

Figure S1. Comparison of nucleotide sequences between WT and *psl* mutant. Nucleotide sequence alignment revealed that there was a deletion of 3 bp in the exon of LOC_Os12g42420 in the *psl*.

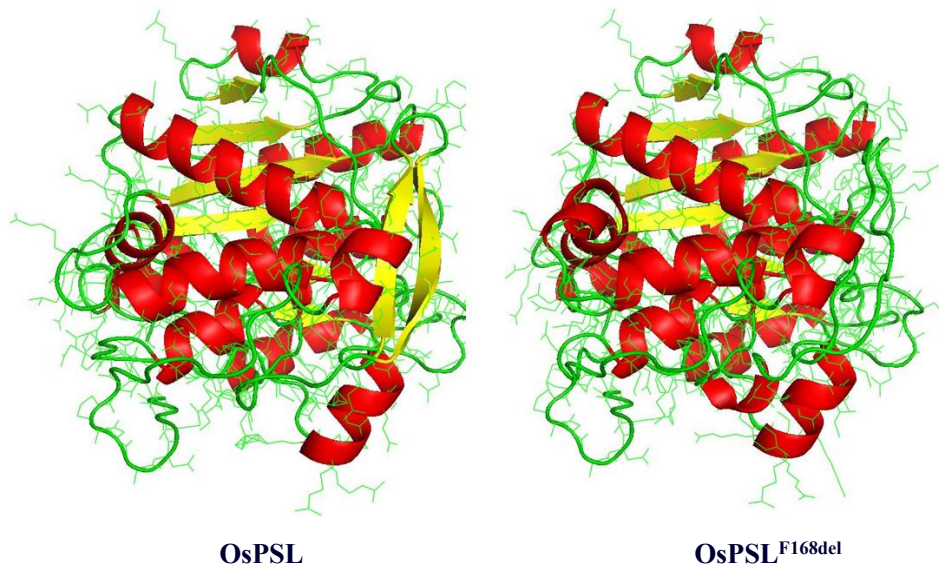


Figure S2. Three-dimensional structure prediction of OsPSL protein. The advanced structure of the OsPSL protein was predicted by using Phyre2 server (<http://www.sbg.bio.ic.ac.uk/phyre2>). A phenylalanine residue (F168) is located in a β -sheet and its deletion leads to the absence of the β -sheet in OsPSL protein

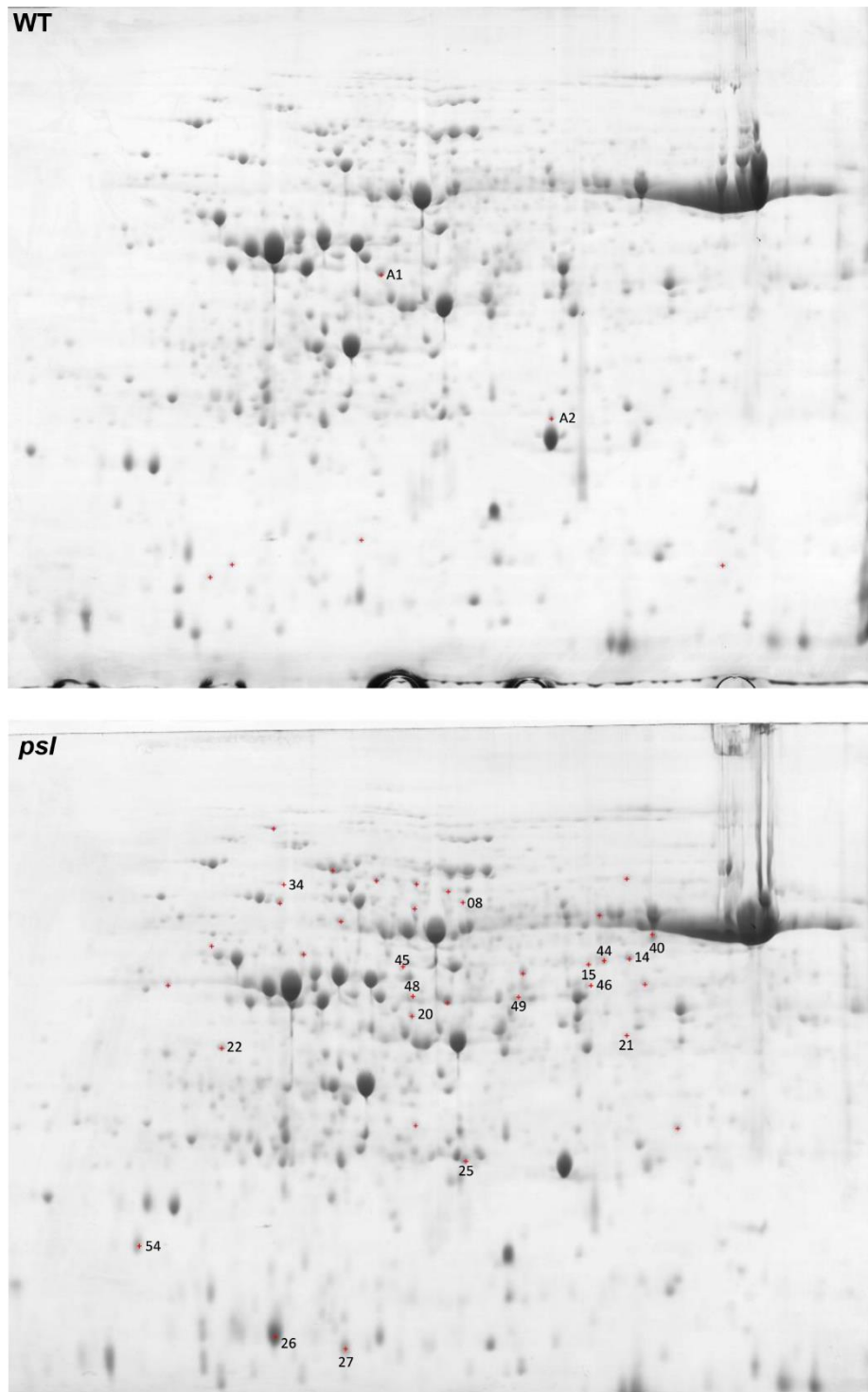


Figure S3. Representative 2-D gel protein profiles of leaves from the *psl* mutant and WT. Coomassie blue stained spots were detected by ImageMaster software in the WT and *psl* gel profiles, respectively. Numbered “+” show proteins selected for mass spectrometry.

Table S1 List of primers used in this study.

Primers	Sequence (5'→ 3')	Locus/Gene	Experiments	Marker's type
PSM183F	GACAAAACCGGCAACAGATT	Chromosome 12	Map-based cloning	SSR
PSM183R	TAGCTTTATTGTGGCAGGGG	Chromosome 12	Map-based cloning	
RM247F	TAGTGCCGATCGATGTAACG	Chromosome 12	Map-based cloning	SSR
RM247R	CATATGGTTTTGACAAAGCG	Chromosome 12	Map-based cloning	
PSM419F	GAGGCAATAGGAGGGGAGA	Chromosome 12	Map-based cloning	SSR
PSM419R	GGCAGCGAAAGCATAAAGTA	Chromosome 12	Map-based cloning	
PSM420F	ACCTATGGCTTGCACGAAC	Chromosome 12	Map-based cloning	SSR
PSM420R	CTGAGTTGACAATATCATCACGGA	Chromosome 12	Map-based cloning	
PSM421F	TTGGCGTGCTGCTGTATTTT	Chromosome 12	Map-based cloning	SSR
PSM421R	GTCCCGGATTCATGGTTCTG	Chromosome 12	Map-based cloning	
RM519F	AGAGAGCCCCTAAATTTCCG	Chromosome 12	Map-based cloning	SSR
RM519R	AGGTACGCTCACCTGTGGAC	Chromosome 12	Map-based cloning	
PSM464F	CCGTTCAAATGTTAATGTCCAG	Chromosome 12	Map-based cloning	SSR
PSM464R	GACCAAAGGTGAGACCAATC	Chromosome 12	Map-based cloning	
PSM189F	TGATAGTTGGACCCGATCCT	Chromosome 12	Map-based cloning	SSR
PSM189R	ATCACCCCTCTGCTCGTCT	Chromosome 12	Map-based cloning	
RM235F	AGAAGCTAGGGCTAACGAAC	Chromosome 12	Map-based cloning	SSR
RM235R	TCACCTGGTCAGCCTCTTTC	Chromosome 12	Map-based cloning	
PSM192F	CTGCAGCCCTGTGATAGGAT	Chromosome 12	Map-based cloning	SSR
PSM192R	TGTGCGGTTGCTTTCATAGA	Chromosome 12	Map-based cloning	
PSM193F	CATCGTCCTCGGTATCATCA	Chromosome 12	Map-based cloning	SSR
PSM193R	GTGAAACGGAGGGAGTAGCA	Chromosome 12	Map-based cloning	
AL732532-2F	AACCCACGGGTTTGACTAGC	Chromosome 12	Map-based cloning	InDel
AL732532-2R	GTCTGGTAGCTGGGATCGTG	Chromosome 12	Map-based cloning	
BX000457-1F	CGGATATACACGGCTGCACT	Chromosome 12	Map-based cloning	InDel
BX000457-1R	TGTTAGAAGGGTGCTGAGGC	Chromosome 12	Map-based cloning	
AL731885-1F	CTGTTTGCTCGTTCGTTGGA	Chromosome 12	Map-based cloning	InDel
AL731885-1R	TCGACCCAACCATCACCTG	Chromosome 12	Map-based cloning	
AL731885-3F	AAGTGACAGGAGTGGCATGG	Chromosome 12	Map-based cloning	InDel
AL731885-3R	GGATAGCTTGGTTCGTCCGT	Chromosome 12	Map-based cloning	
AL845347-11F	GGTGGCCCATCATGTCAGAG	Chromosome 12	Map-based cloning	InDel
AL845347-11R	GCAATGCTAACACCTCGCAT	Chromosome 12	Map-based cloning	
AL845347-13F	TGCTAAGGGAGTCAGAACGC	Chromosome 12	Map-based cloning	InDel
AL845347-13R	AGATCGGAACACGAAAAG	Chromosome 12	Map-based cloning	
AL732532-7F	TGTGTGCCTTACAGCAGAGG	Chromosome 12	Map-based cloning	InDel
AL732532-7R	TCCCGCTAGAGAGGGTCAC	Chromosome 12	Map-based cloning	
AL732532-8F	ATTTTGCCTCGAATTGGGGC	Chromosome 12	Map-based cloning	InDel
AL732532-8R	TCGCACAAAACCTAGAACCG	Chromosome 12	Map-based cloning	
AL732532-5F	AGCGTGAATAAACACACCCA	Chromosome 12	Map-based cloning	InDel
AL732532-5R	TCTCTCCAGAATCGCTCCA	Chromosome 12	Map-based cloning	

Table S1 List of primers used in this study (continued).

Primers	Sequence (5'→ 3')	Locus/Gene	Experiments
PSLF	GGTACCTCTAGAATGGCGCTGCCGCACGC CGCCT	LOC_Os12g42420	Complement assay
PSLR	ACTAGTCTACCATGGGTCTCGCAGGATGA CGGA		Complement assay
PSL-qRTF	CACCCCTTTCCCCACCTTCTACC	LOC_Os12g42420	qRT-PCR
PSL-qRTR	GAACCTTGTTCCACAGCCTCCGA		qRT-PCR
SEC1-F	GAGCACATCAGACGCAGTGC	LOC_Os01g68680	qRT-PCR
SEC1-R	CCATCTCTTCCCAATTCCA		qRT-PCR
SEC2-F	TTCCTGGACACCCCTCTCTG	LOC_Os02g28830	qRT-PCR
SEC2-R	AATCATCTCTTCCCCTAGCCC		qRT-PCR
SPY-F	GAGGCTGGTTGCGAAGTCTG	LOC_Os08g44510	qRT-PCR
SPY-R	TGCGCCACATGTTTCTGTATG		qRT-PCR
EIN2F	TACTGCCTAACTGCGGAGACG	LOC_Os07g06130	qRT-PCR
EIN2R	CCAGGATGCCCTGAAGACG		qRT-PCR
EIN3F	CACGGAGAACAAGCCATCG	LOC_Os03g20790	qRT-PCR
EIN3R	GCCACTTCCCTGTCCAAAAA		qRT-PCR
B14F	ATCAAGCCTGTCAATCCCGA	LOC_Os05g04510	qRT-PCR
B14R	GAGCTCCCCAGCCACCATA		qRT-PCR
B15F	CCATCTTCCACCTCAACCCC	LOC_Os01g22010	qRT-PCR
B15R	CTGGCGACGATGCTCTTGG		qRT-PCR
25SR-F	AAGCCGAAGAGGAGAAAAGGT	25sRNA	qRT-PCR
25SR-R	TTGGCGGGCCGTTAAGCAGAAAAGA		

Table S2 Comparisons of agronomic traits between WT and *psl* mutant.

Trait	WT	<i>psl</i>
Heading date (d)	81.33 ± 0.58	81.67 ± 1.02
Seed setting rate (%)	84.47 ± 3.16	79.56 ± 2.58*
1000-grain weight (g)	26.52 ± 0.16	23.51 ± 0.27**
Plant height (cm)	86.16 ± 2.02	86.07 ± 1.76

Asterisks represent significant difference at p-value < 0.05 (*) or < 0.01 (**).