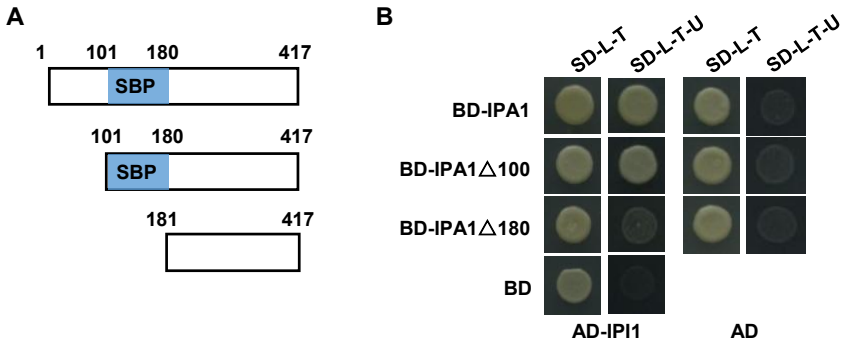
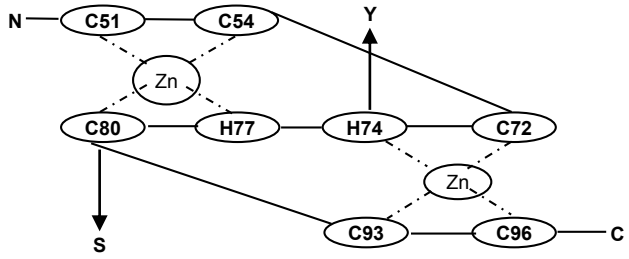


Supplemental Figure 1. The SBP Domain of IPA1 Is Essential for the Interaction between IPA1 and IPI1. (Supports Figure 1)

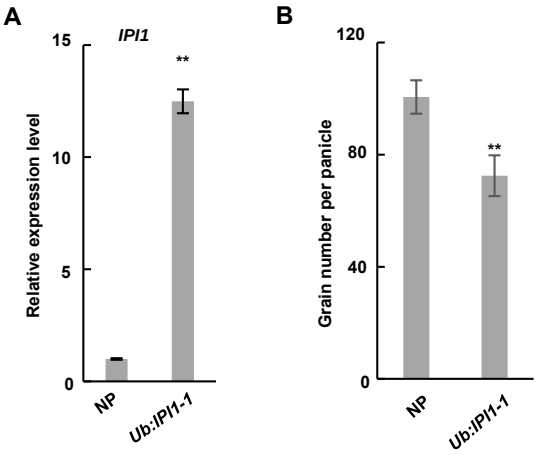
(**A**) Scheme of constructs used for mapping the domain of IPA1 that interacts with IPI1.

(**B**) Interaction between IPI1 and truncated IPA1 in the yeast two-hybrid assay. The full-length or truncated IPA1 was fused to the GAL4 binding domain and IPI1 to the GAL4 activation domain. Yeast cells were grown on SD-L-T-U medium.



Supplemental Figure 2. Scheme of the IPI1 RING Finger Composition. (Supports Figure 2)

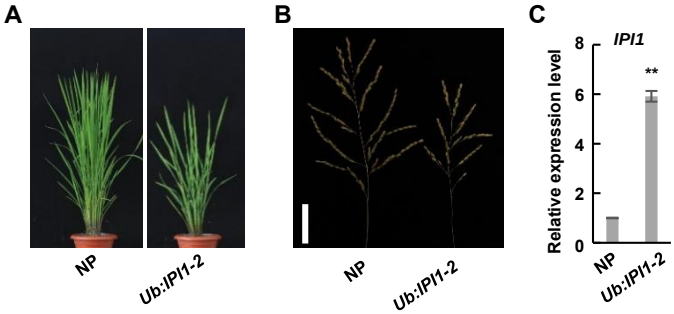
Arrows indicate the sites mutated in the RING finger domain of IPI1.



Supplemental Figure 3. Expression and Phenotype of *Ub:IPI1* Transgenic Plants. (Supports Figure 4)

(**A**) The transcript levels of *IPI1* in Nipponbare (NP) and *Ub:IPI1-1* transgenic plants. Rice ubiquitin was used as reference. Double-asterisk indicates $P < 0.01$ (Student's *t*-test, $n = 3$), and values are means ± SD.

(**B**) Statistical Analysis of grain number per panicle of NP and *Ub:IPI1* Transgenic Plants. Values are means ± SD ($n = 10$ independent plants). Double-asterisk indicates $P < 0.01$ (Student's *t*-test, $n = 3$), and values are means ± SD.

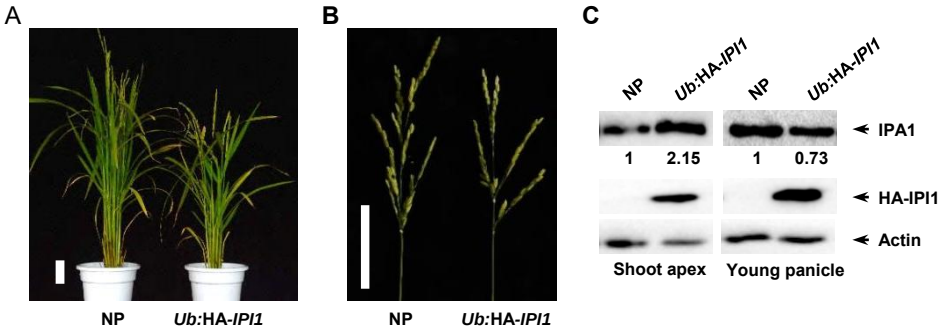


Supplemental Figure 4. Overexpression of *IPI1* Affects Plant Architecture. (Supports Figure 4)

(**A**) The morphological phenotypes of Nipponbare (NP) and *IPI1*-overexpressing transgenic plants (*Ub:IPI1-2*). Bar = 10 cm.

(**B**) Morphologies of main panicles of NP and *IPI1*-overexpressing transgenic plants (*Ub:IPI1-2*). Bar = 5 cm.

(**C**) The transcript levels of *IPI1* in NP and *Ub:IPI1* transgenic plants. Rice Ubiquitin was used as reference. Double-asterisk indicates $P < 0.01$ (Student's *t*-test, n = 3), and values are means ± SD.

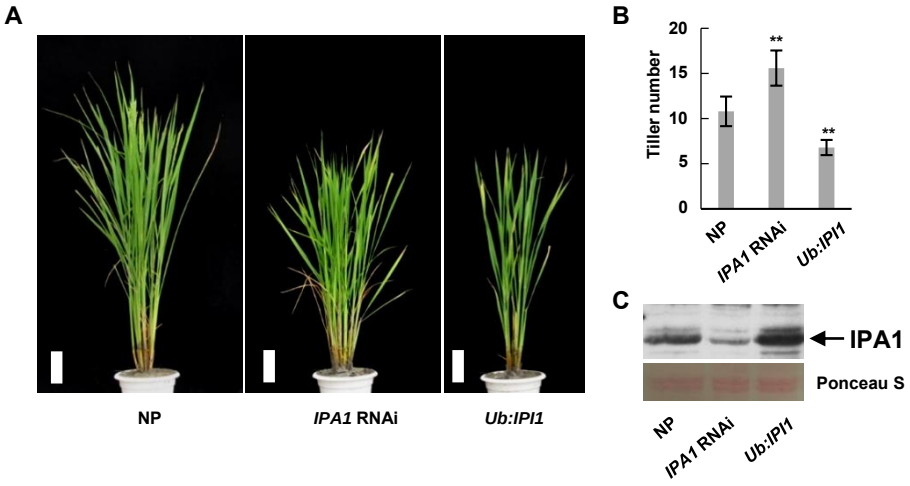


Supplemental Figure 5. Overexpression of *IPI1* Affects Plant Architecture via Modulating IPA1 Abundance. (Supports Figures 4 and 5)

(**A**) The morphological phenotypes of Nipponbare (NP) and *IPI1*-overexpressing transgenic plants (*Ub:*HA-*IPI1*). Bar = 5 cm.

(**B**) Morphologies of main panicles of NP and *IPI1*-overexpressing transgenic plants (*Ub:*HA-*IPI1*). Bar = 5 cm.

(**C**) IPA1 and HA-IPI1 abundance in different tissues, including shoot apexes and young panicles in NP and *IPI1*-overexpressing transgenic plants (*Ub:*HA-*IPI1*). Relative amounts of IPA1 proteins were determined by densitometry and normalized to loadings determined by the actin protein level and expressed relative to the value of the wild type.

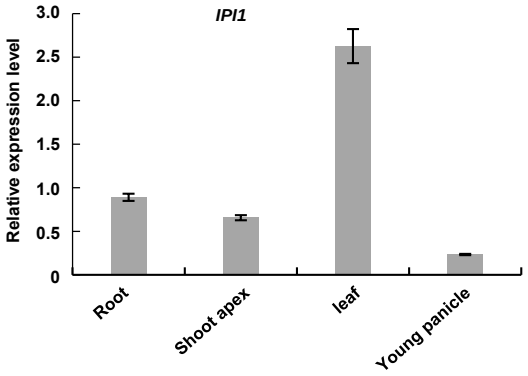


Supplemental Figure 6. IPI1 Negatively Regulates Tiller Number. (Supports Figures 4 and 5)

(A) The gross morphological phenotypes of Nipponbare (NP), *IPA1 RNAi* and *Ub:IPI1* transgenic plants. Bar = 10 cm.

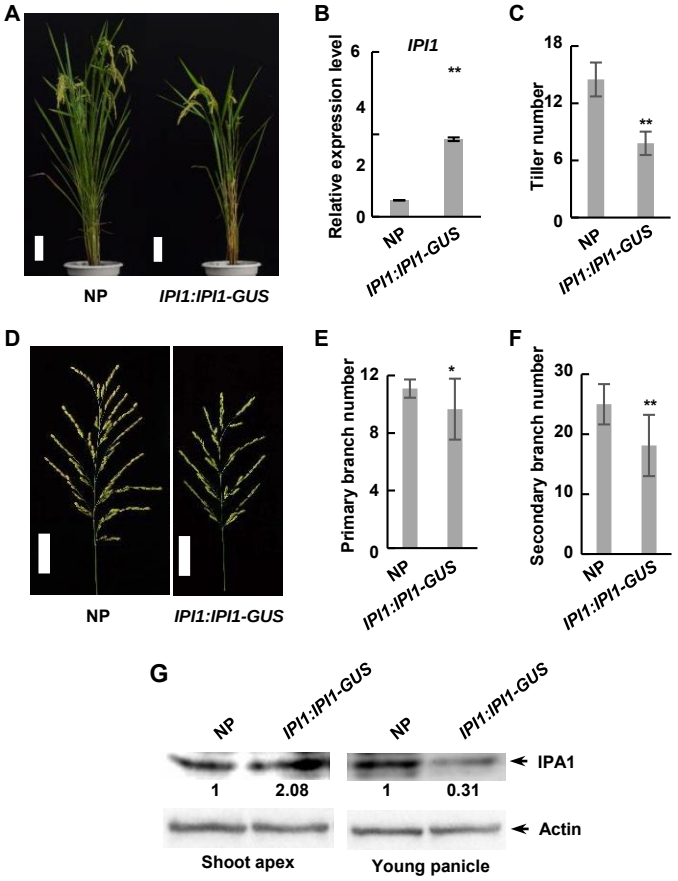
(B) Statistical analysis of tiller numbers and protein levels of IPA1 in NP, *IPA1 RNAi* and *Ub:IPI1* transgenic plants. Double-asterisk indicates $P < 0.01$ (Student's *t*-test, n = 5), and values are means ± SD.

(C) IPA1 abundance in shoot apexes. The protein levels of IPA1 in different plants as indicated. The Ponceau S staining is used as an loading control.



Supplemental Figure 7. The *IPI1* Expression Pattern. (Supports Figures 4 and 5)

Quantitative Real-Time PCR was performed to detect the transcript levels of *IPI1* in various tissues, as indicated.



Supplemental Figure 8. Overexpression of *IPI1* Driven by its Native Promoter Affects Plant Architecture via Modulating IPA1 Abundance. (Supports Figures 4 and 5)

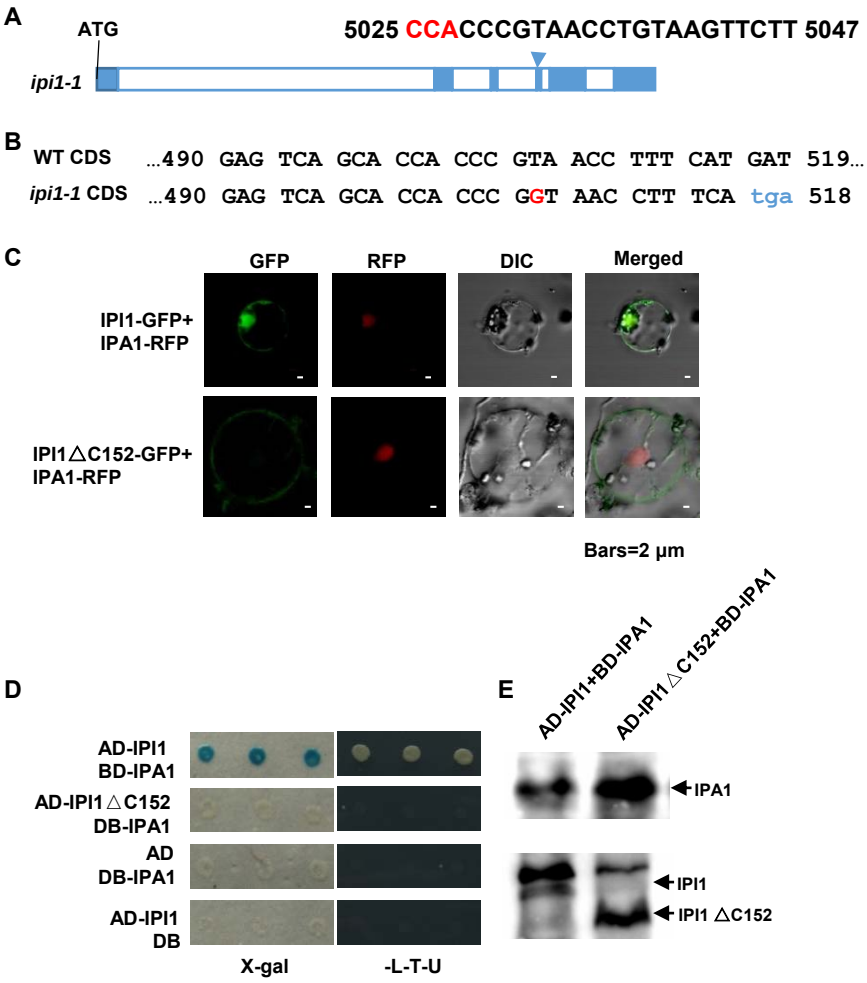
(**A**) The gross morphological phenotypes of Nipponbare (NP) and *IPI1:IPI1*-GUS transgenic plants. Bar = 10 cm.

(**B**) Transcript levels of *IPI1* in NP and *IPI1:IPI1*-GUS transgenic plants. Rice ubiquitin was used as reference. Double-asterisk indicates $P < 0.01$ (Student's *t*-test, n = 3), and values are means ± SD.

(**C**) Statistical analysis of tiller numbers of NP and *IPI1:IPI1*-GUS transgenic plants. Double-asterisk indicates $P < 0.01$ (Student's *t*-test, n = 10 independent plants), and values are means ± SD.

(**D**) - (**F**) Morphologies of main panicles of NP and *IPI1:IPI1*-GUS transgenic plants. Bar = 5 cm (**D**). Primary (**E**) and secondary (**F**) branch numbers were compared. * indicates $0.01 < P < 0.05$, and ** indicates $P < 0.01$, (Student's *t*-test, n = 10 independent plants), and values are means ± SD .

(**G**) IPA1 abundance in different tissues, including shoot apexes (left) and young panicles (right) in NP and *IPI1:IPI1*-GUS transgenic plants. The actin was used as an internal control. Relative amounts of IPA1 protein were determined by densitometry and normalized to loadings determined by the actin protein level and expressed relative to the value of wild type.



Supplemental Figure 9. Identification of *ipi1-1* mutant plants. (Supports Figures 6 and 7)

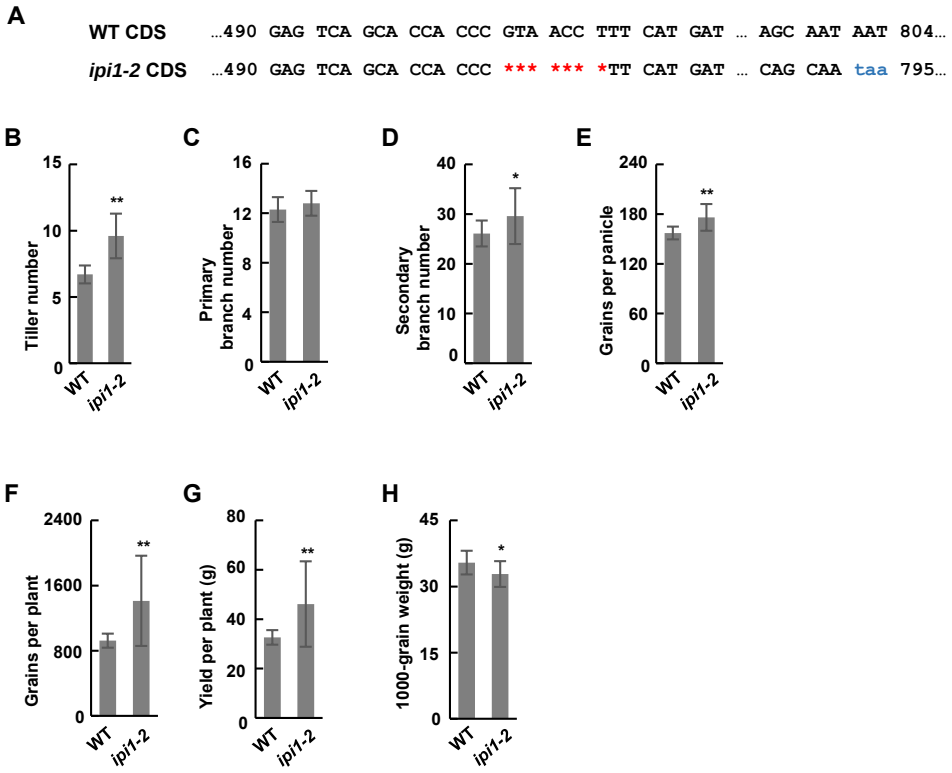
(**A**) Schematic map of the genomic region of *IPI1* and the sgRNA target site; arrows show the sgRNA target site on the *IPI1* genomic; the PAM motif (NGG) is shown in red. The blue box indicates the exon of *IPI1* and the white box indicates the intron of *IPI1*.

(**B**) Sequence alignment of the sgRNA target region showing altered bases of cDNA sequence between wild type and *ipi1-1*. The inserted base is shown in red and the new stop codon in *ipi1-1* is marked with blue.

(**C**) Co-localization of IPI1-GFP or IPI1△C152-GFP with IPA1-RFP. Bars = 2 μm.

(**D**) Interaction between truncated IPI1 and IPA1 in the yeast two-hybrid assay. The full-length IPA1 was fused to the GAL4 binding domain and IPI1 or IPI1△C152 to the GAL4 activation domain. Yeast cells were grown on the SD-L-T medium containing X-gal or SD-L-T-U medium.

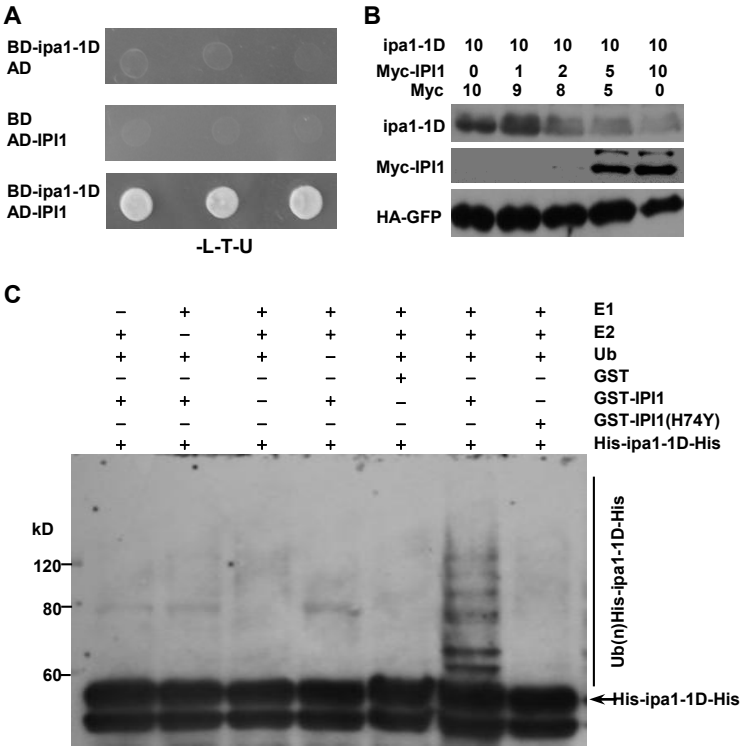
(**E**) Detection of IPA1, IPI1 and IPI1 △C152 in yeast cells.



Supplemental Figure 10. The *ipi1-2* mutant shows altered plant architecture as *ipi1-1*. (Supports Figures 6 and 7)

(**A**) *IPI1* cDNA sequence alignment between the of wild type and *ipi1-2*. The altered base is shown in red and the blue characters indicate the new stop codon in *ipi1-2*.

(**B**) - (**H**) Statistical analysis of plant architecture of wild type plants and *ipi1-2* mutant. Single Double-asterisk indicates 0.01 < P < 0.05 and double-asterisk indicates P < 0.01 (Student's *t*-test, n = 10 independent plants), and values are means ± SD .

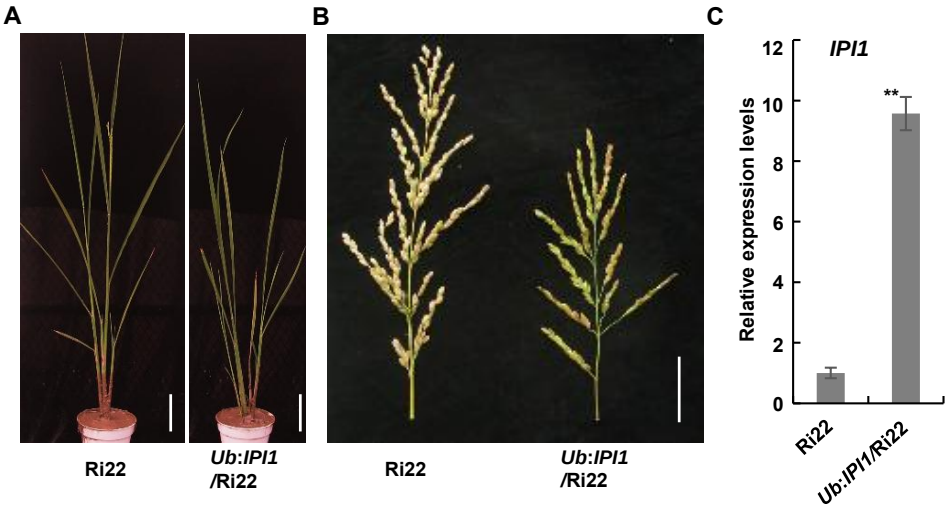


Supplemental Figure 11. Mutation in *ipa1-1D* Has No Effect on Polyubiquitination Mediated by IPI1. (Supports Figure 8)

(**A**) Interaction between IPI1 and ipa1-1D in the yeast two-hybrid assay. The ipa1-1D and IPI1 proteins were fused with the GAL4 DNA binding domain and activation domain, respectively. Clones were grown on the medium SD-L-T-U.

(**B**) Effect of IPI1 levels on the degradation of ipa1-1D. Numbers indicate the ratio of the concentration of agrobacteria used in co-infiltration. HA-GFP was used as an internal control for protein synthesis.

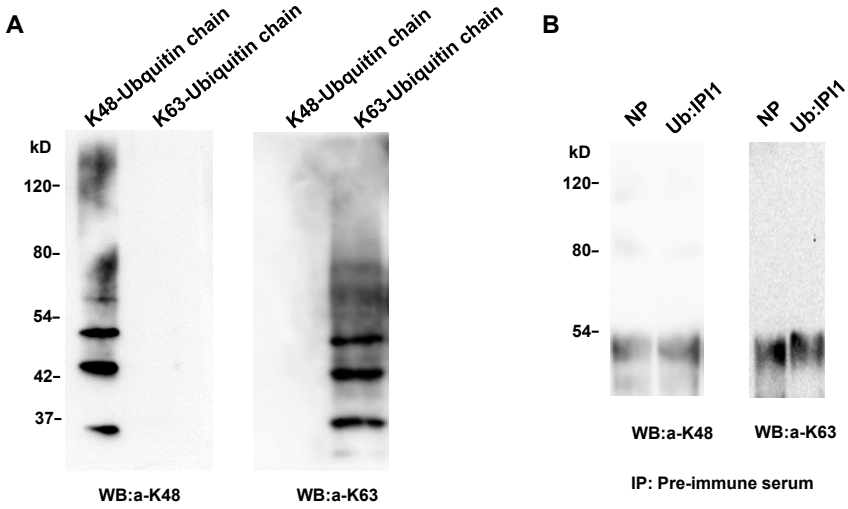
(**C**) *In vitro* polyubiquitination of ipa1-1D by IPI1. GST-IPI1(H74Y) and GST were used as negative controls. Anti-His polyclonal antibodies were used to detect the ipa1-1D tagged with polyubiquitin chain. The presence (+) or absence (-) of components in the reaction mixture is indicated.



Supplemental Figure 12. Overexpression of *IPI1* in the *ipa1-1D* Background Affects Plant Architecture. (Supports Figure 8)

(**A**) - (**B**) Phenotypes of Ri22 (a gain-of-function *ipa1-1D* allele) and *IPI1*-overexpressing transgenic plants in Ri22 (*Ub:IPI1*) of young plants (**A**) and panicles (**B**). Bars represent 10 cm in (**A**) and 5 cm in (**B**).

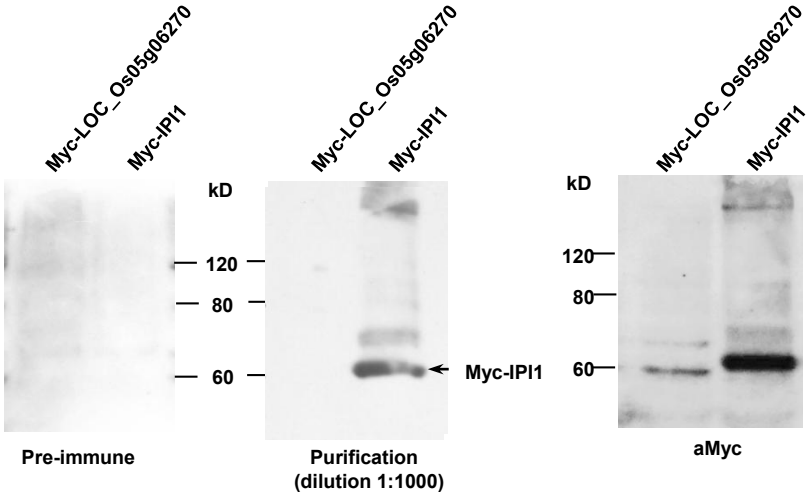
(**C**) Transcript levels of *IPI1* in Ri22 and *Ub:IPI1*. Rice *Ubiquitin* is used as an internal control. Values are means ± SD (n = 3).



Supplemental Figure 13. Specificity of K48- or K63-Polyubiquitin Antibodies. (Supports Figure 8)

(**A**) The K48- or K63- polyubiquitin chain was detected with the anti-K48 or anti-K63 polyclonal antibodies.

(**B**) The total protein extracted from Nippobbare (NP) and Ub:IPI1 was immunoprecipitated with pre-immune serum. Immunoblot was performed with the anti-K48 or anti-K63 polyclonal antibodies.



Supplemental Figure 14. Specificity of IPI1 Polyclonal Antibodies. (Supports Figures 1 and 8)

Immunoblotting was performed with pre-immune serum, anti-IPI1 and anti-Myc polyclonal antibodies. LOC_Os05g06270, a homolog of IPI1, was used as a control.

Supplemental Table 1. Putative Proteins Interacting with IPA1.

Number	Gene ID	Annotation
1	LOC_Os01g24880	RING finger containing protein
2	LOC_Os05g25210	Expressed protein
3	LOC_Os07g33630	HEAT repeat family protein
4	LOC_Os06g06760	protein kinase
5	LOC_Os05g40290	KH domain-containing protein

Supplemental Table 2. Primers Used in This Study.

Primer names	Sequences
Primers for RT-PCR	
IPA1-F	CGGTCGACTAGCTGCATCTGTTGG
IPA1-R	CATCGTGTTGCTGGTTTGGTCGAAG
ACTIN-F	CATCAGGAAGGACTTGTACGG
ACTIN-R	GATGGACCTGACTCGTCATAC
Ubiquitin-F	CCCTCCACCTCGTCCTCAG
Ubiquitin-R	AGATAACAACGGAAGCATAAAAGTC
IPI1-F	CGCTGTTGGCTATCACTATC
IPI1-R	CACCACCCGTAACCTGTAA
Primers for qPCR	
qIPI1-F	ACGAACAATATCAGCAGAA
qIPI1-R	TCCGTCTCCATTGAATTAG
qUbiquitin-F	ACGAACAATATCAGCAGAA
qUbiquitin-R	AGATAACAACGGAAGCATAAAAGTC
Primers for constructs	
IPA1-SmaI1-AF	AACCCGGGAATGGAGATGGCCAGTGGAGGAGGCGCCG
IPA1-Spe1-R	AAACTAGTCTACAGAGACCAATCCATCGTGTTGCTGG
IPA1-BamH1-F	AAGGATCCATGGAGATGGCCAGTGGAGGAGGCGCCG
IPA1-Kpn1-NR	AAGGTACCCAGAGACCAATCCATCGTGTTGCTGG
IPA1-Sac1-NR	AAGAGCTCCAGAGACCAATCCATCGTGTTGCTGG
IPA1-Sac1-R	AAGAGCTCCTACAGAGACCAATCCATCGTGTTGCTGG
IPI1-SmaI1-AF	AACCCGGGAATGGGCGCCGAGGAGGAGGAGGAGCCGG
IPI1-Spe1-R	AAACTAGTCTACATCCGAGGGATGTGCATCTGTCGG
IPI1-BamH1-F	AAGGATCCATGGGCGCCGAGGAGGAGGAGGAGCCGG
IPI1-Xho1-R	AACTCGAGCTACATCCGAGGGATGTGCATCTGTCGG
IPI1-Hind III-NR	AAAAGCTTCATCCGAGGGATGTGCATCTGTCGG
IPI1-SmaI1-NR	AACCCGGGCATCCGAGGGATGTGCATCTGTCGGTAC
IPI1-CF	CATGGGCGCCGAGGAGGAGGAGGAGCCGG
IPI1-R	CTACATCCGAGGGATGTGCATCTGTCGG
IPI1-Sac1-R	AAGAGCTCCTACATCCGAGGGATGTGCATCTGTCGG
IPI1-(H74Y)-F	AGGCTGCAGTGCGGCTATGAGTTCCACCTCGATTGC
IPI1-(H74Y)-R	GCAATCGAGGTGGAACTCATAGCCGCACTGCAGCCT
IPI1-(C80S)-F	GAGTTCCACCTCGATAGCATTGGTTCAGCATTTAATG
IPI1-(C80S)-R	CATTAAATGCTGAACCAATGCTATCGAGGTGGAACTC
Primers for identification of *ipi* mutant	
sg1516-seq(ge)-F	GAAGACTATCTTAGATATG

sg1516-seq(ge)-R	AATCAAAAGTTTGGAGGGT
sg1517-seq(ge)-F	ATGCAATGTCGTCCCTTCCT
sg1517-seq(ge)-R	CAGGTAGGGGGTTCCAGTGA
sg1517-seq(CDS)-F	GTCCTATTGGCCGCTTAG
sg1517-seq(CDS)-R	GGTGCGTCCAGTGGTTAT