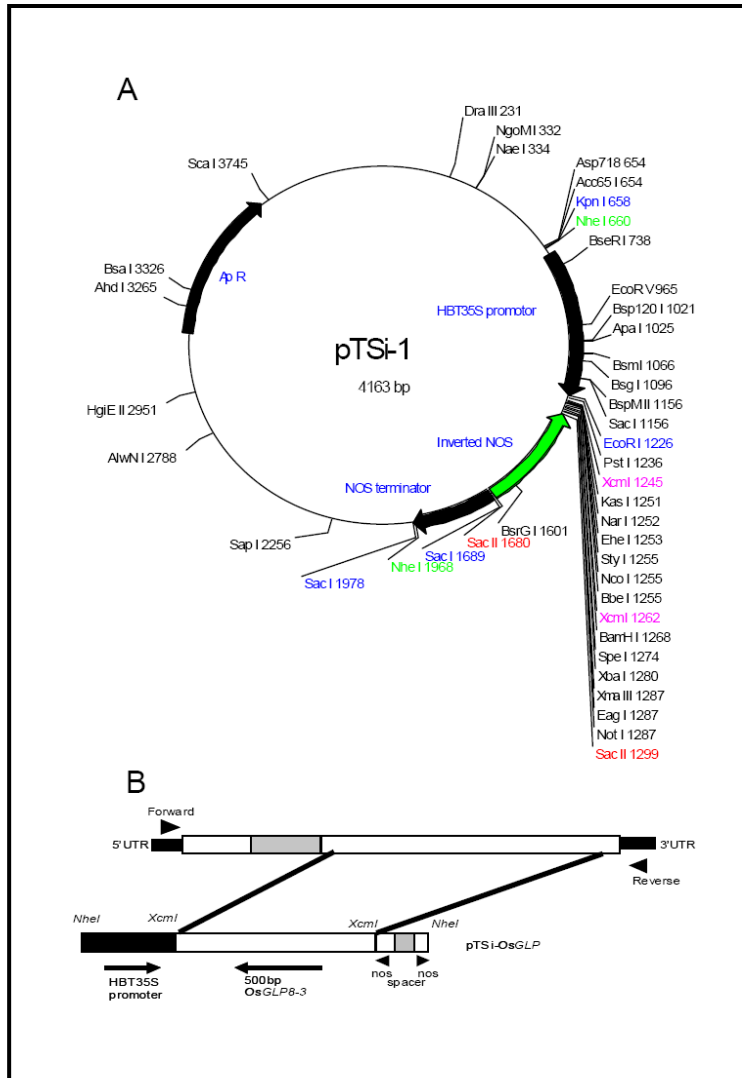


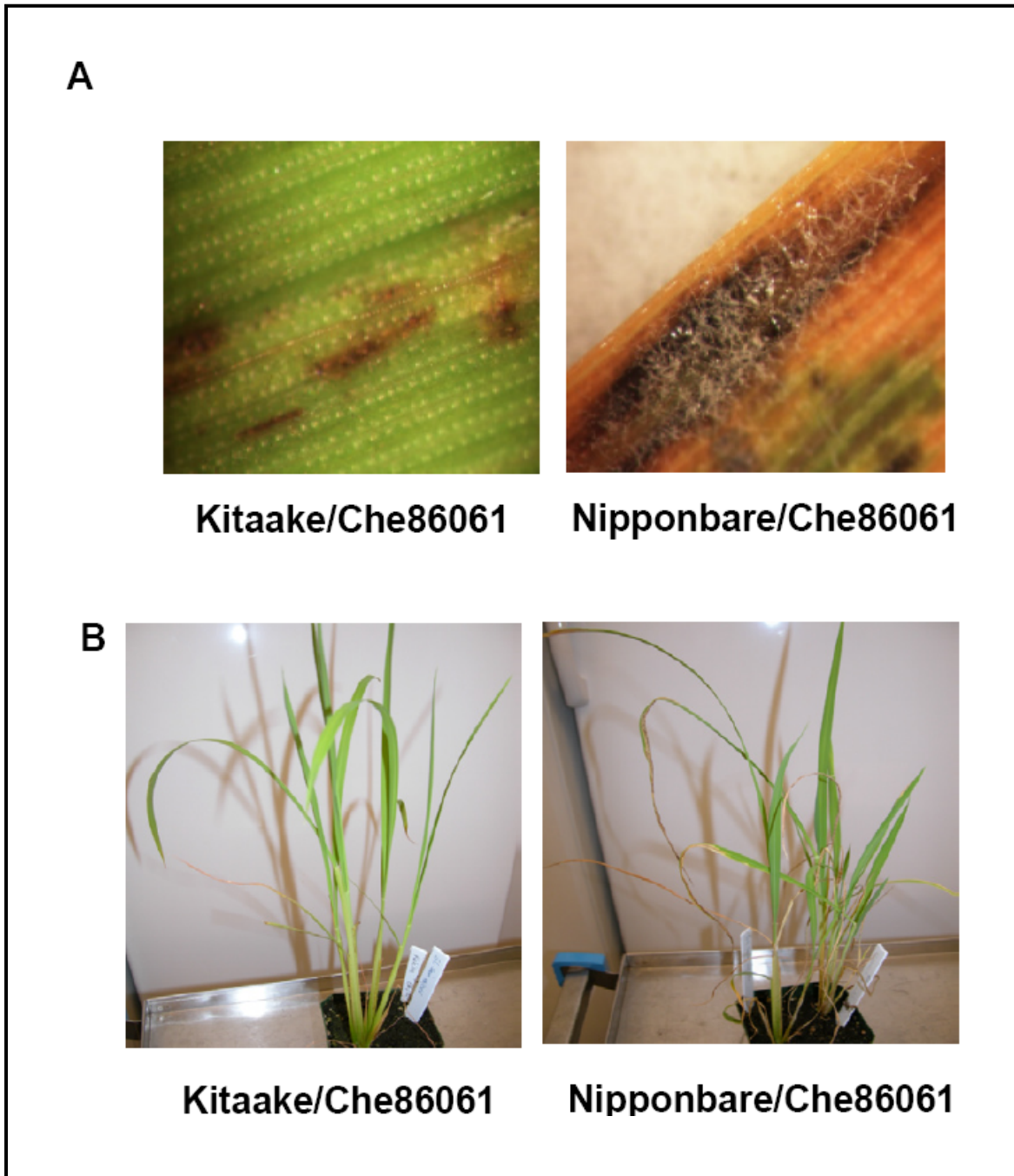


**Figure S2.** RNAi silencing vector pTSi-1 and the *OsGLP* RNAi construct. **(A)** Vector pTSi-1 contains the HBT35S promoter, which includes a minimal CaM35S enhancer plus the 5' UTR of maize *CDDPK* gene (1). The inverted *NOS* carry the antisense sequence of the *Agrobacterium NOS* terminator plus an 81 bp fragment of the 3' end of the *GFP* gene. A pair of *XcmI* sites is used to generate "T" 3' extensions for cloning PCR products. **(B)** RNAi silencing construct pTSi-*OsGLP* was constructed by inserting an antisense 500 bp PCR product of *OsGLP8-3* into the pTSi-1 RNAi vector. *NheI*-digested pTSi-*OsGLP* vector was inserted into *XbaI*-digested pCambia 1305 binary vector.

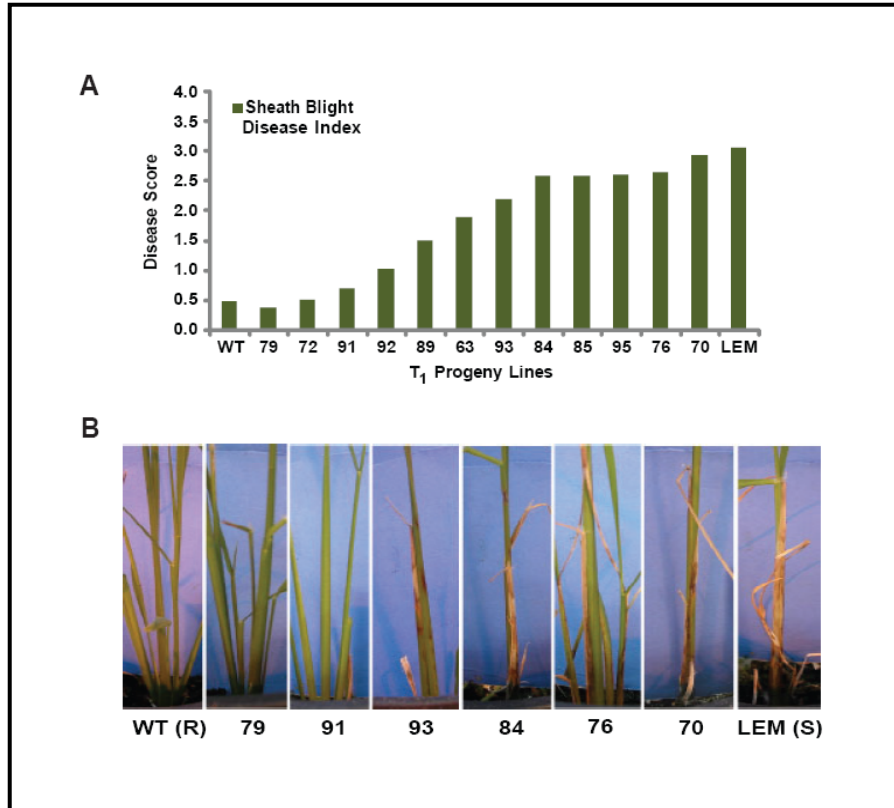




**Figure S4.** Disease phenotypes of Kitaake and Nipponbare after *Magnaporthe oryzae* (*Mo*) inoculation. **(A)** Spot inoculation of rice detached leaves of Kitaake (resistant) and Nipponbare (susceptible) with *Mo* isolate Che86061. **(B)** Spray inoculation of Kitaake and Nipponbare plants with *Mo* isolate Che86061.



**Figure S5.** *OsGLP*-silenced  $T_1$  plants show higher levels of sheath blight disease. **(A)** Sheath blight disease scores of  $T_1$  RNAi transgenic plants assessed using the sheath blight disease index (2). Kitaake (WT, resistant control) and Lemont (LEM, susceptible control). **(B)** Sheath blight disease phenotypes on  $T_1$  silenced plants with different levels of gene suppression.



**Table S1.** Disease ratings for Sanhuangzhan 2 (SHZ-2, donor resistant parent), BC116 (backcross line harboring QTL from SHZ-2) and commercial cultivar Texianzhan 13 (TXZ-13, recurrent susceptible parent) after 7 yr of field evaluation in a rice blast nursery in Yangjiang, Guangdong, China.

Year	Disease Scale <sup>a</sup>			t-value <sup>b</sup>	Significance
	SHZ-2	BC116	TXZ-13		
2001	0.87±0.35	5.40±1.35	9.00±0.00	-11.0227	0.0000
2002	0.67±0.49	4.73±1.83	8.33±0.98	-8.08845	0.0000
2003	0.67±0.49	4.87±1.77	9.00±0.00	-9.05741	0.0000
2004	1.67 ± 0.98	4.02 ± 1.01	6.07 ± 1.49	-3.5000	0.0035
2005	0.87 ± 0.74	2.87 ± 1.63	8.60 ± 0.83	-12.1276	0.0000
2006	0.87 ± 0.74	6.60 ± 0.83	8.70 ± 0.83	-5.9161	0.0000
2007	0.73 ± 0.46	2.73 ± 1.28	7.80 ± 1.01	-11.7671	0.0000

<sup>a</sup> Panicle blast symptoms were evaluated on each rice line using IRRI Standard Evaluation System for Rice (<http://www.knowledgebank.irri.org/ses/SES.htm>). Data are averages of disease for the two crops for each year (mean ± standard error).

<sup>b</sup> t-test between BC116 and TXZ-13.

**Table S2.** Gene members of the barley germin-like protein (*HvGER*) subfamilies used for the phylogenetic analysis of the *OsGER* subfamilies in rice.

Name of gene	TIGR TC number <sup>a</sup>	Predicted protein size (number of aa)
<i>HvOxOa</i>	Y142203	224
<i>HvOXOLP</i>	X93171	229
<i>HvGER1a</i>	TC140112	224
<i>HvGER1b</i>	TC148017	215
<i>HvGER1c</i>	TC141021	223
<i>HvGER1d</i>	TC148015	228
<i>HvGER2a</i>	TC146914	212
<i>HvGER2b</i>	TC147369	212
<i>HvGER3a</i>	TC131410	226
<i>HvGER3b</i>	TC131415	227
<i>HvGER3c</i>	TC131413	226
<i>HvGER4a</i>	TC139505	228
<i>HvGER4b</i>	H011H17	229
<i>HvGER4c</i>	TC139504	211
<i>HvGER4d</i>	TC147149	229
<i>HvGER4e</i>	TC139503	229
<i>HvGER5a</i>	TC147527	216
<i>HvGER5b</i>	TC147526	216
<i>HvGER6a</i>	TC141367	219

<sup>a</sup> TC = Tentative Consensus sequences created by assembling ESTs into virtual transcripts. The TC annotation numbers corresponds to the *Hordeum vulgare* gene index (HvGI):

<http://compbio.dfci.harvard.edu/tgi>

**Table S3.** Oligonucleotide primers used in the study.

Gene	TIGR Locus ID <sup>a</sup>	Primer <sup>b</sup>	Sequence 5' - 3'	T <sub>A</sub> (°C) <sup>c</sup>
8-1	LOC_Os08g08920	GLP1F	CAGGAAACACAAAGCATCTGATCAGG	57
		GLP1R	CTTTGCAACACTATGGGACAATTA	
8-2	LOC_Os08g08960	GLP2F	GAAACCATAAAACACACAGGCATCTG	59
		GLP2R	ATGTAGTATACTGTCCTTGATGGTG	
8-3	LOC_Os08g08970	GLP3F	CTCACCCAAAATAACGATAAACACAGGG	56
		GLP3R	ACGCACAAAGGAACAATCAAG	
8-4	LOC_Os08g08980	GLP4F	GGAGAAACCAACTCATAGTAGCTTAGC	52
		GLP4R	GCATCAATTGATTAGGGAGAATCAG	
8-5	LOC_Os08g08990	GLP5F	GCAGAAATTAATCCAAAGCCGAAT	56
		GLP5R	GTAACACAAAAGCTAATACATTG	
8-6	LOC_Os08g09000	GLP6F	CTTCCCATCAGAGAAAGATAGCAG	58
		GLP6R	GATTCACGGTATGCCAACAAC	
8-7	LOC_Os08g09010	GLP7F	CAAAGCCAAATGGCTTCACCATCTTC	58
		GLP7R	GCAGAATAGAAACTTATACATAGTATAA	
8-8	LOC_Os08g09020	GLP8F	CAAATGGCTTCACCATCCTTCTGCCTA	59
		GLP8R	CATAGAGTCCGTAAGCGGAC	
8-9	LOC_Os08g09040	GLP9F	CAGTAGAGAAGATAGCAGAAACCC	57
		GLP9R	GTATGCATAACAAGTACAAACTCC	
8-10	LOC_Os08g09060	GLP10F	GCCAAGTAAATGGCTTCACCATC	52
		GLP10R	GTACAAACTCCATACCACTTATTTATG	
8-11	LOC_Os08g09080	GLP11F	GCTAATTAAGAAGGGCATTAGAATGGC	59
		GLP11R	GTTATGTGCAGTTACAGAGATCCTGC	
8-12	LOC_Os08g13440	GLP12F	GCTAGCTAACTACCAGAGAGAGATAC	59
		GLP12R	CCTCCCATACACAAAAGCAC	
12-1	LOC_Os12g05840	GLP14F	ATCAACTATAGCTATACAAGAAT	53
		GLP14R	GTAGTGTTATACATTATTGATGCGT	
12-2	LOC_Os12g05860	GLP15F	TAGACTACAGCTATACAAGAAGCAT	53
		GLP15R	CTCTTTTACTACCAATCACTAGTTTTG	
12-3	LOC_Os12g05870	GLP16F	CAAGCTAGCATCGAGTAATACTTC	53
		GLP16R	GATAACTAATTTTCAACAGATAAGCATC	
12-4	LOC_Os12g0580	GLP17F	GACTACTTCTACAGGATCTGTAG	53
		GLP17R	CCTTTTATACCAATCACTAATTCTGA	
<i>EF1α</i>	D63582	EF1α1F	AGCCTCGTTCAAATGGTGGT	57
		EF1α1R	TAGTGCACATTGCGAGCAGA	
<i>Hygromycin</i>	AF354046	HygroF1	GAGCCTGACCTATTGCATCTCC	54.5
		HygroR1	GGCCTCCAGAAGAAGATGTTGG	
<i>CaMV35S</i>	AY234331	CaMVR1	CGTGCTCCACCATGTTGGCAAGC	

<sup>a</sup> TIGR Rice Genome Annotation: <http://www.tigr.org/tdb/e2k1/osa1/>

<sup>b</sup>F = forward primer, R = reverse primer

<sup>c</sup>T<sub>A</sub> = annealing temperature

### References:

1. Zhao B (2004) Isolation and characterization of the maize nonhost resistance gene *Rxo1* and the corresponding bacterial effector gene *avrRxo1* from *Xanthomonas oryzae* pv. *oryzicola*. *Doctorate thesis*.
2. Jia Y, et al. (2007) Rapid determination of rice cultivar responses to the sheath blight pathogen *Rhizoctonia solani* using a micro-chamber screening method. *Plant Dis* 91:485-489.