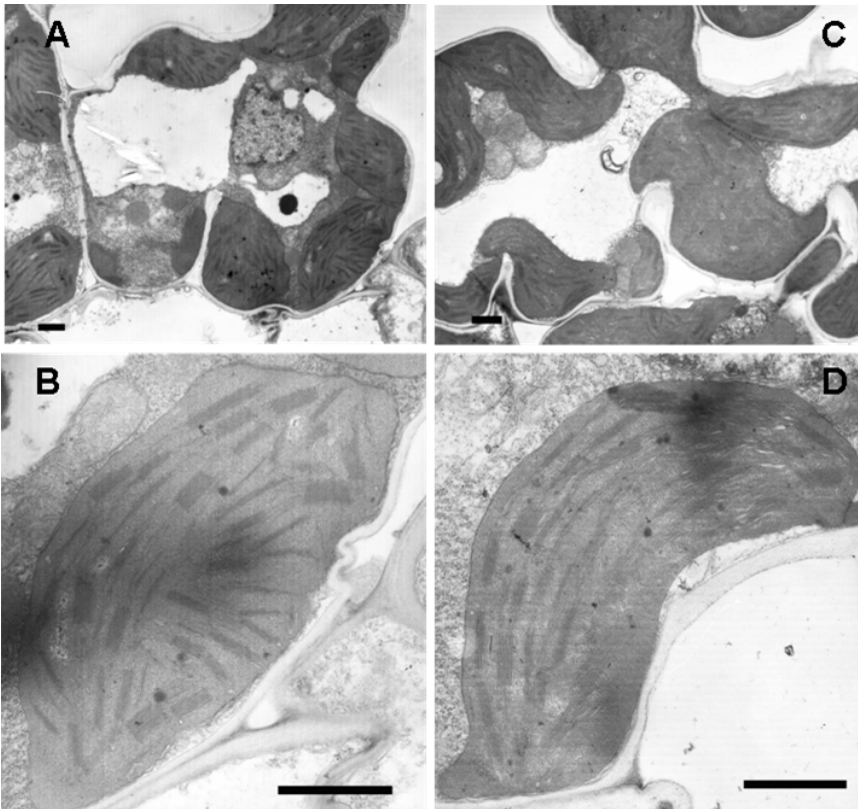


**S. Figure S1**



**Supplemental Figure S1.** Electron microscopic analysis of the rice *824ys* mutant. A and B, Mesophyll cells and chloroplasts of wild-type, respectively. C and D, Mesophyll cells and chloroplasts of *824ys* mutant, respectively. Bar equals 1 μm.

## S. Figure S2

```
1   ATGGCTGCCCTCCTCCTCCTCCCACCTCACCGCCGCTCCTCATCCTCCACCACGTCC
    M A A L L L S S H L T A A S S S S T T S
61  CCCACTGCTCGACCGGCGCCAAGCTTCGTCTCCTTCCGCGCCGCAACGCCGCCCTAAG
    P T A R P A P S F V S F R A A N A A P K
121 GGTGCCCGTCGGGGTTGGCCTTTCCCTTGGCTTCGTTCGGTAGAGCCACCGCCTGCTGCGTCG
    G A R R G W P F L A S S V E P P P A A S
181 GCGGCGCAGCCGTTCCGGTCACTGGCGCCGTCGGAGACCACCGTGTGTCACGGGCGCC
    A A Q P F R S L A P S E T T V L V T G A
241 ACGGGCTACATCGGGCGTTATGTCTCCGCGAGCTCCTCCGCCGCGCCACCCCGTGGTC
    T G Y I G R Y V V R E L L R R G H P V V
301 GCCGTGGCGCGCCCCCGGAGCGGGCTGCGCGGCCCAACGGCCCCGACGAGGTGCTGCGCG
    A V A R P R S G L R G R N G P D E V V A
361 GACCTCGCCCCCGCCGCGTCTCTTCTCCGACGTCACCGACGCGGGCGCGCTCCGCGCC
    D L A P A R V V F S D V T D A G A L R A
421 GACCTGTGCGCCGACGGCCCCATCCACGCCGCGGTGTGCTGCCTCGCCAGCCGCGGGCGG
    D L S P H G P I H A A V C C L A S R G G
481 GCGGTGCGGGACTCGTGGCGCGTGGACTACCGCGCCACGCTGCACACCCTCCAGGCGGGC
    G V R D S W R V D Y R A T L H T L Q A A
541 CGCGGCCTCGGCGCCGCGCACTTCGTCTCCTCCTCCTCCGCGTCTGCGTCCAGAAGCCGCTC
    R G L G A A H F V L L S A V C V Q K P L
601 CTCGAGTTCAGCGCGCCAAGCTCAGGTTTCGAGGGCGAGCTCGCCGCGGAGGCGTCCGCG
    L E F Q R A K L R F E G E L A A E A S R
661 GACCCGTCCTTACCTACAGCATCGTCCGCCCCACCGCCTTCTTCAAGAGCCTGGGCGGC
    D P S F T Y S I V R P T A F F K S L G G
721 CAGGTCGAGACCGTCAAGAACGGCCAGCCCTACGTCATGTTTCGGCGACGGGAAGCTCTGC
    Q V E T V K N G Q P Y V M F G D G K L C
781 GCCTGCAAGCCCATCAGCGAGGAGGACCTCGCCGCGTTCATCGCCGACTGCATCTCCGAC
    A C K P I S E E D L A A F I A D C I S D
841 GAGGGCAAGGCCAACAAGATCCTCCCCATCGGCGGGCCGGGAAGGCGCTGACGCCGCTG
    E G K A N K I L P I G G P G K A L T P L
901 GAGCAAGGGGAGATGCTGTTCCGGCTGCTGGGGCGCGAGCCCAGGTTTCATCAAGGTGCCG
    E Q G E M L F R L L G R E P R F I K V P
961 ATCCAGGTCATGGACGCCCATCTGGGTGCTCGACGCGCTGGCCAAGGTGTTCCCCGGG
    I Q V M D A A I W V L D A L A K V F P G
1021 GTGGAGGACCGGCGGAGTTCGGCAAGATCGGGAGGTAACGCGTTCGGAGAGCATGCTG
    V E D A A E F G K I G R Y Y A S E S M L
1081 GTGCTCGACCCGGACACCGGCGAGTACAGCGACGAGATGACGCCAGCTACGGCAGCGAC
    V L D P D T G E Y S D E M T P S Y G S D
1141 ACGCTCGAGCAGTTCTTCGAGAGGGTGATCAGGGAAGGCATGGCAGGGCAGGAGCTCGGC
    T L E Q F F E R V I R E G M A G Q E L G
1201 GAGCAGACCATCTTCTAG
    E Q T I F *
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**Supplemental Figure S2.** Nucleotide sequence and deduced amino acid sequence of *OsDVR*.

Numbers at left refer to the positions of nucleotides. Letters in the box indicate the nine nucleotides and three amino acid residues deleted in 824ys mutant; Italic letters indicate the putative chloroplast-targeting sequence of 58 amino acid residues at its N terminus.

## S. Figure S3

OsDVR	...MAALLSSHLTAASSSTTS...PTARPAFSVFSRAANAAPKARRGWPFCLASSVEPPAA.S.AAQ.P.FRALPASETTLVLT	78
S.bicolor	...MAALLSSRLPTTGTATPS...SSTRPAPRFLSFPGTATRRRS...PLLASSAAPAPA...AAQP.FRALPASETTLVLT	70
Z.mays	...MATILLSSRLPTTGTATP...SPTRPAPRFLSFPGTALRRRGRG...PLLASSAVSPAP.ASAAQP.YRALPASETTLVLT	74
DVR_At5g18660	MSLCSFNFVASYSPKPKTIFKDSKFISQFQVKSPLASTFFHTNESSTSLKYKRRLKPISSLDGSGIS.EIATSPSFRNKSPKIDINLVV	89
C.reinhardtii	MLANKTSVSRQTAGKASSRAQAAIPLHLISSRVEVRASGVVVFSGVNVKASASAAPARAMAASRQAVRVAADVADYKREPKDVRVLVV	90
SYNW0963	.....MALRHDFSRPPEQVRVVV	20
BciA_CT1063	.....MSSSVLAESC.....GSQKKRFVV	22
R.sphaeroides	.....MSETAP.....LPAPRRITLML	16
OsDVR	GATCYIGRYVRELLRRGHVVAVARPRSGLRGRNPDEVVADLAPARVVESDVTDAGALRADLSPHGP.IHAAVCCCLASRGGVQDSWR	167
S.bicolor	GATCYIGRYVRELLRRGHRVLAVARPRSGIRGRNSPEDVADLAPAQVVESDVTDPAALLADLAPHGP.VHAAVCCCLASRGGVQDSWR	159
Z.mays	GATCYIGRYVRELLRRGHRVLAVARPRSGIRGRNSPDDVADLAPAQVVESDVTDPAALLADLAPHGP.VHAAVCCCLASRGGVQDSWR	163
DVR_At5g18660	GSYCYIGRFVVKEMIKRGNVIAVARREKSGIRGKNDKEETLQQLQGANVCFSDVTELDVLEKSIENLGFQVDDVVVSCLASRNGIKDSWK	179
C.reinhardtii	GPTCYIGKFFVVKELVSRGYNVAFARENAKIKGKMGREDIVKEFPGAVERFGSVLDPASLRDVAFKDPV..DVVVSCLASRTGKKDSWL	178
SYNW0963	GATCYIGRFVVEQELVBERGYQVVAFAFRERSGIGGRSQEQVIIDHKGAEVRFQVTDPAASIAAEAFNQPT..DVVVSCLASRTGGRNDSWA	108
BciA_CT1063	GATCYIGKFFVRELVSRGYEVIISFAFRERSGVNASTTEDETRRQLQGSSEVRFQVGNLESILRDGIRGEH.FDAVVSCLASRNGIKDSWD	111
R.sphaeroides	GATGTIGQATARALLARGHEVVCFLRP.CGTRRQARLP.....DGAVLRVYGDVTDPSLTRDGFCEGER.FDAVVSCLASRTGVRDWA	98
OsDVR	VDMRATLHTLQAARGLGAHFVLLSAICVQKPILEFQRAKLRFEELAAEAASR.DPSFTYSVVRPTAFFKSLGGQVETVKNQGPVVMFGD	256
S.bicolor	VDMRATLHTLQAARGLGAHFVLLSAICVQKPILEFQRAKLRFEELAAEAAR.DPAFTYSVVRPTAFFKSLGGQVDIVKNQGPVVMFGD	248
Z.mays	VDMRATLHTLQAARGLGAHFVLLSAICVQKPILEFQRAKLRFEELAAEAAR.DPSFTYSVVRPTAFFKSLGGQVDIVKNQGPVVMFGD	252
DVR_At5g18660	IDYEATKNSLVAGKFKGAKHFVLLSAICVQKPILEFQRAKLRFEELMDLAQQDSSFTYSVVRPTAFFKSLGGQVETVKNQGPVVMFGD	269
C.reinhardtii	IDYTAATKNSLDVARASGAKHFVLLSAICVQKPILEFQKAKLQFESDLQAAGDI.....TYSVVRPTAFFKSLAGQIDIVKKNQGPVVMFGD	263
SYNW0963	IDHCATLNTYREGRRAGVAHYVLLSAICVQKPILEFQKAKLFAFEELQADGEM.....TYSVVRPTAFFKSLGGQVESCRRKGGPVMVFGG	193
BciA_CT1063	IDYQATRNSLDAGMKAGINHFVLLSAICVQKPILEFQRAKLRFEELRESGVT.....TYSVVRPTAFFKSLAGQIEKVNKNQGPVVMFGD	195
R.sphaeroides	IDHAAHSHALAAARAAGVTQVLLSAICVQKPILEFQCAKLAFAFEELMRSGLA.....WSVVRPTAFFKSLGGQVKRVQGRFVFGD	182
OsDVR	.....***	
S.bicolor	GKLCACKPISEEDLAAFIADCIYDQDKANKVLPVIGGPGKALTPLECGEMLRLLGREPKFKVPEIQVMDAAIHWLDLAKLFFGLEDAAE	346
Z.mays	GKLCACKPISEEDLAAFIADCIYDQDKANKVLPVIGGPGKALTPLECGEMLRLLGREPKFKVPEIQVMDAVIHWLDLAKLFFGLEDAAE	342
DVR_At5g18660	GKLCACKPISEEDLAAFIADCVLEENKINQVLPVIGGPGKALTPLECGELRLKILGREPKFLKVPPEINDFVIGVLDIAKIFPSVGEAAE	359
C.reinhardtii	GNLAACKPISEADLASFADCVTEQNKVNVLPVIGGPGSAFTAKQCADLNFNITCLPPKYPFVPEVALMDGMIGLFDLAKLFFGLEDAE	353
SYNW0963	GETASCKPISEADLAREMADCLREDEKRNQVLPVIGGPGPALSAKQCGEMLRLLGREPKFLKVPPEIADLMDGPIALDEGLSRLFFGLEDAE	283
BciA_CT1063	GKLTACKPISEGDARFITLQLEDPEKQNKILPVGPGPEVNLQCALMLFELLGRKPKLKKVPEIQIFDVIITLPLTLISNPLPSFAEKAE	285
R.sphaeroides	GKLTACKPISEDDDLGRYMLCLEEDPALRNRIILPVGPGPALTPRCAEMLRLLGREPKFKVPEIQVPEVALLDAILAVLSLGRLLLSLRDKAE	272
OsDVR	FGKIGRYAASESMLVLDPTGEMSDEMTPSYGSDTLEQFFERVIREGMAGQBLGEQTI.....	405
S.bicolor	FGKIGRYAASESMLLIDPETGEMSDKTPSYGKDTLEQFFQVIREGMAGQBLGEQTI.....	397
Z.mays	FGKIGRYAASESMLLIDPETGEMSDKTPSYGKDTLEQFFQVIREGMAGQBLGEQTI.....	401
DVR_At5g18660	FGKIGRYAASESMLLIDPETGEMSEKTPSYGKDTLEDFFAKVIREGMAGQBLGEQFF.....	417
C.reinhardtii	FARIGRYAASESMLVYDEARGVLEDETEFGYKDTLEDFFSAVKELGQBLGEQVAVGGQ.....	415
SYNW0963	FRIGRYAASESMLVWDEPERQCDADATPSYGEDTLERFERVVRDGMAGQDLGDAALE.....	342
BciA_CT1063	FARIGRYAASESMLVWDPVKRYDADATPSYGETETLRDHYKRVLKEGLAGQBLGAHAME.....	344
R.sphaeroides	LARIGRYAASESMLVLDPATGRMDAETPSFETETLEDHYRQLL.AGEATVLDGEHAVRERAVTAEGSPGN	343

**Supplemental Figure S3.** Alignment of the deduced amino acid sequence of OsDVR and its homologues. Identical residues were boxed in black, similar residues ( $\geq 75\%$  identical) were highlighted in gray. The deletion of three amino acid residues (Lys, Val and Pro) was indicated with asterisks at the mutation site of 824ys mutant. Accession numbers for the respective protein sequences are as follows: *Oryza sativa* (OsDVR, Os03g22780, ADE43128); *Sorghum bicolor* (XP\_002465274); *Zea mays* (PCB2, NP\_001148282); *Arabidopsis thaliana* (DVR, At5G18660, NP\_197367); *Synechococcus* sp. WH 8102 (SYNW0963, NP\_897056); *Chlamydomonas reinhardtii* (XP\_001690168); *Chlorobium tepidum* TLS (BciA (CT1063), NP\_661954); and *Rhodobacter sphaeroides* (ZP\_00006667).