

Supplementary Tables

Table S1. List of the primers used in this study for gene mapping and sequencing.

Marker	Forward primer (5'→3')	Reverse primer (5'→3')	Use
RM314	CTAGCAGGAACTCCTTTCAGG	AACATTCCACACACACACGC	Mapping
RM50	ACTGTACCGGTCGAAGACG	AAATTCCACGTCAGCCTCC	Mapping
A6K1	TTCCCTCGTTTGATGACTT	GCCCCAATAATAATGGTAAG	Mapping
A6K2	GCTCTGCGACTGATGAACT	AACGTGACAAACCTATTGCT	Mapping
A6K3	ACACATCCGTCGCACTCA	GGAGCCAAGAAGACGTGAAG	Mapping
A6K4	TCTCGGTCTCATGGTCACC	TTGGGAGGATTGGGAAT	Mapping
A6K5	CATCCAAATAGGTTGCGAA	GTGGGACCCACATGTCAT	Mapping
A6K6	AGTGCGGCAATTATTGAT	CTGAAGTCTGAAGACCGAAT	Mapping
A6K7	CATGACAACAATGGGTATGAC	CAGATATTATGAGGAATCAG	Mapping
A6K8	GTTGTCAGGTGGTCTCTCATT	CCGTTGCTGTGTCGGTGT	Mapping
PL1	TCAGTTTCAGAGAGAGGAGTC	TCATTCTTGGACTAGAGTTCA	Sequencing
PL2	TTATCCCTTCAATACCCTTTAC	AAGAACATTGCATATCAGGC	Sequencing
PLM	CTCAGTCTCACACCGCACA	CAAGCTCTCCTCCCCATT	Marker

4 **Table S2. List of the primers used in this study for qRT PCR.**

Name	Genebank accession	Forward primer (5'–3')	Reverse primer (5'–3')
<i>Actin</i>	XM_015774830	GTGGTCGCCCCCTCCTGAAAG	GGCTTAGCATTCTTGGGTCCG
<i>OsPL6</i>	MK636605	CAACGAGCTGGTTTGAGGCGGT	TGTAGAGACCACCTGTTGCCGAG
<i>OsPAL</i>	XM_015769634	AGCTCCGTCAAGAACTGCGTC	CGATGGCGGTGAGGAGGT
<i>OsANS</i>	Y07955	AGCTGCTCGCCATCCTCTCC	GCTGACGTGCGGTGTGTGCC
<i>OsCHS</i>	XM_015762568	GTTACACCGCTGGGGATCT	TCCTCTCCTTGTCAGCCCA
<i>OsDFR</i>	MK636607	GACATCGACTTCTGTGCGCCG	TGACGCTGATGAGGTCCAGC
<i>OsF3'H</i>	XM_015757555	CTACAGTACCAGCCTTCTC	TCATCAGTGTGACCATCC
<i>OsF3H</i>	XM_015779149	TGACCATGCTCACTATCTG	TCTCTATCTTCCTTGCTCTT
<i>OsCHI</i>	XM_034715967	CATCCTCTTCACCCACTC	GATGATGGAATCCAGCAC
<i>CHLI</i>	XM_015772495	AGTAACCTTGGTGCTGTG	AATCCATCAACATTCAACTCTG
<i>CHD</i>	XM_015775598	GCTTGCAGAAAGCTACACAAGC	AGGCCGTGAGCTAAAGGAGA
<i>CHLM</i>	XM_015785870	CCATCCATTGGTCTCCTTATGACA	GTAGCCTACTTACCATCAATGAGC
<i>CAOI</i>	XM_015758600	GACACCTTCATCTGGGCTTCAA	CGAGAGACATCCGGTAGAGC
<i>PORA</i>	XM_015759459	ATCACCAAGGGCTACGTCTC	GAGTTGTTGTTCCAGCTCCA
<i>PSaA</i>	AAS46121	TGGGGTTGATCCTAAGGAGATACCA	CCTCCGCGAAAATAAGAAATTCTG
<i>PSbA</i>	AAS46104	GCGGTTCCCTATTCACTGCTATG	TAACCATGAGCGGCCACAATATT
<i>rbcl</i>	AAS46127	GGAGGGACGTATGTCACCACAA	GAGTTACTCGGAATGCTGCCAAG
<i>rbclS</i>	X07515	GTGGCAACTAAGCCGTCATCGTC	TGCCTCACCCAACAACATATAGTC
<i>atpA</i>	AAP54723	TGAATCTCCTGCTCCGGGTATAA	TGCTGTTTTGCCGGTTTGTCT
<i>atpG</i>	AGT42322	AGGTGGAGCTCCTCTACTCCAAG	TCAGCTTCCCTTCCTTGGTGGT

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6 **Table S3. The genes information between 36 kb target region**

Gene locus	Genebank accession	Putative function	Sequence alignment result
<i>LOC_Os06g10290</i>	BAS96685	F-box domain containing protein	No difference
<i>LOC_Os06g10300</i>	BAS96686	LRR containing protein	No difference
<i>LOC_Os06g10310</i>	BAS96688	Growth regulating factor protein	No difference
<i>LOC_Os06g10330</i>	N/A	Myb-related protein	No difference
<i>LOC_Os06g10340</i>	BAS96689	Autophagy-related protein	No difference
<i>LOC_Os06g10350</i>	BAF19004	MYB family transcription factor	Mutation in promoter region including SNPs at -612, -508 -360 and insertion at -29 as well as mutation in 5'-UTR region including 3 SNPs and 6-bp deletion

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9 Supplementary Figures

10 Fig. S1. Sequence analysis of the promoter and 5' UTR regions of WT and *pl6* in PLACE
11 database.



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13 Normal black boxes show induction of new cis elements in *pl6* and bold black box show deletion
 14 of cis element from *pl6*. Black arrow showed start codon of gene.