

Figure S1 *OsGELP77* expression is induced by different pathogens. (a) Relative transcript levels of *OsGELP77* after bacterial pathogen *Xoo* infection. Rice leaves were inoculated with *Xoo* strain PXO99 at the booting stage. (b) Relative transcript levels of *OsGELP77* after bacterial pathogen *Xoc* infection. Rice leaves were inoculated with *Xoc* strain GX01 at the tillering stage. (c) Relative transcript levels of *OsGELP77* after fungal pathogen *M. oryzae* infection. Rice leaves were inoculated with *M. oryzae* isolate 99-20-2 at the seedling stage. hpi, hours post infection. dpi, days post infection. (d) Activation of *OsGELP77* expression in two-week-old seedlings treated with 1 mM SA or 250 μ M JA. H_2O inoculation was used for mock treatment. hpt, hours post treatment. Data represent means \pm SD ($n = 3$). Gene expression analysis was performed by RT-qPCR and normalized to *Actin*. Asterisks in (a, b, c, d) present significant differences between H_2O inoculation and pathogen infection or hormone treatment, as determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

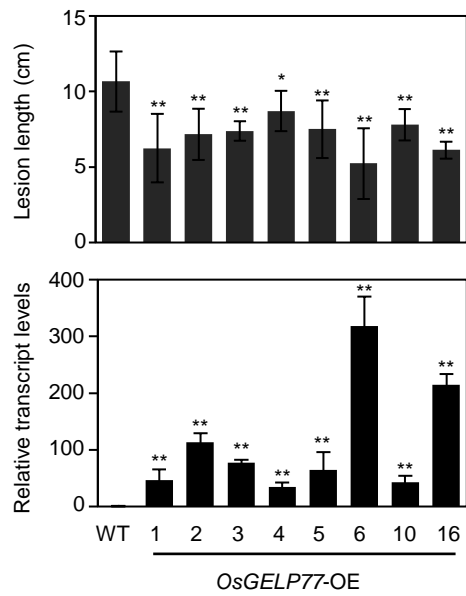


Figure S2 Enhanced resistance to *Xoo* of *OsGELP77*-OE plants. Plants were inoculated with *Xoo* strain PXO99 at the booting stage. Data represents mean \pm SD ($n = 3$). Gene expression analysis was performed by RT-qPCR and normalized to *Actin*. Asterisks indicate significant differences between the *OsGELP77*-OE plants and wild type (WT) determined by two-tailed Student's *t*-test at ** $P < 0.01$ or * $P < 0.05$.



Figure S3 Generation of *OsGELP77* knockout lines. (a) The target sites designed for knocking out *OsGELP77* by the CRISPR/Cas9-mediated gene editing. The target site nucleotides are shown in capital letters, and the PAM sites are indicated as red capital letters. (b) Gel electrophoresis of PCR products amplified from the mutant region. (c) Sequence alignment of the target regions showing large fragment deletions in the two independent *osgelp77* mutants.

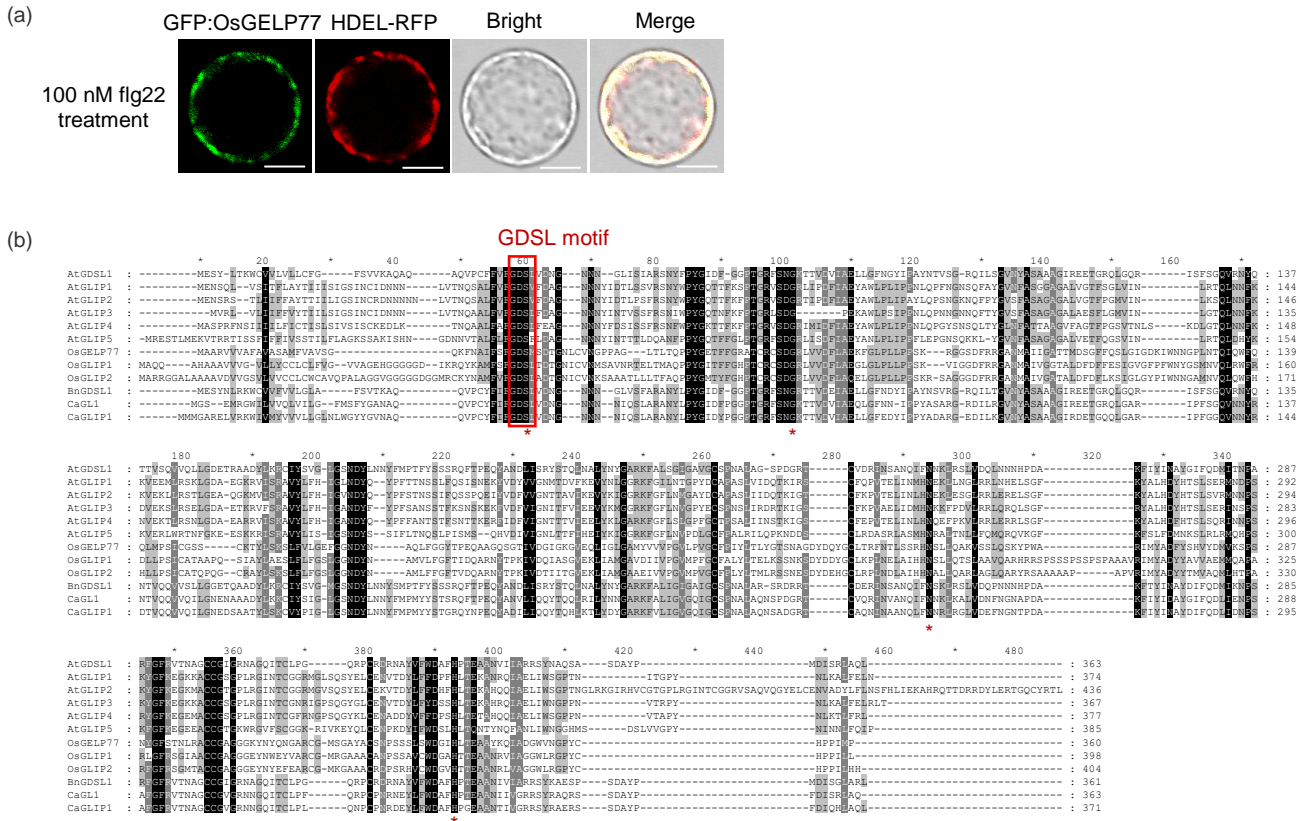


Figure S4 Alignment of amino acid sequences of functionally characterized plant GDSL proteins. (a) Subcellular localization of OsGELP77 in rice protoplasts after flg22 treatment. HDEL protein fused to RFP was used as an endoplasmic reticulum marker. Scale bars: 10 μ m. (b) Sequences were aligned using Clustal Omega. The red box indicates conserved GDSL motif, and the red asterisks indicate invariant key catalytic residues. The GDSL proteins were from *Arabidopsis thaliana* (AtGDSL1, NP_174260.1; AtGLIP1, AED94623.1; AtGLIP2, NP_175797.1; AtGLIP3, NP_175801.1; AtGLIP4, NP_188039.1; AtGLIP5, NP_175795.2), *Oryza sativa* (OsGLIP1, APX55003.1; OsGLIP2, BAS96245.1), *Brassica napus* (BnGDSL1, KC489464), and *Capsicum annuum* (CaGL1, AAZ23955.1; CaGLIP1, NP_001311634.1).

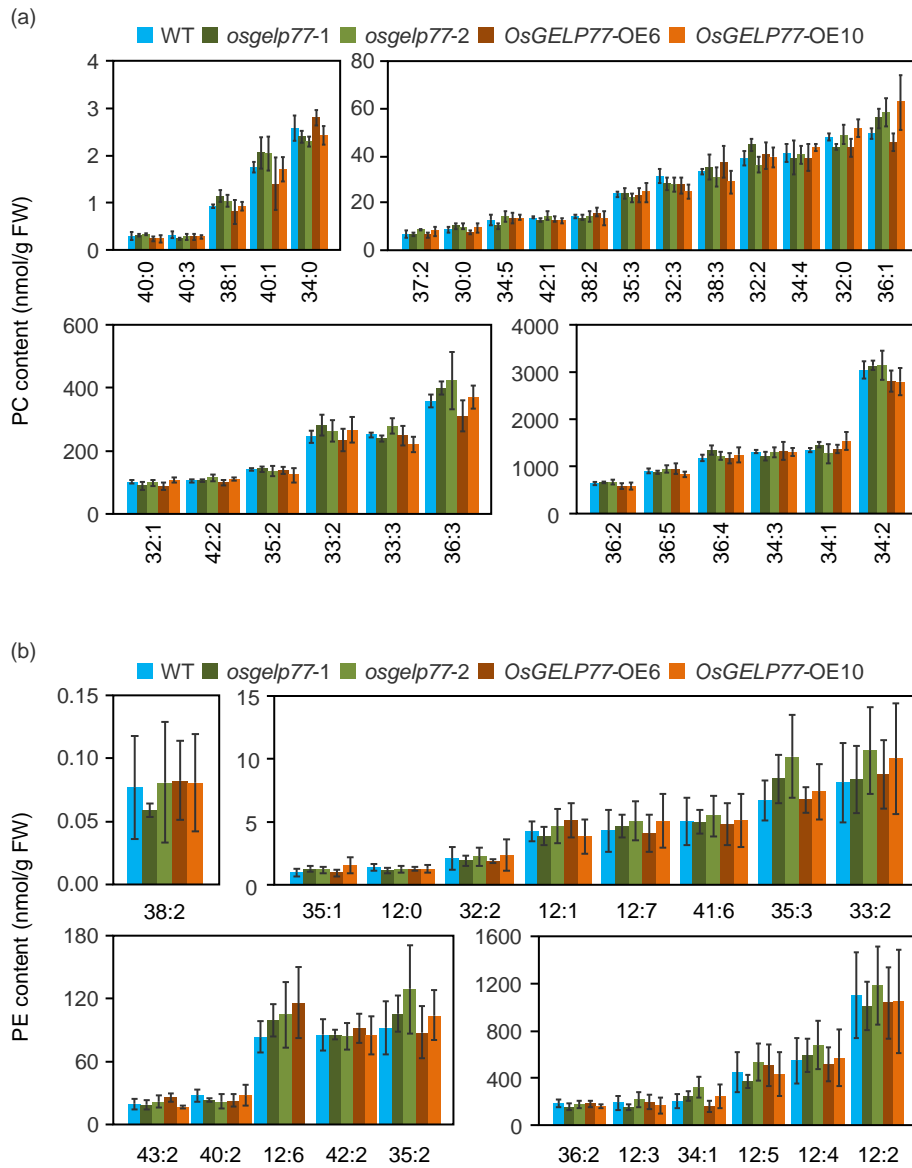


Figure S5 Contents of individual PC and PE species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. (a) Contents of 29 PC species. (b) Contents of 20 PE species. Data represents mean \pm SD ($n = 3$).

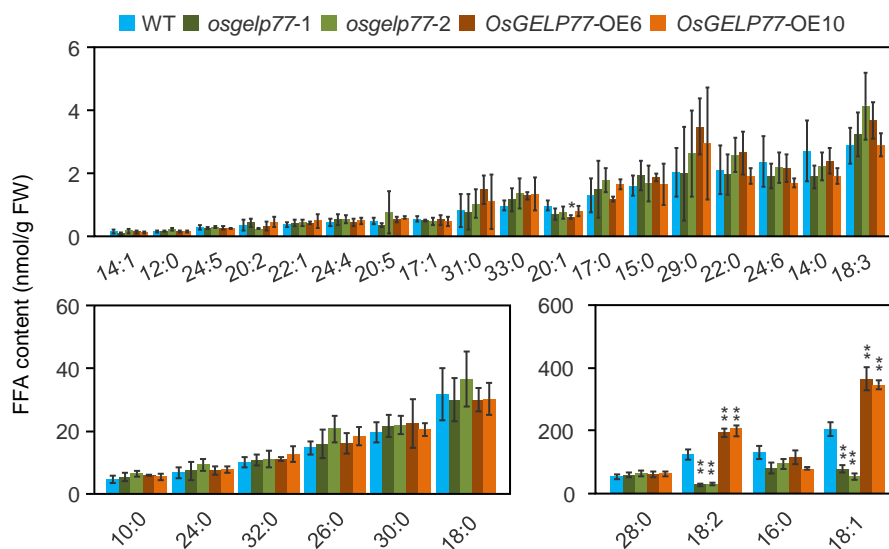


Figure S6 Contents of 28 FFA species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *OsGELP77*-OE plants or *osgelp77* mutants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

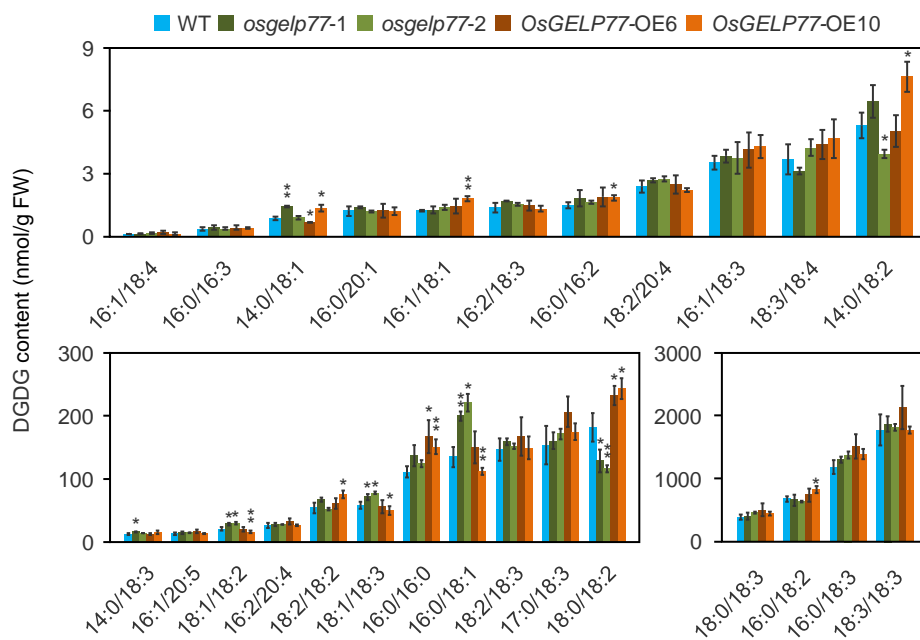


Figure S7 Contents of 26 DGDG species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *OsGELP77*-OE plants or *osgelp77* mutants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

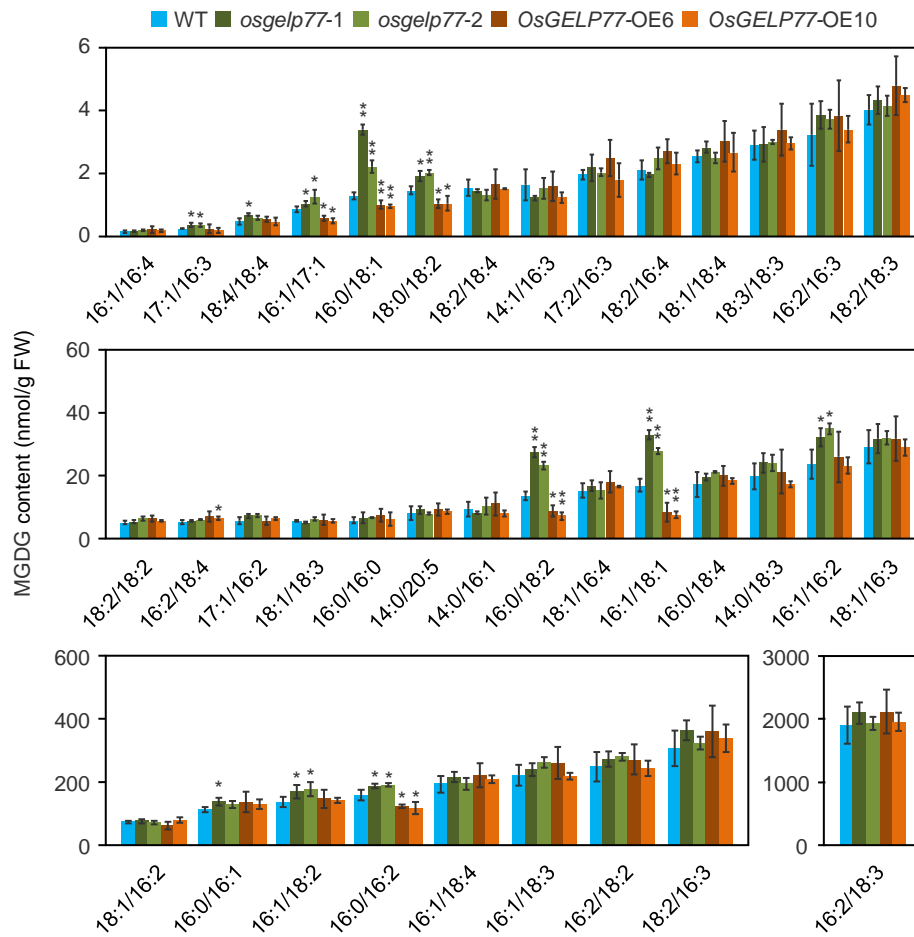


Figure S8 Contents of 37 MGDG species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *OsGELP77*-OE plants or *osgelp77* mutants determined by two-tailed Student's *t*-test at ** $P < 0.01$ or * $P < 0.05$.

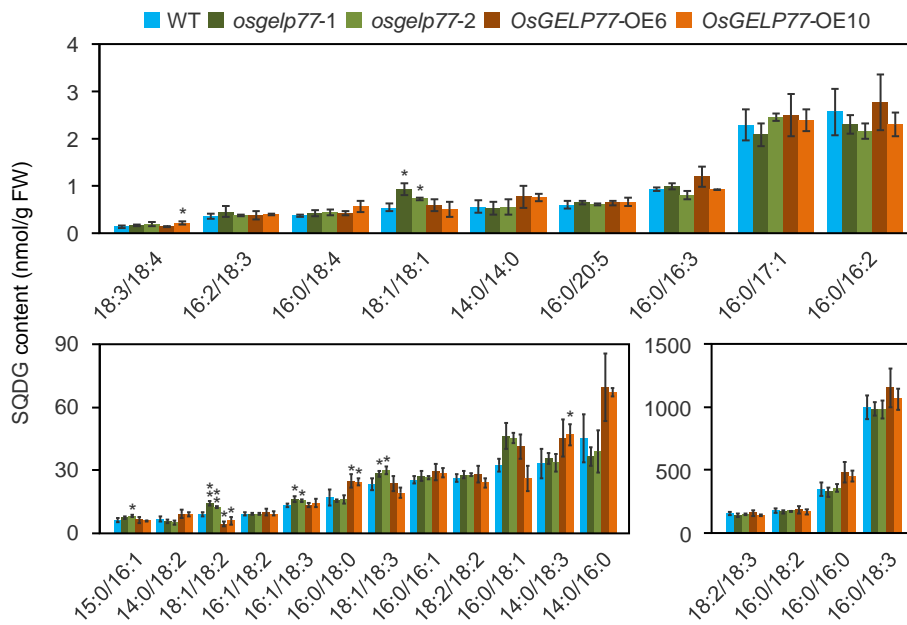


Figure S9 Contents of 25 SQDG species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *OsGELP77*-OE plants or *osgelp77* mutants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

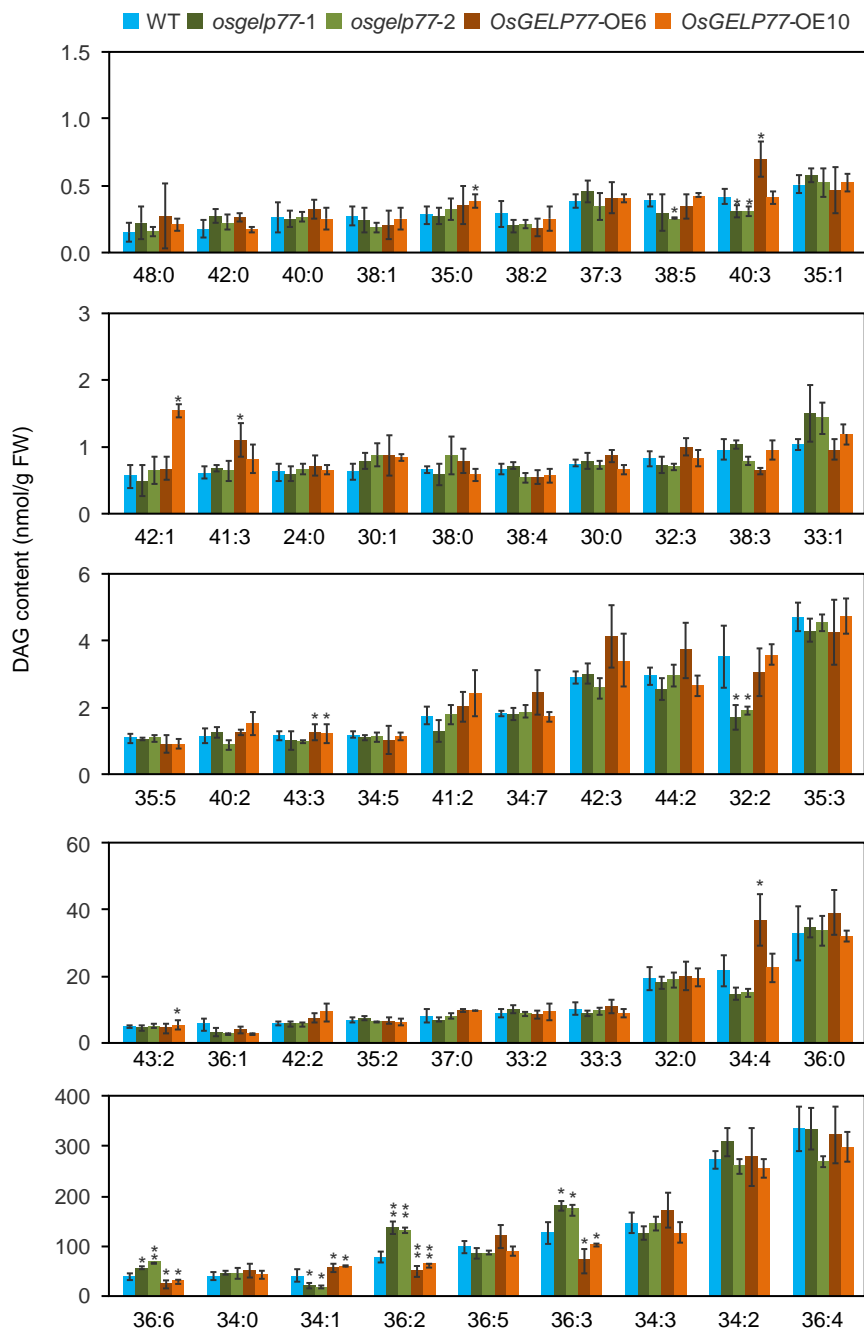


Figure S10 Contents of 49 DAG species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *OsGELP77*-OE plants or *osgelp77* mutants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

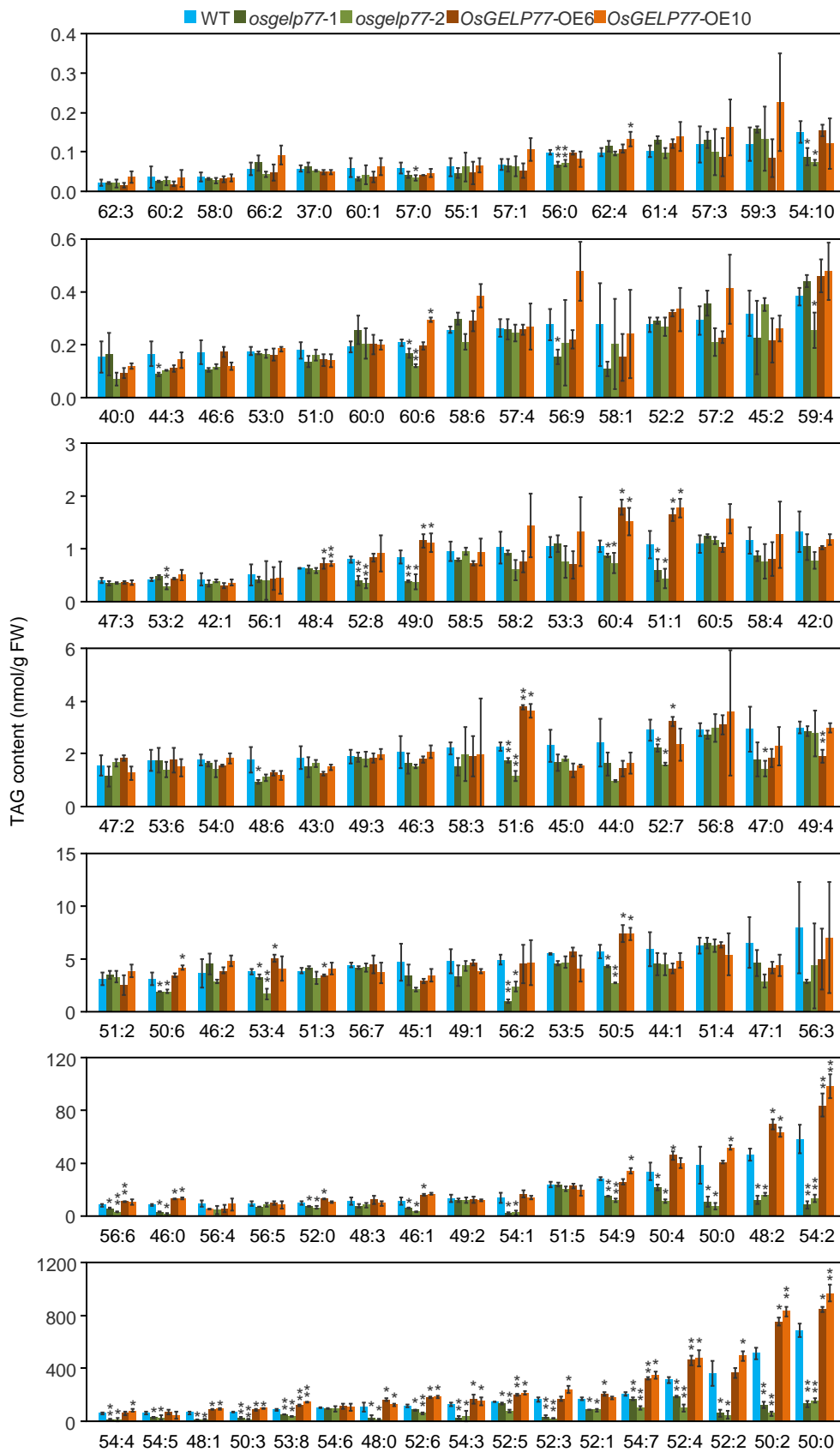


Figure S11 Contents of 107 TAG species in the leaves of *OsGELP77*-OE plants and *osgelp77* mutants. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *OsGELP77*-OE plants or *osgelp77* mutants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

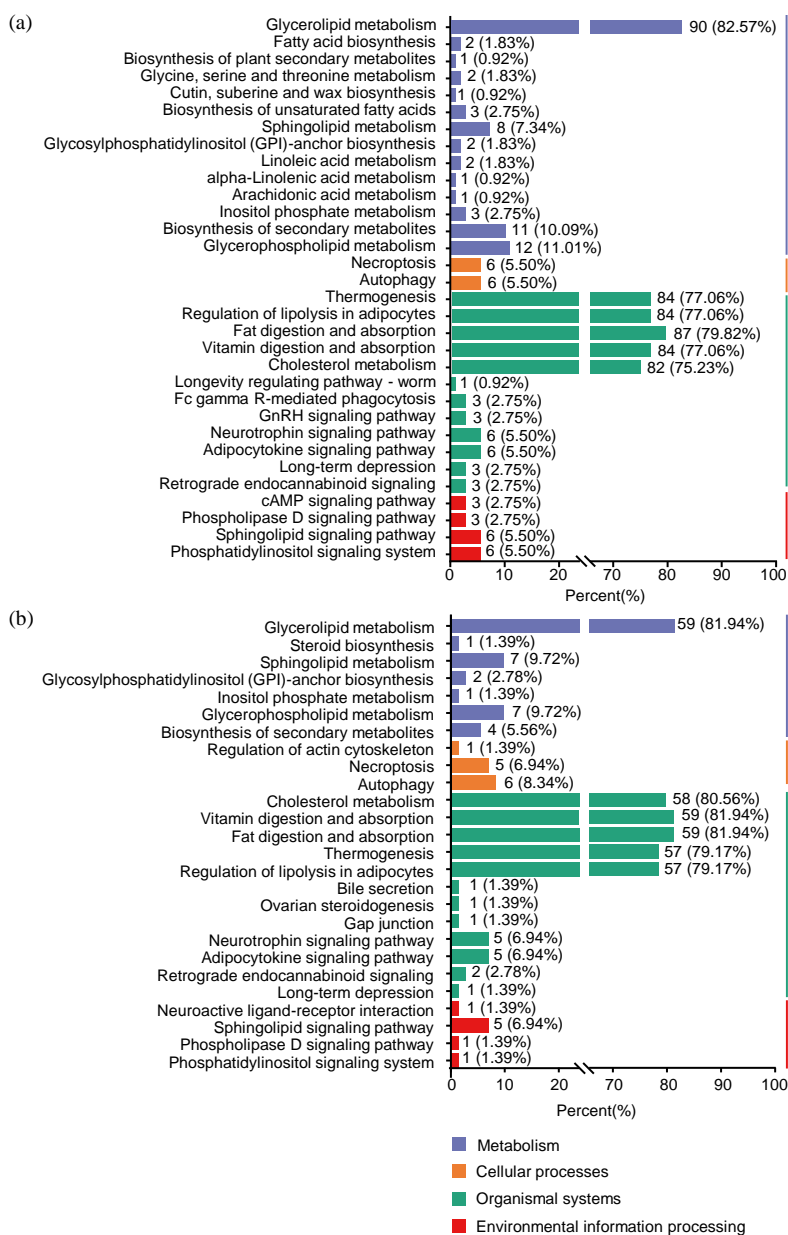


Figure S12 KEGG enrichment analysis of differential lipids between the *osgelp77* mutant and wild type (a) or between the *OsGELP77*-OE plant and wild type (b). The ordinate is the name of the KEGG metabolic pathway, the abscissa represents the ratio of the number of metabolites annotated to the pathway and number of metabolites on the annotation.

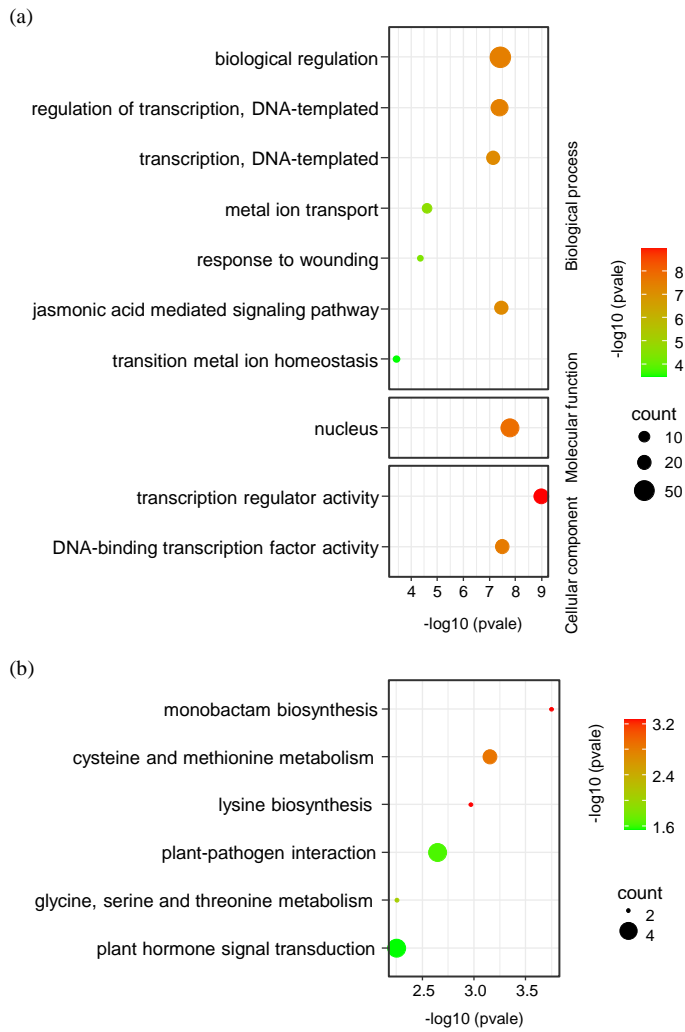


Figure S13 GO enrichment and KEGG pathway analysis of *osgelp77* mutant DEGs. (a) GO enrichment analysis of DEGs. (b) KEGG enrichment analysis of DEGs. DEGs, differentially expressed genes.

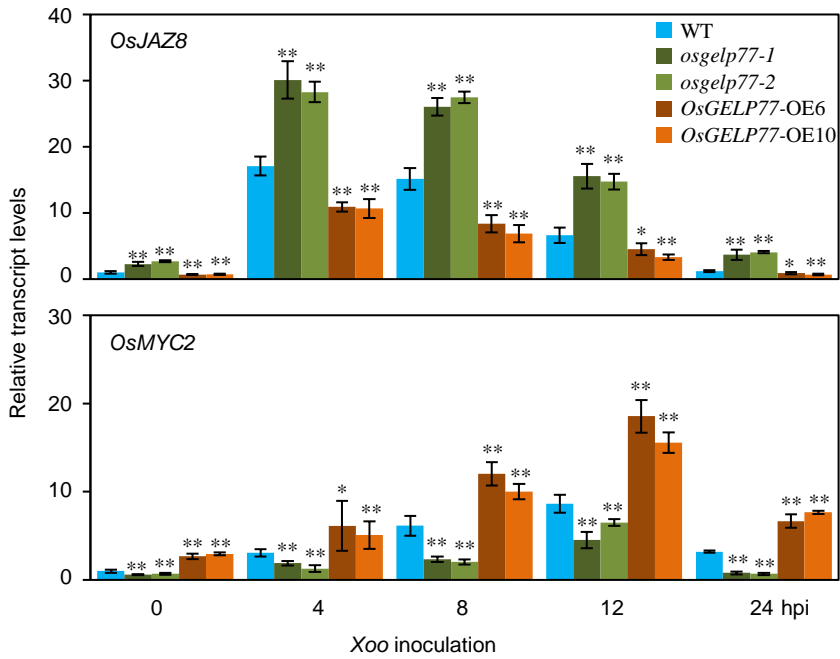


Figure S14 Modulating *OsGELP77* expression influenced the expression of JA signaling pathway genes. Samples were collected at different time points after inoculation with *Xoo* PXO99. hpi, hours post infection. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between wild type (WT) and the *osgelp77* mutants or *OsGELP77*-OE plants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$.

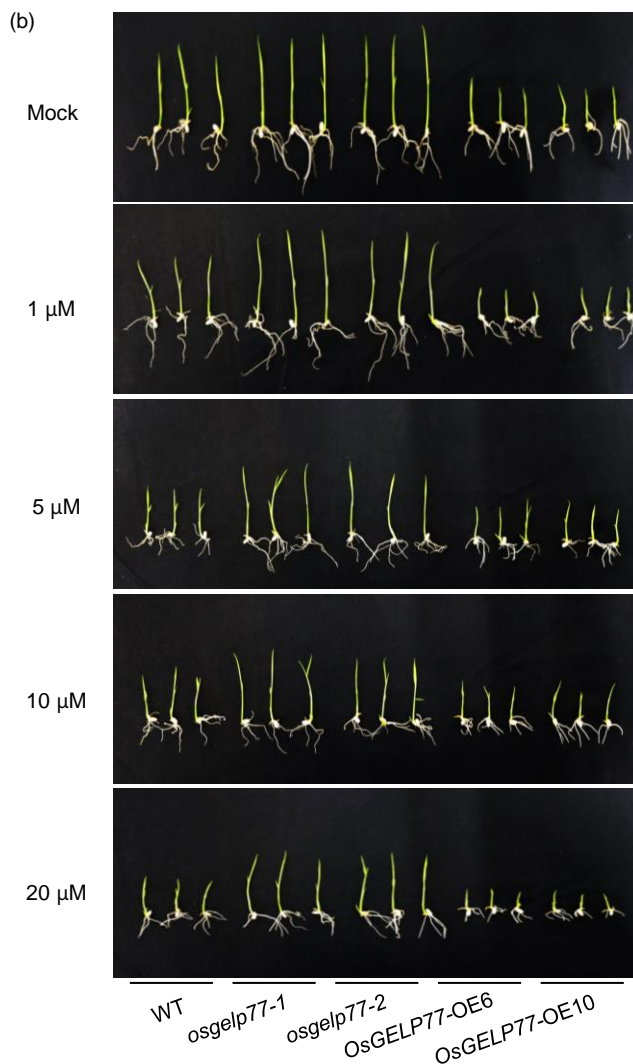
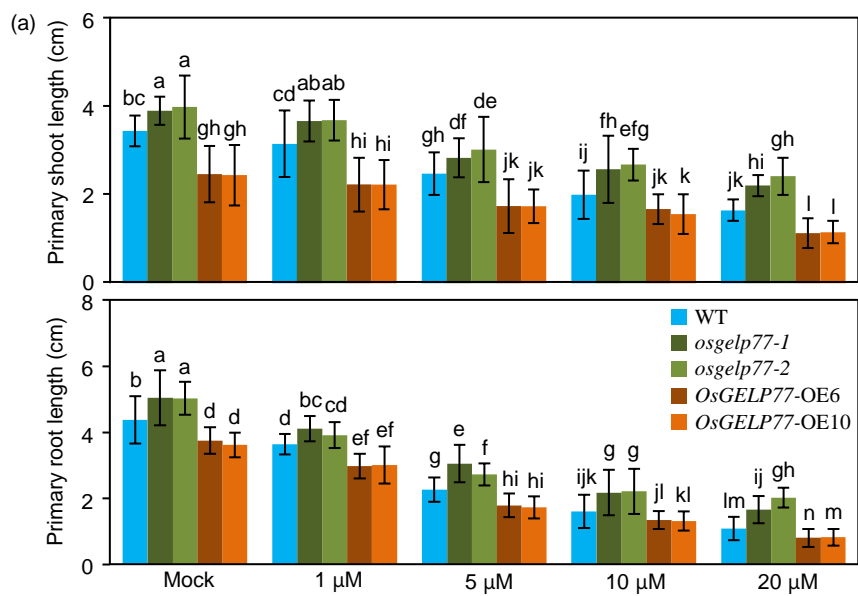


Figure S15 The *OsGELP77*-OE and *osgelp77* mutant plants showed opposite responses to MeJA treatment in primary shoot and root development. (a) The lengths of primary shoot and primary root for *OsGELP77*-OE and *osgelp77* mutant plants after different concentrations of MeJA treatment. Mock, without supplementation of MeJA. Data represents mean \pm SD ($n = 30$). The different letters above each bar indicate statistically significant differences, as determined by one-way ANOVA analysis followed by Tukey's multiple test ($P < 0.05$). (b) Phenotypes of *OsGELP77*-OE and *osgelp77* mutant plants after different concentrations of MeJA treatment. Scale bars: 1 cm.

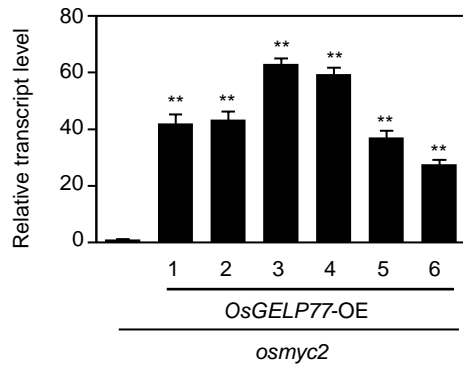


Figure S16 Relative transcription of *OsGELP77* in the *osmyc2* mutant. Data represents mean \pm SD ($n = 3$). Asterisks indicate significant differences between the *OsGELP77*-OE plants and *osmyc2* mutant determined by two-tailed Student's *t*-test at $**P < 0.01$.

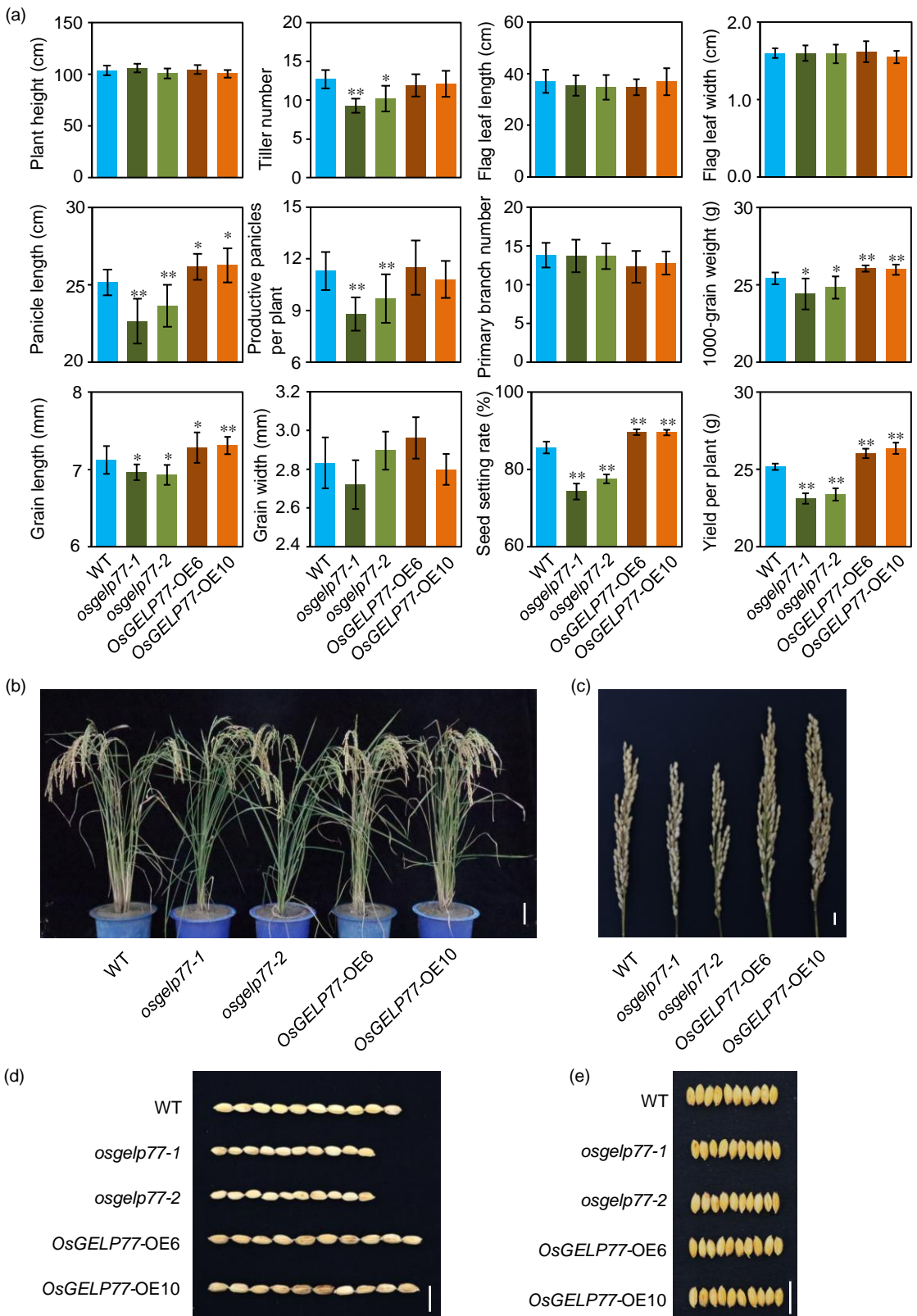
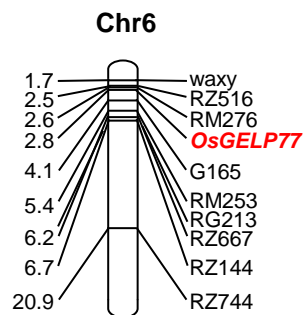


Figure S17 Agronomic traits of *OsGELP77* transgenic lines grown in field. (a) Statistical analysis of agronomic traits of the *osgelp77* mutant, *OsGELP77*-OE plant, and wild type (WT). Data are means \pm SD ($n = 30$). Asterisks indicate significant differences between WT and the *osgelp77* mutants or *OsGELP77*-OE plants determined by two-tailed Student's *t*-test at $**P < 0.01$ or $*P < 0.05$. (b) Plant height of *OsGELP77* transgenic lines. Scale bar: 10 cm. (c) Panicle length of *OsGELP77* transgenic lines. Scale bar: 1 cm. (d) Grain length of *OsGELP77* transgenic lines. Scale bar: 1 cm. (e) Grain width of *OsGELP77* transgenic lines. Scale bar: 1 cm.



QTL1: RZ516-RZ144. Causse et al., 1994. *Genetics*, 138, 1251-1274.

QTL2: RZ516-G165. Xu et al., 2004. *Chin. Sci. Bull.*, 49, 337-342.

QTL3: RZ516-RM253. Talukder et al., 2005. *New Phytol.*, 168, 455-464.

QTL4: RZ516-RG213. Talukder et al., 2005. *New Phytol.*, 168, 455-464.

QTL5: RM276-RZ667. Sallaud et al., 2003. *Theor. Appl. Genet.*, 106, 794-803.

QTL6: waxy-RZ744. Wang et al., 1994. *Genetics*, 136, 1421-1434.

Figure S18 Colocalization of *OsGELP77* loci with previously reported disease-related QTL derived using different genetic populations. Data of disease-related QTL were retrieved from PubMed, Q-TARO, and RiceQTLPro.

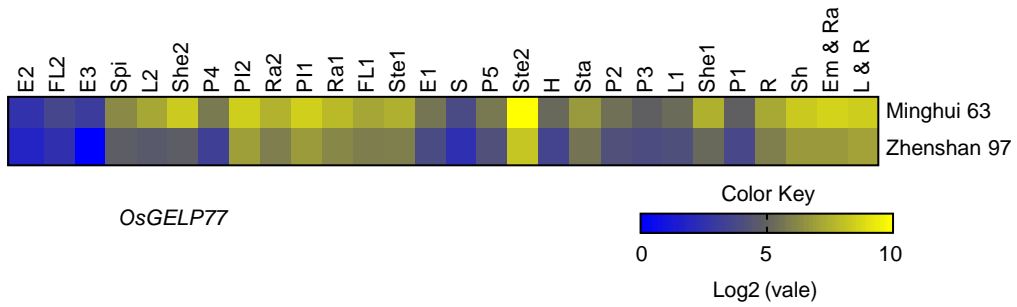


Figure S19 Expression profiles of *OsGELP77* in different tissues of rice varieties Minghui 63 and Zhenshan 97. Data were obtained from a microarray database (<http://www.ncbi.nlm.nih.gov>; accession number GSE19024; Wang et al. Plant J. 61:752-766, 2010). E2, endosperm at 14 days after pollination; FL2, flag leaf at 14 days after heading; E3, endosperm at 21 days after pollination; Spi, spikelet at 3 days after pollination; L2, leaf at 4- to 5-cm young panicle stage; She2, sheath at 4- to 5-cm young panicle stage; P4, panicle at 4- to 5-cm young panicle stage; P12, plumule at 48 h after emergence under dark; Ra2, radicle at 48 h after emergence under dark; P11, plumule at 48 h after emergence under light; Ra1, radicle at 48 h after emergence under light; FL1, flag leaf at 5 days before heading; Ste1, stem at 5 days before heading; E1, endosperm at 7 days after heading; S, germinating seed at 72 h of imbibitions; P5, panicle at heading stage; Ste2, stem at heading stage; H, hull at 1 day before flowering; Sta, stamen at 1 day before flowering; P2, panicle at pistil and stamen primordium differentiation stage; P3, panicle at pollen–mother cell formation stage; L1, leaf at secondary branch primordium stage; She1, sheath at secondary branch primordium stage; P1, panicle at secondary branch primordium stage; R, root of seedling with two tillers; Sh, shoot of seedling with two tillers; Em & Ra, embryo and radicle at 3 days after germination; L & R, leaf and root at three-leaf stage. Expression levels (log₂ transformations of average signal values) are color-coded: yellow and blue denote high and low expression, respectively.

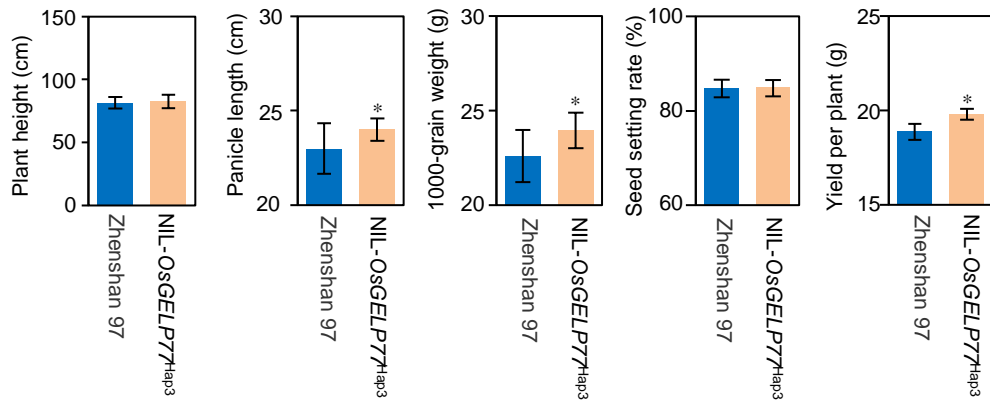


Figure S20 Agronomic traits of NIL-*OsGELP77*^{Hap3} and Zhenshan 97 grown in field. Data represents mean \pm SD ($n = 30$). Asterisks indicate significant differences determined by two-tailed Student's *t*-test at $*P < 0.05$.