

Supplementary material

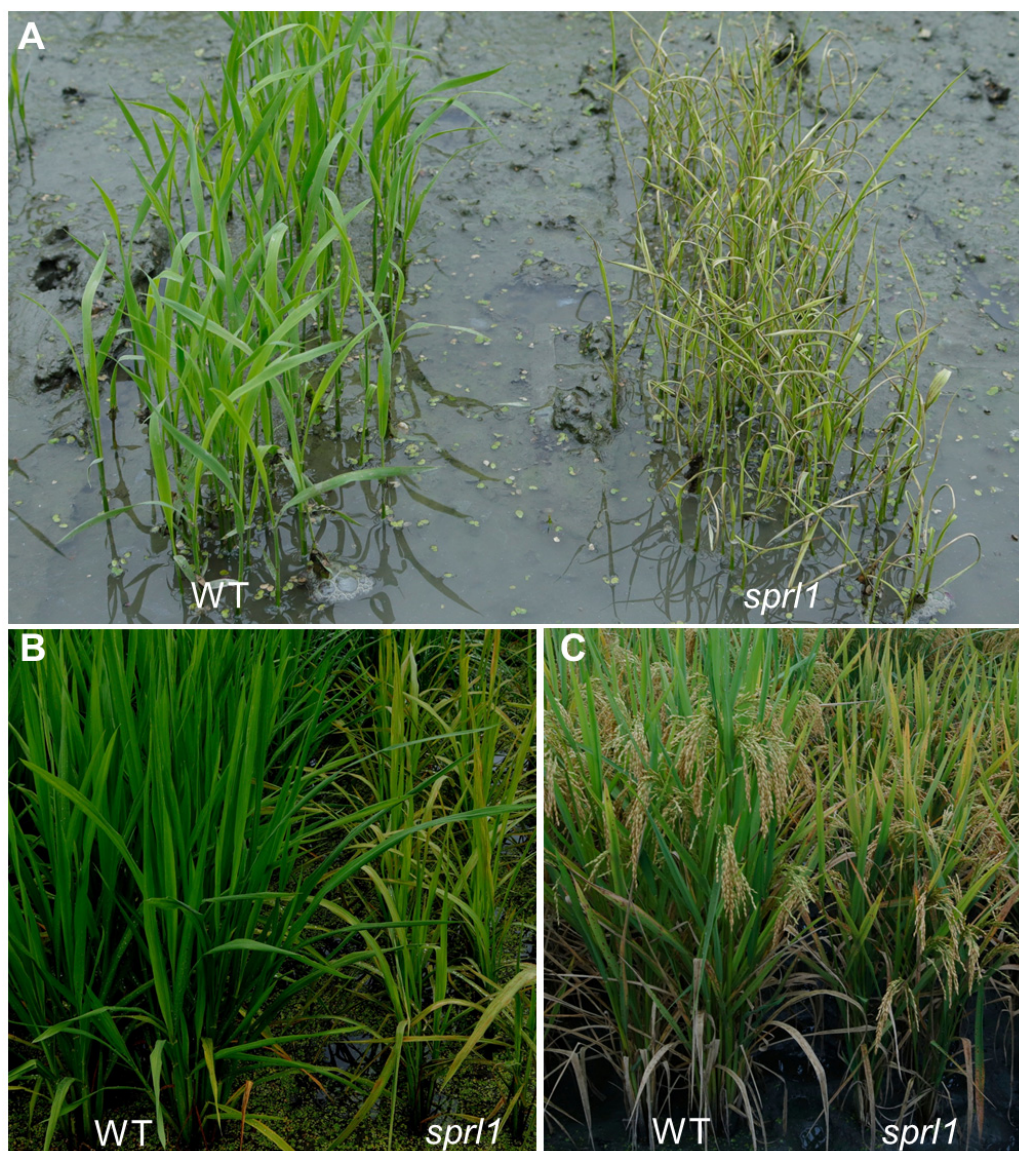


Figure S1. Plant phenotypes of the *spr11* mutant and its wild type (WT). (A) Seedlings at the three-leaf stage. (B) Plants at the tillering stage. (C) Plants at the mature stage.

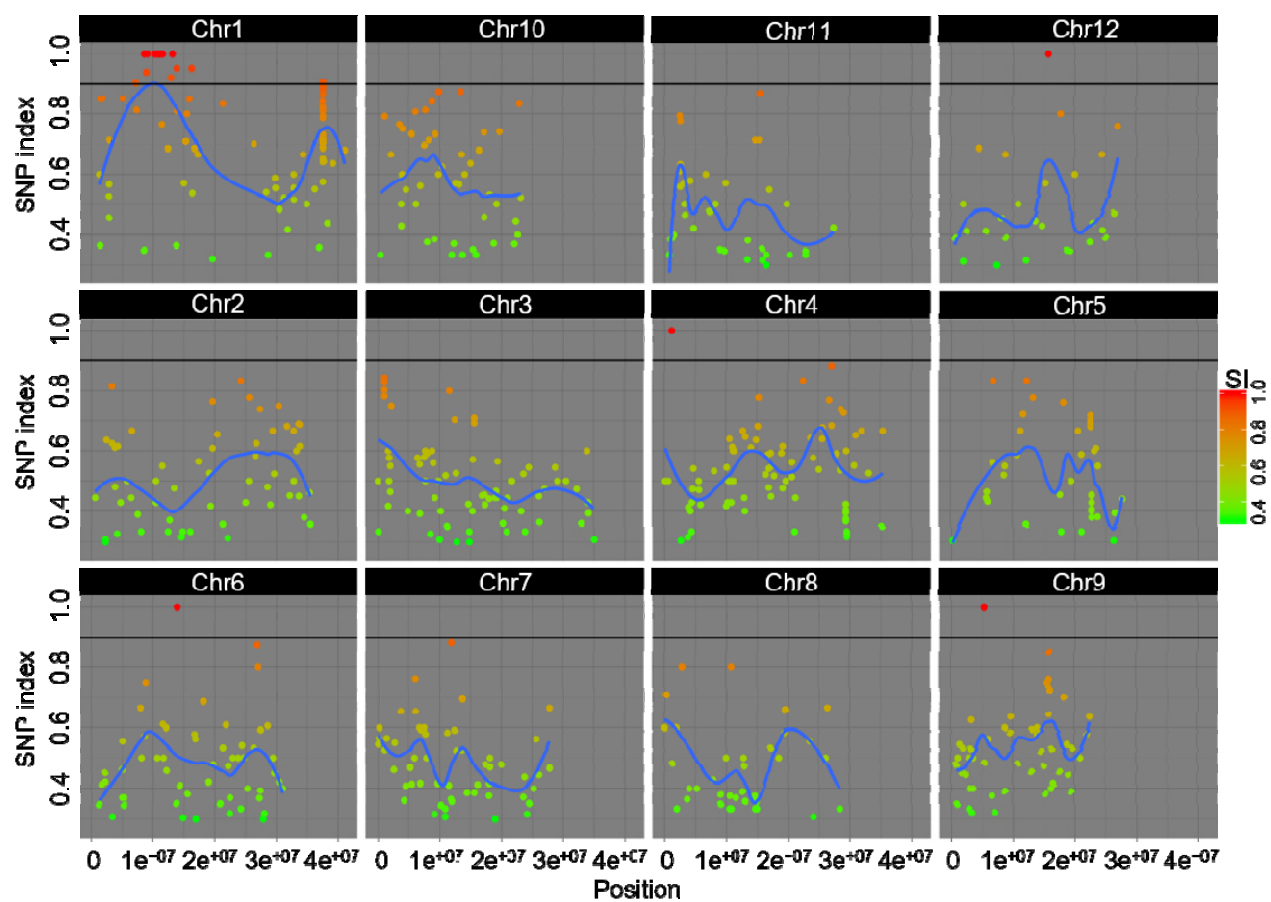


Figure S2. Δ (SNP-index) plot of the whole genome generated using MutMap.

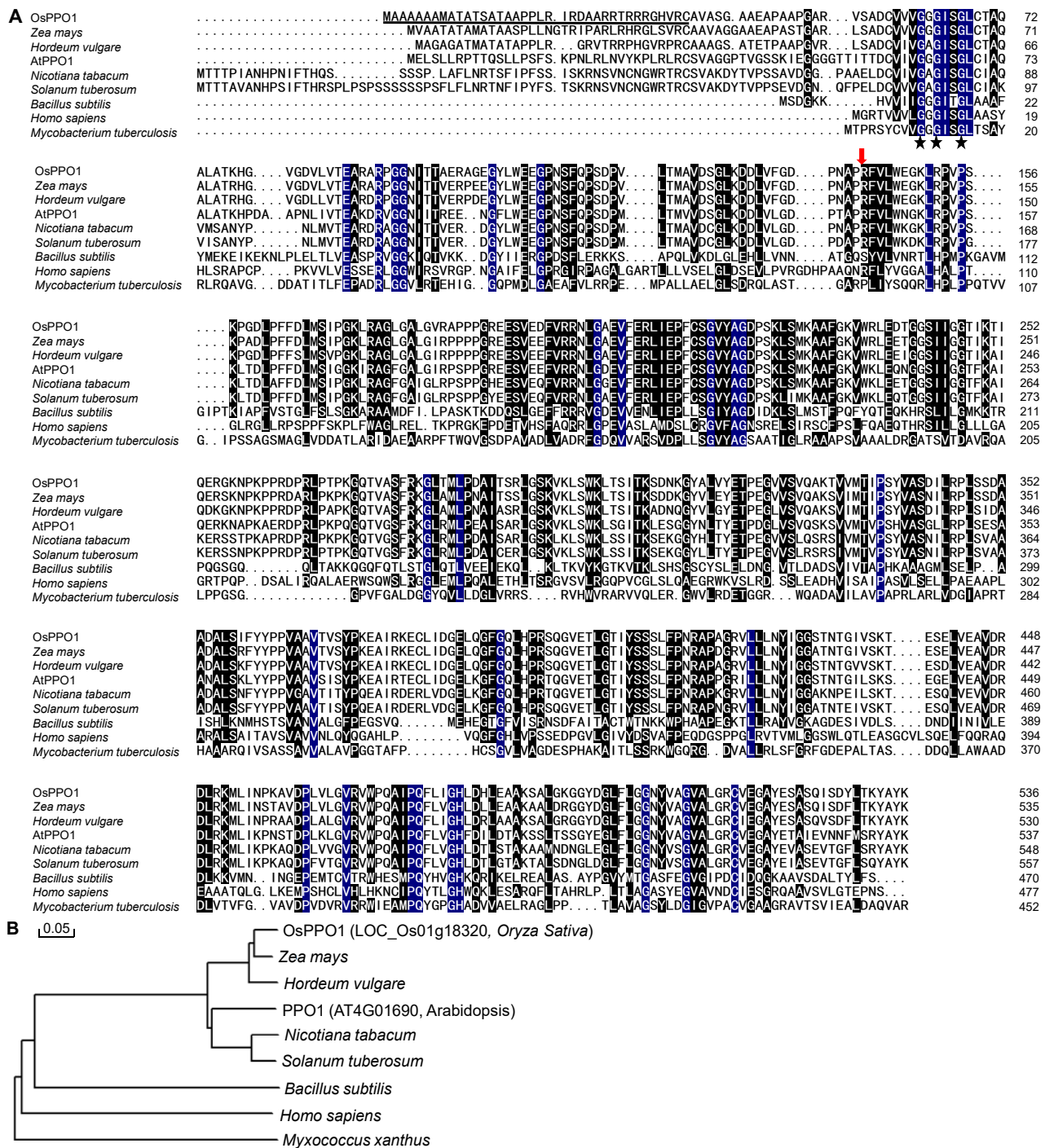


Figure S3. Sequence alignment and phylogenetic analysis of OsPPO1 and its homologues. **(A)** Sequence alignment. Identical residues in blue, similar residues ($\geq 75\%$ identical) are highlighted in black. A black underline shows the putative chloroplast signal peptides. The red arrow indicates the mutant site of *sprl1*. The black asterisks shows the Gly-rich motif. **(B)** Phylogenetic tree representing alignment of *OsPPO1* homologs. The unrooted neighbor-joining tree using percentage identities was constructed based on a multiple sequence alignment produced with the program DNAMAN. Accession numbers for the respective sequences are as follows: rice (OsPPO1, LOC_Os01g18320), *Zea mays* (AAF26417.1), *Hordeum vulgare* (KAE8789512.1), Arabidopsis (PPO1, AT4G01690, BAA11820.1), *Nicotiana tabacum* (CAA73865.1), *Solanum tuberosum* (NP_001275224.1), *Bacillus subtilis* (AOT51497.1), *Homo sapiens* (BAA07538.1), *Myxococcus xanthus* (WP_003413871.1). Scale represents percentage substitution per site.

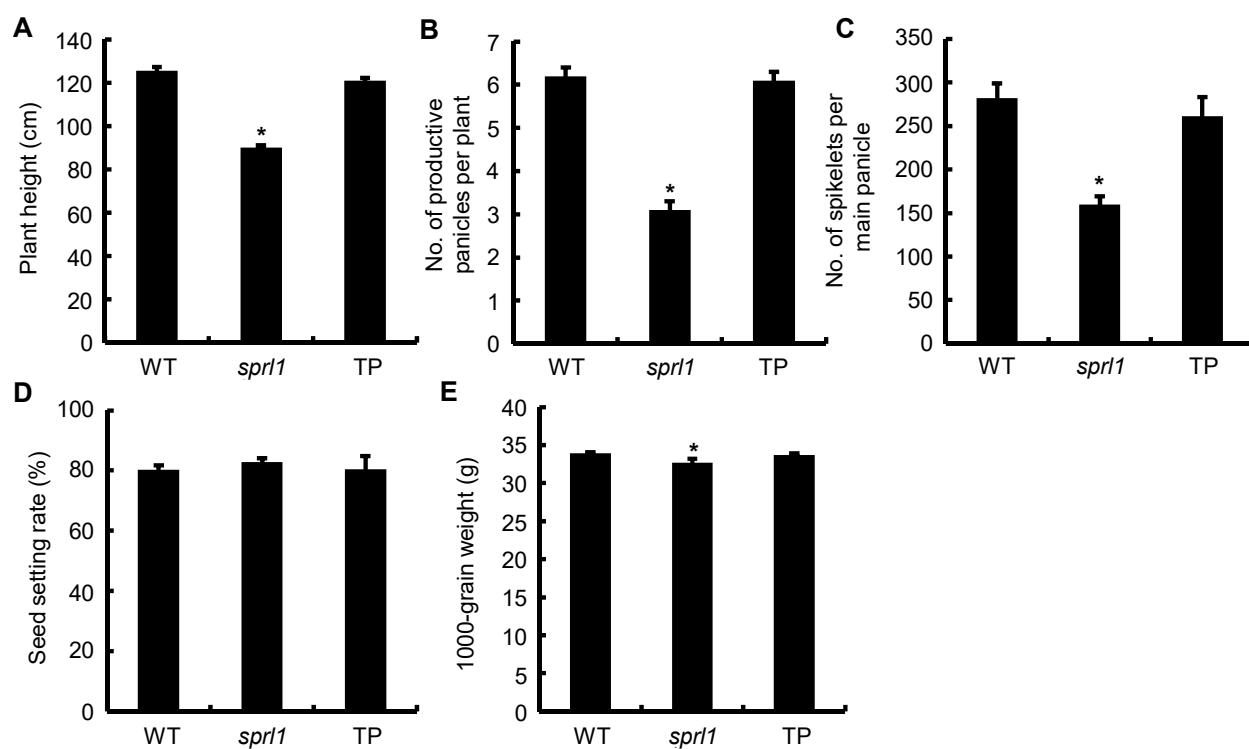


Figure S4. Major agronomic traits of complementation lines. Error bars represent standard errors of three independent experiments. The asterisk indicates statistically significant differences compared with the wild type at $* p < 0.05$. WT, wild type; TP, transgenic plants.

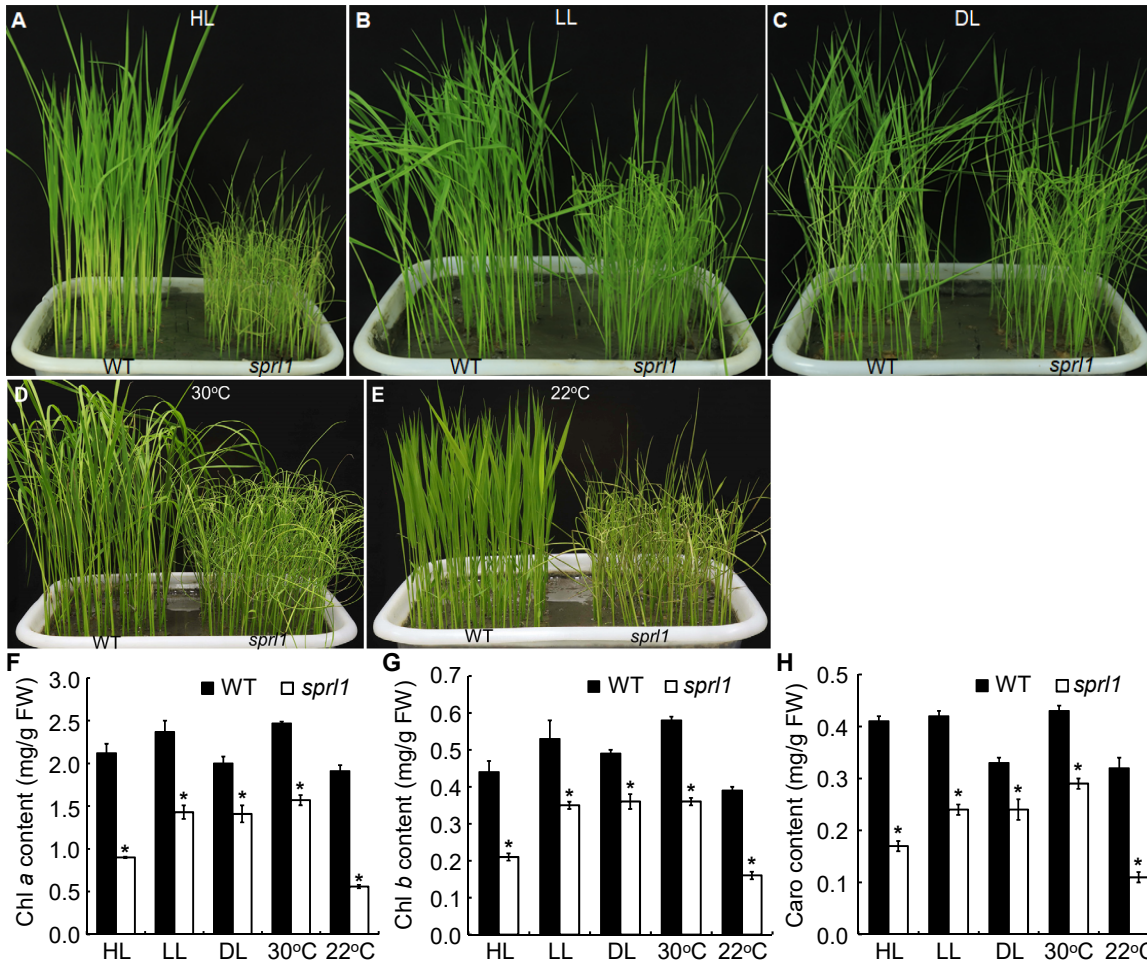


Figure S5. Phenotypic characterization of the *spr11* mutant and WT grown in the growth chamber under various light intensity and temperature conditions. (A,B,C) 12-day-old seedlings grown under 12 h of high light (HL, 300 $\mu\text{mol m}^{-2} \text{s}^{-1}$), low light (LL, 80 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and dim light (DL, 20 $\mu\text{mol m}^{-2} \text{s}^{-1}$) conditions at 28°C respectively/12 h of darkness at 26°C. (D,E) 12-day-old seedlings grown under constant 30°C and 22°C conditions respectively under 12 h of low light (LL, 80 $\mu\text{mol m}^{-2} \text{s}^{-1}$)/12 h of darkness. (F,G,H) Contents of Chl *a*, Chl *b* and Caro respectively in WT and *spr11* under various light intensity and temperature conditions. Data are means \pm SD of three independent experiments. Asterisks indicate statistically significant between WT and *spr11* mutant at * $p < 0.05$ by Student's *t* test.

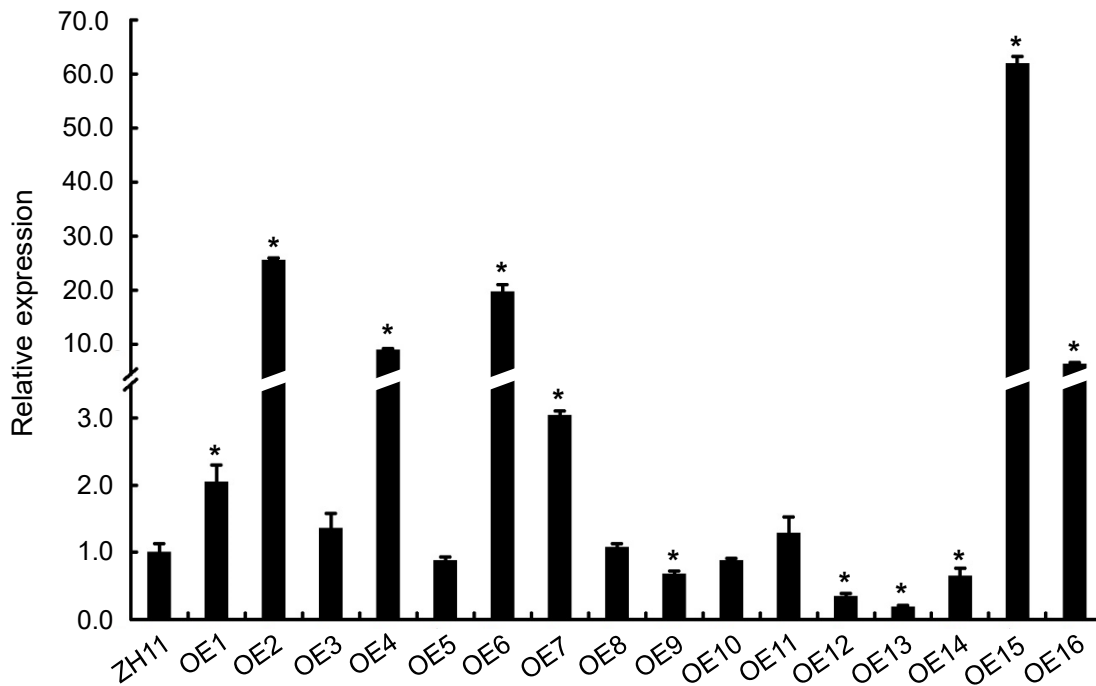


Figure S6. Relative expression levels of *OsPPO1* gene in the over-expressing lines. OE1-OE16 indicate transgenic lines overexpressing *OsPPO1* gene. The expression level in the control ZH11 was set to 1.0, and those in the over-expressing lines were calculated accordingly. Error bars represent standard errors of three independent biological replicates. Asterisk indicates statistically significant difference compared with the control ZH11 at $*p < 0.01$.

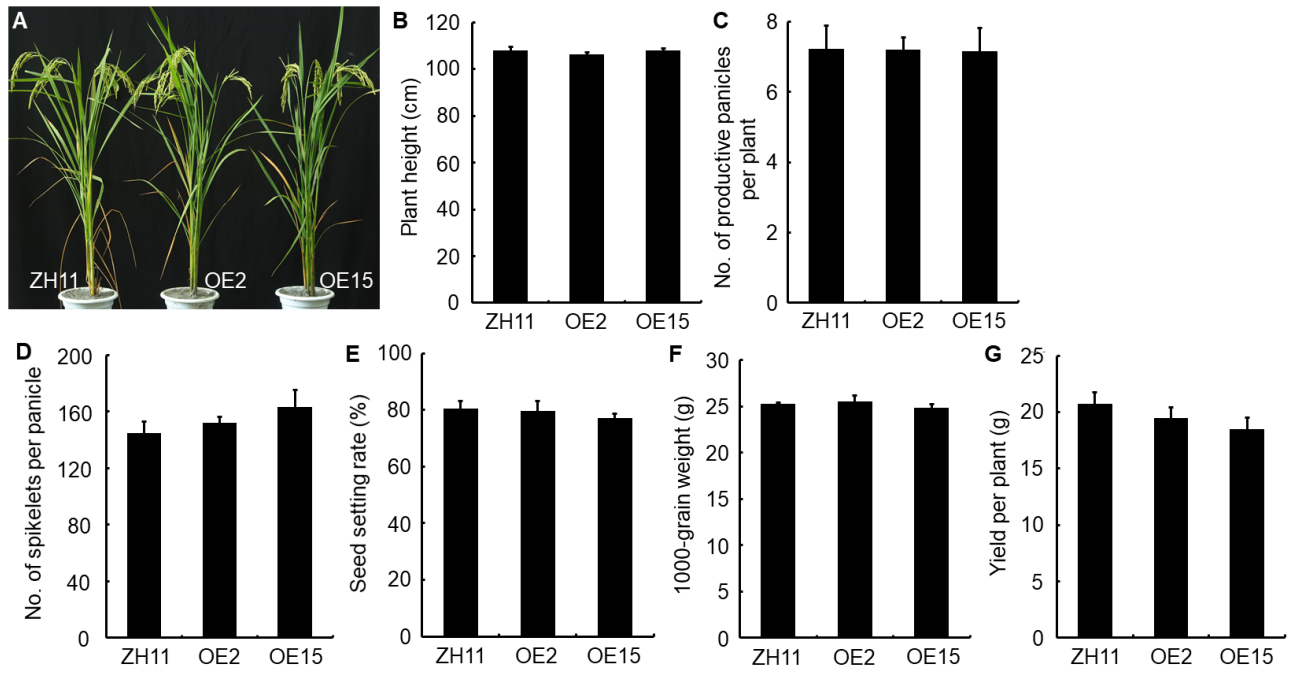


Figure S7. Comparison of major agronomic traits between the over-expressing lines and the control ZH11. Error bars represent standard errors of three independent experiments. The statistically significant differences were performed by Student's *t* test. * $p < 0.05$.

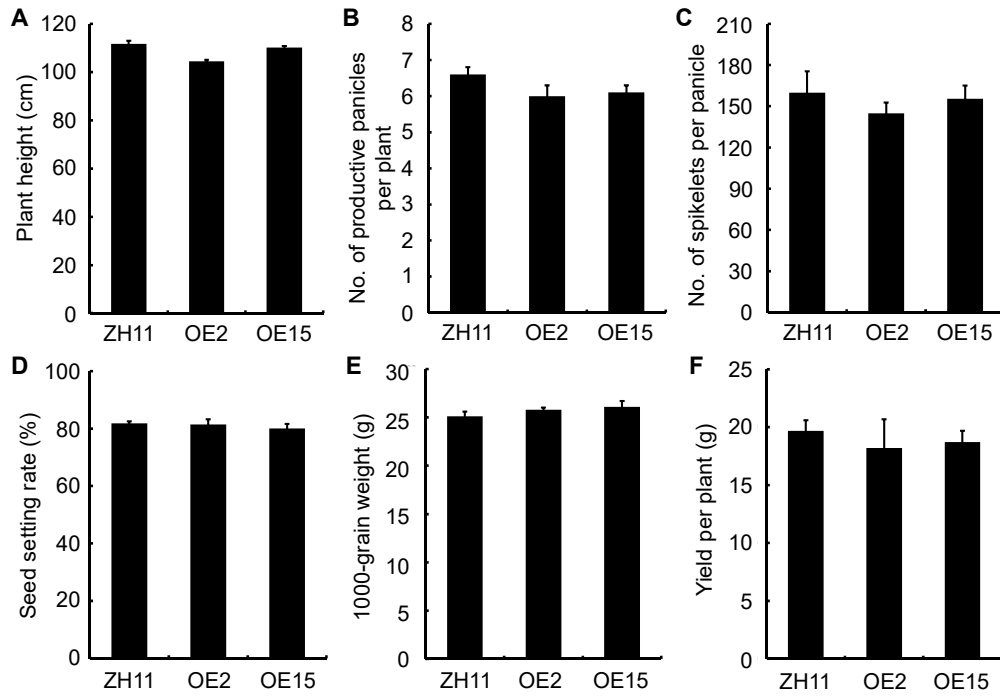


Figure S8. Comparison of major agronomic traits between the over-expressing plants with oxyfluorfen treatment and the control ZH11 without oxyfluorfen treatment. The 3-week-old seedling overexpressing *OsPPO1* gene were sprayed with 125 μ M of oxyfluorfen, and wild-type ZH11 plants were sprayed with water as control. Error bars represent standard errors of three independent experiments. The statistically significant differences were performed by Student's *t* test. * $p < 0.05$.

Table S1. Primers used in vector construction and detection

Marker	Forward primer (5'-3')	Reverse primer (5'-3')
<i>OsPPO1</i> -Com F/R	GAGCTCGGTACCCGGGGATCCAGGG CTGAGGCTGACATACGG	CAGGTCGACTCTAGAGGATCCGTCTGG GAAGAGTCTAAACAG
<i>OsPPO1</i> -Tra F/R	TCGTATGTTGTGTGGAAT	CGTCCAATATGCTGCAGT
<i>OsPPO1</i> -OE F1/R1	GGACAGGGTACCCGGGGATCCATGG CCGCCGCCGCCGCAGCC	AGAGCCCTGGCATGCCTGCAGTCACTT GTAGGCGTACTTGGT
<i>OsPPO1</i> -OE F2/R2	ATCCACCAGTTGCTGCTG	AATCAGTAAATTGAACGG
<i>OsPPO1</i> -Gfp F/R	CGGGGATCCTCTAGAGTCGACATGG CCGCCGCCGCCGCAGCC	CACCATGGTACTAGTGTCGACCCACTT GTAGGCGTACTTGGT

Table S2. Primers used in qRT-PCR

Gene name	Forward primer (5'–3')	Reverse primer (5'–3')	Reference
<i>OSPP01</i>	AGGTGTGTATGCTGGTGA	AGCATAGTCAGACCCTTC	
<i>rbcL</i>	CTTGGCAGCATTCCGAGTAA	ACAACGGGCTCGATGTGATA	Su et al., 2012
<i>rbsS</i>	CAGCAATGGCGGCAGGAT	AGGGCACCCACTTGGAACG	Li et al., 2015
<i>psaA</i>	GGAGGTGGCGAGTTAGTA	GATTTGCTTTATCGGGTAT	Li et al., 2015
<i>psbA</i>	TATGGGTCGTGAGTGGGA	TTATGCTCTGCCTGGAAT	Li et al., 2015
<i>FC1</i>	GGTCAACAGGGTGTAAGAG	GTGCATCCAAGAGCTGGAAC	Inagaki et al., 2015
<i>FC2</i>	CTTGCCTTATGTTGGTGCTA	AGCCCCACTCCCATACAGTC	Inagaki et al., 2015
<i>HEMA1</i>	CGCTATTCTGATGCTATGGGT	TCTTGGGTGATGATTGTTTGG	Su et al., 2012
<i>GSAM</i>	TGGACGTAAGGACATCAT	GTCCAAGTAATCGTAGGT	Wang et al., 2021
<i>HEMB</i>	ACCTGGATTGCCATACTT	TTCGTCGATCATGTTCACTG	Wang et al., 2021
<i>CHLD</i>	CAAGGGTCGCCCCAAGTAAA	CTTCAGGTCCGAGAGTGCAG	Li et al., 2019
<i>CHLH</i>	CCAATCCGTAACCCGAAGGT	CAATAATTTTGGCGCTCTTCAA	Inagaki et al., 2015
<i>CHLI</i>	TTCGACAGGGATCCAAAGGC	ACAGCACCAAGGTTACTCCG	Li et al., 2019
<i>DVR</i>	CCATTGCCAGTTTCTTGGTG	AATTGAATGGCTAATGGCGT	Inagaki et al., 2015
<i>PORA</i>	TGTACTGGAGCTGGAACAACAA	GAGCACAGCAAAATCCTAGACG	Su et al., 2012
<i>YGL</i>	GGCACTGCTAGGACTCAC	CCCAAGACGAAGAACGGT	Li et al., 2019
<i>CAO1</i>	GATCCATACCCGATCGACAT	CGAGAGACATCCGGTAGAGC	Su et al., 2012
<i>CatA</i>	CAACCGCAACGTCGACAACCTTCTT	TTCACCGGCAGCATCAGGTAGTTT	Yang et al., 2020
<i>CatB</i>	GCTTGCTTTCTGCCCAGCGATAAT	AAATAGTTTGGGCCAAGACGGTGC	Yang et al., 2020
<i>APX1</i>	AGGTGCCACAAGGAAAGATCTGGT	TCAGCAGGGCTTTGTCACTAGGAA	Yang et al., 2020
<i>APX2</i>	TGGGAAGATGCCACAAGGAGAGAT	TCCGCAGCATATTTCTCCACCAGT	Yang et al., 2020
<i>POD1</i>	ACGTCGGGGTCGCCAACAAC	CGAACTCGTCCACCGACGCC	Yang et al., 2016
<i>AOX1a</i>	CTTCGCATCGGACATCCATTA	TCCTCGGCAGTAGACAAACATC	Yang et al., 2020
<i>AOX1b</i>	CCTGCTCAGTTCATCACCATCA	GCATAAAACGGAGTGACAATAGC	Yang et al., 2020
<i>ROC5</i>	ACGAGCTCTTCTTCGTTGGG	GCAAAACACCACGGCGTAAA	
<i>ZHD1</i>	CAGTTCTGTGACGAGGTCGG	ATGCATTTGCTCCCGGTCAT	
<i>REL1</i>	GCACTCCAGCTTGGAACCTCT	CTGAGTGCAGTGATCGGAGG	
<i>REL2</i>	TTGCCTTGTTGGGAGTTGGT	TGCACTTCACAGGACAAGCA	
<i>SRL1</i>	TCCTCATCTCCTGCCTCCTC	GAACCAAGGGGTTGGGAGAG	
<i>Actin 1</i>	TGTATGCCAGTGGTCGTACCA	CCAGCAAGGTCGAGACGAA	Li et al., 2015

Table S3. Segregation of F₂ populations from the crosses between *spr11* and its wild-type parent 188R

Combination	No. of total plants	No. of normal plants	No. of mutant plants	Expected ratio	χ^2	$\chi^2_{0.05}$
<i>spr11</i> ×188R	453	345	108	3:1	0.27	3.84

Table S4. Insertion/deletion (InDel) markers used for mapping of the *spr11* locus

Marker	Forward primer (5'-3')	Reverse primer (5'-3')
L1	CAGAAGCCGCTCTTACTC	AAACCCAAATTCCAACAC
L2	GATTTTCATGGTAGGGTTT	TACAGCGAGTGAGGTCTT
L3	GTTGGAGATGGCATTAGA	AAGGTAGACGGCAGTGAG
L4	GGTGTACCTACAAGCCCA	TCTGCTCAGATCCTGCGA
L5	TGGTGAAAGGCACCTAGC	TTGCTCCACACCTGTCTG