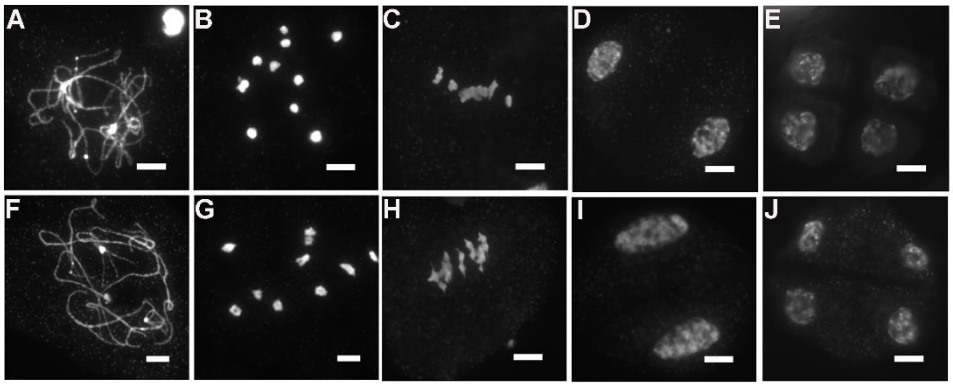
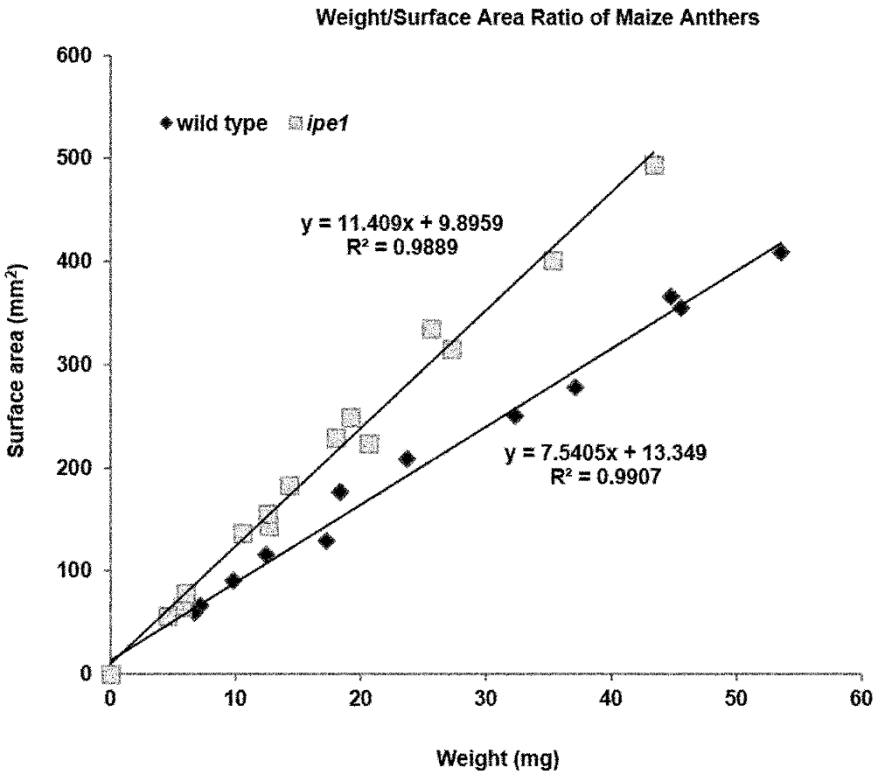
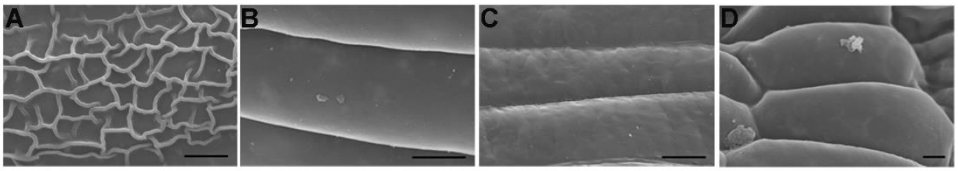


Supplemental Figure S1. DAPI Staining of Chromosomes of Wild Type and *ipe1* in Meiosis.

Compared with the wild type ([A] to [E]), meiosis was normal in the *ipe1* mutant ([F] to [J]). (A) and (F), Pachytene; (B) and (G), Diakinesis; (C) and (H), Metaphase I; (D) and (I), Telophase I; (E) and (J), Telophase II. Bars = 10 μm.

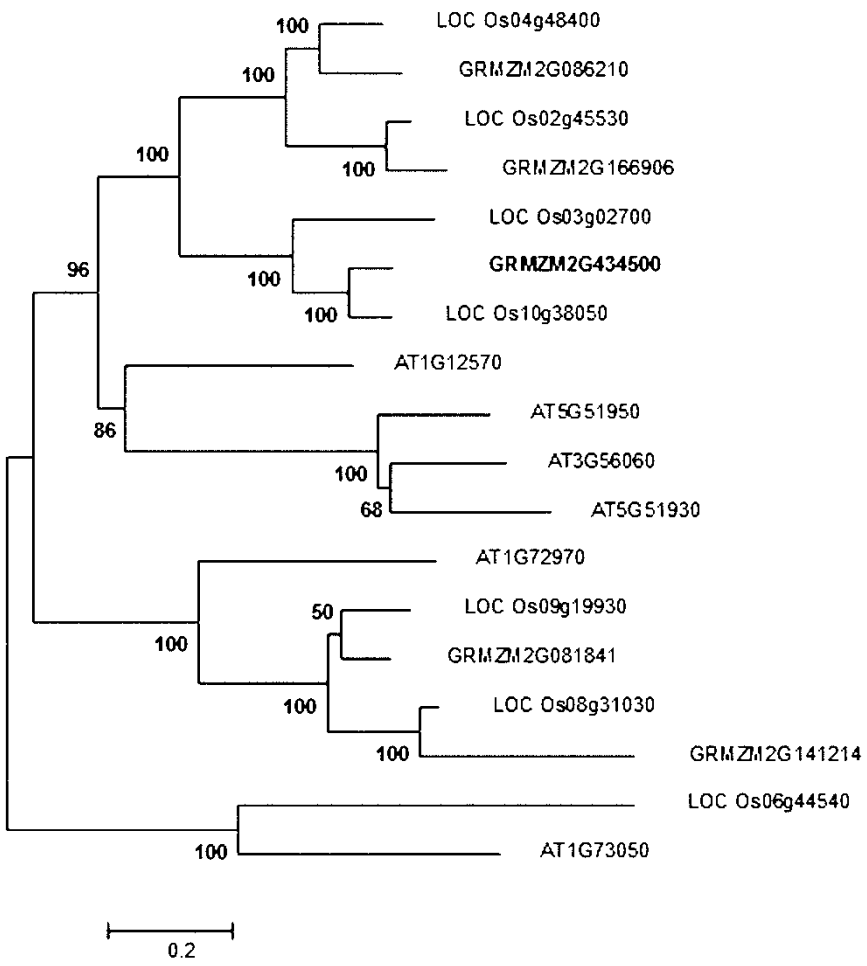


Supplemental Figure S2. Weight/Surface Area Ratio of the Wild Type and *ipe1* Anthers.



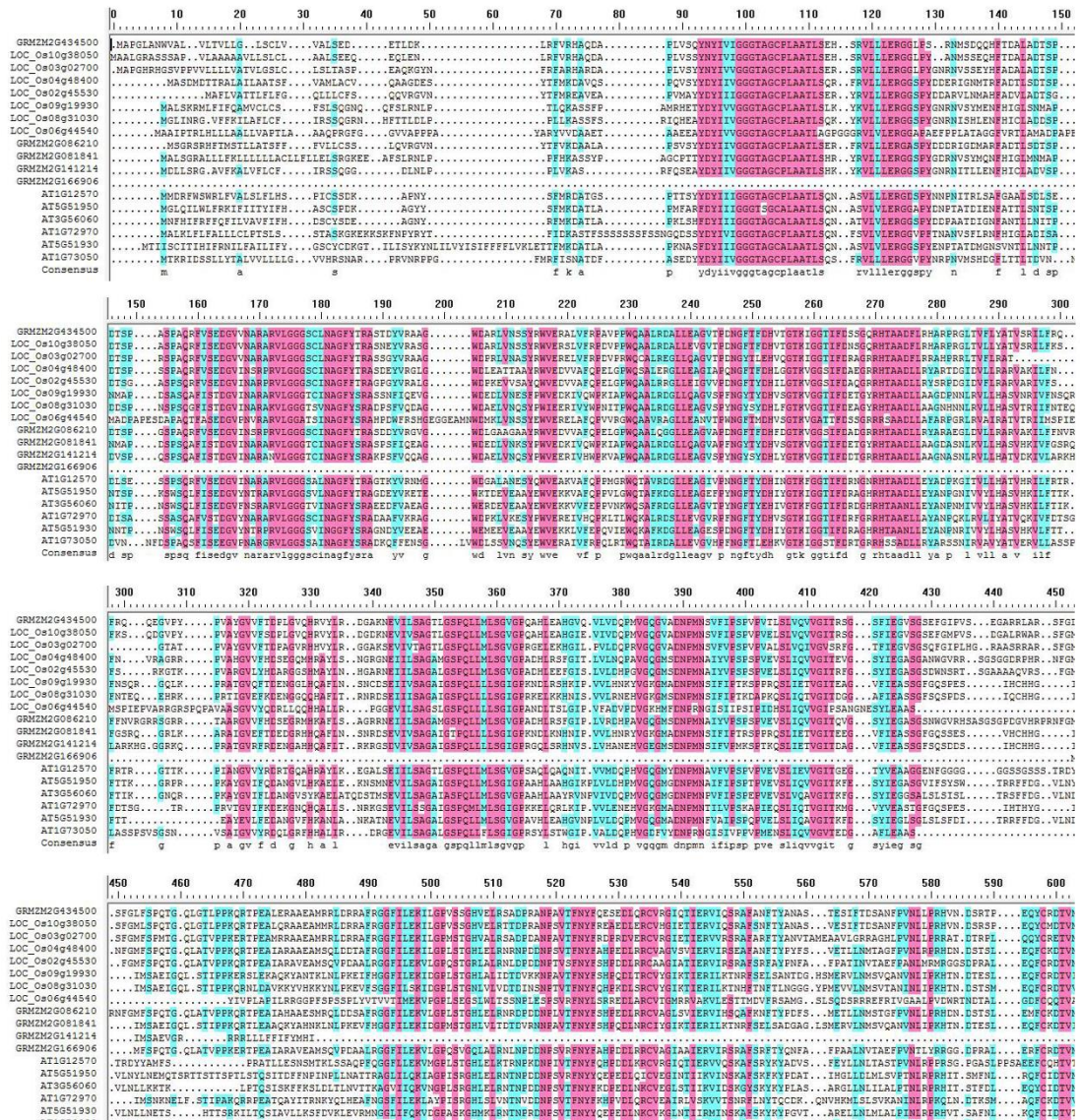
Supplemental Figure S3. SEM Observation of the Anther Surface.

The wild-type anther surface consists of the reticular anther cuticle (A), whereas the surface is smooth in *ipe1-1* (B), *ipe1-2* (C), and *ipe1-3* (D). Bars = 5 μm.

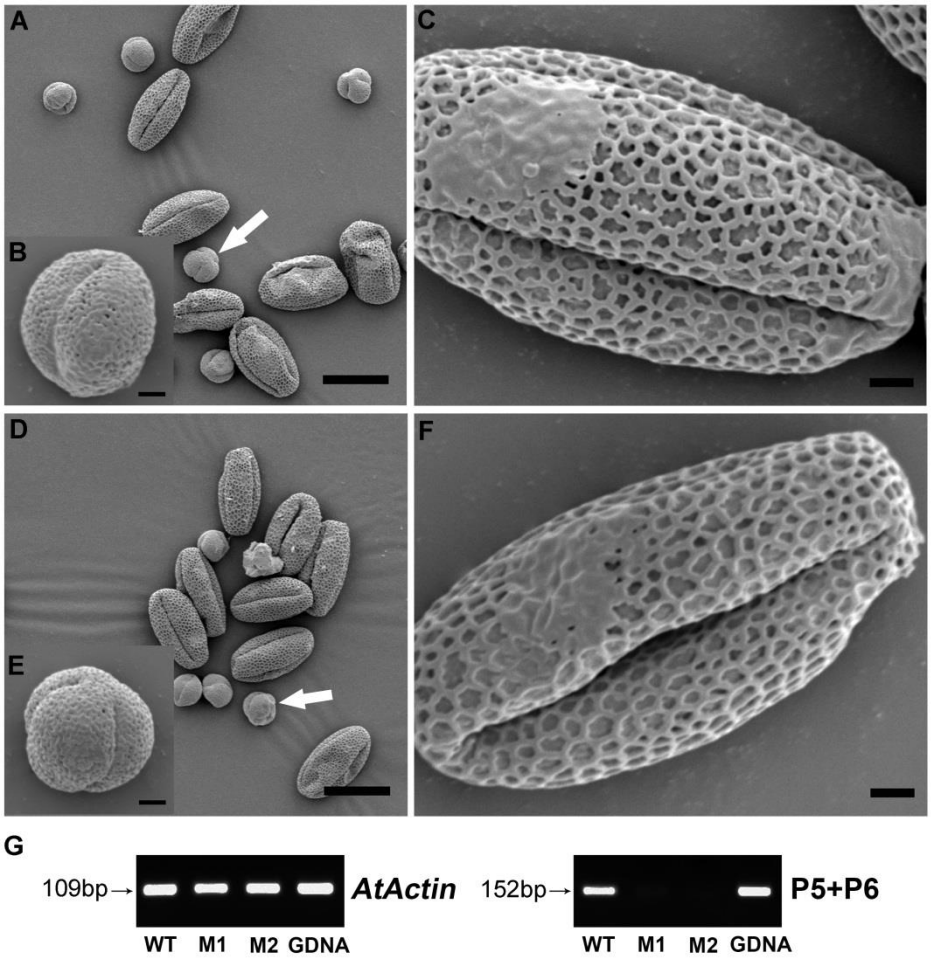


Supplemental Figure S4. The Phylogenetic Tree of IPE1-Related Proteins.

A neighbor-joining phylogenetic tree summarizes the evolutionary relationships between the IPE1-related proteins (E value of BLASTP result is < 1E-100). The proteins are named according to their gene names or Phytozome accession numbers. The numbers under the branches refer to the bootstrap value of the neighbor-joining phylogenetic tree. The length of the branches is proportional to the amino acid variation rates. Os, *Oryza sativa*; Zm, *Zea mays*; At, *Arabidopsis thaliana*. The bar indicates the estimated number of amino acid substitutions per site.



Supplemental Figure S5. The Sequence Alignment of IPE1 and 17 IPE1-Related Proteins



Supplemental Figure S6. Phenotypes of Two Additional T-DNA Insertional Lines of *AT1G12570.*

(A) to (C) Phenotypes of the T-DNA insertional line SALK-112758.

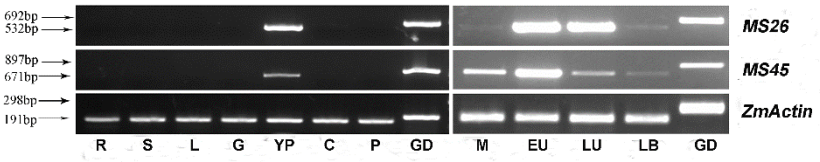
(D) to (F) Phenotypes of the T-DNA insertional line SALK-031400.

(A) and (D) Smaller pollen grains appeared in the two T-DNA insertional line(arrowhead). Bars = 20 μm.

(B) and (E) The magnification of a smaller pollen grain. Bars = 2 μm.

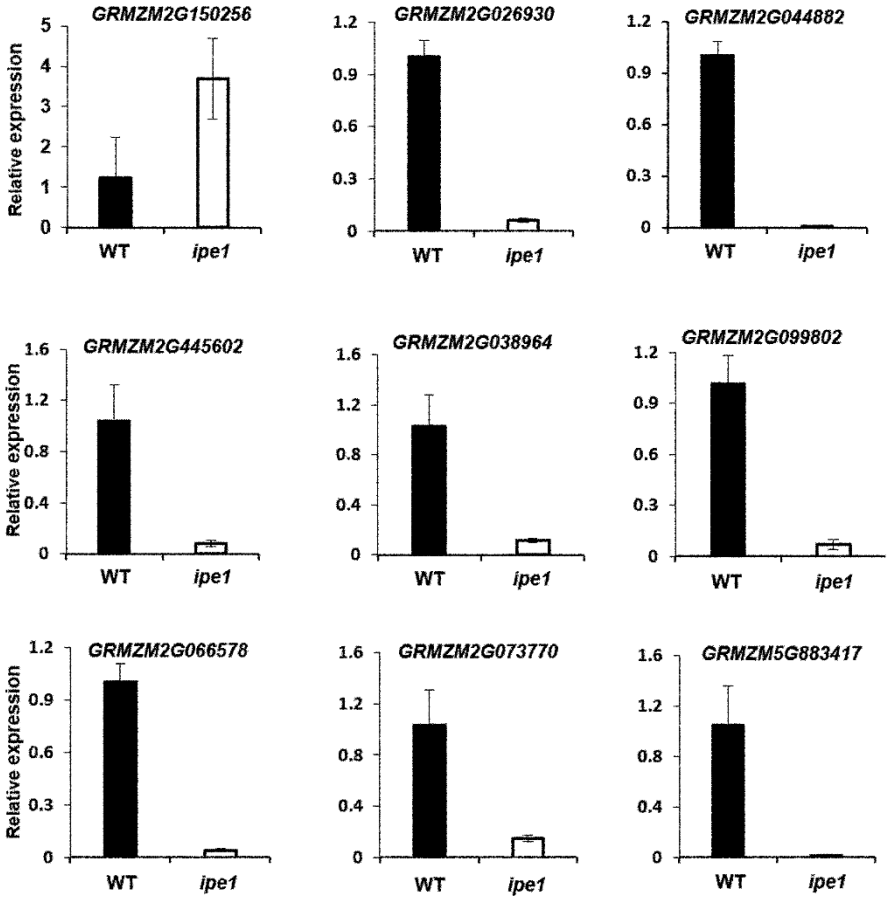
(C) and (F) The defective pollen exine. Bars = 2 μm.

(G) RT-PCR anlysis of the two additional T-DNA insertional lines. WT, wild type; M1, the line SALK-031400; M2, the line SALK-112758; GDNA, genomic DNA.

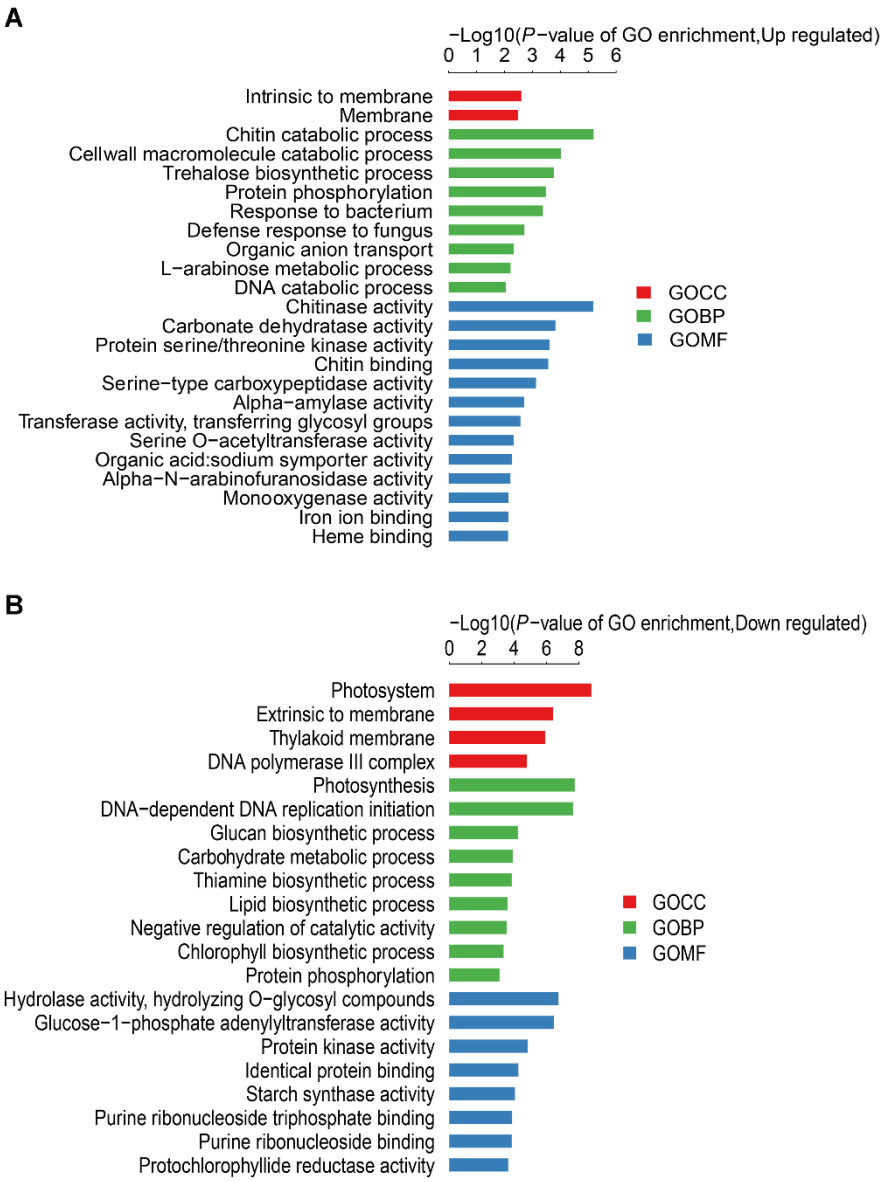


Supplemental Figure S7. The Spatial and Temporal Expression of *MS26* and *MS45* by RT-PCR.

The transcripts of *MS26* and *MS45* were only detected in young spikelets, and the level peaked in anthers at the early uninucleate microspore stage. R, roots; S, stems; L, leaves; G, glumes; YP, young spikelets; C, cobs; P, pistils. GD, genomic DNA. M, anthers in the meiosis stage; EU, anthers in early uninucleate microspore stage; LU, anthers in late uninucleate microspore stage; LB, anthers in late binucleate microspore stage. *ZmActin* was used as a positive control.

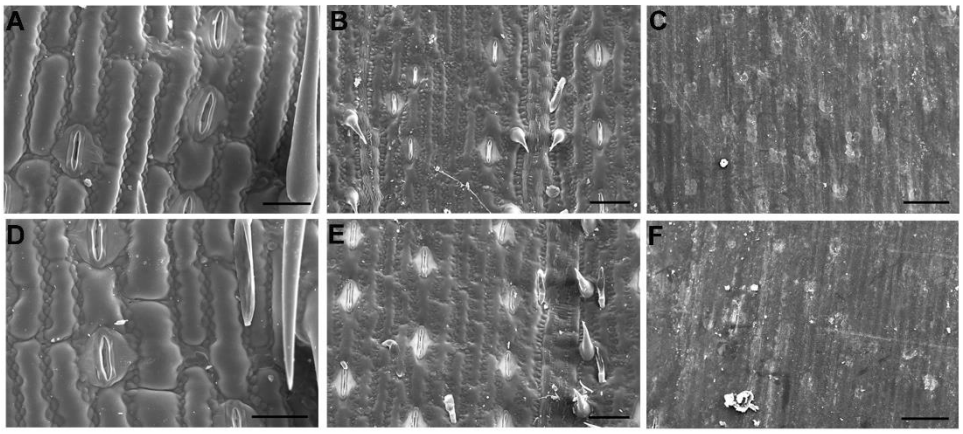


Supplemental Figure S8. qRT-PCR Analysis of Randomly Selected Nine Differential Expressed Genes in *ipe1*(n=3).



Supplemental Figure S9. Significantly Enriched Gene Ontology (GO) Terms of the Up-Regulated Genes (A) and Down-Regulated (B) in *ipe1*.

GO terms belonging to cellular components (GOCC), biological processes (GOBP), and molecular functions (GOMF) are shown in red, green, and blue, respectively.



Supplemental Figure S10. SEM Analysis of the Surface of Glume, Leaf and Stem in Wild Type and *ipe1*.

The normal surface structures of glume [(A) and (D)], leaf [(B) and (E)] and stem [(C) and (F)] are shown in wild type ([A] to [C]) and *ipe1* mutant ([D] to [F]). Bars = 30 μm in (A) and (D); 60 μm in (B), (C), (E) and (F).

Cutin monomers	Wild Type	*ipe1*	Up
	Mean ± SD (ng mm^{-2})		
C16:1 acid	0.460 ± 0.286	0.118 ± 0.068	-290.86%
C16:0 acid	63.795 ± 10.238	14.812 ± 2.112	-330.70%
C18:0 acid	5.571 ± 3.631	1.098 ± 0.805	-407.45%
C18:1 acid	2.995 ± 1.513	0.557 ± 0.285	-437.99%
C18:2 acid	110.962 ± 23.858	25.079 ± 5.269	-342.46%
C18:3 acid	153.555 ± 9.809	40.746 ± 2.113	-276.86%
C20:0 acid	4.274 ± 2.729	0.780 ± 0.537	-447.81%
C22:0 acid	1.612 ± 1.292	0.331 ± 0.324	-387.43%
C24:0 acid	1.163 ± 0.967	0.185 ± 0.244	-528.33%
C26:0 acid	0.455 ± 0.336	0.065 ± 0.081	-599.12%
C16:0 β-OH acid	0.525 ± 0.065	0.129 ± 0.021	-306.68%
C18:0 β-OH acid	0.308 ± 0.128	0.061 ± 0.019	-406.82%
C22:0 β-OH acid	1.592 ± 1.757	0.235 ± 0.319	-578.34%
C24:0 β-OH acid	5.674 ± 3.998	0.815 ± 0.777	-596.88%
C26:0 β-OH acid	3.266 ± 2.078	0.496 ± 0.432	-558.57%
C16:0 ω-OH acid	48.643 ± 9.592	7.593 ± 1.860	-540.67%
C18:1 ω-OH acid	54.536 ± 20.574	7.495 ± 3.059	-627.62%
C18:2 ω-OH acid	18.368 ± 5.262	2.751 ± 0.998	-567.71%
C18:0 9/10 di-OH acid	0.941 ± 0.648	0.224 ± 0.333	-320.85%
C18:0 9/10 di-OH diacid	96.746 ± 25.601	11.761 ± 4.298	-722.63%
C18:0 9/10/18 tri-OH acid	22.122 ± 5.187	3.396 ± 1.492	-551.47%
C16:0 diacid	2.271 ± 0.648	0.318 ± 0.102	-613.53%
C18:2 diacid	1.957 ± 0.711	0.190 ± 0.132	-932.20%

Supplemental Table S1. The Detailed Cutin Compositions of the Wild-type and *ipe1* Anthers.

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Primer Name	Forward primers	Reverse primers	Usage
S1	GAGAAGGGCGGGAGGAATAAC	CGAAGAGCACGATGTTGACG	
S2	GGTAGACAGCTGCCGCCACG	ACCACCGCCGTAACACGCAG	
S3	CGGCAAAGCAGCTGATTCCGGT	GGCACAAATGCACCAATCACGGA	
S4	AAACCGCCCTGTTCTGTTCA	AGTCTGGTGCATTTGCCACT	
S5	TCGTGATGGTTGTCGGATCG	GTACAGGACGACACGACTGG	
S6	TTCACCTACGCCAACGCTTC	TGGGCTTGGTCTTGTTCAGTT	*IPE1*
S7	GGCTGGCGGGTAGAAGTAGA	CTCGGTTGCTCTCAACACGG	mapping
S8	GCCAGAGTCGCAGGGCGAAG	TCGCTGTGGCTGCCAAGACT	
S9	GCGGCAAGCCCATCTGCGAG	CCGAAGCGCTCCGACCACGC	
S10	TTTAGGCGCGTCGTTCCTCGG	CTCGGCGACACAGCCTCGTC	
S11	GGCGTCGCTTTAGCCGTTGC	AGCACCATCGTTTCGCCCCG	
IPE1	TTCACCTTCGACCACGTCAC	CCGAGTTCATCGGGTTGTCA	
ZmActin	TCACCCTGTGCTGCTGACCG	GAACCGTGTGGCTCACACCA	
MS26	ATGCACGACTGGCTTGTCGGGTACC	CGTGGAAGAACCTCTTGATGCGCCACA	
MS45	CGAGGGCGTGATGGCATCGT	GTGCCTTCCTCCTTCTAACAGGATGTTCAG	RT-PCR
P1/P2	TTTTTGACCGCAACGGCAAT	AGAAGGAACGAACACGGCAT	
P3/P4	GCTCAAGACCCGAAACCCAA	ACTTCTTGGTGAGTCTCTCTCTC	
P5/P6	TTGAATCGGATCAGGGGTTT	TCCGTATACATCTCAGTTTGGTC	
AtActin	GGTAACATTGTGCTCAGTGGTGG	AACGACCTTAATCTTCATGCTGC	
qIPE1	TCTTCAGACAGCAAGAGGG	CCGACAGGATCACCTCGT	
qMS26	GGACGAGTTCACCTACAGC	AAGTTGAGCACCACGTCCC	
qMS45	GCCTCAGCCCAACAAGC	ATGACATGAAACGGTGCCTT	
qGRMZM2G150256	TGATCTGTAATGCACGAAGCAC	CCAAATCACTTATTCCATCGGTT	
qGRMZM2G026930	TCTCCCCGTCGATGATGCT	CCAGGGGATAAAACAATTCGT	
qGRMZM2G044882	CTCTTCAACCCGCAGATGG	TCGTGAACCCGAAGTCCTG	qRT-PCR
qGRMZM2G445602	GCACCAAGTGTTACTATACCG	TCCCTCCCTTAACCGCTAC	
qGRMZM2G038964	AAGAAGAACTGACGCACGTA	TGAACATGTCAACCCATCGC	
qGRMZM2G099802	ACTTCAGAAATTGCTAAGCGGTA	CTTGTACCCCAAAAGTTCAGG	
qGRMZM2G066578	TCATGTACACACCCTCGTTT	TTCTCATACAACGTGTCCGAT	
qGRMZM2G073770	GTTCGCTGTATGTTTCTCGAC	AGCAGCATGATGTAAATTCGT	
qGRMZM5G883417	GGCCCAATCTGTCAGCATC	GTGCATTTCCAACGCCTCC	
GFP-F	GTGTTACTTCTGCAAAGCTTATGGCGCCTGCGCTTGCGAACT		
GFP-R	CCCTTGCTCACCATGGATCCTTTCCTCCATCTCTCGGCCTGA		Subcellular
ΔSP-GFP-F	GTGTTACTTCTGCAAAGCTTCTGGACAAGCTGCGGTTCGTGC		localization
SP-GFP-R	CCCTTGCTCACCATGGATCCTGTTTCATCCTCCGAGAGCGCG		
IPE1-Sp6	GATTTAGGTGACACTATAGaatGCTTCACCGTGTTCCTCTACGCTA		
IPE1-T7	tgTAATACGACTCACTATAGGGCTCTGCTTCGGCGGCAAC		Probe

Supplemental Table S2. Primers Used in This Study

♀ × ♂	Fertile plants	Sterile plants
ipe1-1ipe1-1/IPE1ipe1	51	46
ipe1ipe1/IPE1-1ipe1-1	132	120
ipe1-2ipe1-2/IPE1ipe1	36	35
ipe1ipe1/IPE1-2ipe1-2	59	65
ipe1-3ipe1-3/IPE1ipe1	52	48
ipe1ipe1/IPE1-3ipe1-3	28	32

Supplemental Table S3. Fertile and Sterile Plants Analysis of F_1 Plants from Genetic Crosses among *ipe1, ipe1-1, ipe1-2* and *ipe1-3*. *ipe1-1ipe1-1/IPE1ipe1* indicates progeny of the homozygous *ipe1-1* plants crossed with heterozygous *IPE1* plants. *ipe1ipe1/IPE1-1ipe1-1* indicates progeny of the homozygous *ipe1* plants crossed with heterozygous *IPE1-1* plants. *ipe1-2ipe1-2/IPE1ipe1* indicates progeny of the homozygous *ipe1-2* plants crossed with heterozygous *IPE1* plants. *ipe1ipe1/IPE1-2ipe1-2* indicates progeny of the homozygous *ipe1* plants crossed with heterozygous *IPE1-2* plants. *ipe1-3ipe1-3/IPE1ipe1* indicates progeny of the homozygous *ipe1-3* plants crossed with heterozygous *IPE1* plants. *ipe1ipe1/IPE1-3ipe1-3* indicates progeny of the homozygous *ipe1* plants crossed with heterozygous *IPE1-3* plants.

Gene	The Tissue of High-Level Expression
LOC_Os10g38050	Pre-emergence inflorescence
LOC_Os03g02700	Pre-emergence inflorescence
LOC_Os04g48400	Pre-emergence inflorescence
LOC_Os02g45530	Pre-emergence inflorescence
LOC_Os09g19930	Pre-emergence inflorescence
LOC_Os08g31030	Shoots
LOC_Os06g44540	Pre-emergence inflorescence
GRMZM2G086210	Meiotic tassel
GRMZM2G081841	Immature tassel
GRMZM2G141214	Silks
GRMZM2G166906	Meiotic tassel
AT1G12570	Flower stage 12, petals
AT3G56060	Flower stage 15, petals
AT5G51950	Flower stage 15, stamen
AT1G72970	Flower stage 12, petals
AT5G51930	Mature pollen
AT1G73050	Flower stage 9

Supplemental Table S4. The Putative Expression Patterns of *IPEI* Homologous Genes