

Supplementary file S1

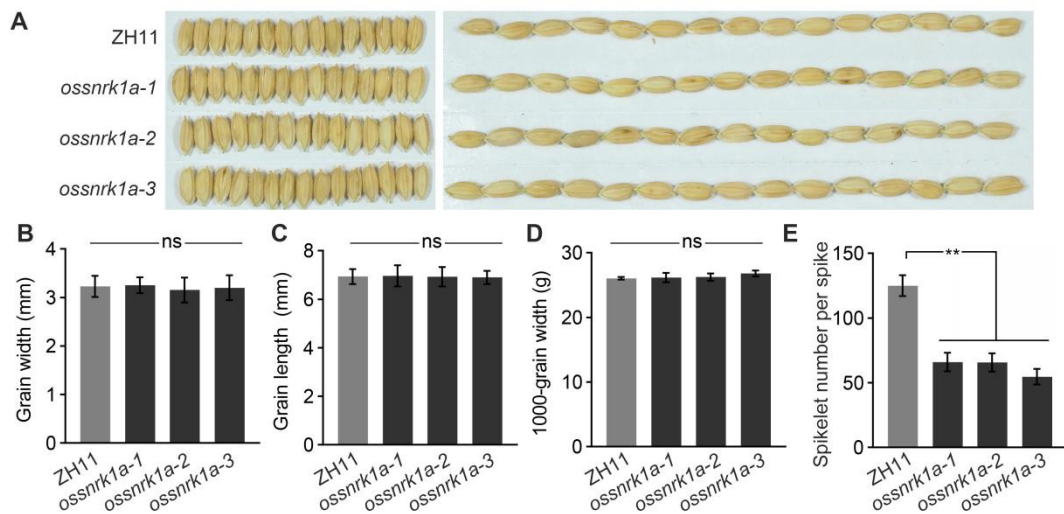


Figure S1. The *ossnrk1a* mutants displayed no obvious defects in grain size and weight, compared with the wild type. **(A)** Morphology of mature grains from ZH11 and the *ossnrk1a* mutants. **(B)** and **(C)** Measurement of grain width, and grain length of ZH11 and *ossnrk1a* mutant seeds, respectively. with bars representing mean values \pm SD ($n = 15$). **(D)** 1000-grain weight of ZH11 and *ossnrk1a* mutants with bars representing means \pm SD ($n = 3$). **(E)** The spikelet number per spike of ZH11 and *ossnrk1a* mutants with bars representing means \pm SD. “ns” means no significance by Student’s *t*-test.

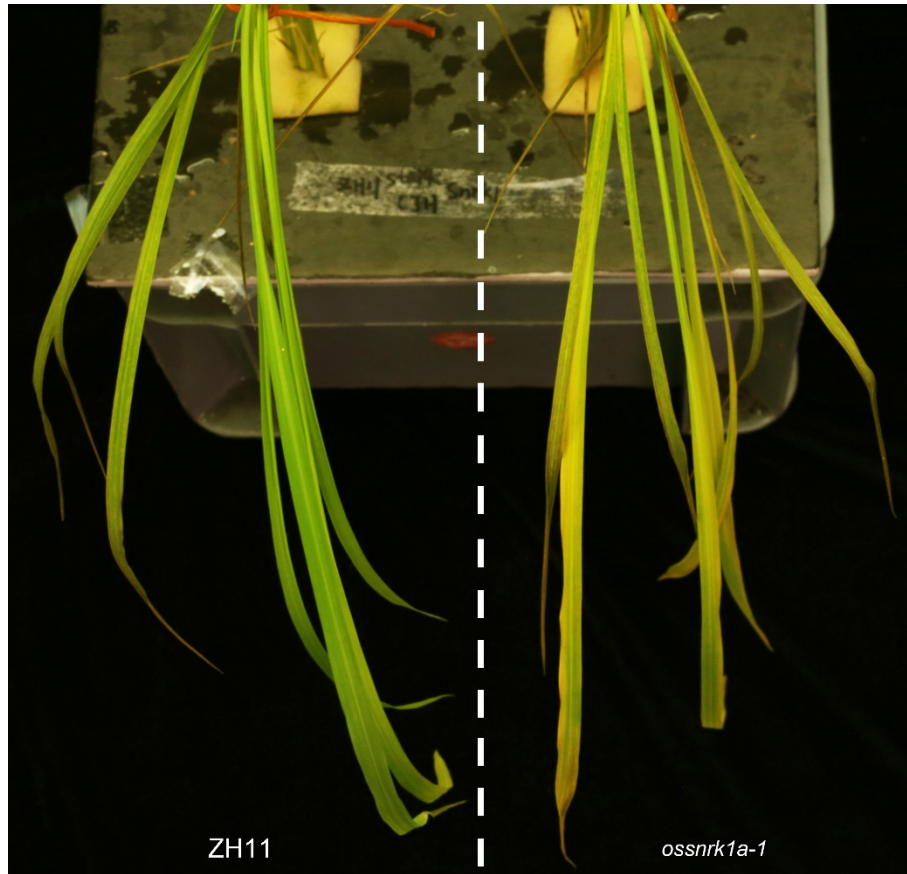


Figure S2. Phenotypes of ZH11 and *ossnrk1a-1* under starvation/continuously dark stresses. After 4-day continuously dark treatment, the water-culturing ZH11 (left) and *ossnrka-1* (right) plants were imaged.

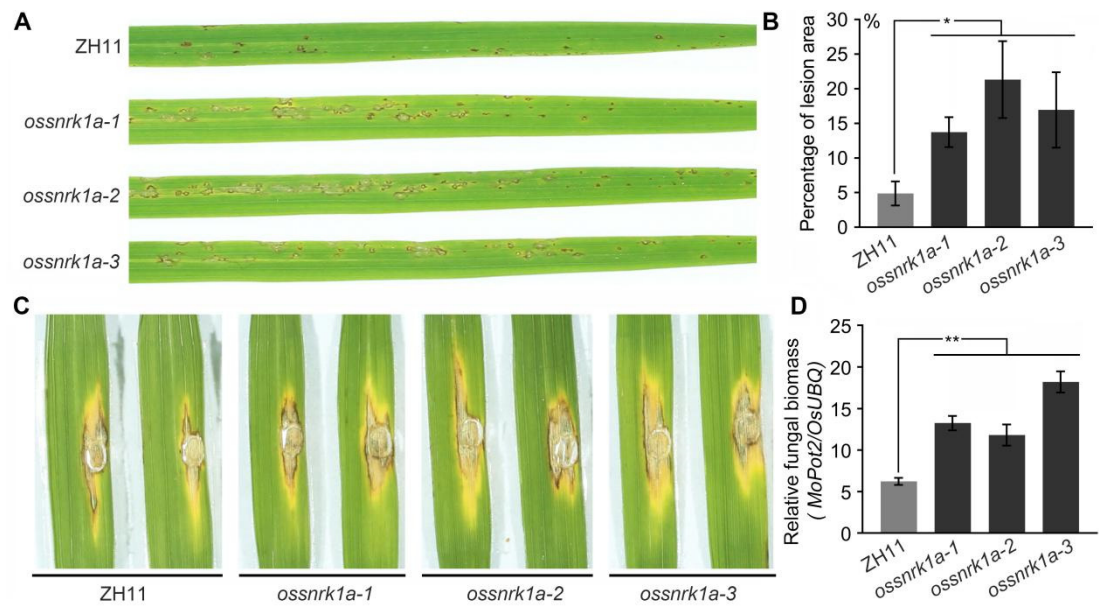


Figure S3. The *ossnrk1a* mutants showed more susceptibility to *M. oryzae* infection. **(A)** and **(B)** Spraying inoculation on 3-week-old ZH11 and *ossnrk1a* mutants seedlings with Guy11 conidia. The leaves of *ossnrk1a* mutants at 5 dpi displayed larger diseased lesion area, compared to those of ZH11. **(C)** Five-week-old plants of ZH11 and *ossnrk1a* mutants were subjected to punch inoculation with Guy11 conidia. The diseased leaves were photographed at 9 dpi. **(D)** Fungal biomass of the punch-inoculation leaves was measured by qPCR analysis (*MoPot2/OsUBQ*) with extracted genomic DNA as templates. Bars in **(B)** and **(D)** are means \pm SD from three biological replicates. Significant differences were determined by Student's *t*-test (*, $p < 0.05$ and **, $p < 0.01$).

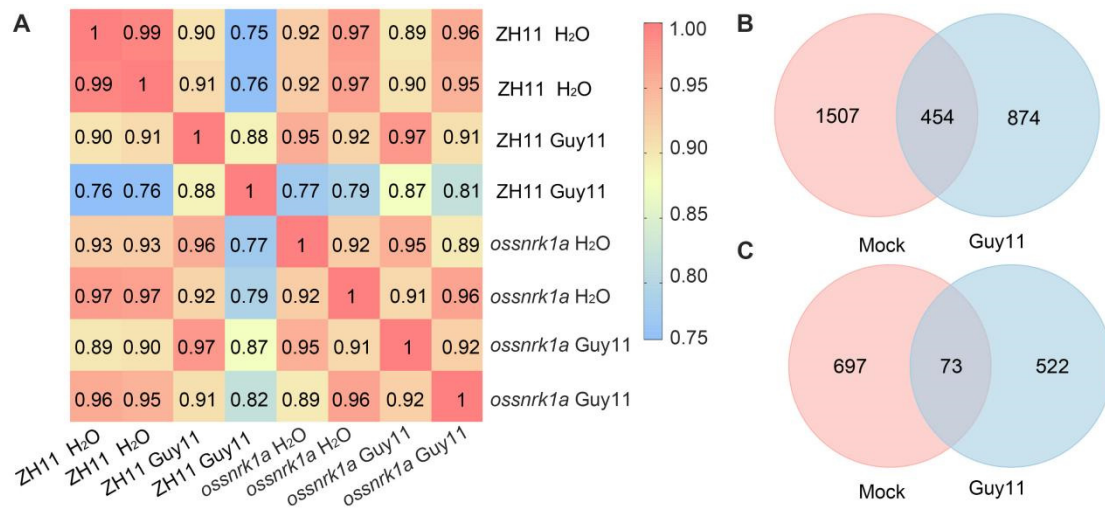


Figure S4. Correlation analysis of the transcriptome replicates and venn plots of the DEGs in *ossnrk1a-1* and ZH11. **(A)** Correlation analysis using Pearson correlation coefficient indicating high correlation coefficients of the biological replicates for each sample in RNA-seq. **(B)** and **(C)** are the venn diagrams indicating the upregulated (B) and downregulated (C) DEGs numbers from *ossnrk1a-1* vs. ZH11 with non-pathogen (pink pie) and Guy11 infection treatments (blue pie), respectively.

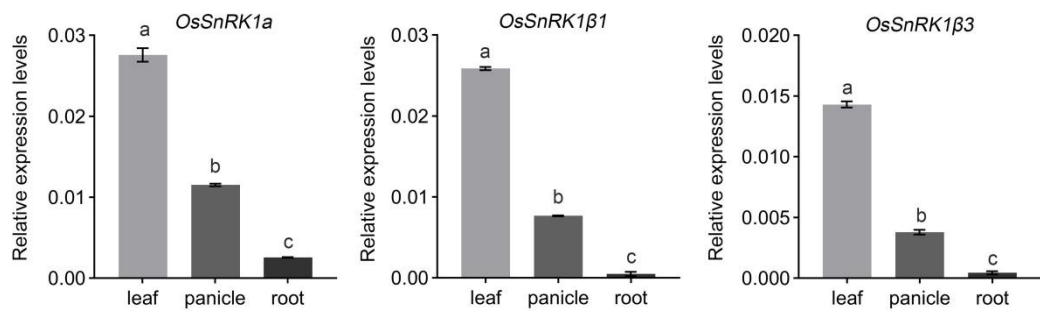


Figure S5. Transcript levels of *OsSnRK1a*, *OsSnRK1β1* and *OsSnRK1β3* in leaf, young panicle and root tissues of ZH11 at heading stage. Data are means \pm SD ($n = 3$). Statistically significant differences were indicated by Mann-Whitney test (Different letters mean significant difference among treatments ($p < 0.05$)).

Table S1. List of primer pairs used in this study.

Plasmid construction		
Gene	Forward Sequence (5'-3')	Reverse sequence (5'-3')
OsSnRK1a-GFP	ACTGGGATCCATGGAGGGAGCT GGCAGAGA	ACTGGAATTCAAGGACTCTC AGCTGAGTTA
OsSnRK1 β 1-GFP	CGCTCTAGAACTAGTGGATCCAT GGGGAACGCGAGCGGGC	GATAAGCTTGATATCGAATTC TCGTTCAATGGGCTTATACAG
OsSnRK1 β 3-GFP	ACTGGGATCCATGGGGAACGCG AGCGGCAA	ACTGGTCGACACCACCATTCT TTGTTGCTTC
OsSnRK1a-HA	ACTGGGATCCATGGAGGGAGCT GGCAGAGA	ACTGGAATTCAAGGACTCTC AGCTGAGTTA
OsSnRK1a-nLUC	GGGGACAAGTTTGTACAAAAA GCAGGCTTCATGGAGGGAGCTG GCAGAGA	GGGGACCACTTTGTACAAGA AAGCTGGGTCAAGGACTCTC AGCTGAGTTA
OsSnRK1 β 1-cLUC	GGCGGTACCCGGGATCCAATGG GGAACGCGAGCGGGC	GAAAGCTCTGCAGGTCGACC TAtCGTTCAATGGGCTTATACA G
OsSnRK1 β 3-cLUC	GGGGACAAGTTTGTACAAAAA GCAGGCTTCATGGGGAACGCGA GCGGCAA	GGGGACCACTTTGTACAAGA AAGCTGGGTCAACCACCATTCT TTGTTGCTTC
pGADT7-OsSnRK1 β 1	GTACCAGATTACGCTCATATGAT GGGGAACGCGAGCGGGC	ATGCCCACCCGGGTGGAATTC CTACTATCGTTCAATGGGCTT

		ATACAG
pGADT7- OsSnRK1 β 3	ACTGCATATGATGGGGAACGCG AGCGGCAA	ACTGGGATCCTTAACCACCAT TCTTTGTTC
qRT-PCR		
Gene	Forward Sequence (5'-3')	Reverse sequence (5'-3')
OsAOS2	CGTCCAAAGTTTCGGGAGTT	CTCCATGGCGCCTAGCTAA
OsJAMyb	GAGGACCAGAGTGCAAAAGC	CATGGCATCCTTGAACCTCT
osWRKY45	GGACGCAGCAATCGTCCGGG	CGGAAGTAGGCCTTTGGGT
OsNADHG OGAT2	CCTGTCTGAAGGATGATGAAGGT GAAACC	TGCATGGCCCTACTATCTTCG CATCA
OsPR1b	ACGGGCGTACGTACTGGCTA	CTCGGTATGGACCGTGAAG
OsSnRK1 β 1	TGTGGACGCTTGGAGGAAA	CCGATGGAAGTATCAACAGG AG
OsSnRK1 β 3	GGACATCAAGGAGGGTGTTAGA	CATCAGCCACATGAGGTAGTT C
OsSnRK1a	CGAATCACTTCACAAGAGACTG	CTGGAGTTACTTGAGCGAGA G
OsUBQ	TTCTGGTCCTTCCACTTTCAG	ACGATTGATTTAACCAGTCCA TGA
MoPot2	ACGACCCGTCTTTACTTATTTGG	AAGTAGCGTTGGTTTTGTTGG AT

Table S2. Gene ID, FPKM, and functions of DEGs in Fig 3 and Fig 4.

GO name	Gene ID	FPKM								Functions
		ZH11_H ₂ O (Mock)		ZH11_Guy1 1 (48 hpi)		ossnrk1a- 1_H ₂ O (Mock)		ossnrk1a- 1_Guy11 (48 hpi)		
response to biotic stimulus	LOC_Os06g34400	7.97	7.38	23.86	14.45	8.59	5.75	6.57	6.95	zinc finger, C3HC4 type domain containing protein
	LOC_Os07g08300	16.81	13.14	29.94	15.46	14.25	9.91	15.58	12.47	major facilitator superfamily antiporter, putative, expressed
	LOC_Os01g41750	0.88	0.79	2.50	2.84	1.31	0.94	1.42	0.97	expressed protein
	LOC_Os05g29710	0.66	1.11	11.15	1.87	0.66	0.62	0.97	0.77	RING-H2 finger protein, putative, expressed
	LOC_Os03g03700	0.56	0.21	4.12	0.14	0.55	2.82	2.15	1.61	MLO domain containing protein, putative, expressed
	LOC_Os05g28770	0.49	0.57	2.28	1.64	0.60	0.36	0.57	0.64	GCRP9 - Glycine and cysteine rich family protein precursor, expressed
	LOC_Os01g713	2.64	7.92	39.98	27.70	25.39	5.29	20.13	13.54	glycosyl hydrolases family 17, putative,

	50									expressed
	LOC_Os10g39700	0.65	1.39	1.72	3.28	2.57	0.91	1.26	0.84	CHIT15 - Chitinase family protein precursor, putative, expressed
	LOC_Os05g51610	3.49	3.68	24.34	8.59	3.16	2.10	5.56	5.64	sodium/calcium exchanger protein, putative, expressed
	LOC_Os10g13700	1.53	1.13	3.84	2.45	1.09	1.04	1.50	1.08	phosphoenolpyruvate carboxykinase, putative, expressed
	LOC_Os03g55670	53.14	81.03	358.81	112.07	70.03	67.68	96.48	60.93	expressed protein
	LOC_Os07g13100	1.41	2.73	9.18	2.37	1.72	1.47	1.19	1.48	DNA binding protein, putative, expressed
	LOC_Os12g44070	0.04	0.00	2.35	1.15	0.38	0.32	0.43	0.19	nodulin, putative, expressed
	LOC_Os05g45980	0.83	0.67	2.07	1.08	0.56	0.37	0.64	0.61	expressed protein
	LOC_Os02g10120	7.09	7.68	4.98	5.20	3.69	5.64	1.19	0.96	lipoxygenase gene
	LOC_Os03g23050	0.17	0.00	0.29	0.20	0.05	0.07	0.16	0.04	expressed protein
	LOC_Os01g713	4.27	20.65	96.84	161.8	50.50	22.74	56.68	22.38	glycosyl hydrolases family 17, putative,

	40				9					expressed
	LOC_Os01g28450	0.11	0.43	2.25	2.01	0.92	0.00	1.10	1.01	pathogenesis-related protein 1b, OsPR1b
Energy metabolism	LOC_Os10g21212	0.88	1.03	1.09	0.68	0.81	0.36	0.93	0.79	photosystem II 44 kDa reaction center protein, putative, expressed
	LOC_Os10g21310	2.65	1.53	2.44	2.29	2.31	1.06	1.14	1.78	photosystem II P680 chlorophyll A apoprotein, putative, expressed
	LOC_Os04g16770	16.13	11.80	17.93	10.96	12.90	4.17	8.10	10.86	photosynthetic reaction center protein, putative, expressed
	LOC_Os01g64120	49.73	35.61	354.79	124.09	29.86	10.69	30.21	38.88	Ferredoxin, OsFd5
	LOC_Os08g15322	0.72	0.38	0.73	0.64	0.79	0.32	0.15	0.34	cytochrome b559 subunit alpha, putative, expressed
	LOC_Os10g13700	1.53	1.13	3.84	2.45	1.09	1.04	1.50	1.08	phosphoenolpyruvate carboxykinase, putative, expressed
	LOC_Os08g10020	67.21	25.69	46.05	84.54	61.70	95.72	67.62	27.98	photosystem II 10 kDa polypeptide, chloroplast precursor,
	LOC_Os05g48200	31.19	37.52	103.53	42.72	16.17	7.87	21.02	13.19	NADH-glutamate synthase 2 gene, OsNADH-GOGAT2
	LOC_Os01g580	13.55	24.04	25.47	8.76	8.06	4.50	22.04	9.12	NADPH-dependent oxidoreductase, putative,

Energy metabolism	22									expressed
	LOC_Os10g21324	2.06	1.47	2.35	1.63	0.70	1.26	1.61	0.91	cytochrome b6, putative, expressed
	LOC_Os05g48200	31.19	37.52	103.53	42.72	16.17	7.87	21.02	13.19	NADH-glutamate synthase 2 gene, <i>OsNADH-GOGAT2</i>
	LOC_Os02g53130	23.05	2.88	6.07	9.26	2.08	1.52	2.35	4.44	nitrate reductase gene
	LOC_Os08g14860	6.32	7.19	22.08	8.03	5.39	7.55	13.59	4.611	Hydroxyacid oxidase 1
	LOC_Os11g13890	513.37	318.09	49.27	387.65	306.84	330.30	215.02	155.31	light-harvesting complex II protein
	LOC_Os10g38276	2.50	2.19	0.97	0.42	1.09	0.47	1.10	0.60	chloroplast ATP synthase a chain precursor, putative, expressed
	LOC_Os01g57945	8.00	5.35	6.70	4.14	2.40	2.41	4.57	2.93	cytochrome b6-f complex subunit 4, putative, expressed
	LOC_Os01g59920	15.49	10.64	4.17	8.25	6.18	2.91	2.06	3.85	cysteine synthase, chloroplast precursor, putative, expressed
	LOC_Os01g11054	12.20	7.67	13.90	12.02	8.98	4.31	11.10	11.15	phosphoenolpyruvate carboxylase
	LOC_Os10g212	2.97	1.52	1.55	1.61	1.13	0.44	1.17	1.57	ATP synthase subunit beta, putative, expressed

	66									
	LOC_Os04g16848	4.53	3.71	4.16	3.48	3.80	1.70	2.26	3.12	photosystem II reaction center protein H, putative
	LOC_Os08g36480	215.28	122.94	212.15	134.45	75.89	75.76	94.87	83.29	nitrate reductase
	LOC_Os12g44150	64.37	53.00	28.16	37.89	28.16	37.89	36.22	31.68	plasma membrane H ⁺ -ATPase, <i>OsA3</i>
	LOC_Os01g25484	6.45	4.09	13.55	6.03	4.50	0.66	1.72	2.31	leaf ferredoxin-nitrite reductase; promoter of shoot regeneration 1, <i>OsNiR1</i>