	-		1	(0.3)	Bingala
		C	G	G	C	T	C		T		A	T	CGGCTCTAT	C	Pib_H24	-		1	(0.3)	Jena 035

Locus	Assay name / No. / IRGSP-1.0 (Chr. 6)	FA5376 / 1 / 10361215	10372676	FA4676 / 2 / 10379796	FA4678 / 3 / 10382967	FA4679 / 4 / 10384890	FA4680 / 5 / 10385269	FA5378 / 6 / 10389855	FA4697 / 7 / 10421778	FA4698 / 8 / 10422671	FA4683 / 9 / 10422831	FA4702 / 10 / 10426588	FA4703 / 11 / 10427313	FA4704 / 12 / 10427757	10471201	Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]		No. of varieties	(%)	Representative varieties[d]
Piz		G	*Piz* locus_US	A	C	C	T	C	G	T	A	A	C	T	*Piz* locus_DS	GACCTCGTAACT	CTCTC	Piz_H01	*Piz*		13	(3.5)	**Fukunishiki**, Zenith, **Hanaechizen**
		G		G	C	C	G	T	G	T	A	A	G	T		GGCCGTGTAAGT	CGTTG	Piz_H02	*Piz-t*	*	5	(1.4)	**Toride 1**, **IRBLzt-T**, Yumetoiro, Nona Bokra
		A		G	C	C	G	C	G	T	A	A	G	T		AGCCGCGTAAGT	CGCTG	Piz_H03	*Piz-5*		3	(0.8)	**IRBLz5-CA[LT]**, **IRBLz5-TA[LT]**, IRBLz5-CA
		G		A	C	T	T	C	G	T	A	A	G	T		GACTTCGTAAGT	TTCTG	Piz_H04	*Pi9*		3	(0.8)	**IRBL9-W[LT], IRBL9-W[US], Koshihikari Kanto BL1**
		G		G	G	C	T	C	G	T	G	T	G	T		GGGCTCGTGTGT	CTCTG	Piz_H05	-	*	207	(56.1)	Nipponbare, Koshihikari, Fukuhibiki, Kasalath
		G		A	C	C	T	C	G	T	A	A	G	A		GACCTCGTAAGA	CTCTG	Piz_H06	-		74	(20.1)	Kusahonami, Momiroman, Asahinoyume
		G		G	C	C	T	C	G	A	A	A	G	T		GGCCTCGAAAGT	CTCAG	Piz_H07	-	*	10	(2.7)	Hokuriku 193, Takanari, IR 64
		G		G	C	C	T	C	A	T	G	T	G	T		GGCCTCATGTGT	CTCTG	Piz_H08	-	*	16	(4.3)	Sensho, Owarihatamochi, Naba
		G		G	C	C	T	C	G	T	A	A	G	T		GGCCTCGTAAGT	CTCTG	Piz_H09	-		19	(5.1)	IR 24, Te-tep, Hokurikumochi 181
		G		G	C	C	T	C	G	T	G	T	G	T		GGCCTCGTGTGT	CTCTG	Piz_H10	-		2	(0.5)	K59, Kanto 51
		G		A	C	C	T	C	G	T	G	T	G	T		GACCTCGTGTGT	CTCTG	Piz_H11	-	*	2	(0.5)	Khao Nam Jen, Khau Mac Kho
		G		G	C	C	T	C	G	A	A	A	C	T		GGCCTCGAAACT	CTCAC	Piz_H12	-		2	(0.5)	IRBL5-M[US], IRBLkh-K3[US]
		G		G	C	C	T	C	G	T	A	T	G	T		GGCCTCGTATGT	CTCTG	Piz_H13	-	*	3	(0.8)	Bingala, Bleiyo, Ryou Suisan Koumai
		G		G	C	T	T	C	G	T	G	T	G	T		GGCTTCGTGTGT	TTCTG	Piz_H14	*Pi9*	*	3	(0.8)	Pokkali, Rafhandam, Shwe Nang Gyi
		G		A	C	C	T	C	G	T	A	A	G	T		GACCTCGTAAGT	CTCTG	Piz_H15	-		2	(0.5)	Chin Galay, Rambhog
		-		G	C	-	-	C	G	-	-	-	-	-		-GC--CG-----	--C--	Piz_H16	-		3	(0.8)	Badari Dhan, Jhona 2, Local Basmati
		G		G	C	C	T	T	G	T	G	T	G	T		GGCCTTGTGTGT	CTTTG	Piz_H17	*Piz-t?*	*	1	(0.3)	Menaragala
		G		A	C	C	T	T	G	-	-	T	G	T		GACCTTG--TGT	CTT-G	Piz_H18	-	*	1	(0.3)	Bei Khe

(Continued)

Locus	Chr. 6											Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]	No. of varieties	(%)	Representative varieties[d]
Assay name		FA5269	FA5270	FA5271	FA5280	FA5294	FA5283	FA5288	FA5292	FA5293								
No.		1	2	3	4	5	6	7	8	9								
IRGSP-1.0	11677578	17096200	17105485	17121368	17159082	17161116	17166899	17174653	17186714	17240935	19614430							
Pi13	*Pi13* locus_US	G	G	G	A	G	T	G	G	G	*Pi13* locus_DS	GGGAGTGGG	AGTG	Pi13_H01	*Pi13*	6	(1.6)	**Kasalath**, **Koshihikari Toyama BL7**, Anjana Dhan
		G	G	G	A	G	C	G	G	A		GGGAGCGGA	AGCG	Pi13_H02	-	76	(20.6)	Nipponbare, Koshihikari, Hamasari
		G	G	G	A	G	C	G	G	G		GGGAGCGGG	AGCG	Pi13_H03	-	159	(43.1)	Fukuhibiki, Kusahonami, Sensho, Sasanishiki
		A	G	C	A	G	C	G	G	G		AGCAGCGGG	AGCG	Pi13_H04	-	22	(6)	Ishikarishiroke, Yumepirika, Kitayukimochi
		A	G	G	A	G	C	G	G	G		AGGAGCGGG	AGCG	Pi13_H05	-	20	(5.4)	Fujisaka 5, Hoshiaoba, Ochikara
		G	G	G	G	G	C	A	T	G		GGGGGCATG	GGCT	Pi13_H06	-	30	(8.1)	Yumetoiro, IR 64, Guizhao 2
		G	G	G	A	A	T	G	G	G		GGGAATGGG	AATG	Pi13_H07	-	27	(7.3)	Hokuriku 193, Takanari, Mochidawara
		G	A	G	A	G	C	G	G	G		GAGAGCGGG	AGCG	Pi13_H08	-	9	(2.4)	Momiroman, Mizuhochikara, Yamadawara
		G	G	G	G	G	T	G	G	G		GGGGGTGGG	GGTG	Pi13_H09	-	6	(1.6)	Mizuhatamochi, Kahei, Nerica 1
		G	G	G	A	A	T	A	G	G		GGGAATAGG	AATG	Pi13_H10	-	6	(1.6)	Toride 1, IRBLzt-T, Bingala
		G	G	G	A	G	T	G	T	G		GGGAGTGTG	AGTT	Pi13_H11	-	3	(0.8)	ARC 5955, ARC 7047, Pusur
		G	G	G	A	G	C	A	T	G		GGGAGCATG	AGCT	Pi13_H12	-	2	(0.5)	Hong Cheuh Zai, Keiboba
		G	G	G	A	A	C	G	T	G		GGGAACGTG	AACT	Pi13_H13	-	2	(0.5)	Nepal 555, Shoni
		G	G	G	A	A	C	G	G	G		GGGAACGGG	AACG	Pi13_H14	-	1	(0.3)	Modan

Locus	Chr. 9											Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]		No. of varieties	(%)	Representative varieties[d]
Assay name	FA4515	FA4505		FA4494	FA4495	FA4501		FA4526	FA4527	FA4533	FA4536								
No.	1	2		3	4	5		6	7	8	9								
IRGSP-1.0	9657397	9663840	9667216	9667330	9668417	9672424	9674617	9787343	9787450	9834576	9859957								
Pii	G	G	*Pii* CDS_US	G	G	T	*Pii* CDS_DS	G	A	A	T	GGGGTGAAT	GGT	Pii_H01-1	*Pii*		101	(27.4)	**Fujisaka 5**, **Ishikarishiroke**, Hitomebore
	G	G		G	G	T		G	T	T	T	GGGGTGTTT	GGT	Pii_H01-2	*Pii*		4	(1.1)	**Nerica 1**, Hoshiyutaka, AC 540
	A	G		T	G	C		G	T	T	T	AGTGCGTTT	GTC	Pii_H02	*Pi5/Pi3*	*	14	(3.8)	**IRBL5-M[LT]**, **IRBL5-M**, **IRBL3-CP4[LT]**, **IRBL3-CP4**, Hokuriku 193, Basilanon
	G	C		G	C	C		T	T	T	G	GCGCCTTTG	CGC	Pii_H03	-		166	(45)	Nipponbare, Koshihikari, Fukuhibiki, Kusahonami
	G	C		G	C	C		G	T	A	T	GCGCCGTAT	CGC	Pii_H04	-	*	44	(11.9)	Takanari, Hokurikumochi 181, IR 64
	G	C		G	C	C		G	T	T	G	GCGCCGTTG	CGC	Pii_H05	-		6	(1.6)	Hokkai 188, Kitaake, Akage
	G	C		G	C	C		G	T	T	T	GCGCCGTTT	CGC	Pii_H06	-	*	4	(1.1)	Sensho, Owarihatamochi, Gaisen mochi
	G	C		G	C	C		T	T	T	T	GCGCCTTTT	CGC	Pii_H07	-	*	9	(2.4)	Moroberekan, Tadukan, Bleiyo, LAC23
	G	C		G	G	C		G	T	A	T	GCGGCGTAT	CGC	Pii_H08	-	*	15	(4.1)	Modan, Pusur, Kasalath, Tupa 121-3
	G	C		G	G	C		G	T	A	-	GCGGCGTA-	CGC	Pii_H09	-		3	(0.8)	Yumetoiro, Anjana Dhan, Lebed
	G	G		G	G	C		G	T	A	T	GGGGCGTAT	GGC	Pii_H10	*Pii*	*	2	(0.5)	Jinguoyin, Naba
	G	G		G	G	T		G	A	T	G	GGGGTGATG	GGT	Pii_H11	*Pii*	*	1	(0.3)	Khau Mac Kho

(Continued)

Locus	No. IRGSP-1.0	Chr. 11										Haplotype		Haplotype ID	Genotype[c]		No. of varieties	(%)	Representative varieties[d]
		6521353	6540957	6542301	6543100	6544401	6561363	6634911	6638905	6656541	6707030								
	Assay name	1	2		3	4		5	6	7	8	Standard set	Core set[b]						
		FA4608	FA4605	*Pia* CDS_US	FA4598	FA4615	*Pia* CDS_DS	FA4617	FA4620	FA4624	FA4625								
		C	G		C	C		C	A	A	G	CGCCCAAG	C	Pia_H01-1	*Pia*		99	(26.8)	**Sasanishiki**, **Aichiasahi**, Fukuhibiki, Momiroman
		C	G		C	C		C	A	A	C	CGCCCAAC	C	Pia_H01-2	*Pia*		22	(6)	Bozu, Ochikara, Tachiaoba, Kitamizuho
		G	G		G	C		A	A	A	G	GGGCAAAG	G	Pia_H02	-		4	(1.1)	Nipponbare, Hanaechizen, Koganemasari
		G	G		G	C		A	A	A	C	GGGCAAAC	G	Pia_H03	-		122	(33.1)	Koshihikari, Kusahonami, Hoshiyutaka
		G	T		C	C		A	G	C	C	GTCCAGCC	C	Pia_H04	*Pia*	*	30	(8.1)	Hokuriku 193, Takanari, Mochidawara, Deng Pao Zhai, Bei Khe
		G	T		C	C		-	-	C	C	GTCC--CC	C	Pia_H05	*Pia*	*	17	(4.6)	Te-tep, Tadukan, Zenith, Basilanon, Qiu Zhao Zong
		G	G		G	T		A	A	-	-	GGGTAA--	G	Pia_H06	-		13	(3.5)	Sensho, Owarihatamochi, Yumenohatamochi
		G	T		C	C		A	A	C	-	GTCCAAC-	C	Pia_H07	*Pia*		2	(0.5)	Guizhao 2, Taporuri
		G	G		G	C		A	A	A	-	GGGCAAA-	G	Pia_H08	-	*	17	(4.6)	Bleiyo, Muha, Tupa 121-3, Kasalath
		G	G		G	C		A	A	C	-	GGGCAAC-	G	Pia_H09	-	*	7	(1.9)	Leafstar, Nona Bokra, Saltstar
Pia		G	G		G	T		A	A	A	C	GGGTAAAC	G	Pia_H10	-	*	2	(0.5)	Khao Nam Jen, Reishiko
		C	G		G	C		A	A	A	-	CGGCAAA-	G	Pia_H11	-		6	(1.6)	Milyang 42, IR 36, Pokkali
		G	G		G	T		A	A	-	C	GGGTAA-C	G	Pia_H12	-		6	(1.6)	IRBL19-A, IRBLkh-K3, IRBLks-B40[LT]
		-	G		G	C		A	A	A	-	-GGCAAA-	G	Pia_H13	-		4	(1.1)	Asu, Co 13, Puluik Arang
		G	G		G	C		-	-	A	-	GGGC--A-	G	Pia_H14	-		4	(1.1)	Anjana Dhan, Hong Cheuh Zai, Keiboba
		G	G		G	C		A	A	-	C	GGGCAA-C	G	Pia_H15	-	*	3	(0.8)	Badari Dhan, Khau Mac Kho, Nerica 1
		G	G		C	C		-	-	A	G	GGCC--AG	C	Pia_H16	*Pia*	*	3	(0.8)	ARC 7098, Pusur, Shoni
		G	G		G	C		A	-	-	C	GGGCA--C	G	Pia_H17	-		3	(0.8)	IRBL5-M[US], IRBL9-W[US], IRBLkh-K3[US]
		G	G		C	C		A	-	-	C	GGCCA--C	C	Pia_H18	*Pia*	*	2	(0.5)	IRBL5-M[LT], Jinguoyin
		G	G		G	C		A	A	C	C	GGGCAACC	G	Pia_H19	-		1	(0.3)	AC 540
		G	G		C	C		-	A	C	G	GGCC-ACG	C	Pia_H20	*Pia*	*	1	(0.3)	Modan
		G	G		C	C		-	-	A	S	GGCC--AS	C	Pia_H21	*Pia*	*	1	(0.3)	Naba

(Continued)

Locus	Assay name	IRGSP-1.0 No.	Chr. 11																			Haplotype		Haplotype ID	Genotype[c]		No. of varieties	(%)	Representative varieties[d]
			1 27817940	2 27818557	3 27820870	4 27823073	5 27823722	6 27828066	27978523	7 no hit	8 no hit	9 no hit	10 no hit	11 no hit	12 no hit	13 no hit	14 no hit	27988874	15 27992151	16 27993468	17 27995372	18 27995713	19 27996426	20 28006310	Standard set	Core set[b]					
			FA4742	FA4740	FA4737	FA4735	FA4734	FA4732		FA4710	FA4712	FA5375	FA4717	FA4718	FA4721	FA4723	FA4726		FA4729	FA4750	FA4751	FA4752	FA4753	FA4758							
			A	G	T	C	G	C	*Pik* CDS_US	C	A	C	G	T	A	A	T	*Pik* CDS_DS	T	C	G	G	A	G	AGTCGCCACGTAATTCGGAG	GGCCACTAATT	Pik_H01-1	*Pik*		12	(3.3)	**Kusabue**, Hamaasahi, Kirara 397
			A	G	T	C	G	C		G	A	C	G	T	A	A	T		T	C	G	G	A	G	AGTCGCGACGTAATTCGGAG	GGCGACTAATT	Pik_H01-2	*Pik*		4	(1.1)	**Kanto 51**, Iwaidawara, Yukigesho
			G	C	C	C	G	C		C	C	G	G	T	A	A	C		T	C	G	G	G	T	GCCCGCCCGGTAACTCGGGT	CGCCCGTAACT	Pik_H02	*Pik-m*		13	(3.5)	**Tsuyuake**, **Hinohikari Kanto BL2**, Himenomochi
			G	C	C	C	G	C		C	A	-	C	C	T	A	C		T	C	G	G	A	T	GCCCGCCA-CCTACTCGGAT	CGCCA-CTACT	Pik_H03	*Pik-p*	*	5	(1.4)	**K60**, **IRBLkp-K60**, Pusur
			G	C	C	C	G	C		C	C	C	G	T	A	A	C		T	C	G	G	G	T	GCCCGCCCCGTAACTCGGGT	CGCCCCTAACT	Pik_H04-1	*Pik-s*		127	(34.4)	**Shin2**, Koshihikari, Hokuriku 193
			A	G	C	C	G	C		C	A	-	C	T	A	A	T		T	C	G	G	A	G	AGCCGCCA-CTAATTCGGAG	GGCCA-TAATT	Pik_H04-2	*Pik-l*	*	12	(3.3)	**IRBLks-B40[LT]** , Qiu Zhao Zong, IRBLta-CP1, Lijiangxintuanheigu
			G	G	C	C	A	C		C	A	-	C	T	T	A	C		T	C	A	G	A	T	GGCCACCA-CTTACTCAGAT	GACCA-TTACT	Pik_H04-3	New gene	*	11	(3)	**IRBLks-Zh[LT]**, Mochidawara, IR 64, Yumetoiro
			G	G	C	C	G	A		C	A	-	C	C	T	A	C		T	C	G	G	A	T	GGCCGACA-CCTACTCGGAT	GGACA-CTACT	Pik_H05	*Pik-h*	*	3	(0.8)	**IRBLkh-K3**, **IRBLkh-K3[LT]**, IRBLkh-K3[US]
			G	C	C	C	G	A		C	A	-	C	C	T	A	C		T	C	G	G	A	T	GCCCGACA-CCTACTCGGAT	CGACA-CTACT	Pik_H06	*Pi7*	*	4	(1.1)	**IRBL7-M[LT]** , ARC 5955, Rambhog
			G	G	C	C	G	C		C	C	C	G	T	A	T	C		T	C	G	G	G	T	GGCCGCCCCGTATCTCGGGT	GGCCCCTATCT	Pik_H07	*Pi1*	*	2	(0.5)	**IRBL1-CL[LT]**, Te-tep
			G	G	C	C	G	A		-	-	-	-	-	-	-	-		C	T	A	G	A	T	GGCCGA--------CTAGAT	GGA-------C	Pik_H08	-		73	(19.8)	Nipponbare, Moroberekan, Sensho
			A	G	C	C	G	A		-	-	-	-	-	-	-	-		C	C	A	G	A	T	AGCCGA--------CCAGAT	GGA-------C	Pik_H09	-		15	(4.1)	Tomoemasari, Kitaaoba, Hoshimaru
			G	C	C	C	G	C		C	A	C	C	T	T	A	C		T	C	G	G	A	T	GCCCGCCACCTTACTCGGAT	CGCCACTTACT	Pik_H10	*Pik-s*		13	(3.5)	Momiroman, Tachisugata, Yamadawara
			G	C	C	T	G	C		C	A	C	C	T	T	A	C		T	C	G	G	A	T	GCCTGCCACCTTACTCGGAT	CGCCACTTACT	Pik_H11	*Pik-s*	*	9	(2.4)	Takanari, IR 24, Davao 1
			G	G	C	C	G	C		C	A	-	C	T	T	A	C		T	C	A	C	A	T	GGCCGCCA-CTTACTCACAT	GGCCA-TTACT	Pik_H12	New gene	*	6	(1.6)	Kusahonami, Hoshiyutaka, Akenohoshi, Modan
			G	G	C	C	G	A		-	-	-	-	-	-	A	C		C	C	A	G	A	T	GGCCGA------ACCCAGAT	GGA-----ACC	Pik_H13	-		2	(0.5)	Kusanohoshi, Tachisuzuka
			G	G	C	C	G	C		-	-	-	-	-	-	-	-		C	T	A	G	A	T	GGCCGC--------CTAGAT	GGC-------C	Pik_H14	-	*	16	(4.3)	Hamasari, Leafstar, Tadukan, Basilanon, Kasalath
			G	G	C	C	G	C		-	-	-	-	-	-	-	-		C	C	A	G	A	T	GGCCGC--------CCAGAT	GGC-------C	Pik_H15	-	*	5	(1.4)	Deng Pao Zhai, Toboshi, IRBL5-M[US]
			G	G	C	C	G	A		-	-	-	-	-	-	-	-		C	C	A	G	A	T	GGCCGA--------CCAGAT	GGA-------C	Pik_H16	-		13	(3.5)	Milyang 42, Taporuri, IRBL3-CP4, IRBLta-CT2
			G	G	C	T	G	C		-	-	-	-	-	-	-	-		C	T	A	G	A	T	GGCTGC--------CTAGAT	GGC-------C	Pik_H17	-	*	6	(1.6)	Muha, Tupa 121-3, Anjana Dhan
			A	G	C	C	G	C		C	A	C	C	T	T	A	C		T	C	G	G	A	T	AGCCGCCACCTTACTCGGAT	GGCCACTTACT	Pik_H18	*Pik-s*	*	3	(0.8)	Deejiaohualuo, Hong Cheuh Zai, Keiboba
			G	G	C	C	G	C		-	-	-	-	-	-	A	C		C	C	A	G	A	T	GGCCGC------ACCCAGAT	GGC-----ACC	Pik_H19	-		3	(0.8)	Neang Menh, Tupa729, Zenith
			-	-	-	-	-	-		-	-	-	-	-	-	-	-		C	T	A	G	A	T	----------CTAGAT	----------C	Pik_H20	-		2	(0.5)	Puluik Arang, Ratul
			G	G	C	C	G	C		C	A	C	G	T	A	A	C		T	C	G	G	G	T	GGCCGCCACGTAACTCGGGT	GGCCACTAACT	Pik_H21	-		1	(0.3)	Padi Kuning
			G	G	C	C	G	C		C	A	-	C	T	T	A	C		T	C	A	G	A	T	GGCCGCCA-CTTACTCAGAT	GGCCA-TTACT	Pik_H22	*Pik-s*	*	1	(0.3)	Kaluheenati
			G	-	C	C	G	C		C	A	-	C	T	T	A	C		T	C	G	G	A	T	G-CCGCCA-CTTACTCGGAT	-GCCA-TTACT	Pik_H23	*Pik-s*	*	1	(0.3)	Guizhao 2
			G	C	C	C	A	C		C	A	-	C	T	T	A	C		T	C	A	G	A	T	GCCCACCA-CTTACTCAGAT	CACCA-TTACT	Pik_H24	*Pik-s*	*	1	(0.3)	Naba
			A	G	C	C	G	C		-	-	-	-	-	-	-	-		C	C	A	G	A	T	AGCCGC--------CCAGAT	GGC-------C	Pik_H25	-		1	(0.3)	Mairangphoe
			A	G	C	C	G	A		-	-	-	-	-	-	A	C		C	C	A	G	A	T	AGCCGA------ACCCAGAT	GGA-----ACC	Pik_H26	-		2	(0.5)	Urasan 1, Kahei
			G	C	C	C	G	C		-	-	-	-	-	-	A	C		C	C	A	G	A	T	GCCCGC------ACCCAGAT	CGC-----ACC	Pik_H27	-		1	(0.3)	Calotoc
			G	G	C	T	G	C		-	-	-	-	-	-	-	-		C	C	A	G	A	T	GGCTGC--------CCAGAT	GGC-------C	Pik_H28	-		1	(0.3)	Jhona 2
			G	C	C	C	G	C		-	-	-	-	-	-	-	-		C	T	A	G	A	T	GCCCGC--------CTAGAT	CGC-------C	Pik_H29	-		1	(0.3)	Tsuyaotome

(Continued)

Locus	Chr. 12 IRGSP-1.0 No.	10607519	1 10607554	2 10611244	3 10611754	10611770	4 10612903	5 10614915	6 10635507	Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]		No. of varieties (%)		Representative varieties[d]
	Assay name	*Pita* CDS_US	FA4541	FA4544	FA4546	*Pita* CDS_DS	FA4553	FA4556	FA4569								
Pita		C	T	A		C	C	G		CTACCG	CC	Pita_H01	*Pita*	*	34	(9.2)	**Yashiromochi**, **IRBLta-CP1**, PiNo.4, Ikuhikari, Deng Pao Zhai, Qiu Zhao Zong
		A	T	C		G	C	G		ATCGCG	AG	Pita_H02	*Pi20*	*	28	(7.6)	**IR 24**, Hokuriku 193, Takanari, Bleiyo
		A	A	C		C	T	G		AACCTG	AC	Pita_H03	-	*	110	(29.8)	Nipponbare, Hamasari, Akidawara, IRBL19-A
		A	A	C		C	T	A		AACCTA	AC	Pita_H04	-		60	(16.3)	Koshihikari, Leafstar, Tachiharuka
		A	A	C		C	C	G		AACCCG	AC	Pita_H05	-		95	(25.7)	Fukuhibiki, Sensho, Tachiaoba
		A	T	C		C	C	G		ATCCCG	AC	Pita_H06	-	*	19	(5.1)	Yatanomochi, Naba, Khau Mac Kho
		A	T	A		C	C	G		ATACCG	AC	Pita_H07	-	*	19	(5.1)	Kasalath, Muha, Tupa 121-3
		A	T	C		-	C	G		ATC−CG	A−	Pita_H08	-		3	(0.8)	Kaluheenati, Mal Marso, Pokkali
		A	-	C		C	C	G		A−CCCG	AC	Pita_H09	-		1	(0.3)	Asu

Locus	Chr. 12 IRGSP-1.0 No.	1 10801324	10824087	2 10830872	3 10833033	4 10833370	10833494	5 10849598	6 10853113	Haplotype: Standard set	Haplotype: Core set[b]	Haplotype ID	Genotype[c]		No. of varieties (%)		Representative varieties[d]
	Assay name	FA4580	*Pita-2* CDS_US	FA4571	FA4572	FA5655	*Pita-2* CDS_DS	FA4585	FA4588								
Pita-2		G		G	T	[B]		C	A	GGT[B]CA	GT[B]C	Pita-2_H01	*Pita-2*		12	(3.3)	**PiNo.4**, **Ikuhikari,** Tadukan, Reihou, Te-tep
		A		G	T	[A]		G	G	AGT[A]GG	GT[A]G	Pita-2_H02	*Pi19*		249	(67.5)	**Nipponbare**, **Koshihikari**, Leafstar, Fukuhibiki
		G		G	T	[A]		C	A	GGT[A]CA	GT[A]C	Pita-2_H03	-	*	24	(6.5)	Yashiromochi, IRBLta-CP1, IRBLta-CT2, Deng Pao Zhai, Qiu Zhao Zong
		G		A	C	-		G	A	GAC−GA	AC−G	Pita-2_H04	*Pi20*	*	36	(9.8)	**IR 24**, Hokuriku 193, Takanari, Kusahonami, Bleiyo, Muha
		-		A	T	-		G	A	−AT−GA	AT−G	Pita-2_H05	-	*	26	(7)	Akage, Khau Mac Kho, Kitayukimochi
		G		G	T	[A]		G	A	GGT[A]GA	GT[A]G	Pita-2_H06	*Pi19*	*	7	(1.9)	Yatanomochi, Naba, Khao Nam Jen, Bei Khe
		G		G	T	[A]		G	G	GGT[A]GG	GT[A]G	Pita-2_H07	*Pi19*	*	14	(3.8)	AC 540, Anjana Dhan, Deejiaohualuo, Kaluheenat, Shoni
		A		A	T	-		G	A	AAT−GA	AT−G	Pita-2_H08	-		1	(0.3)	Khau Tan Chiem

Positions of end of the coding sequence (CDS) of respective resistance locus are indicated in white on black background. US, Upstream; DS, Downstream.

[a] At the FA5655 marker locus, the allele-type [A] indicates "AAAAACCAG" and [B] indicates "TG".

[b] The core set was chosen from the standard set to distinguish between resistant alleles and others; red letters indicate the core set.

[c] Genotypes for blast resistance; minus signs indicate absence of resistance alleles. Genotypes followed by an asterisk were validated by using varieties indicated in red in the column on the right, or chromosomal substitution lines containing the allele from donors indicated in blue.

[d] Variety names in bold represent the donors of respective resistance alleles.

Supplemental Table 5. Reactions of differential varieties harboring *Pik* alleles to 19 different races of blast isolates

Differential lines	SNP haplotype	Resistance alleles	Isolate name	1804-4	H09-187-1	H05-72-1	H08-174-1	Kyu92-22	Ina168_Hokudai	H13-098-1	P-2b	H09-225-1	H05-99-1	Kyu9439013	MA79-6-1	H11-223-1	H10-163-1	H09-219-1	H10-044-1	H10-060-1	H09-117-1	H07-195-1
			Code[b]	k177	k147	k137	k107	k107	k107	k106	k106	k101	k101	k100	k056	k046	k007	k007	k007	k007	k006	k000
			Origin	Japan (Niigata)	Japan(Hokkaido)	Japan(Ibaraki)	Lao PDR	Japan(Kumamoto)	Japan(Aichi)	Kenya	Japan (Mutant)	Japan (Ibaraki)	Japan (Ibaraki)	Japan(Kochi)	Malaysia	Bangladesh	Japan(Fukui)	Japan(Ibaraki)	Vietnam	Vietnam	Uganda	Lao PDR
IRBLks-F5	Pik_H04-1	*Pik-s*		S	S	S	S	S	S	S	S	S	S	S	R	R	R	R	R	R	R	R
IRBLk-Ka	Pik_H01-2	*Pik*		S	S	S	S	S	S	R	R	S	S	R	R	R	S	S	S	S	R	R
IRBLk-Ku	Pik_H01-1	*Pik*		S	S	S	S	S	R	R	R	S	S	R	R	R	S	S	R	R	R	R
IRBLkm-Ts	Pik_H02	*Pik-m*		S	R	S	R	R	R	R	R	R	R	R	S	R	R	R	R	R	R	R
IRBL1-CL	Pik_H07	*Pi1*		S	R	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
IRBL1-CL[LT]	Pik_H07	*Pi1*		S	R	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
IRBLkp-K60-19F	Pik_H03	*Pik-p*		S	S	S	S	S	S	S	S	R	R	R	S	S	S	S	S	S	S	R
IRBL7-M	Pik_H06	*Pi7*		S	S	S	S	S	S	S	S	R	R	R	S	S	S	S	S	S	S	R
IRBLkh-K3	Pik_H05	*Pik-h*		S	S	R	R	R	R	R	R	R	R	R	S	S	R	R	R	R	R	R
IRBLk*-F66[LT]	Pik_H12	[a]New gene		S	S	R	S	R	R	R	R	R	R	R	S	S	S	S	R	R	R	R
IRBLk*-F25[LT]	Pik_H12	[a]New gene		S	S	R	S	S	R	S	R	R	R	R	S	S	S	S	S	S	S	R
IRBLk*-F14[LT]	Pik_H12	[a]New gene		S	S	R	S	R	R	S	R	R	R	R	R	S	S	S	R	R	R	R
IRBLk-Ka[LT]	Pik_H12	[a]New gene		S	S	R	S	R	R	R	R	R	R	R	R	S	S	S	R	R	R	R
IRBLks-Zh[LT]	Pik_H04-3	[a]New gene		S	S	S	S	S	S	S	S	S	S	S	R	S	S	S	S	S	S	R
Lijiangxintuanheigu	Pik_H04-2	*Pik-l*		S	S	S	S	S	S	S	S	S	S	S	R	S	S	S	R	R	S	S
IRBLks-S[LT]	Pik_H04-2			S	S	S	S	S	S	S	R	S	S	R	R	S	S	S	R	R	S	R
IRBLks-B40[LT]	Pik_H04-2			S	S	S	S	S	S	S	R	S	S	R	R	S	S	S	S	R	S	R
US-3(H)	-	(Susceptible check)		S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S

S, Susceptible, infection type 4–5

R, Resistant, infection type 0–2 and intermediate, infection type 3

[a] New gene: the alleles that differ from known resistance alleles against 19 blast isolates tested.

[b] Codes that represent reaction types of rice blast isolates to the differentials for *Pik* locus genes.

Supplemental Table 6. Detailed information of the PCR-based markers developed in this study

Target locus	Marker name[a]		Forward primer sequence (5′ to 3′)	Reverse primer sequence (5′ to 3′)	Marker type	Chr.	Position of 5′ end of forward and reverse primers		Product size (bp)[b, c]	Expected product size of the other variety (bp)[d]	Number of alleles[e]	Annealing temperature (°C)[f]			Note in PCR conditions[g]	Agarose gel (%)	Position of CDS start[h]	Distance from CDS start (kb)[i]	Note
							Start	End				50	55	60					
Pit	Pit-ID004		GCGAGCTCATTTATACCTCTCC	CTCCCTCTCCAACCAGCAA	InDel	1	2588798	2588890	93	104	2	-	○	-	-	4	2682019	-93.2	
Pit	Pit-ID005		CTGATTAGATGGAACTGGACGC	CCCCTATATTATCCTGTCCATGGT	InDel	1	2593530	2593646	117	103	3	-	○	-	-	4	2682019	-88.5	
Pit	Pit-ID006		CGCACAACGTATCTTAAGATGGT	AAGCATATCGTGGACTTTCTGC	InDel	1	2598062	2598161	100	87	2	-	○	-	-	4	2682019	-84.0	
Pit	Pit-ID007		ATCGTTTAGATGCAGGCAG	ATCATCGAGGGTTTGGCCTTA	InDel	1	2627002	2627108	107	95	4 ‡	-	○	-	-	4	2682019	-55.0	
Pit	Pit-ID008		TCTCTGATTCATCTCGCACGTA	GAACTTGGAGGGGCATTTCATC	InDel	1	2673971	2674066	96	106	5	-	×	○	-	4	2682019	-8.0	
Pit	Pit-ID001		TGGAGCATGGATGTTTGGAGTT	ACTAACCAATTCACAACTCTTCTTT	InDel	1	2675422	2675541	120	184	3 ‡	-	○	×	-	4	2682019	-6.6	
Pit	Pit-ID002		GCAGGATGCTGCTACACTAG	CACAAGAGTTTGGACAAAGAACC	InDel	1	2675706	2675961	256	116	3	-	○	○	-	4	2682019	-6.3	
Pit	Pit-ID003	†	CCTGAAACACATTATCTATGTTG	AGAAAGAAGCATAAGTTTAAAATAGA	InDel	1	2676307	2676466	160	190	2	-	○	-	-	4	2682019	-5.7	
Pit	Pit-ID009		GGCTTAGGTTGGTTCTAGTTGT	AGTATGAAAACAGTGAAGCAATTT	InDel	1	2724180	2724299	120	105	2	-	○	-	-	4	2682019	42.2	
Pit	Pit-ID010		TGAAGGCCTTCTGTCCCGTTTG	AGGAAGAGGAGCACCATCGACA	InDel	1	2742038	2742128	91	105	2	-	○	-	-	4	2682019	60.0	
Pit	Pit-ID011		TGTTTCAGCTATTAGAACATATCCCA	CAATTTCTGCCGCTTTGGTTTG	InDel	1	2745995	2746074	80	90	2	-	○	-	-	4	2682019	64.0	
Pit	Pit-ID012		CCTTCTCTAGGCGCACCAAGAT	GGGTAGCAGGCATGACCGATG	InDel	1	2757976	2758067	92	81	3 ‡	-	×	○	-	4	2682019	76.0	
Pit	Pit-ID013		TGCTCTTCCTTTCATGGAGATG	CAAGATTCATTATGAAATGGAGGCG	InDel	1	2760881	2760961	81	92	2	-	○	-	-	4	2682019	78.9	
Pit	Pit-ID014		GATGGGACGTTTTCAAGTATAA	CCTCTGTCCTAAATGAAACT	InDel	1	2769914	2770005	92	81	2	-	○	-	-	4	2682019	87.9	
Pit	Pit-ID015		GGTTCAGGATTGCTAAGATTGGT	TCCACGAACTTACATGACTCCA	InDel	1	2770718	2770824	107	94	2	-	○	-	-	4	2682019	88.7	
Pit	Pit-ID016		TCCACGGGATGCTCACCG	GGGCCTAATCGATGCCGT	InDel	1	2781269	2781368	100	89	2	-	○	-	-	4	2682019	99.3	
Pish	Pish-ID001		GGTGCTGCATTTGGGAGAAACG	ACGTAGCAATGTAGTTAATGCCAT	InDel	1	32964710	32964799	90	75	2	-	○	-	-	4	33141127	-176.4	
Pish	Pish-ID002		CCATGCCAAGGATCTTCGAC	CGGGAAGCGAGGTGGTGG	InDel	1	32979522	32979626	105	117	2	-	○	-	-	4	33141127	-161.6	
Pish	Pish-ID003		AAATGTACTCCCATCCCACGAT	AGGATAAAACATATTGTACTGTTTAAAT	InDel	1	32999102	32999193	92	80	2	×	○	-	-	4	33141127	-142.0	
Pish	Pish-ID004		GCTTGTGATTTTGTGAAGGCAC	TACTCTCGTACTGGTCATTGGG	InDel	1	33030685	33030784	100	87	2	-	○	-	-	4	33141127	-110.4	
Pish	Pish-ID005		TGAGAAGCAACCATTAGATCCTGCT	AATCTCGCATATACCCTCGAACA	InDel	1	33049598	33049686	89	76	2	-	○	-	-	4	33141127	-91.5	
Pish	Pish-ID006		TCCTATGTTGGGTTGTAGGCTT	GGAGAATTCCACTCTATGAAACATCCT	InDel	1	33069775	33069870	96	83	2	-	○	-	-	4	33141127	-71.4	
Pish	Pish-ID007	†	TACACCGCTCGGCTTTTCACC	ATGCCCCTCGTTGCAGCC	InDel	1	33085522	33085621	100	87	2	-	○	-	-	4	33141127	-55.6	
Pish	Pish-ID008		CACTTGGAAGTTGAAAGTGCAC	ATCTGAAGAAGCAGGACCGAT	InDel	1	33085548	33085646	99	87	3 ‡	-	○	-	-	4	33141127	-55.6	
Pish	Pish-ID009		CAAGCGGCCCAACGTTTGTT	GGGAGGATCACGTTACGCCG	InDel	1	33182369	33182467	99	84	2	-	○	-	-	4	33141127	41.2	
Pish	Pish-ID010	†	TGCTACATATATATGATAATTGTCGAGG	TCAATCTACACCGTTAGATCAT	InDel	1	33206534	33206627	94	81	2	○	×	-	-	4	33141127	65.4	
Pish	Pish-ID011	†	AGCACTTGACACTCCACAGCAG	GGCAAAACCCGTGTTTCTGACG	InDel	1	33229984	33230085	102	116	2	-	○	-	-	4	33141127	88.9	
Pish	Pish-ID012		ATGGGTTTGGATTGATACCAA	TGATGGTTTGATTTGGAGCCA	InDel	1	33260968	33261086	119	108	2	-	×	○	-	4	33141127	119.8	
Pish	Pish-ID013		CCGCTAGGTCTCGGTTATGAAAA	TCGGTTGTAGGGCGGACTAGAC	InDel	1	33299166	33299264	99	86	2	-	○	-	-	4	33141127	158.0	
Pish	Pish-ID014		GTGCCTCCCACTTGCTGAACTG	AGGACGCCGTCAAGAGCTTTG	InDel	1	33330985	33331065	81	93	2	○	○	-	-	4	33141127	189.9	slightly weak band
Pib	Pib-ID07		AAGGTATGGAGGAGGCGC	CGAAAACCCAAACCACCTCTAA	InDel	2	35013753	35013853	101	87	2	-	○	-	-	4	35108842	-95.1	
Pib	Pib-ID08		ATCTTGTGTTGGTCAAGGCAAC	GTTTAGCAGCATTTCCCTTGGA	InDel	2	35016942	35017047	106	95	2	-	○	-	-	4	35108842	-91.9	
Pib	Pib-ID09		TGAAGGTGACTCTTGTGTCCTA	CCTGCAATCACCTTATTGACGT	InDel	2	35020876	35020992	117	104	2	-	○	-	-	4	35108842	-88.0	
Pib	Pib-ID10		ACACCGATTTGTACACGAGGGC	AGGCAAAGCTCCATGGCGATC	InDel	2	35086284	35086388	105	95	2	-	○	-	-	4	35108842	-22.6	
Pib	Pib-ID11	†	AGAGTGGTTGGTTGGAGGTG	GCCCATATTGCTTTGCTCCAAA	InDel	2	35090751	35090853	103	92	2	-	○	-	-	4	35108842	-18.1	
Pib	Pib-ID01		CATCCATCCAATGCAGGTCA	ATCCAATCAAGATGATATTTGTGCA	InDel	2	35111917	35112061	145	119	2	-	○	-	-	4	35108842	3.1	
Pib	Pib-ID12		ATCATCATGGCCCGCTCC	GAGGGATGGAGAAGGGGAAAG	InDel	2	35117756	35117844	89	99	3 ‡	-	×	○	-	4	35108842	8.9	weak band in 89-bp long
Pib	Pib-ID02		TTGCCTCTCACACTCGGTGC	AATGGGTTGGTGCGCTTTGT	InDel	2	35118755	35118873	119	145	3	-	○	-	-	4	35108842	9.9	
Pib	Pib-ID13		TCTCAAGCTCCATGGAAAGCTA	ATCACCCTTTCAGTGCCTCTAA	InDel	2	35144462	35144554	93	85	3	-	○	-	-	4	35108842	35.6	
Pib	Pib-ID14		CTTCGTCTCCGTTGGTTAGTTT	GTGATTCATGGCGAGCTAATCT	InDel	2	35176847	35176931	85	75	2	-	○	-	-	4	35108842	68.0	
Pib	Pib-ID15		GCTTACAAAATCACCAGACAGC	GGTTATCATCTCTTTTCATATTGCGT	InDel	2	35183346	35183445	100	94	3	-	○	-	-	4	35108842	74.5	86-bp long is genotype C.
Piz	Piz-ID16		GGGTACAATGTTGGCCAACTGC	GGGGTAACATTGAGTGCTTTTCT	InDel	6	10356451	10356548	98	111	2	-	○	-	-	4	10372676	-16.2	
Piz	Piz-ID17		CAGATCGGCCGCCAATTC	GCTCCTCCTCCTCTCAGATTAG	InDel	6	10358203	10358301	99	88	4	-	○	-	-	4	10372676	-14.5	
Piz	Piz-ID18	†	CTGCTGCTACCGTTTGGAAGTCA	CTCCTGGCCCCACGCGTC	InDel	6	10358427	10358524	98	84	2	-	○	-	-	4	10372676	-14.2	
Piz	Piz-ID19		ACCATGGCTACGTTTGAAACTACA	ACACACGTCGTTTTACAGTTTCAA	InDel	6	10370810	10370906	97	107	2	○	○	-	-	4	10372676	-1.9	slightly weak band
Piz	Piz-ID20		TTTCCACTTCGATTCCTCTCCC	GGATGAGAGGAGCACGCA	InDel	6	10372159	10372256	98	110	3	-	○	-	-	4	10372676	-0.5	
Piz	Piz-ID21		CGACCTCGGCTTCCATGGC	TGATCCTGAATCCGTTGGAATCACC	InDel	6	10376083	10376164	82	100	2	-	×	-	*	4	10372676	3.4	40 cycles (55°C), weak band
Piz	Piz-ID22	†	ATGTGGGGTTTCTGATTCCAAT	CTTGATTAGTGAGATCCATTGTTCC	InDel	6	10381442	10381568	127	100	3	-	○	-	-	4	10372676	8.8	118-bp long is genotype C (*PI9* type, see Supplemental Fig. 11-4B).
Piz	Piz-ID23		TCTTATAGTGGGTAGTGGAGCC	GAAGAGAATCATATTCCCCCTAACT	InDel	6	10381739	10381834	96	106	2	-	○	-	-	4	10372676	9.1	
Piz	Piz-ID24		CGAGAAGGACATCTGGTACGTA	GCACAAGGATGATCAATGTCGA	InDel	6	10382105	10382292	188	289	3	-	○	-	-	4	10372676	9.4	
Piz	Piz-ID25		AGGACATCTGGTACGTACTGCA	TCTTTCCTAGTCTTCGAGCTCTCT	InDel	6	10382110	10382226	117	218	3	-	○	-	-	4	10372676	9.4	
Piz	Piz-ID26		ATTGCCGAGGCTCCTAAGTGTG	GGCGATGGCAGATGAAGCAGAA	InDel	6	10382995	10383098	104	93	2	-	○	-	-	4	10372676	10.3	
Piz	Piz-ID27		TGCTTCATCTGCCATCGCCGTA	AGAGCGACGACGATAGGGGTCA	InDel	6	10383080	10383222	143	92	2	-	○	-	-	4	10372676	10.4	
Piz	Piz-ID28		AGTTCAAGTTGTCGCTGTGGCA	TCTCACAGCATGTTGGACCTGC	InDel	6	10383104	10383329	226	176	2	-	○	-	*	4	10372676	10.4	40 cycles (55°C), weak band
Piz	Piz-ID06		TTTGCAATGGCAAGAATTGTTCA	GTACCAAGCTCAACCAAGCAA	InDel	6	10387071	10387225	155	196	2 ‡	-	○	-	-	4	10372676	14.4	155-bp long was very weak (almost absent).
Piz	Piz-ID29		ATGACCTCTCGCGCATGGAAAT	GGAGCCCAGTTAAGTTGGAATGGT	InDel	6	10418509	10418620	112	81	3 ‡	-	○	-	-	4	10372676	45.8	
Piz	Piz-ID30		CGCCTGGAAACAAATTAGTGTG	AGGGTTAAAATGAAATGACCTACCA	InDel	6	10432418	10432516	99	113	2	-	○	-	-	4	10372676	59.7	
Piz	Piz-ID31	†	CCAATTTCAGGCTTAGTTTGAT	AGCTATTTATTAAGCTGATTTCTCA	InDel	6	10434241	10434347	107	84	2	-	○	-	-	4	10372676	61.6	
Piz	Piz-ID32		AGTCAACGGGATGCTCGATTCG	ACTGCAGGAGATCAGTCAGCCT	InDel	6	10436065	10436310	246	216	3	-	○	-	-	4	10372676	63.4	
Piz	Piz-ID33		GGGATGCTCGATTCGTTACATT	GGCCAATTCCGAGTGCTTTTAT	InDel	6	10436072	10436274	203	173	3	-	○	-	-	4	10372676	63.4	
Piz	Piz-ID34		AGCCATGTAATGTCCTAAAATTGTCCT	CCATCTCTTCAGCTGTCATCAGG	InDel	6	10437522	10437601	80	97	2	-	○	-	-	4	10372676	64.8	
Piz	Piz-ID08		GCCATGTAATGTCCTAAAATTGTCC	TTGCTCCACCCACGCTTTCA	InDel	6	10437523	10437639	117	134	2	-	○	-	-	4	10372676	64.8	
Piz	Piz-ID35		GCTAACCTCCAAAGCCTCGAGA	ATGATGCGCACTTTGGCTCTGA	InDel	6	10440133	10440231	99	117	3 ‡	-	○	-	-	4	10372676	67.5	
Piz	Piz-ID12		CGCGCGAAACAGAGGGAGAG	TTGCCGGCCGTGACTTGATT	InDel	6	10444239	10444920	682	252	3 ‡	-	×	○	-	3 or 4	10372676	71.6	
Piz	Piz-ID36		AACAGAGGGAGAGGGGTT	GAGATGGATTCGGCCTGA	InDel	6	10444246	10444332	87	97	3 ‡	-	○	-	-	4	10372676	71.6	
Piz	Piz-ID15		TGCTGTGCAATTTTGCTTTTGACC	GGCAATCCGATGGCGATCCT	InDel	6	10446600	10447378	779	415	3 ‡	-	×	○	-	3 or 4	10372676	73.9	
Piz	Piz-ID37		CGATTCTAGTGATAACTGGAATTC	GCTCGGCTCGTTACGAAA	InDel	6	10459030	10459149	120	142	3 ‡	○	○	-	-	4	10372676	86.4	weak band
Piz	Piz-ID39		GATTTTCCCTCGGTAGATTGCC	CCGCCGATTCAATCTCGTTC	InDel	6	10478219	10478313	95	83	3 ‡	○	○	-	-	4	10372676	105.5	very weak band in 83-bp long

(Continued)

Pi13	Pi13-ID001		ACGCTAGGAGCAAGCTAATAAA	TTGCTATTGGAACTTAGCGT	InDel	6	16972636	16972746	111	99	2	○	×	-	-	4	17160636	-188.0	
Pi13	Pi13-ID002		GGTCTGCAAAGAAACTTGCAAA	GGCACTTCTCTCCCAACTTTAC	InDel	6	17005386	17005498	113	126	3 ‡	-	×	○	-	4	17160636	-155.3	
Pi13	Pi13-ID003		AAATTAAGCACAGGTTTACACC	GCAGATGAGTTTATCGGTTTC	InDel	6	17043979	17044073	95	85	2	-	○	-	-	4	17160636	-116.7	
Pi13	Pi13-ID004		TTTACCGAGCTTAGCTTGAG	GTGCAAACACATGCTAATTTTAT	InDel	6	17092963	17093061	99	89	2	○	×	-	-	4	17160636	-67.7	
Pi13	Pi13-ID005		CGGCTAGCTGCTCGATTAATC	TGATGTGACTTAATGAGAGAAGAGA	InDel	6	17101929	17102023	95	85	2	○	×	-	-	4	17160636	-58.7	
Pi13	Pi13-ID006		ACCTGGTACACCATTACAGTCA	AAGTACTAAACTTTTCACATGCCT	InDel	6	17108731	17108839	109	95	2	-	○	-	-	4	17160636	-51.9	
Pi13	Pi13-ID007		AGAATAAGCTATGAACTATTTGT	TTCTCTGGATGAGCTTTT	InDel	6	17109367	17109467	101	91	2	○	×	-	-	4	17160636	-51.3	slightly weak band
Pi13	Pi13-ID008	†	GTGAGCTGGAATACTAGATCGA	GTCAAAGTTCCTGCAATTTTGTGA	InDel	6	17126121	17126234	114	88	2	-	○	-	-	4	17160636	-34.5	
Pi13	Pi13-ID009		TGACTTAGTCCTCGTCATACGT	TGACATGTGGGACTCATATTTTGT	InDel	6	17144666	17144758	93	82	2	-	×	○	-	4	17160636	-16.0	
Pi13	Pi13-ID010		TCTACTTTCACAATCTCTAATTTAACAA	ACGGGTAAAATTTGCTACTCCC	InDel	6	17155715	17155804	90	104	2	-	○	-	-	4	17160636	-4.9	slightly weak band
Pi13	Pi13-ID011		CCATACGACAGACAGGCAATCCC	GGGTGGTTCACGGGGAAGAAAA	InDel	6	17155951	17156044	94	80	2	-	○	-	-	4	17160636	-4.7	
Pi13	Pi13-ID012		AAGAATAACAATCGCCCGGAAC	TGGATCTTTCTTTGCTAGCTCG	InDel	6	17164450	17164557	108	87	2	-	○	-	-	4	17160636	3.8	
Pi13	Pi13-ID013		AAATCCGCTAGCTTATTCTGGG	CTTGCCCAAGTGTTAGCTCAA	InDel	6	17215797	17215915	119	156	2	-	×	○	-	4	17160636	55.2	
Pi13	Pi13-ID014		CTTCATCTAAAAGCCACAACAT	TTCTTATCTACTATACAATTTTCTTTCA	InDel	6	17289117	17289227	111	97	2	○	×	-	-	4	17160636	128.5	
Pi13	Pi13-ID015		AGAGATTTGAAACTTAACTTGAAGTAAG	TCATGCACACGAACATGAGAA	InDel	6	17313656	17313808	153	173	2	-	○	-	-	4	17160636	153.0	
Pi13	Pi13-ID016		GCTGCCTGACCTGTTTTC	CCAGTTTGACGTCCACTTTG	InDel	6	17358343	17358442	100	90	2	-	○	-	-	4	17160636	197.7	
Pii	Pii-ID02		TCTGAATTCTTGTAGTCCTCCATGC	TGGCAACGCGTATTGGTGTC	InDel	9	9632867	9633449	583	266	2	-	○	-	-	3 or 4	9667216	-34.3	
Pii	Pii-ID01		CCTCCATGCATTGGTAGAAA	TCCCTCGTCGGCCTCTGTAG	InDel	9	9632883	9633513	631	314	2	-	○	-	-	3 or 4	9667216	-34.3	
Pii	Pii-ID04		CAGCCCAAACCATGCACAAC	TTCTCGTGCATGTGCTGCAA	InDel	9	9640689	9640960	272	294	2	-	○	-	-	4	9667216	-26.5	
Pii	Pii-ID18		TGAAATCTCCATTACCTTTAAAA	AGTTCACCCACTTTCGATAAAA	InDel	9	9648658	9648776	119	106	2	○	×	-	-	4	9667216	-18.6	
Pii	Pii-ID07	†	TTCGGTCATTAGCCGGTGCT	GGCGGCAGGTATGGTACTTCA	InDel	9	9667928	9668377	450	289	3	-	○	-	-	3 or 4	9667216	0.7	493-bp long is genotype C (see Supplemental Fig. 11-6B).
Pii	Pii-ID19		TATCTATGTTACTATATCACATGA	ACATGTTGTTATAGCGTATGAA	InDel	9	9763380	9763467	88	99	3 ‡	○	×	-	-	4	9667216	96.2	slightly weak band
Pii	Pii-ID20		AGGCTTACCAGTTCACTCTGAA	ATTTTGGGCGAGATTTGAGCAT	InDel	9	9781213	9781307	95	82	3 ‡	-	○	-	-	4	9667216	114.0	
Pii	Pii-ID21	†	AAGCGAACGACTCTAGCTAGAA	TCTCCATATGTATGTATAACTGGCTT	InDel	9	9789035	9789118	84	96	2	-	○	-	-	4	9667216	121.8	
Pii	Pii-ID22		TGGATCTGGACGGTTTCATTTG	AACTCCGTAAGAATTGTCGGTG	InDel	9	9792715	9792808	94	81	3 ‡	-	○	-	-	4	9667216	125.5	
Pii	Pii-ID23		TGGACGGTTTCATTTGTTTCCCT	ACAACCACCAAACTCCGTAAGA	InDel	9	9792721	9792818	98	85	3 ‡	-	○	-	-	4	9667216	125.5	
Pii	Pii-ID24	†	ATGAGGAGATGACAACGAGGAG	GAAGAGGGGAACGCCGAG	InDel	9	9839676	9839775	100	88	2	-	○	-	-	4	9667216	172.5	
Pii	Pii-ID25		CGGAGAGCCAGCCACGGC	GCCAGATGATCGCAGCGGC	InDel	9	9839705	9839804	100	88	2	-	×	○	-	4	9667216	172.5	
Pii	Pii-ID26		AGGTTTGGAACGTGATGGCGTA	TCGGGCACTCAATTCCTAGTCTC	InDel	9	9848951	9849053	103	91	3 ‡	-	○	-	-	4	9667216	181.7	
Pia	Pia-ID02		GTAGCGTTTCTCCCACCACTT	TCTGGAAGGGTGCCGCAC	InDel	11	6375786	6375885	100	89	2	-	○	-	-	4	6542301	-166.5	
Pia	Pia-ID03		TGCTTCCAGGCGTCTGCAG	CTCCAGGATGTAGTTCGCCGTC	InDel	11	6400787	6400901	115	101	2	-	○	-	-	4	6542301	-141.5	
Pia	Pia-ID04		CCGAATTCTAACGGCAGATG	CGACGAAGACAAAGACTCAAAT	InDel	11	6522517	6522610	94	84	2	-	×	○	-	4	6542301	-19.8	
Pia	Pia-ID05		ATAATTTTGAGTCCAAACAATACGTGT	TCAATCCATGCTTGAATTCAACCT	InDel	11	6523786	6523865	80	92	2	-	○	-	-	4	6542301	-18.5	slightly weak band
Pia	Pia-ID01_2	†	ACGGTAGAGCAATTTAGAAGCAGTGA	AGTGCGACTGACACTTTCAATAGCA	InDel	11	6544602	6544796	195	152	2	-	○	-	-	4	6542301	2.3	
Pia	Pia-ID06		TAGTGTCCATATGTTTGCTGCG	ACATCGGCTACCTATCAAACCA	InDel	11	6562152	6562231	80	91	3 ‡	○	○	-	-	4	6542301	19.9	
Pik	Pik-ID001	†	CTTCTTAGCCTCCAGATTTGCA	TCATGTGCATCAAAATGGGCTA	InDel	11	27743108	27743207	100	88	2	-	○	○	-	4	27978523	-235.4	slightly weak band
Pik	Pik-ID002		CATGCTGATACCTATAGCGA	TCCAACAGAATACCTTATGTGATGA	InDel	11	27778163	27778267	105	95	3 ‡	-	○	-	-	4	27978523	-200.4	
Pik	Pik-ID003		GTGCGCAAGTGTTCGATGGATG	CGATCGACTCACTGCAGCATCT	InDel	11	27785048	27785151	104	89	3 ‡	-	○	○	-	4	27978523	-193.5	
Pik	Pik-ID004		TCAAGCTTGTTCATGGCGGC	GAGGTGATGTATCTTCTACCTCCTCT	InDel	11	27791894	27791977	84	94	2	-	×	○	-	4	27978523	-186.6	
Pik	Pik-ID005		CTCACTGAGCTGTGCATTTCAT	TGTCTGCGATCAGTTTGAGGTA	InDel	11	27796760	27796859	100	90	2	-	○	-	-	4	27978523	-181.8	
Pik	Pik-ID006		CACGGTAATACTCTTCTCATCACA	ACTTTGAAAAGTCTAAAACGTAAA	InDel	no hit	(27017)	(27124)	108	120	3 ‡	○	○	-	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID007	†	AACGAATATTTATGACTAAAGAAAGT	AGAAGCTTGACTCCGTTAG	InDel	no hit	(28817)	(28936)	120	406	3 ‡	-	○	-	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID008		GGCGAGATCACCGCGGTG	AATATGTACGCCGCCATCGA	InDel	11	27844029	27844120	92	80	2	-	×	-	*	4	27978523	-134.5	2 STEP-PCR (see footnote g), weak band
Pik	Pik-ID009		CGATCACGGCGGAGAACGG	CTGTCGTCATCGCGTCCAGAC	InDel	11	27844228	27844342	115	133	5	-	×	-	*	4	27978523	-134.3	2 STEP-PCR (see footnote g), weak band
Pik	Pik-ID010		GCCCACCTTCTTCCGGAGC	GATGCTTCACGATGGCGCAAG	InDel	no hit	(44233)	(44600)	368	396	3 ‡	-	○	○	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID011		GGTTAAATAGGACTCCCTCTA	GCATCCAATAGAATCAGAGA	InDel	no hit	(45995)	(46163)	169	150	3 ‡	-	○	-	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID012		CAAGGCCCCAATCTTCCCACC	ACCCATGGAACTGAACCCTCCT	InDel	no hit	(46412)	(46543)	132	102, 104	3 ‡	-	×	○	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID013		GTGCAGTATTATTGGCCTCCG	AACCCTCCTCCGACCAGA	InDel	no hit	(46374)	(46530)	157	127, 129	3 ‡	-	○	○	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID014	†	TTCTTCTTTATCCCGTCTTCTT	ATGAGGAAAACGAAGATGAGAG	InDel	no hit	(51647)	(51990)	344	149, 150	3 ‡	-	○	-	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID015		TTATCCCGTCTTCTTCCCGCAC	CCAGATCTGGTGAGAGAGGGCC	InDel	no hit	(51654)	(52053)	400	205, 206	3 ‡	-	○	○	-	4	27978523	Not available	The positions in parentheses are based on 'Kanto 51' sequence (AB616659)
Pik	Pik-ID017		GAGGGTGGACATATGCAACAA	GAGACAAGGCTGACTATATTAAAT	InDel	11	27995163	27995281	119	108	2	-	○	-	-	4	27978523	16.6	
Pik	Pik-ID018	†	ATCCTCTGTGTCTGAAGCCAT	AGGCTTCTCTGCTCCTATAACA	InDel	11	27996941	27997050	110	100	2	-	○	-	-	4	27978523	18.4	
Pik	Pik-ID019		TGCATACATTGTGCATGAATCAAC	TTTGTTCGTGTTCACCCGTAAA	InDel	11	27997324	27997408	85	95	2	-	○	-	-	4	27978523	18.8	slightly weak band
Pik	Pikm-ID06		TCGTTGCCAACAAATCCATCA	TGCTTGTCCAATGGTGGAACC	InDel	11	28002956	28003115	160	360	2	-	○	-	-	4	27978523	24.4	
Pik	Pik-ID021		CAGTGCCCTTTTCTTCCTCATT	AAGACCAAATAATGTCGCAGCA	InDel	11	28004960	28005069	110	96	2	-	○	-	-	4	27978523	26.4	
Pik	Pik-ID022		GGTGTACGATGTAGAATGGTGG	TCACAGCAAAGACCATACAACC	InDel	11	28004994	28005113	120	107	2	-	○	-	-	4	27978523	26.5	
Pik	Pikm-ID07		TCATTCCAATCTCGCTCCTCCT	TGCAGGTGGAGAGGGTTCTCTT	InDel	11	28005464	28005557	94	103	3	-	○	-	-	4	27978523	26.9	
Pik	Pikm-ID08		GAAAGCAAAATAAAAAGGCAACACG	CAACTTTGCAAAATACAACTTGCAGC	InDel	11	28012610	28012721	112	88	2	-	○	-	-	4	27978523	34.1	

(Continued)

Pita	Pita-ID13	†	AGGCAAGAGTACAATGGAAAC	TGCCCTCTGAAAATAAAGTTT	InDel	12	10467644	10467743	100	112	2	-	○	-	-	4	10607519	-139.9	slightly weak band
Pita	Pita-ID14		TCATGTAGTTGTAAACACATGTT	TGTTGGTGATTATGGCATGTTT	InDel	12	10470430	10470549	120	105	2	○	○	-	-	4	10607519	-137.1	slightly weak band
Pita	Pita-ID15		CCCTTACCTAGATCGAATGGGAT	GGTCTGATCACTCCCTCCATAA	InDel	12	10485998	10486117	120	134	2	-	○	-	-	4	10607519	-121.5	
Pita	Pita-ID16		TGGCAGAGTATAACAGCTCTCACT	TCTACGTTCTTAACATACTGATACTGT	InDel	12	10508155	10508273	119	96	2	-	○	-	-	4	10607519	-99.4	
Pita	Pita-ID17		TTTCTTACTGTCTTTGCGCGAT	ACCACTAGTAAAGAGCACTGTAGT	InDel	12	10531581	10531690	110	89	2	-	○	-	-	4	10607519	-75.9	
Pita	Pita-ID18		AAAAGGTTTTAAAATCTCCCTTTT	GCTGGTGGGCTAACTTGG	InDel	12	10560821	10560909	89	79	2	○	×	-	-	4	10607519	-46.7	
Pita	Pita-ID04	†	CGTGAAGAGGATTCCGGTAGCA CAAGTCAGGTTGAAGATGCATtGC	TGCCGTGGCTTCTATCTTTACgTT CCGACGCCGAGCACTCTTAT	PCR-CTPP	12 12	10607441 10607531	10607577 10607746	137	216	2	-	-	-	*	4 4	10607519 10607519	-0.1 0.0	306-bp long is the common band between both alleles.
Pita	Pita-ID03		GATTCATCATCATCAGTGCCC CTCGTTGGCATTGAACCTTAGATTTtAC	CAATGCCGAGTGTGCAATGA CCCAGGATGACCTTGACACT	PCR-CTPP	12 12	10607796 10607891	10607937 10608105	142	215	2	-	-	-	*	4 4	10607519 10607519	0.3 0.4	310-bp long is the common band between both alleles.
Pita	Pita-ID19		CGTCTTAGATCCGTGTTATCGC	GAGCATATCTGAGACGGGGAA	InDel	12	10615423	10615525	103	122	2	-	○	-	-	4	10607519	7.9	
Pita	Pita-ID20		AGAAAACAATTCGGGTTCACCA	TATTCGCATGGATTTTACGGCT	InDel	12	10618603	10618705	103	119	2	-	○	-	-	4	10607519	11.1	
Pita	Pita-ID21		CGATGGAATATGATCGATGTCAGT	AAGTGATTAGGGTAACATTGGCA	InDel	12	10623210	10623310	101	91	2	-	○	-	-	4	10607519	15.7	
Pita	Pita-ID22		GCGACCGCATTTGAGGATTTAA	CTCCGATCCTGGGACGTG	InDel	12	10652892	10652981	90	109	3 ‡	-	○	-	-	4	10607519	45.4	
Pita	Pita-ID23		GTGAATTGTCCATATTTTCTTATCAGCT	CAAGGGAGTTGGAGACAGTGAT	InDel	12	10691846	10691963	118	142	2	-	○	-	-	4	10607519	84.3	
Pita	Pita-ID24		GGAGTGTCAAAGGCCTATTGG	TCCACAGTATTAGGGAAGCTTCT	InDel	12	10703096	10703214	119	83	2	○	○	-	-	4	10607519	95.6	slightly weak band
Pita-2	Pita-2-ID001		CGAAGGCGTCATCCATGGAAGA	CTGGCATTGGTGGAGCTAGTGT	InDel	12	10725835	10725939	105	93	2	-	×	○	-	4	10824087	-98.3	
Pita-2	Pita-2-ID002		CCCCACCAAAACAGATTTAGGG	TGCTTAGATCCAACATAGAACCAC	InDel	12	10736661	10736764	104	143	3 ‡	-	○	-	-	4	10824087	-87.4	
Pita-2	Pita-2-ID003		ATCTGTTTCCCCTTTCTTGTGC	TCATAAAGGTGCAGTAACTTAGCG	InDel	12	10745092	10745187	96	84	2	-	○	-	-	4	10824087	-79.0	
Pita-2	Pita-2-ID004		TGTTCTGATTGTGCCAAACCAT	CCCTTAGAAGAATGCTGGCATG	InDel	12	10760837	10760947	111	144	2	-	○	-	-	4	10824087	-63.3	
Pita-2	Pita-2-ID006		TGCTGTTTCGATGCGTATTTCT	CAATAATGATGATGTGCGTGCG	InDel	12	10771016	10771119	104	79	3 ‡	-	×	○	-	4	10824087	-53.1	
Pita-2	Pita-2-ID007		ATCCTCAACATGTGTGCAAGTG	GAACGGGAAGACTTGCAATGAG	InDel	12	10797537	10797637	101	118	2	-	○	-	-	4	10824087	-26.6	
Pita-2	Pita-2-ID008		AATCCAGATCGAGTCTCCGTC	TGACAGAGTAGAATGACCTAGCA	InDel	12	10810754	10810855	102	112	2	-	○	-	-	4	10824087	-13.3	
Pita-2	Pita-2-ID009	†	CACATAGCATTAGAGCACTAAACT	AACCATCATACCGGCCTATTTA	InDel	12	10815778	10815879	102	114	2	-	○	-	-	4	10824087	-8.3	
Pita-2	Pita-2-ID016_3	†	AAAGTTCATCGCATCGAATTTA	ACACGCGTTGGGATCTTCCTC	InDel	12	10833348	10833482	135	123	2	○	○	×	-	4	10824087	9.3	
Pita-2	Pita-2-ID010		GGTGTTTCGGAGCTATTTTCCA	ACAGTTGTGCATGAAACCTAACA	InDel	12	10853142	10853251	110	138	2	-	○	-	-	4	10824087	29.1	
Pita-2	Pita-2-ID011	†	TGCAATTAGTCTGGTGTTGTTGA	ACATGAATCAGTCTGACGTCAT	InDel	12	10853795	10853909	115	85	3	-	○	-	-	4	10824087	29.7	
Pita-2	Pita-2-ID012		TGGGATTACACTACACAGGGAGAGG	GAGAAGGGGAACTGGGATGGGA	InDel	12	10862608	10862712	105	95	2	-	○	-	-	4	10824087	38.5	
Pita-2	Pita-2-ID013		GACGACGAGAAGTGCGTC	CTTCAGGGAGCAGTGCTG	InDel	12	10876975	10877134	160	127	3 ‡	-	○	-	-	4	10824087	52.9	
Pita-2	Pita-2-ID014		TTTTGGGGAGGGATAGAATGGG	CCCCTAACCCTAGAATTCCACG	InDel	12	10894020	10894125	106	116	2	-	○	-	-	4	10824087	69.9	
Pita-2	Pita-2-ID015		ACGAAAAGGGCAATTGATCGC	TGAGAACATCCGAACGATAGAAGTT	InDel	12	10896196	10896306	111	101	2	-	○	-	-	4	10824087	72.1	

Chr., chromosome number; CDS, coding sequence.

[a] The markers with a dagger (†) are recommended for distinguishing resistance alleles from the others (also see Table 5).

[b] Size is based on the reference genome, 'Nipponbare' IRGSP-1.0.

[c] Product sizes of the markers for the *Pik* locus in gray boxes were estimated from 'Kusabue' (HM048900) or 'Kanto 51' (AB616659), because these sequences are absent in the 'Nipponbare' genome.

[d] The variants correspond to genotype B in Supplemental Fig. 11A. The variants obtained by the four markers for the *Pik* locus include amplicons of two sizes that cannot be clearly discriminated from each other on the gel.

[e] Number of alleles identified under respective PCR condition. The double dagger (‡) indicates a marker genotype for which an amplicon was not detected.

[f] A circle or cross indicates that the result was or was not acceptable, respectively, in terms of amplification and/or balance between the alleles; a minus sign indicates that the condition was not tested.

[g] Asterisks mark the conditions that differ from the standard, as described in Materials and methods:
Piz-ID21 and Piz-ID28, additional 5 cycles of PCR; Pik-ID008 and Pik-ID009, denaturation at 98°C for 10 s and extension at 65°C for 1 min; Pita-ID04 and Pita-ID03, initial denaturation at 95°C for 2 min, and cycle conditions of 94°C for 30 s, 55°C for 1 min 30 s, and 72°C for 1 min.

[h] Positions of the respective resistance loci indicated in "Map position (bp)" in Table 1.

[i] Distance between CDS start and 5′ end of the forward primer.

Supplemental Table 7. Detailed information of the 96 SNP genotyping assays, BRA1, for the Fluidigm genotyping platform

Locus	Assay name	Serial number in this set	Serial number for each locus	Chr.	Target SNP Position (bp)[a]	Allele1	Allele2	Direction[b]	Allele 1–specific primer[c]	Allele 2–specific primer[c]	Locus-specific primer	Specific target amplification primer
Pit	FA4467	1	1	1	2680046	A	G	+	TGAGGTTAAGCGTATAAGCGACAA	TGAGGTTAAGCGTATAAGCGACAG	CCGAAGTAGATATAATTAAGGCCTAGTGGATT	TGTGTTCTGAAAGAACCTTCAAATGA
	FA4453	2	2	1	2681202	A	G	+	GGATTATTGGTTATGTCACCCCACA	GATTATTGGTTATGTCACCCCACG	ACAACGATCGAAGTACATCTGTTTCAGT	GCACAATCGGGGTAAGAGGAT
	FA4455	3	3	1	2682651	C	T	-	CAACGACTGCACTTCATGTTCAG	CAACGACTGCACTTCATGTTCAA	GCAGTTCTGGCATCTGGCCT	AAATTTGGGTCATATGCACCTCAA
	FA4461	4	4	1	2683065	C	A	-	GAACAGACTGCAATCGACCATG	AGAACAGACTGCAATCGACCATT	TTGCTGCAACTTTGCCAACTCCT	TCGAACATAAGTTTCCTAGAGCTAGA
	FA4482	5	5	1	2688550	C	T	-	GGAGGAACACAAGGTTGCG	TGGAGGAACACAAGGTTGCA	CAGTGGCATGCATCTAAGCTTAATGA	CAGTGTTGATGATTGTACCAGGAATAA
	FA4483	6	6	1	2688828	A	T	-	CAATCTGGCTTCATGAAGAAGAAAATGT	CAATCTGGCTTCATGAAGAAGAAAATGA	GCACTGTTGAATAATTCTTGTTTTTATGCTTTCAT	GCTGATCCAACAATCTGGCT
Pish	FA4649	7	1	1	32985740	G	T	-	CTAGTATAGACTTTATGTATTTAATCTCTCTCTCTC	CTAGTATAGACTTTATGTATTTAATCTCTCTCTTA	TCCACTTAGCTTTCTAAATTGTAAATATAATTTCTAAATA	AGCTAGTATAGACTTTATGTATTTAATCTCTCTCTC
	FA4645	8	2	1	33074934	G	A	-	GTATTGTAGATGATGCTAAATTTTACTCTCTCC	GGTATTGTAGATGATGCTAAATTTTACTCTCTCT	TGATAAGTAGAATTAGATGAAATATGACTATCAAAAGTAA	TGAAACTAATTTGGTATTGTAGATGATGCT
	FA4644	9	3	1	33075459	C	T	+	ATTGCAAAGCCTGCGGC	GATTGCAAAGCCTGCGGT	TAGTGACACAAGTTAATGAAAATCCAGCA	TGGGCTGCCATCTTGGA
	FA4636	10	4	1	33080208	C	T	-	CATAGAGAAGTGCATCGGCTTTG	TCATAGAGAAGTGCATCGGCTTTA	ATCTGGTCTAATTCTTTATTCTTTGAAGTTTCTCTATTTT	TGCAAAAGCTCATTGTCATAGAGAA
	FA4627	11	5	1	33101529	A	T	+	CAACCACTGTTCGACATCTATCTGTA	AACCACTGTTCGACATCTATCTGTT	CTTTGCTTATGGAATTTCATACTCTCAACACG	GGGTGAAAGAGATACCAACCAC
	FA4650	12	6	1	33146248	C	T	+	TCTCCCTCTAGCGATAGCCTCC	TTCTCCTCTAGCGATAGCCTCT	GAGAATCCAAAACGAGGTGGCA	GGTTTTTGCCGTACGTTCCTT
	FA4651	13	7	1	33146996	A	C	-	TGGTAGGGCTCGCCCT	GGTAGGGCTCGCCCG	AAATTTAACAATCTTTATAATACGAATTTCGTGTGCCT	GAATCACGCCGCGCC
	FA4652	14	8	1	33148998	C	T	-	ATGCTCATTTTCTGACAAACCAGTG	CATGCTCATTTTCTGACAAACCAGTA	GGCACGTCAATTTTCTAGTGATTTGCTT	CAGGCAATAGTAGGCATGCTC
	FA4654	15	9	1	33151594	G	C	+	TCAAGAGAAGACGCCACCTG	TCAAGAGAAGACGCCACCTC	GACCCGGTATCAGGGGCA	CCATCGTAGCGCGCAAG
	FA4665	16	10	1	33174003	A	G	-	CGTATAAGTTCTGAAAGTAATTCTACAATATTTCTT	CGTATAAGTTCTGAAAGTAATTCTACAATATTTCTC	CCAACTGGCCATGCATGATCAA	CCATGCGCGTATAAGTTCTGAA
	FA4667	17	11	1	33174848	C	A	-	TCATCTGGTTCCCCAAAGTCTG	TTCATCTGGTTCCCCAAAGTCTT	TCACTTTCGCTCTTGCTGTCACT	CAGCTGACAGCTTCAAGGATT
Pib	FA4424	18	1	2	35089605	C	T	-	GCTCCCATTAAGCCACGTG	TGCTCCCATTAAGCCACGTA	ACCGGCGCCAATGTTGC	GGATCCCATGGCCATCGT
	FA4422	19	2	2	35090234	T	G	-	GGTCGGCTGTCGGAACA	GGTCGGCTGTCGGAACC	TGAGATCGCCGCAGCTCG	CCTCCCGCTCCGGTTG
	FA4416	20	3	2	35092033	G	T	-	GCAAGCTGAAGATGACTATTTTGCATATTC	GCAAGCTGAAGATGACTATTTTGCATATTA	TCTCAATCTAATTACTAAGTTTCAGCCAAACCT	GGATCTGCAAATTGCAAGCTGA
	FA4408	21	4	2	35095702	C	T	+	GATTGTGGCTATGCACATGCC	GATTGTGGCTATGCACATGCT	CTTCATGTGATTCGTATTAATTTAGTGCTAATGCT	TGACTGCCTTATGCACTTTCTAAG
	FA4407	22	5	2	35095970	G	T	-	CATTAGCTCTTTATTTGGATGCACCTTATC	CATTAGCTCTTTATTTGGATGCACCTTATA	TGTCTACTGATTTTTGTAGTAGAAAGCAGAAACTAA	ATTAGCTCTTTATTTGGATGCACCT
	FA4404	23	6	2	35097776	T	C	+	GCAAGAGCTTCATTGACCTTCT	GCAAGAGCTTCATTGACCTTCC	GAAAGATATTTCCCCGCGGCA	CATCAAGAGTCTTATTTATCAGCGCA
	FA4401	24	7	2	35111607	C	T	+	CTGGATTCATTTCCAACTCAGCAC	CTGGATTCATTTCCAACTCAGCAT	ACCCCAGAAGAGTGGAGAAAATTGA	CGGTTCTTATCATTCCAAGCTCTG
	FA4439	25	8	2	35133756	G	A	+	GGCCAACGAATGCGACG	AGGCCAACGAATGCGACA	CTCCTGCTGCTGCTGCTT	ACGACAACGACAACAAGAACAA
	FA4446	26	9	2	35138569	G	T	+	GGGTAACCTATATTTAGGACGAATCATAGG	GGGTAACCTATATTTAGGACGAATCATAGT	CAACACAACTCAACTCTAATTGACATGCATT	CTCTTTTCAAAAACAAATTATGGGTAACCT
Piz	FA5376	27	1	6	10361215	G	A	-	CCATGCATGTATCGATAATTAGGAATCAC	TCCATGCATGTATCGATAATTAGGAATCAT	ACTATTGTATCTAGAAAAGTTATGTATTTAAAACACAGCA	GACAAGTCTCCATGCATGTATCG
	FA4676	28	2	6	10379796	G	A	+	GGCACCTCGCCAACG	GGGCACCTCGCCAACA	CCTGATTCCAACCTGCAACCAT	AGCAACTTAGAGAGATAAGATTTGAGGA
	FA4678	29	3	6	10382967	G	C	-	ATGATAACTTGGGCTAGGGCC	TGATAACTTGGGCTAGGGCG	CCACCGCCGCCGCAT	CTCGGCAATTGCCACGA
	FA4679	30	4	6	10384890	C	T	+	ACAGTCAAGCCCTCATTCCC	GATACAGTCAAGCCCTCATTCCT	GGCAGCACAGTAGTGGCAT	CCCACCAACCAACCACAGA
	FA4680	31	5	6	10385269	T	G	-	CAAGGCTTTATCACTTAACATACAACGAAA	AAGGCTTTATCACTTAACATACAACGAAC	GGAGGCTGCGAATGAGTTTTCTT	GGTAGCATTTCTTACCAAGGCTTT
	FA5378	32	6	6	10389855	C	T	+	CCTAACTGGATTGAGCAGCTCAC	CCTAACTGGATTGAGCAGCTCAT	GCTCCTCAATAAGTAGATCTTCTTCAGGT	TGGAATTCTTGAGGAGATGCCTA
	FA4697	33	7	6	10421778	G	A	-	GAAAAAATGCCCATGCGTTACAAC	AGAAAAAATGCCCATGCGTTACAAT	TCACCTAATTAAACCGTATAACAATAATAAGAAATAACC	ACTAGAAAAAATGCCCATGCGT
	FA4698	34	8	6	10422671	T	A	-	GTAGTTTAAGAGTGATTTTTCAATCTTTGAGGA	GTAGTTTAAGAGTGATTTTTCAATCTTTGAGGT	ACCGTAGATACCAAATTTTATATTAGAAAATATATTCGGT	CATGTGTGTAGTTTAAGAGTGATTTTTCAA
	FA4683	35	9	6	10422831	G	A	+	AACCCTCTTTAGTCCCGGTTG	CAACCCTCTTTAGTCCCGGTTA	TGCTTTGGGCGTCTCGGT	CCCATCTTTAGTCCCAGTTTGC
	FA4702	36	10	6	10426588	T	A	-	TTAAGCACTTCACCGGGTGA	AAGCACTTCACCGGGTGT	GCACTCTTCGTTGTACAAGGGTATCTAAT	AGGCAGACACATTGTGTTAGTTAAG
	FA4703	37	11	6	10427313	G	C	-	TCCCTATTTCCAACCTGCAGTATC	TCCCTATTTCCAACCTGCAGTATG	GACAGCTCGCCCCTATTGGA	CCTCATAAGGTTAGAGATACCAATAATCC
	FA4704	38	12	6	10427757	T	A	+	CGGCCAATGATGTGGATAATCCT	CGGCCAATGATGTGGATAATCCA	AACATTTTCATCTCTTCTCTCGAAGTCTTTCT	TGCTTTCTAAAAGGAAATCTATCACCG
Pi13	FA5269	39	1	6	17096200	G	A	+	GAAGAGCTTTTAAACAAAACAATTCCTTCTG	AGAAGAGCTTTTAAACAAAACAATTCCTTCTA	TGCAGTATGCTGATGACACAATCAATGTTTTT	TGAAAGTGTGCAGAAGAGCTTT
	FA5270	40	2	6	17105485	G	A	+	GGATTTTAGTGTGGGAGATTGGG	GGGATTTTAGTGTGGGAGATTGGA	CAGCCACAAAGATCTGAACATAAAGTTGT	ACAAGAAGCGAAGTGTTAGGGA
	FA5271	41	3	6	17121368	G	C	-	GTTGCCCAAAACTAGCACTAATTCC	TTGCCCAAAACTAGCACTAATTCG	ACTACTGCCGACCAACCCA	CTGCCGATTACGGTTGCC
	FA5280	42	4	6	17159082	A	G	-	GCTCAATATCATTCTAAATACTTTAGCTTTGGT	GCTCAATATCATTCTAAATACTTTAGCTTTGGC	GGGATACAGCAGCAATGCACA	ACAATTTTACTACAGGTTAATATGCTCAATATCAT
	FA5294	43	5	6	17161116	G	A	+	TCAGGTGCAAGGTACCCG	CTCAGGTGCAAGGTACCCA	AGGGAGCAGAGCCATGTTTTCA	GGCATAGTTGGTGAGCCAC
	FA5283	44	6	6	17166899	C	T	+	AGCAATTGAGTTCGGGCAAAC	AAGCAATTGAGTTCGGGCAAAT	TTCCTGTTAAATACGTACTCACGTATGTATGG	CGTGTGATTATCACTCAACTGACA
	FA5288	45	7	6	17174653	G	A	+	ATGAACCATTGTTAAATAGCGGCG	CATGAACCATTGTTAAATAGCGGCA	GGTTCCGCCGCTATTCAATAGG	GATAGTGCCAAAAAACATGAACCA
	FA5292	46	8	6	17186714	G	T	-	CGAGCCTCACGAGACACC	CGAGCCTCACGAGACACA	GATCCCGTATCATGTAGAATTGACTCGT	TCAAAGGATTAGATTGACTGGCAAG
	FA5293	47	9	6	17240935	A	G	+	ACCCCCAAGCCTGCA	ACCCCCAAGCCTGCG	GCCAGCGGAAAGGCGA	GCAGCCGGAGAGGCAT
Pii	FA4515	48	1	9	9657397	G	A	-	AGCAGGGAACCCAAGTTAGC	TTAAGCAGGGAACCCAAGTTAGT	GTTGGCAGGCTGCAGGT	TCTGGAAAATGCATGTAGTAACATGTTAA
	FA4505	49	2	9	9663840	C	G	+	ATTGCACTCTTCTGTTAGATGATCTCTAC	ATTGCACTCTTCTGTTAGATGATCTCTAG	GCTATTGACAAGCAATATGTTGAGGGAA	GCCATCTTTCCTTAATATCATTGCACT
	FA4494	50	3	9	9667330	G	T	-	TGACAGTTCCTCGGTCCAAC	TTGACAGTTCCTCGGTCCAAA	GCCATCTTTTACCGGCATGGG	GGTTTATTTTCTTGACAATGCAGCT
	FA4495	51	4	9	9668417	C	G	+	GCTCACTTGTTGAGGTGTCCC	GCTCACTTGTTGAGGTGTCCG	GCATCAAGCTCAGCGCCAT	GCCTCTTCATTAGGCACTGGAT
	FA4501	52	5	9	9672424	C	T	-	TTGGCAAGCTGCAAAGGATG	GATTTGGCAAGCTGCAAAGGATA	GGGATAATCTTCCTCTATCTTCCACATTTCT	CAACGACAAAGGCGTGAGAT
	FA4526	53	6	9	9787343	T	G	-	GTTGTGTCGGTCACTTTTGCATA	TTGTGTCGGTCACTTTTTGCATC	GGAACATTTTCATTTATACCTACTCTTTAAATCCCAAA	GTGTCATTTTAAAGTTGTGTCGGTC
	FA4527	54	7	9	9787450	T	A	-	CCATTATAACCTACCGCTTAACATTTGTTAA	CCATTATAACCTACCGCTTAACATTTGTTAT	TGTCAAAATAAGTGCTTCCAAACATATGTAAATAGTG	TCCATTATAACCTACCGCTTAACATTTG
	FA4533	55	8	9	9834576	T	A	+	TGGATGAATCGGCAATGAACTCT	TGGATGAATCGGCAATGAACTCA	GATCATCTTTATCAATTGGCTTGCCTATAGC	CGAGTACGTTGCCAAGATGTG
	FA4536	56	9	9	9859957	G	T	-	AGCTTCCCGTTGTCTAACAGTATC	CAGCTTCCCGTTGTCTAACAGTATA	CGTTTGCTTGTGAACAATGGATCATAGA	ACCACTAAATGCATATCAGCTTCC
Pia	FA4608	57	1	11	6521353	G	C	+	TCGTCTCTGCAAACTCGGG	TCGTCTCTGCAAACTCGGC	GAGAAGGCGTGCCAGCAA	GGCCCTTGGCGTCTTT
	FA4605	58	2	11	6540957	G	T	-	CCCTGTTGTGATCTCGATAATTAGAAGAC	CCCTGTTGTGATCTCGATAATTAGAAGAA	CGAGGTGAAATCTCCACTCAATCAGA	GGGAAGTTTTTCTCCCCTGTTG
	FA4598	59	3	11	6543100	G	C	+	TCGCATCTTCAGAGCATCCAG	TCGCATCTTCAGAGCATCCAC	TGGTACCCGTTCTTTATCGCTTCA	AGCAGGGTTCTTTTAAGGAATTTATCG
	FA4615	60	4	11	6544401	C	T	-	GCAGCAGAATAGTGGTCACG	GGCAGCAGAATAGTGGTCACA	GCAGAACAGCAGGCATTAGCT	TTTTCCGACTGATAAGGATATTGGC
	FA4617	61	5	11	6634911	A	C	-	AATTACTCTATGGACACGGTGCAT	ATTACTCTATGGACACGGTGCAG	TGGTCCACTGTGAGAAAAGAAATAATGGT	AGATCATAGATGCTTGTGGTAAAAGAATT
	FA4620	62	6	11	6638905	A	G	-	CAAGGAATGAGAATGAGCCACTT	CAAGGAATGAGAATGAGCCACTC	TGGAACTTGGCTTGAGAGCCT	TTCCAGTTTGCTTCTTTCTGCA
	FA4624	63	7	11	6656541	A	C	+	GAGACTGCTGACAGAATGGCTATATTA	AGACTGCTGACAGAATGGCTATATTC	CCATTCCTGACACCGTTATCACC	AGGACAATAGGAGACTGCTGAC
	FA4625	64	8	11	6707030	G	C	-	GCTGGTAATGCATGGTAGCTTAC	AGCTGGTAATGCATGGTAGCTTAG	TGGCCAAAAATGATGATGTCAAGGC	AGAAGCAGTTCTTTTGGTCAGC
Pik	FA4742	65	1	11	27817940	G	A	-	CCATGCCATGTTCTGCAGC	CCATGCCATGTTCTGCAGT	GCTATGCCATTGCCACCGA	CCAGGACGCGCTCAAAC
	FA4740	66	2	11	27818557	G	C	-	GTGATCAGAAGCCATCCAACTTC	GTGATCAGAAGCCATCCAACTTG	TGAACTAATCAGAGGAAACACGACAGTT	GCCTCAATCGTTGATGCTATTGT
	FA4737	67	3	11	27820870	C	T	-	CGATGGAGATGACCCTCATTCG	CGATGGAGATGACCCTCATTCA	GCTCCTCTCGCTGCTGGATG	CCAATCCACCGAATCCCAC
	FA4735	68	4	11	27823073	C	T	+	CTGCATAAAGATGACCTGAAGAATGTC	CTGCATAAAGATGACCTGAAGAATGTT	GTTTCTTGCAAGGATTTAGTTTACTCATCTTGT	TGTTTGGAAAGTTTATGCTGCATAAAG
	FA4734	69	5	11	27823722	G	A	-	CGACAGAGCAGATGAAGTGAGAC	CGACAGAGCAGATGAAGTGAGAT	TCAAGCAAGGAGCTCTGCCA	CGGATAGTCCGACTAAACCTCG
	FA4732	70	6	11	27828066	A	C	+	TCGAACCAAACTGTGGCATGTA	CGAACCAAACTGTGGCATGTC	GGCCTTAATTATTAGTCAAATCAAATCAACATTATA	GATGTTTGCCAAAGCGATATGTTTAT
	FA4710	71	7	11	No hit	C	G	Unknown	ACATTTTTTCACTTCAGCACCACC	ACATTTTTTCACTTCAGCACCACG	CTGTCGTCAGCATTGGTTGGA	CCTCTATGTGTCTCAAATCCCTACA
	FA4712	72	8	11	No hit	A	C	Unknown	CTATCCCCCAAGACAACGACA	ATCCCCCAAGACAACGACC	TGTTTTTGTCTACGAAGTTGGGGATCT	TGCCCCAGACTTTGTTGC
	FA5375	73	9	11	No hit	C	G	Unknown	GCCGGTGACCTAAGAGACG	GCCGGTGACCTAAGAGACC	AGTCAATGCCATCACCGACCA	GCACTCGGTTGCAATCGC
	FA4717	74	10	11	No hit	G	C	Unknown	GCACTCAACGCAAAAGGGC	GCACTCAACGCAAAAGGGG	CCATCCCTACTCGCGCCTC	GAGGTGAGAGAGTAGCACTCA
	FA4718	75	11	11	No hit	T	C	Unknown	TCAGTTCCATGGGTGCGT	CAGTTCCATGGGTGCGC	GGCGAGATCTCAAGACGAAAGTAGAA	CAGCTCTGGTCGGAGGAG
	FA4721	76	12	11	No hit	A	T	Unknown	CAGCATTGTACAGAAAAGTCAGTGAA	CAGCATTGTACAGAAAAGTCAGTGAT	AGACACAGCTACTGATGCCCG	GACTACCATTGCCACAGCA
	FA4723	77	13	11	No hit	A	T	Unknown	GCTTTCATTGCGCCTTTACCTTTTT	GCTTTCATTGCGCCTTTACCTTTTA	AGGAGCCCGCAAAGAAAGGA	TGACAGTACACGGAGTGCTT
	FA4726	78	14	11	No hit	T	C	Unknown	CCCCACAGCCTCACCT	CCCCACAGCCTCACCC	GGAGTGATGAGGGTAGGAGGG	TGGAGCTTCGCGTGGA
	FA4729	79	15	11	27992151	C	T	+	CCTCCCATCATTCCTGTGAACTC	CCTCCCATCATTCCTGTGAACTT	CGAACAGGATGGCTTGGCTT	ACAATCAGCAGCATCATTGATCC
	FA4750	80	16	11	27993468	T	C	+	TGTTCAGAGACTTCCTCAGAAAGTTT	TGTTCAGAGACTTCCTCAGAAAGTTC	TGCAATTGGTCAGAAAGAAGTTGCAC	TCATTTGGATTCTCATGCTTGTTCA
	FA4751	81	17	11	27995372	A	G	+	CTCAATCTATGGCATCTACCGTACA	CTCAATCTATGGCATCTACCGTACG	TCCATGGTACAAGCATCGGTCC	GAGAGAAAATCAATTTTGTTGTTTCTCTCA
	FA4752	82	18	11	27995713	G	C	+	AGCATGTGAGAATTAATATTCAAGCGTG	AAGCATGTGAGAATTAATATTCAAGCGTC	AATTATTACAGAAGGAAATATCATTCCCCTAAATGTTTTC	AGTAGTACCCTCAATCAAGCATGT
	FA4753	83	19	11	27996426	A	G	-	GTGATTGGGGCAATCATACGTT	GTGATTGGGGCAATCATACGTC	TCTTTGCGTTGCAATTGGACAATCA	AGCGTGCTATTCCTTTATCTCTTTG
	FA4758	84	20	11	28006310	T	G	-	GTTCCCCTGACATATTCATCCCA	TTCCCCTGACATATTCATCCCC	GCAACACTGGTTTAGGCATTTCTCTATTA	ACCCTGTGTGGCCGTT
Pita	FA5541	85	1	12	10607554	A	C	+	ATCAAGTCAGGTTGAAGATGCATAGA	CAAGTCAGGTTGAAGATGCATAGC	TCTTTCTCTGCCGTGGCTTCT	GGTTTCAAACAATCATCAAGTCAGG
	FA5544	86	2	12	10611244	A	T	-	TCGAGGCCGAGAGAAGAAGT	TCGAGGCCGAGAGAAGAAGA	TCGTTGCCGGCGGAGT	AGGCGCACCTCGAGC
	FA5546	87	3	12	10611754	C	A	+	TGACACCCTGCGATGCAC	TGACACCCTGCGATGCAA	CGAGCTGCAGAGGTCTCCA	CGTCAGGGACCGCATGAT
	FA5553	88	4	12	10612903	C	G	-	AATGTTGATGCCGTTATTGTAAGGAAG	AATGTTGATGCCGTTATTGTAAGGAAC	GCATTAGAGTTACGTCTCGGGAACA	GGGATGGAAAATGTTGATGCC
	FA5556	89	5	12	10614915	T	C	+	CAATCACCAGAATCACCACATGAATT	CAATCACCAGAATCACCACATGAATC	TCACATTCTTGCTACTATGATCGATGATTCC	CCAACAAAACCACATGAATGTCAATC
	FA5569	90	6	12	10635507	G	A	-	CACAACTGCGGTTGCTCAC	CACAACTGCGGTTGCTCAT	CGAAATCGTACGCCCCAACC	CGAGTATGCTGCAATGTGACATTC
Pita-2	FA4580	91	1	12	10801324	A	G	+	CGGTTATGGGTGACCAGAACAA	CGGTTATGGGTGACCAGAACAG	AACATGTCATCAGGGAGCCA	ACAAATATGCTGGGATACATCTTCG
	FA4571	92	2	12	10830872	G	A	+	GGGTACTCATTGAAGCGCTTG	TGGGTACTCATTGAAGCGCTTA	GATGAAGCGTGCGGCCT	CTGAATGGAAAAGTAAGCCACATTG
	FA4572	93	3	12	10833033	T	C	+	CAGAGTAGTCTCCAAAAGATGGGAT	CAGAGTAGTCTCCAAAAGATGGGAC	CTTTCGGTCATTCCGATATAAATAGGATGC	TCCATGCTTACTGAATATCCATCAGA
	FA5655	94	4	12	10833370-10833387	AAAAACCAG [A]	TG [B]	+	TTCATCGCATCGAATTTAAAAAACCAG	CTGTAAAAGTTCATCGCATCGAATTTATG	ATTTCGCAGGCATAAACTCGTACG	ATGACCTTCGCAGACCTCATC
	FA4585	95	5	12	10849598	G	C	+	GCTTCTAAGCTCAGAGATCCTCATG	GCTTCTAAGCTCAGAGATCCTCATC	AGGAGTTGTTCGTGGGCCTT	ATTCACTCATTGAATCAACAGCTTCT
	FA4588	96	6	12	10853113	G	A	-	ACCTGTTTGACGTATGGTAGTGC	ACCTGTTTGACGTATGGTAGTGT	GCCACCTTAAAATTTGCAACAATAAAATTAACTGT	GCTCCGAAACACCACTAACAC

Chr., chromosome number.

[a] Position of the SNPs in the 'Nipponbare' reference genome (IRGSP-1.0); "no hit" indicates that the marker did not have a BLASTN match in the 'Nipponbare' reference genome (IRGSP-1.0).

[b] "+" and "-" indicate that the allele-specific primers were designed on the plus and minus strand of the 'Nipponbare' reference genome (IRGSP-1.0), respectively.

[c] Tag sequences for the fluorescent label are not shown.