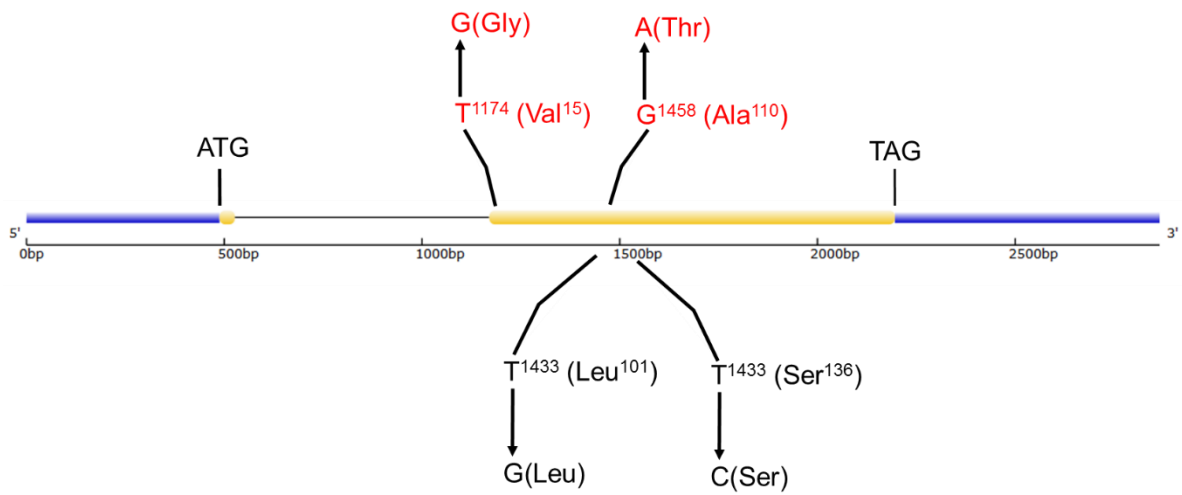


# Supplementary Materials: **Overexpression of *OsGID1* Enhances the Resistance of Rice to the Brown Planthopper *Nilaparvata lugens***

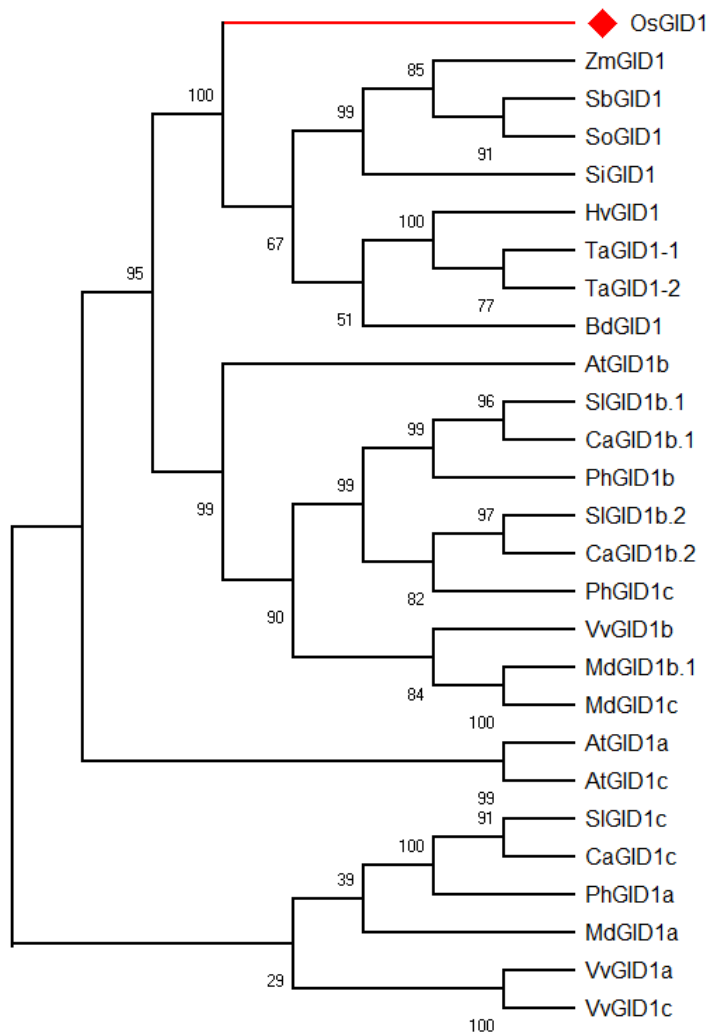
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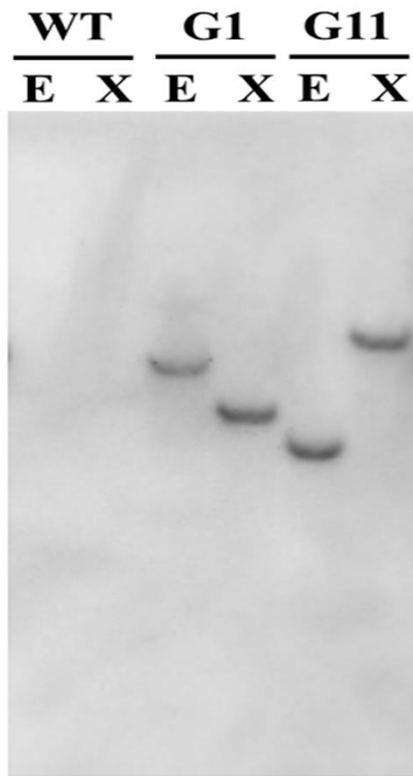
Correspondence: Prof. Yonggen LOU, [yglou@zju.edu.cn](mailto:yglou@zju.edu.cn)



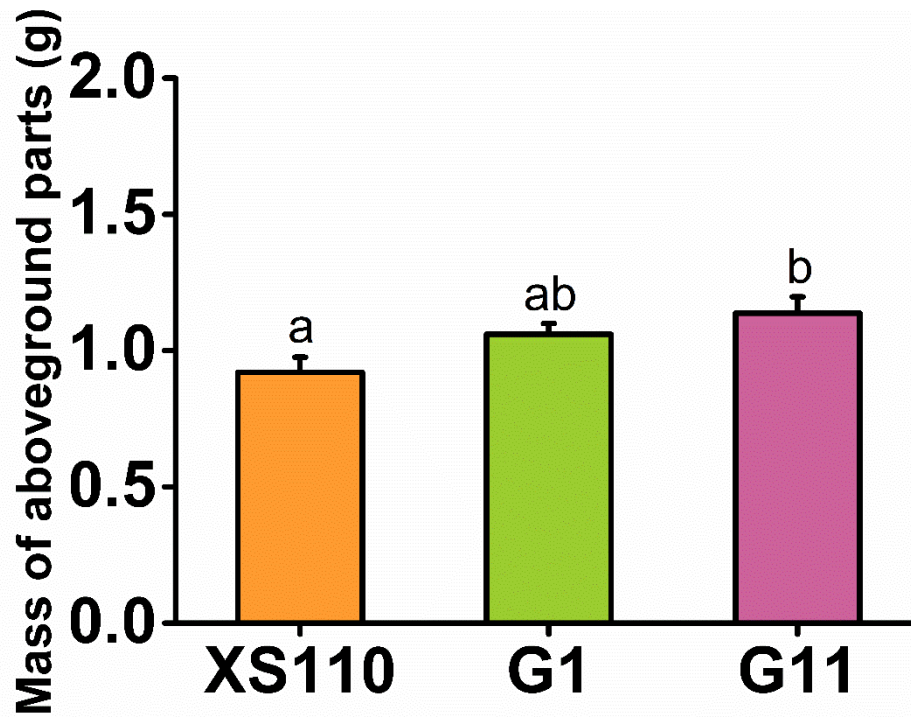
**Supplemental Figure S1.** The structure of *OsGID1* and single nucleotide polymorphisms (SNPs) in its coding sequence. The *OsGID1* consists of two exons (yellow boxes) and one intron (thin line); upstream and downstream regions, including untranslated regions, are showing in blue boxes. Missense and synonymous nucleotide substitutions of the four SNPs are indicated in red and dark.



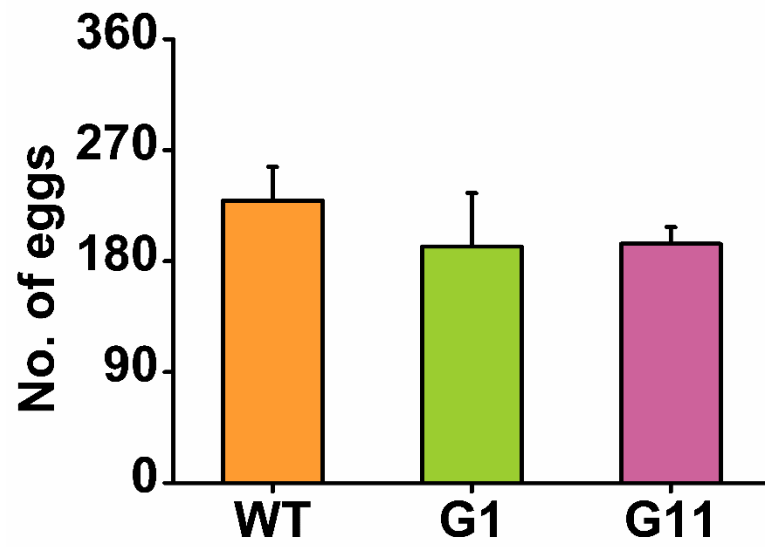
**Supplemental Figure S2.** Phylogenetic analysis of GID1 proteins from different plant species. The unrooted tree was constructed with a neighbor-joining method on the basis of the alignment of protein sequences and confirmation of the tree topology by bootstrap analysis (1,000 replicates) were performed with MEGA X software (default settings except the replicates of the bootstrap value). Species acronyms are included before the protein name: Os, *Oryza sativa*; At, *Arabidopsis thaliana*; Zm, *Zea mays*; Hv, *Hordeum vulgare*; Si, *Setaria italic*; Sb, *Sorghum bicolor*; So, *Saccharum officinarum*; Bd, *Brachypodium distachyon*; Ta, *Triticum aestivum*; Sl, *Solanum lycopersicum*; Vv, *Vitis vinifera*; Md, *Malus domestica*; Ca, *Capsicum annum*; Ph, *Petunia x hybrid*. Sequence data in the phylogenetic tree can be found in the GenBank/EMBL data libraries under accession numbers: OsGID1 (NP\_001055520.1); AtGID1a (NP\_187163.1), AtGID1b NP\_191860.1, AtGID1c (NP\_198084.1); ZmGID1 (CAP64327.1); HvGID1 (CAO98733.1); SiGID1 (XP\_004962116.1); SbGID1 (XP\_021303311.1); SoGID1 (CAP64326.1); BdGID1 (XP\_003568469.1); TaGID1-1 (CBW30246.1), TaGID1-2 (CBW30247.1); SIGID1b.1 (XP\_004240525.1), SIGID1b.2 (NP\_001234767.2), SIGID1c (XP\_004230154.1); VvGID1a (AFG17072.1), VvGID1b (XP\_002271700.1), VvGID1c (XP\_002265764.1); MdGID1a (NP\_001281280.1), MdGID1b (AFD32891.1), MdGID1c (AFD32892.1); CaGID1b.1 (ALY05368.1), CaGID1b.2 (ALY05369.1), CaGID1c (ALY05370.1); PhGID1a (AGN72648.1), PhGID1b (AGN72649.1), PhGID1c (AGN72650.1). The OsGID1s is indicated with red ♦.



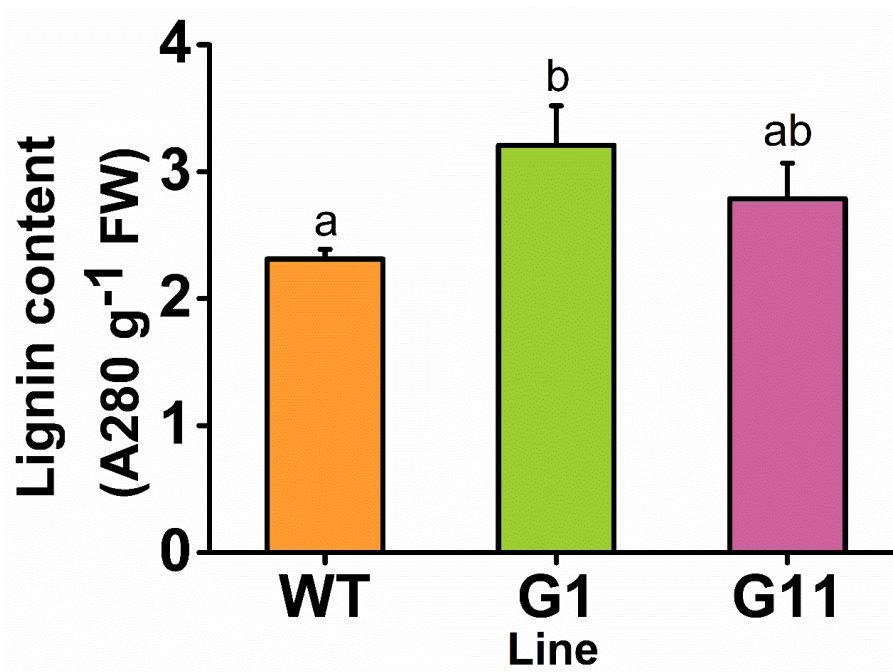
**Supplemental Figure S3.** DNA gel-blot analysis of oe-GID1 lines, G1, G11 and WT plants. Genomic DNA extracted from oe-GID1 and WT plants was digested with *EcoR* I (E) and *Xba* I (X). The blot was hybridized with a probe specific for reporter gene *GUS*. All overexpression lines have a single insertion of *OsGID1*.



**Supplemental Figure S4.** Mean mass (+ SE,  $n = 20$ ) of the above-ground part of 38-day-old plants of *oe-GID1* and WT lines. Different letters indicate significant differences among lines (Duncan's multiple range test,  $P < 0.05$ ).



**Supplemental Figure S5.** Mean number (+ SE, n = 5) of eggs laid by 15 gravid BPH females on oe-GID1 and WT plants for 12 h.



**Supplemental Figure S6.** Constitutive levels of Lignin in WT and oe-GID1 plants.

Mean constitutive levels (+SE, n = 5) of lignin in leaf sheaths of 4-week-old plants of oe-GID1 and WT lines. Different letters indicate significant differences among lines (Duncan's multiple range test,  $P < 0.05$ ).

Table S1. Primers and probes used for qRT-PCR of target genes

Gene	TIGR ID	Primer (5'-3')	Probe (5'-3')
<i>ACTIN</i>	Os03g50885	FP: TGGACAGGTTATCACCAATTGGT RP: CCGCAGCTTCCATTCTATG	CGTTCCGCTGCCCTGAGGTCC-BHQ1
<i>OsWRKY13</i>	Os01g54600	FP: GCGCAAGTACGGCCAGAA RP: CCTTGGAGCTACTGCACCTGTA	CCCATCAAGGGCTCTCCCTACCCA
<i>OsWRKY30</i>	Os08g38990	FP: AACAGTGGCCACCCAAGCT RP: GTTCAGGTCTCCGGTGAAGAAG	AGGCTCAGCCGCTGCACCACA
<i>OsWRKY33</i>	Os03g33012	FP: AGGCAAGCACAGCCATGAC RP: GAAGACGATACGTTGGCATTAGC	CCAGCAGCCAGGAACAGTAGCCATTC
<i>OsGID1</i>	Os05g33730	FP: ACCGCAACGAGTGCAAGAC RP: TTGTACGACAGCTTGAAGTTGGA	CCGCTCCACACATGGGTGCTCA
<i>OsICS1</i>	Os09g19734	FP: ACCAATTATGTTCCGATCAATCA RP: CGTCGCCTTCTTGATTTATG	ACACCTCCTACATACGCAGCCGCTGA
<i>OsC4H</i>	Os01g60450	FP: GTGTACCGCATCATGTTT RP: GAAGTCGCCGTAGTTGTA	
<i>OsACS2</i>	Os04g48850	FP: CACCCGAGGCATCCAT RP: ATTGGCGATCCTCTTGAAGT	TGCACACCGGAGGGCGTCT