

**Table S1.** The three comprehensive FNP marker systems for deeper allele mining, and the primers and markers for transformation test of the *Pid* family.

Gene (accession number) / Marker name / Primer sequence (5'→3') <sup>a</sup>	Annealing temp (°C) <sup>b</sup>	Restriction enzyme (°C) <sup>c</sup>	Expected size (bp) <sup>d</sup>
<b>Set I. <i>Pid2</i> (FJ915121.1)</b>			
<b>Pid2-F/N<sup>C1022T</sup></b> F: acagttccggcagactttgtgacat R: agtttgc当地aaacggccggggct	62	<i>Taq</i> I (65)	109/85
<b>Pid2-F/N<sup>A1383G</sup></b> F: ggaatacacaactcggttcgcatt R: ctatgatagccaaagttagcgc	56	<i>Mlu</i> I (37)	126/104
<b>Pid2-DIG<sup>T2058C</sup></b> F: agttgatgaccaggaggcaga R: ctttcctccagcttcttgaa	58	<i>Hha</i> I (37)	226/174
<b>Pid2-ZS<sup>A555G</sup></b> F: gccacaccttatgcaactactg R: accagacagaaggtgtctgc	53	<i>Hpa</i> II (37)	111/88
<b>Set II. <i>Pid3</i> (FJ745364.1)</b>			
<b>Pid3-F/N<sup>G2009A</sup></b> F: gcagtcgttgtttctaagcaatttg R: cacaagagagcctaggtgtgaaac	58	<i>Bsl</i> I (55)	138/104
<b>Pid3-F/N<sup>C2209T</sup></b> F: aagggtcgaagtgcattgt R: cgtgaggattttagattgttacag	62	<i>Bam</i> HI (37)	216/145
<b>Pid3-DIG<sup>G775A</sup></b> F: aagagttcgcaagaatgtcgg R: cattccatacatcatctaggacaagg	56	<i>Bsr</i> I (65)	138/102
<b>Pid3-DIG<sup>G2695A</sup></b> F: atctgaagttcctgctctgtccaa R: acgtcacaaatcattcgctct	58	<i>Hpy</i> 99I (37)	148/121
<b>Pid3-TTP<sup>C1136T</sup></b> F: aatgagataaggaattgtccgg R: aatgacagaaggcggtccaatgtgc	57	<i>Apa</i> LI (37)	110/85
<b>Pid3-TTP<sup>C1623G</sup></b> F: agcacccgttatcaactca R: ggtaatgactgaagcgaactg	60	<i>Dde</i> I (37)	120/102
<b>Pid3-ZS<sup>G477A</sup></b> dF: gayrgcggaaaggaggagctt R: cacactgaccaccatgcggc	60	<i>Mse</i> I (37)	145/125
<b>Pid3-ZS<sup>C525T</sup></b>	62	<i>Hpa</i> II (37)	125/104

F: caagagggaggatgagcttgc

R: ccgtcttgcgattccac

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**Set III. *Pid4* (MG839283.1)**

**Pid4-F/NC<sup>1217G</sup>** 57 *Mnl* I (37) 107/73

F: cataattcaaaaactgtgcttattccct

R: cctcataacttttatgtatttctca

**Pid4-F/N<sup>A1452G</sup>** 60 *Bsp* HI (37) 115/97

F: gcagctatcttcagggctcat

R: gctaaggtaaaaaacatggct

**Pid4-DIG<sup>A1149T</sup>** 53 *Xba* I (37) 160/136

F: ttaatgaatctgttttctgactctag

R: gattttctcagcagcaaatgttttagc

**Pid4-DIG<sup>A1898G</sup>** 62 *Bsr* I (65) 114/72

dF: gggagacaggaktcawacctaagc

R1: gagcatccttagctgtggtaac

R2: gatcatccttagttgggacggac

**Pid4-NPB<sup>G1362A</sup>** 59 *Aci* I (37) 130/82

F: aggctgagaagggtttgata

R: gaagatagctgcagagacagt

**Pid4-NPB<sup>C1554A</sup>** 53 *Aci* I (37) 118/97

F1: ttctgtacaccttagcattttcg

F2: ttctgtatcttagcgtttccg

R: caacatcctccatagccattcca

**Pid4-SN/CO<sup>T1841A</sup>** 57 *Hph* I (37) 195/161

F: catcaatagaagcatgattcaacc

R: tcctgtctccatcaatagaaag

**Pid4-SN/CO<sup>C2250G</sup>** 56 *Apa* I (25) 120/92

F1: gtcacttcgaatttactaccgtgg

F2: gatactccgatttcaatatctatgg

dR: ggaactcygccaccaccwscga

**Set IV. Transformation test**

**Pid2 cloning** 62 *Asc* I (37) 6,259

F: attggcgccgccatcaacatagacgtacgtgg

R: attggcgccgccattttacagatcactgtgccat

**Pid3 cloning** 62 *Asc* I (37) 6,237

F: attggcgccgcccccacacattgtacacacctacgaccac

R: attggcgccgcgaacgacaagtgcgacatgattg

**HYG** 58 *n/a* 879

F: ctctcgccccgatttg

R: cagcgtctccgacactgat

<b>Vector_F/Pid2_R</b>	56	<i>n/a</i>	4,738
F: aattaattctaggccaccatgttg			
R: ctatgatagccaaagtacgcg			
<b>Pid2_F/Vector_R</b>	56	<i>n/a</i>	2,114
F: ggaataacaactcgttcgcatct			
R: gtctggaccgatggctgttag			
<b>Vector_F/Pid3_R</b>	60	<i>n/a</i>	4,209
F: aattaattctaggccaccatgttg			
R: aatgacagaaggcgatgtcaatgtgc			
<b>Pid3_F/Vector_R</b>	60	<i>n/a</i>	2,919
F: aagagttcgcaagaatgtcgg			
R: gtctggaccgatggctgttag			

<sup>a</sup> F, forward; R, reverse; PCR with multiple primers was designed with F1, F2, or R1, R2, if any; and degenerate primer sequences were labelled dF and dR, where r=a/g; w=a/t; k=g/t; s=c/g; and y=c/t. For transformation test, sequence unlined was responding to the common restriction enzyme *Asc* I for ligating fragments (resistance genes) into the binary vectors, pYLTAC380H.

<sup>b</sup> Each PCR was initiated by a 94°C/3 min denaturation, followed by 35 cycles of 94°C/30 s, 50-62°C/30 s (temperature dependent on choice of primers), 72°C/25-30 s (time dependent on amplicon size) and a final extension step of 72°C/5 min. Amplicons were electrophoresed through a 10-12% polyacrylamide gel. For transformation test, each PCR was initiated by a 95°C/3 min denaturation, followed by 35 cycles of 95°C/15 s, 50-62°C/15 s, 72°C/2-8 min and a final extension step of 72°C/5 min. Amplicons were electrophoresed through a 1% agarose gel.

<sup>c</sup> The number shown in parentheses refers to the temperature at which the restriction digestion reaction was run.

<sup>d</sup> Only the critical bands were sized.