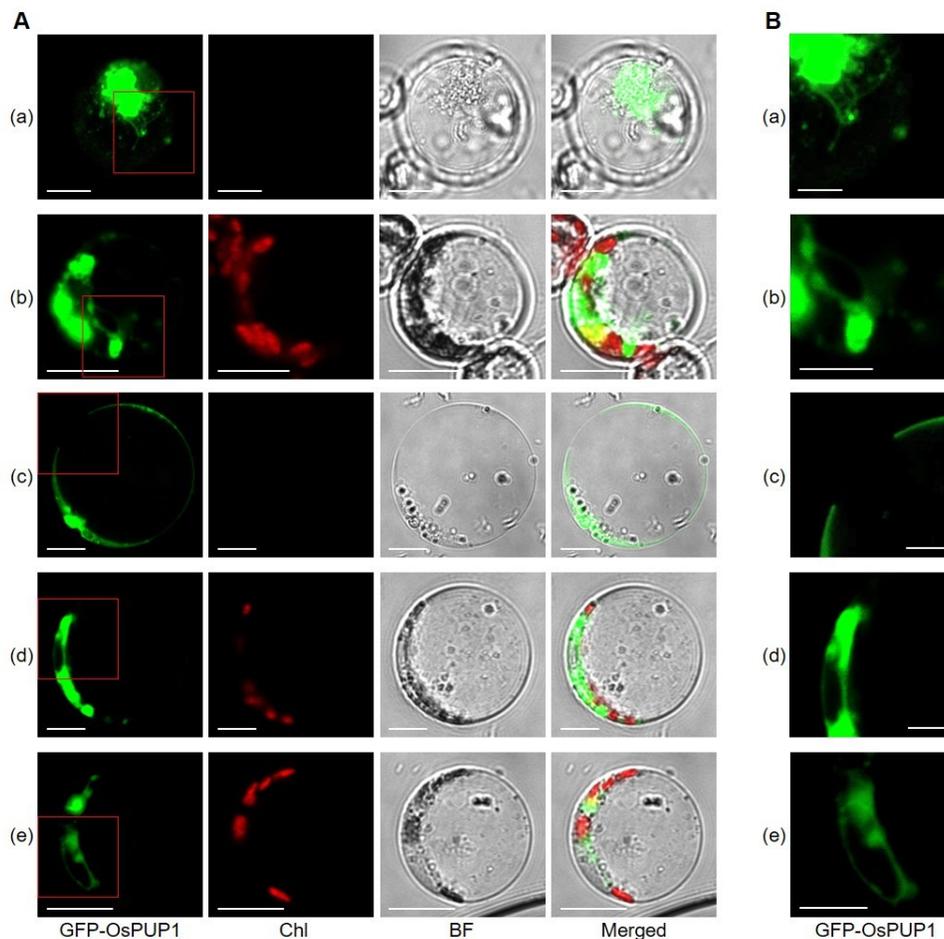
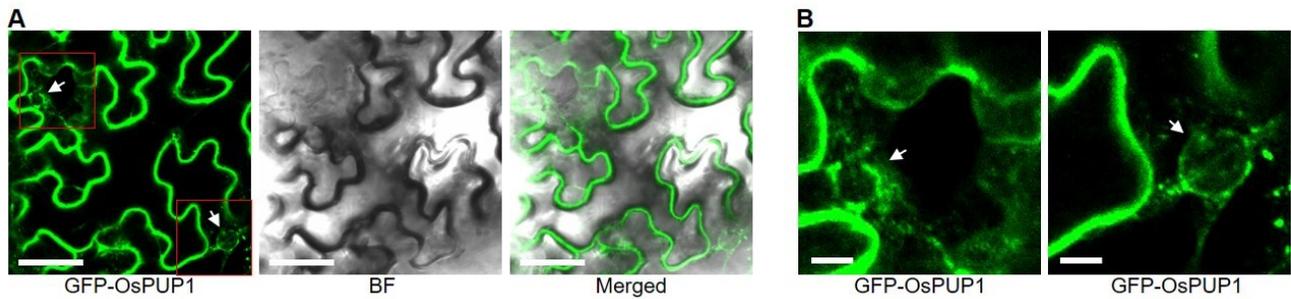


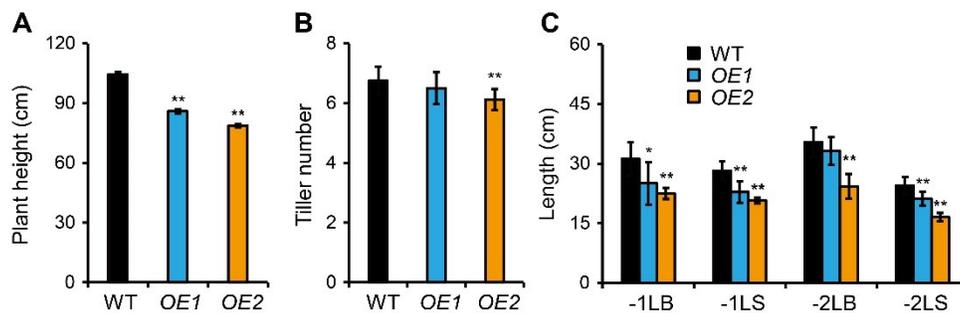
**Supplementary Figure 1.** Effect of different kinds of phytohormones on *OsPUP1* expression in shoots and roots of the wild-type seedlings. The roots of 8-day-old seedlings grown in 1/2 strength MS hydroponic medium were treated by different phytohormones, including brassinolide (BL), gibberellin (GA<sub>3</sub>), abscisic acid (ABA), 1-aminocyclopropane-1-carboxylic acid (ACC), indole-3-acetic acid (IAA), and jasmonic acid (JA), at 10  $\mu$ M concentrations for 4 h. After treatment, the shoot and root tissues were separately collected for gene expression analyses. *Ubiquitin2* gene was used as the internal reference.  $n = 3$ , bar = SD, \* $P < 0.05$  and \*\* $P < 0.01$  in Student's  $t$ -test.



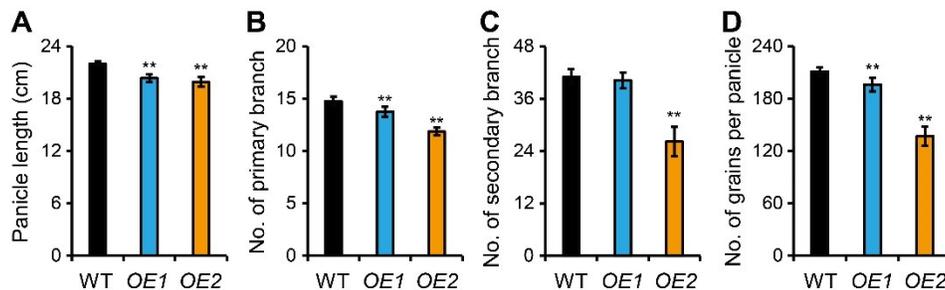
**Supplementary Figure 2.** Subcellular localization analyses of *OsPUP1* in rice protoplasts. **(A)** Multiple cells expressing GFP-*OsPUP1*. **(B)** Amplification of the red-framed regions of the respective cells in **(A)**. Chl, chloroplast fluorescence; BF, bright field. Scale bars: 10  $\mu$ m in **(A)**, 5  $\mu$ m in **(B)**.



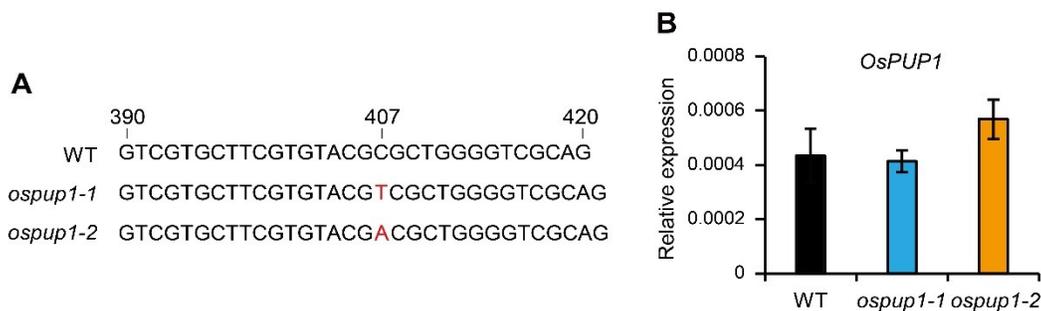
**Supplementary Figure 3.** Subcellular localization analyses of OsPUP1 in tobacco epidermal cells. **(A)** Multiple cells expressing GFP-OsPUP1. **(B)** Amplification of the red-framed regions of the respective cells in **(A)**. White arrowheads mark ER surrounding the nuclei. BF, bright field. Scale bars: 50  $\mu\text{m}$  in **(A)**, 10  $\mu\text{m}$  in **(B)**.



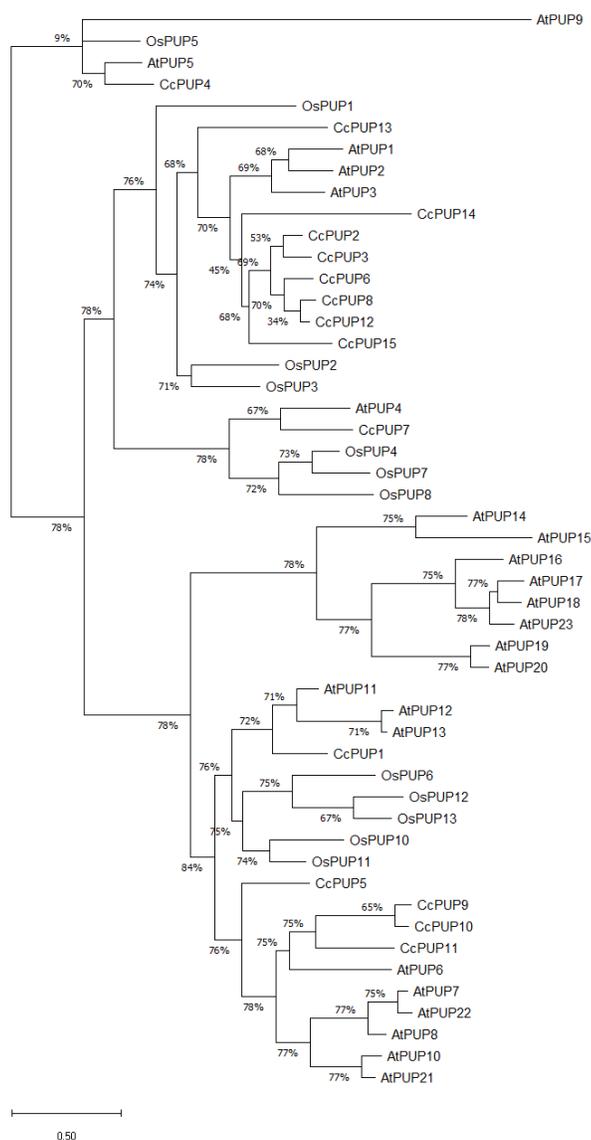
**Supplementary Figure 4.** Comparison of the plant height, tiller number, and leaf length of wild-type and *OsPUP1*-overexpressing plants. **(A-C)** Statistical data of the plant height **(A)**, tiller number **(B)**, and leaf length **(C)** of *OsPUP1*-overexpressing plants at mature stage, compared with the wild type (WT).  $n = 8$ , bar = SD, \* $P < 0.05$  and \*\* $P < 0.01$  in Student's  $t$ -test. -1 and -2 mean the first (also named flag leaf) and the second leaf counted from the top, respectively. LB, leaf blade; LS, leaf sheath.



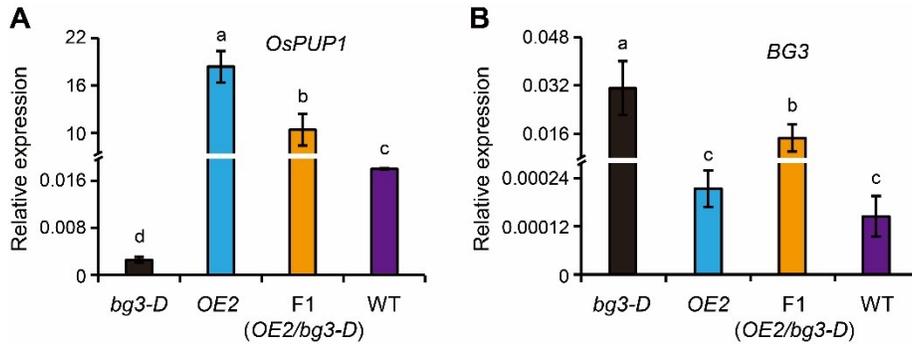
**Supplementary Figure 5.** Panicle characteristics of *OsPUP1*-overexpressing plants. **(A-D)** Statistical data of the panicle length **(A)**, number of primary branch **(B)**, secondary branch **(C)**, and grains per panicle **(D)** of *OsPUP1*-overexpressing plants (OE), compared with wild type (WT).  $n = 8$ , bar = SD, \*\* $P < 0.01$  in Student's  $t$ -test.



**Supplementary Figure 6.** Mutation information in the knockout mutants of *OsPUP1*. (A) The mutation sites in the coding sequence of *OsPUP1* were marked in red letter. (B) Relative expression of *OsPUP1* in shoots of 6-day-old overexpressing plants seedlings tested by qRT-PCR, compared with the wild type (WT). *Ubiquitin2* gene was used as the internal reference.  $n = 3$ , bar = SD.



**Supplementary Figure 7.** Phylogenetic analysis of PUP family proteins in *Arabidopsis* (At), coffee (Cc), and rice (Os). The phylogenetic tree was constructed by software MEGA. The distance mode was observed divergence. Percentage indicated the data coverage.



**Supplementary Figure 8.** Gene expression analyses of *OsPUP1* and *BG3/OsPUP4*. **(A,B)** Gene expression of *OsPUP1* **(A)** and *BG3/OsPUP4* **(B)** in the 5-day-old seedlings of *bg3-D* mutant, *OsPUP1*-overexpressing plant, their F<sub>1</sub> progeny, and the wild type (WT). *Ubiquitin2* gene was used as the internal reference.  $n = 3$ , bar = SD. Different letters above the columns indicate statistically significant differences between groups ( $t$  Test LSD,  $P < 0.05$ ).

**Supplementary Table 1.** Quantification of various cytokinin forms in shoots, roots, and panicles of the wild-type (WT) and *OsPUP1*-overexpressing plants (*OE2*).  $n = 3$ , value = means  $\pm$  SD (pmol $\cdot$ g<sup>-1</sup> F.W.). FW, fresh weight. n.d., not detected. Asterisks indicate statistically significant difference compared with WT. \* $P < 0.05$  and \*\* $P < 0.01$  in Student's  $t$ -test.

Analyte	WT-Shoot	<i>OE2</i> -Shoot	WT-Root	<i>OE2</i> -Root	WT-Panicle	<i>OE2</i> -Panicle
iP	0.44 $\pm$ 0.00	0.30 $\pm$ 0.05**	n.d.	n.d.	1.13 $\pm$ 0.00	0.98 $\pm$ 0.00**
iPR	0.45 $\pm$ 0.05	0.37 $\pm$ 0.23	1.13 $\pm$ 0.03	0.98 $\pm$ 0.14	9.61 $\pm$ 0.17	7.69 $\pm$ 0.21**
iP7G	0.25 $\pm$ 0.03	0.26 $\pm$ 0.02	0.27 $\pm$ 0.00	0.26 $\pm$ 0.09	1.32 $\pm$ 0.06	1.74 $\pm$ 0.07**
iP9G	1.04 $\pm$ 0.07	1.32 $\pm$ 0.48	0.47 $\pm$ 0.00	0.24 $\pm$ 0.02**	2.03 $\pm$ 0.06	2.97 $\pm$ 0.06**
tZ	0.61 $\pm$ 0.03	0.36 $\pm$ 0.05**	0.14 $\pm$ 0.00	0.12 $\pm$ 0.03	0.21 $\pm$ 0.03	0.18 $\pm$ 0.00
tZR	0.23 $\pm$ 0.00	0.14 $\pm$ 0.00**	0.39 $\pm$ 0.04	0.26 $\pm$ 0.03*	0.79 $\pm$ 0.02	0.78 $\pm$ 0.02
tZ7G	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
tZ9G	3.91 $\pm$ 0.70	2.96 $\pm$ 0.33	4.04 $\pm$ 0.07	4.08 $\pm$ 0.12	2.00 $\pm$ 0.07	1.80 $\pm$ 0.08*
tZOG	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
cZ	7.28 $\pm$ 0.05	7.66 $\pm$ 0.53	2.31 $\pm$ 0.03	4.33 $\pm$ 0.00**	0.29 $\pm$ 0.03	0.33 $\pm$ 0.03
cZR	4.34 $\pm$ 0.33	5.30 $\pm$ 1.42	7.65 $\pm$ 0.14	9.46 $\pm$ 0.29**	5.76 $\pm$ 0.09	4.87 $\pm$ 0.09**
cZ9G	0.68 $\pm$ 0.12	0.59 $\pm$ 0.03	0.62 $\pm$ 0.02	0.65 $\pm$ 0.04	n.d.	n.d.
cZOG	2870.01 $\pm$ 40.98	3561.89 $\pm$ 164.04**	1931.92 $\pm$ 36.15	2661.59 $\pm$ 71.14**	430.49 $\pm$ 18.43	411.44 $\pm$ 22.00
DHZ	0.21 $\pm$ 0.03	0.15 $\pm$ 0.03*	n.d.	n.d.	0.00 $\pm$ 0.00	0.05 $\pm$ 0.00**
DHZR	0.09 $\pm$ 0.02	0.08 $\pm$ 0.05	0.09 $\pm$ 0.02	0.15 $\pm$ 0.02*	0.03 $\pm$ 0.00	0.06 $\pm$ 0.00**
DHZOG	0.23 $\pm$ 0.03	0.17 $\pm$ 0.02	0.05 $\pm$ 0.00	0.10 $\pm$ 0.03*	n.d.	n.d.

iP, N<sup>6</sup>-( $\Delta^2$ -isopentenyl) adenine (or isopentenyladenine); iPR, isopentenyladenine riboside; iP7G, isopentenyladenine riboside 7-glucoside; iP9G, isopentenyladenine riboside 9-glucoside; tZ, *trans*-zeatin; tZR, *trans*-zeatin riboside; tZ7G, *trans*-zeatin 7-glucoside; tZ9G, *trans*-zeatin 9-glucoside; tZOG, *trans*-zeatin O-glucoside; cZ, *cis*-zeatin; cZR, *cis*-zeatin riboside; cZ9G, *cis*-zeatin 9-glucoside; cZOG, *cis*-zeatin O-glucoside, DHZ, dihydrozeatin; DHZR, dihydrozeatin riboside; DHZOG, dihydrozeatin O-glucoside.

**Supplementary Table 2.** Primers used for analyses. Additional bases used for plasmid construction are underlined.

Name	Forward (5'-3')	Reverse (5'-3')
<b>For vector construction:</b>		
<i>OsPUP1-OE</i>	<u>CCGGGGATCCTCTAGA</u> ATGGCCACCATTACTG CT	<u>AAAGCAGGGCATGCCTGCAGCTA</u> AGGCGCCGC TGA
<i>pOsPUP1::GUS</i>	<u>TACGCCAAGCTTGGCTGCAGCTTCTAGGCTT</u> TAGCACT	<u>GAATCCCAGGGATCCGATCAAATGAAGCAGTG</u> CT
GFP- <i>OsPUP1</i>	<u>CAAGGAGCTCGGATCC</u> ATGGCCACCATTACTG CT	<u>GCAGGTCGACTCTAGACTA</u> AGGCGCCGCTGAC TC
<b>For qRT-PCR:</b>		
<i>OsPUP1</i>	TCGCCGTCATCTTCCTCCA	CGTCTGCGGTCTTCTGTG
<i>Ubiquitin2</i>	GAGCCTCTGTTCGTCAAGTA	ACTCGATGGTCCATTAAACC
<i>BG3/OsPUP4</i>	ATGGTGACCTCACGTCGT	TCTTCTGCGTGGTATACT
<i>OsRR1</i>	AGGATCAGCAGATGCATGAATG	GAGACGCTGTACGTCCTTGCTT
<i>OsRR2</i>	CATGGTGATGAATGCATCC	TGCTGCCATTGGACCATCT
<i>OsRR4</i>	TGAAGCTGCAACAGCTCA	AGTGGAGGACAATCTTGG