



```

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      |||
      Tyr
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661 TTCTTCGCGGACAGCAGCTCAATCATGCGGTGCAACTACTACCCGCCATGCCCGGAGCCG

721 GAGCGGACGCTCGGCACGGGCCCCGCACTGCGACCCACCGCCCTCACCATCCTCCTCCAG
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721 GAGCGGACGCTCGGCACGGGCCCCGCACTGCGACCCACCGCCCTCACCATCCTCCTCCAG

781 GACGACGTCGGCGGCCTCGAGGTCCTCGTCGACGGCGAATGGCGCCCCGTGAGCCCCGTC
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781 GACGACGTCGGCGGCCTCGAGGTCCTCGTCGACGGCGAATGGCGCCCCGTGAGCCCCGTC

841 CCCGGCGCCATGGTCATCAACATCGGCGACACCTTCATGGCGCTGTGAAACGGGAGGTAT
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901 AAGAGCTGCCTGCACAGGGCGGTGGTGAACCAGCGGCGGGAGCGGCGGTGCTGGCGTTC
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901 AAGAGCTGCCTGCACAGGGCGGTGGTGAACCAGCGGCGGGAGCGGCGGTGCTGGCGTTC

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961 TTCCTGTGCCCGCGGGAGGACAGGGTGGTGCGGCCGCCCGGAGCGCCGCCACGCCGAG
      Gln
      Arg
1021 CACTACCCGGACTTCACCTGGGCCGACCTCATGCGCTTCACGCAGCGCCACTACCGCGCC
      |||
1021 CACTAGCCGGACTTCACCTGGGCCGACCTCATGCGCTTCACGCAGCGCCACTACCGCGCC
      Stop codon
1081 GACACCCGCACGCTCGACGCCTTCACGCGCTGGCTCGCGCCGCCGGCCGCCGACGCCGCC
      |||
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      |||
5 1141 GCGACGGCGCAGGTCGAGGCGGCCAGCTGA

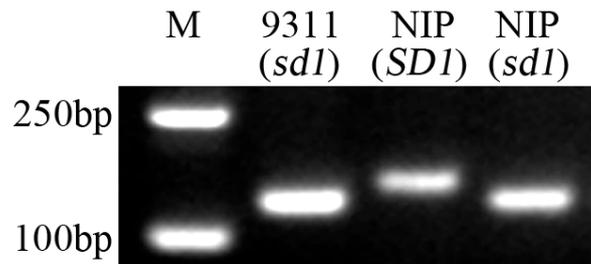
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5  
6 Figure S1. Alignment of *SD1/OsGA20ox2* CDS from Nipponbare (Nip; top) and 9311  
7 (bottom). Four SNPs were detected (shown in red). The genetic codon associated with  
8 each SNP is labelled by a coloured box as follows: grey = no change in the encoded

9 amino acid (aa); light blue = a change in aa; yellow = a change from an aa to a stop  
10 codon.

11

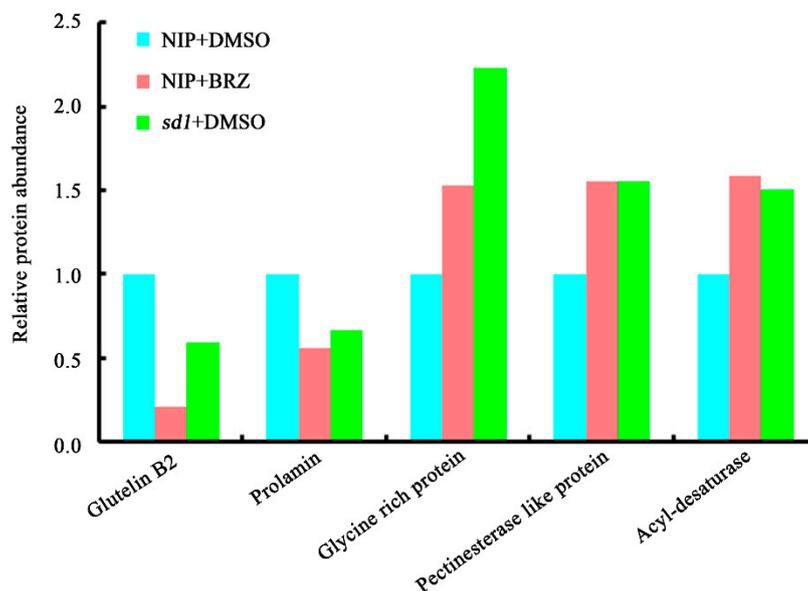
12



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14 Figure S2. Genotyping the *sd1* mutant. A pair of primers (SD1-F and SD1-R) were used  
15 to differentiate Nip-type *SD1* and the 9311-type mutated *sd1* allele.

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18 Figure S3. Five selected target proteins displaying consistent prominent changes in  
19 protein abundance (fold change ratios  $\geq 1.5$  or  $\leq 0.67$ ) in response to both BR and GA

20 deficiency.

21 **Table S1.** Primers and SG sequence used in this study

Primer Names	Sequence ( 5' → 3' )	Usage
Os02g0587000-SG-seq	GAACGCGATGAGAGCCTGCC	SG sequence
Os02g0587000seq-F	GGACTATGAGCAAGCGTCGT,	Primers for sequencing
Os02g0587000seq-R	CACCTTGGTGTCTCCTTCT	
Os02g0587000qRT-F	GCGGCGCGTATGATCTCTAT	Primers used for qRT-PCR analysis
Os02g0587000qRT-R	ACATCGGTCACACACACAGT	
Os03g0774200qRT-F	CCTACATGGGCGCAGGGAA	
Os03g0774200qRT-R	TTGAGTGTCAGCATCAAACCG	
Os03g0799000qRT-F	CGAGCGAGCAATCTAGGGC	
Os03g0799000qRT-R	CCCCTCCTCGCAACTAACAA	
Os07g0119400qRT-F	AGCGAGGCATACAGTTCAGG	
Os07g0119400qRT-R	TACCGCAGAGTATGGCGTTG	
Os02g0249000qRT-F	CAAAGACAGAGCGACCAAGC	
Os02g0249000qRT-R	TTGCCCTCTCTGGTTGTTACC	
Os03g0240700qRT-F	GGAAGAACGAGCACAGGTTG	
Os03g0240700qRT-R	GAGGCGTTTCTCAGTCTCCT	
Os03g0812000qRT-F	CCTGAATGCACAAGAGCTGC	
Os03g0812000qRT-R	TCATCATCCCCACAACGACG	
Os01g0880800qRT-F	AGACCGTCCAGTACCTCATCG	
Os01g0880800qRT-R	GGCATGGTGATCCGCTTGTG	
Os02g0209300qRT-F	GATCAATCGGCTCAGGGAGG	
Os02g0209300qRT-R	GAAGTGCAGGTTGGTAGGGG	
Os04g0390800qRT-F	TCCCTCACCTGAAGAAGACGC	
Os04g0390800qRT-R	GGTGATCTCCGACTCGACCA	
Os06g0675700qRT-F	CAGGTACACCGCTCACTGG	
Os06g0675700qRT-R	GAGTGATCCCTCGAGAACGG	
Os011g0582400qRT-F	GAGAGAGAGCAAACTGCCG	
Os011g0582400qRT-R	TTACTACTGCCTGGAGGATGG	
Os01g0233000qRT-F	GACCAAGGTTTCTCACTGGAC	
Os01g0233000qRT-R	CGGGGAAATCAATCTTAGCCA	
Os03g0379100qRT-F	CGCCTGATTTCTCCTCCCCG	
Os03g0379100qRT-R	GCTATGCTGTCTCCTCTTCCG	
Os03g0700400qRT-F	CTGTGCTGGTGGAGCAGAT	
Os03g0700400qRT-R	CGCCTTGATCGAGTAGCCCA	
OsUBCqRT-F	CCGTTTGTAGAGCCATAATTGCA	
OsUBCqRT-R	AGGTTGCCTGAGTCACAGTTAAGTG	