

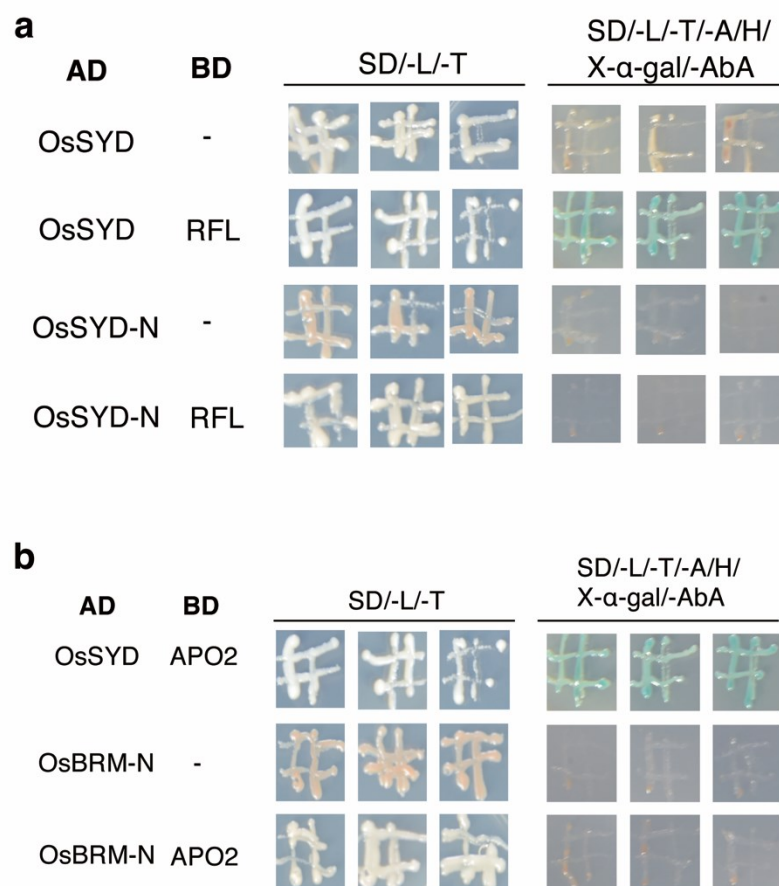


Figure S1. Yeast-two-hybrid test for the interaction between RFL and truncated OsSYD or OsBRM. The yeast two-hybrid experiment was performed thrice for every combination. OsSYD (amino acids 260–846); OsSYD-N (amino acids 487–846) (**a**) and OsBRM-N (amino acids 476–900) (**b**), both truncated with deleted QLQ domain at the N-terminus. AD, pGADT7; BD, pGBKT7; AbA, aureobasidin A.

Table S1. Segregation analysis in germinated seeds of *syd-20/+* mutant lines. The seeds were sown in the soil, and the genotypes were determined using leaf samples after growing for 3 weeks. The theoretical values (E) were calculated according to Mendel's genetic law of segregation. χ^2 tests were performed to evaluate the relationship between the actual data and the predicted ratio of 2:1.

	WT	Heterozygote
Actual Value (O)	38	80
Theoretical Value (E)	39.33	78.67
O-E	-1.33	1.33
χ^2	0.06746091	
<i>P</i>	0.9	

Table S2. Segregation ratio of the source of the mutant allele via DNA sequencing in the endosperm of *syd-20/+* mutant lines. The theoretical values (E) were calculated according to Mendel's genetic law of segregation. χ^2 tests were performed to evaluate the relationship between the actual data and the predicted ratio of 1:1.

Source of mutation allele (n=1)	Male Parent	Female Parent
Actual Value (O)	29	35
Theoretical Value (E)	32	32
χ^2		0.56
<i>P</i>		0.5

Table S3. Sequence information of the primers used in this study.

Primer Name	Sequence (5' to 3')	Experiment
QPCR-OsSYD-F	CCCGCCGATACTGCTATTCA	qPCR
QPCR-OsSYD-R	AGCATCAGCGCTGCTATCAAT	qPCR
QPCR-OSH1-F	AGCTCAACACGCTCTCCATC	qPCR
QPCR-OSH1-R	AGCTGTTGACGAGCATCCTT	qPCR
QPCR-OSH6-F	CGAAGACCAGTGCTCGGGGG	qPCR
QPCR-OSH6-R	AACCAATTGTTGATCTGCTT	qPCR
QPCR-OSH15-F	GTTCTTCTGAGGATGACATG	qPCR
QPCR-OSH15-R	AACCAGTTGTTGATCTGCTT	qPCR
QPCR-OSH71-F	CGCGATCGGCATTATGGAC	qPCR
QPCR-OSH71-R	AACCAGTTGTTGATCTGCTT	qPCR
QPCR-Roc1-F	ACAGCAACCCCTCAGTAGTAG	qPCR
QPCR-Roc1-R	GTTTGAGGTGCGTTCTTGAC	qPCR
QPCR-OsSCR-F	CGATGGATACACGCTTATTGAG	qPCR
QPCR-OsSCR-R	GATCAAGTGATACTTCAGCTC	qPCR
QPCR-OsPNH1-F	AAGACAGAAGTAGCACGGAC	qPCR
QPCR-OsPNH1-R	TCTTCACCTTCTCCTTCACC	qPCR
QPCR-RAmy1A-F	CAAAGATTGGACCAAGATACG	qPCR
QPCR-RAmy1A-R	GAAGTACTTCGTGGACAATTG	qPCR
OsSYDN-Y2H-F	GAATTC CGGAAGGTACATCTTGAAATTGC	Y2H
OsSYDN-Y2H-R	GGATCC TTATTTCTGTTCAATTTTTTCAAG	Y2H
OsBRMN-Y2H-F	CATATG TCTGGACCACCACCTGATTAC	Y2H
OsBRMN-Y2H-R	GAGCTC ACTGTGCTCGGGCAGCAGCAGC	Y2H
RFL-Y2H-F	CATATG GATCCCAACGATGCCT	Y2H
RFL-Y2H-R	GAATTC TTAGAACAAGGGCGGC	Y2H
RFLN-Y2H-F	CATATG GATCCCAACGATGCCT	Y2H
RFLN-Y2H-R	GAATTC TTAATGGTGGCGGCCG	Y2H
OsSYD-20F	GGACCAAATAGGAGCGATGT	Detect of mutant
OsSYD-20R	AGGAGGAACTGTGGGGTAAT	Detect of mutant
OsBRM-F	TTCGCAAATGGTTTGGCTCG	Detect of mutant
OsBRM-R	TCAGCATTGGAATGACCCCC	Detect of mutant
RFL-F	AAGGCGAGGAGGAAGAAGAAGGT	Detect of mutant
RFL-R	CGAGCATAGTAGGGTAGGAG	Detect of mutant