

10.1071/FP18241\_AC

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Supplementary Material: *Functional Plant Biology*, 2019, 46(5), 482–491.

## Supplementary Material

### **Heterologous expression of rice RNA-binding glycine-rich (RBG) gene *OsRBGD3* in transgenic *Arabidopsis thaliana* confers cold stress tolerance**

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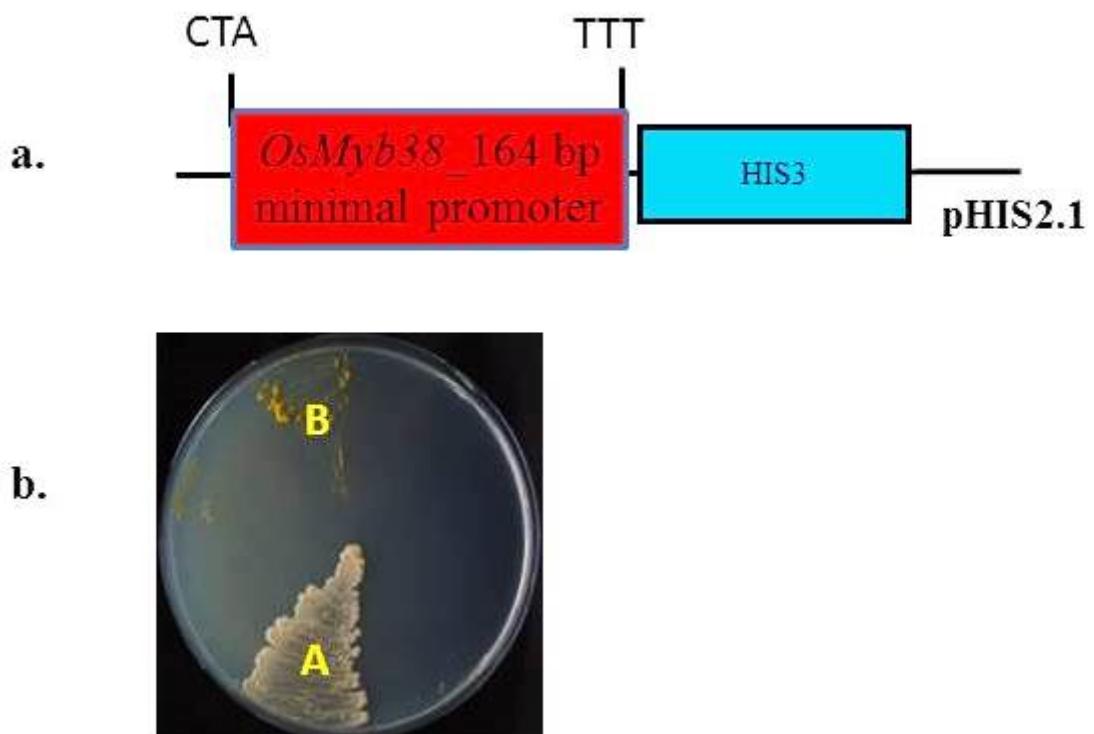
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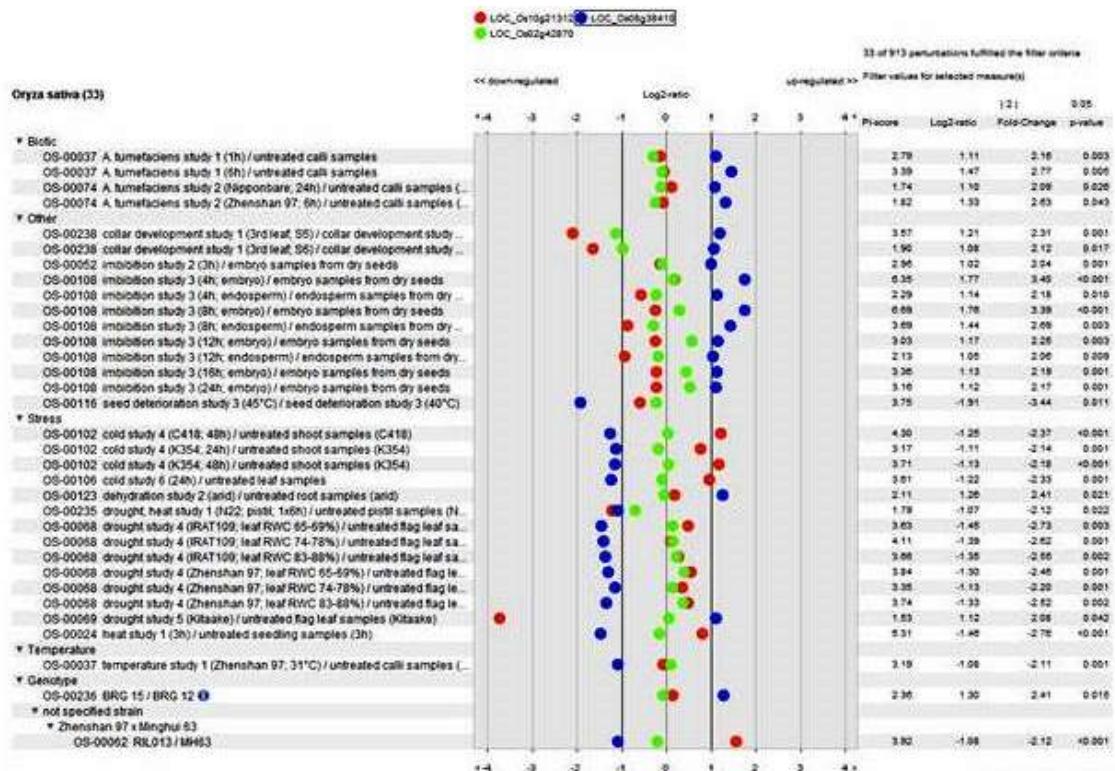
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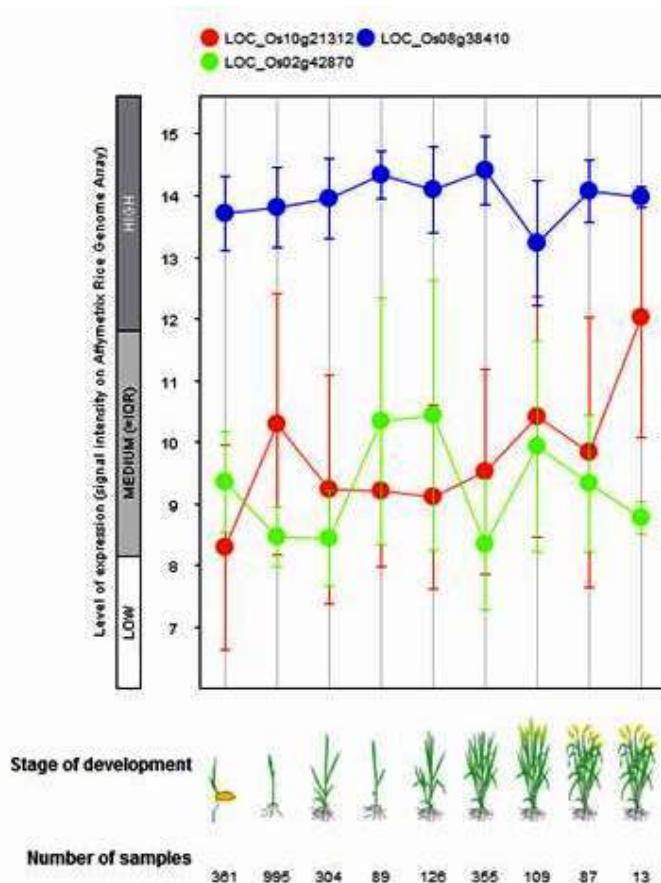


**Fig. S1.** Isolation of five ORFs by Y1H screen using minimal *OsMYB38* promoter. (a) *OsMYB38* minimal promoter (Os02g42870 promoter, -590 to -753 from ATG) was used to drive HIS operon as bait. (b) Y187 colonies growing on TDO/100mM 3-AT (SD/-His/-Leu/-Trp/3-AT) plates harbouring OSMYB38 and corresponding protein factors interacting with OSMYB38 directly or indirectly (via native yeast DNA binding protein). (A) OsRGBD3. (B) Negative control.

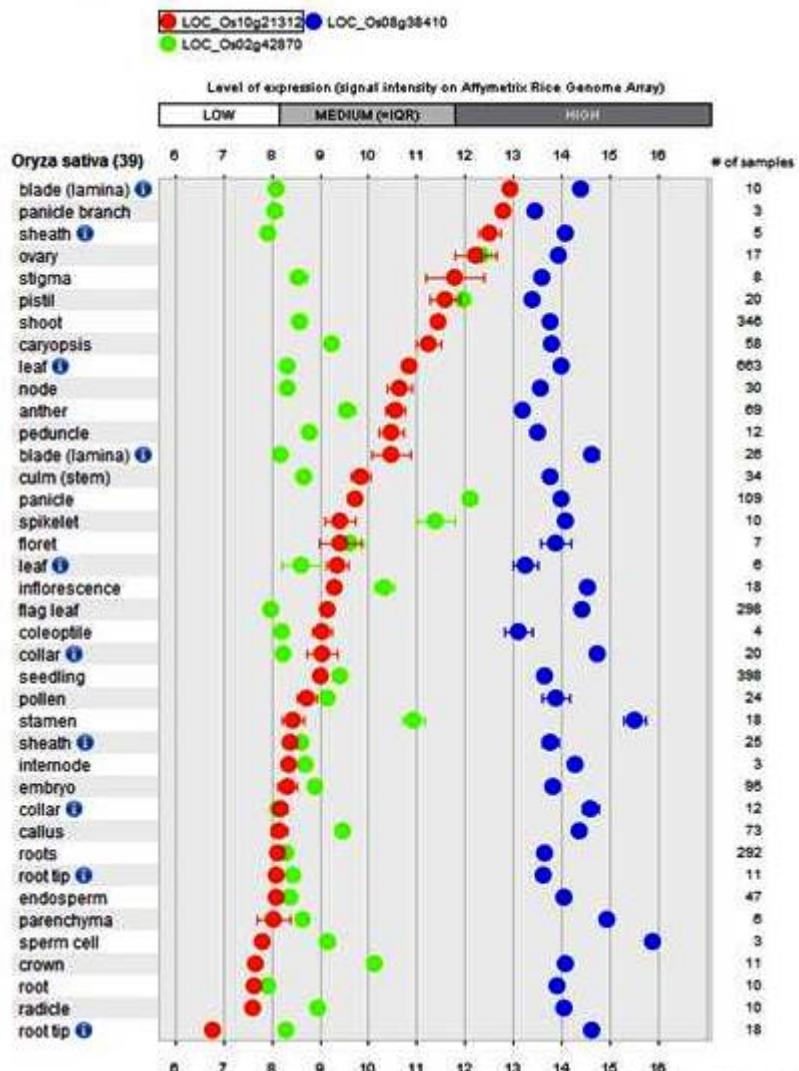
(a)



(b)



(c)



**Fig. S2.** Expression analysis of *OsMYB38* and *OsRGD3* was analysed under different environmental conditions (a) at different developmental stages (b), and in various tissues (c ) of rice using publicly available gene expression data through Genevestigator software. Os10g21312 (chloroplast 30S ribosomal protein S18) is considered as a reference gene.

b)

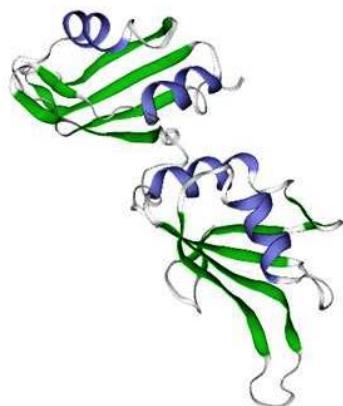
Model\_01 MGKAEARSREHGGGGGGGSAGTTFVQGLPRDTTEADFVKHPQQYGEIVDSVIVWDKHTSQPRGFGEFTVSNPAVVDRVWDD-IHEENGKOMVIRNTIPKDSVQS--KD 107  
4yoel.A -----EFGDIDFEGLSEFTT-----HEQG-----D-----VMDNTIPEQGFTV-----VAT-----VDA-----M-----A-----P-----G-----W-----AVSREDSQAPGAK 103

Model\_01 FKTKEKLVQGLPQALTEDDFKHPFQKYGPVVDHOTMHDHQTKRERGFGEFTVSSDQVVDLLAQNMIIDAGENVYVIFDCEPKKSNNPPSSHGSASRSAYGRDSRGHSS 217  
4yoel.A LTVK-----GKEDTC-----HEQYGP-----D-----VMDGSGANPGF-----VAT-----VDA-----M-----A-----P-----G-----W-----VQSKQEPASRL 192

Model\_01 GNDYGGIANAYSNYNNSGGFGPYRNHHGVYGGGSLSGYGGIGEYGVQYGRYYFGLGGSGSMPSTGVASRVGPFYGGGFEDGYAGGNLSGYRRGGDESTGGLSSSSFGGAMYGG 327  
4yoel.A -----

Model\_01 AAYDPALGGYASGSTPERSRGNLAGGSGRYNYGR 362  
4yoel.A -----

a)



**Fig. S3.** (a) Swiss model was used for secondary structure prediction using DSSP. The top hit template: found was “4yoel.A” with sequence identity 33.53%. QMEAN Z-scores -0.93 (around zero) indicate good agreement between the model structure and experimental structures of similar size. (b) Based on model-Template Alignment, 4 alpha helix (in purple) and 8 beta (green) sheets; one each for each RRM domain (as discussed in Daubner *et al.* 2013).

4 alpha helix:

Glu 36A-Phe43A

Pro74A-Met81A

Glu124A-Phe131 A

Asp162A-Asn 171 A

8 Beta sheet:

Lys 24A-Gly 28A

Ile49A-Arg56A

Pro63A-Try71 72A

Glu93-Arg96A

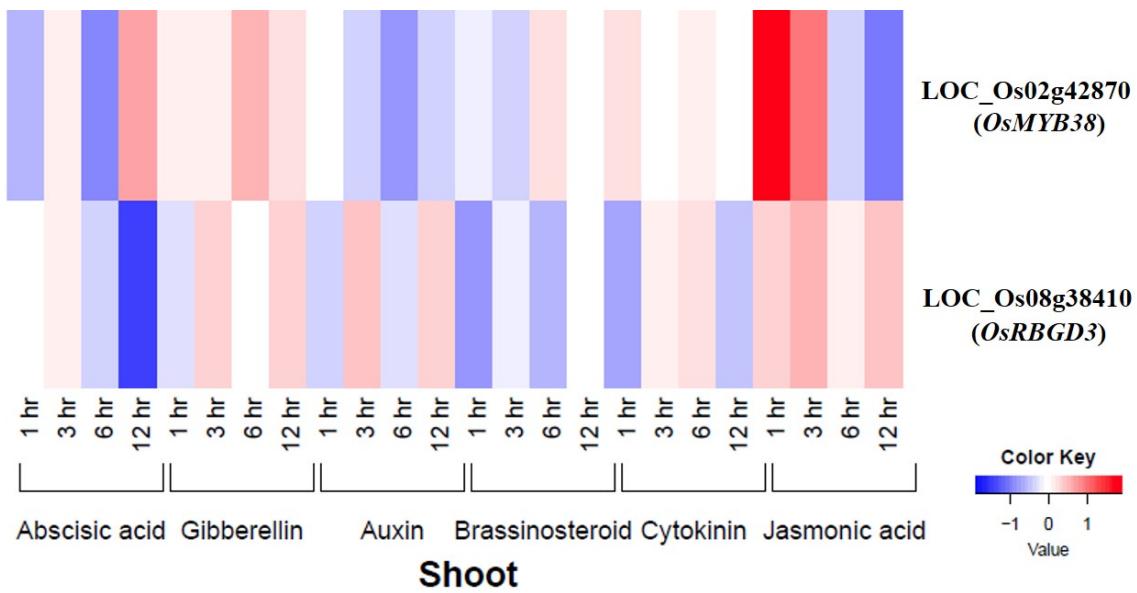
Lys112A-Gly116A

Val137A-Arg144A

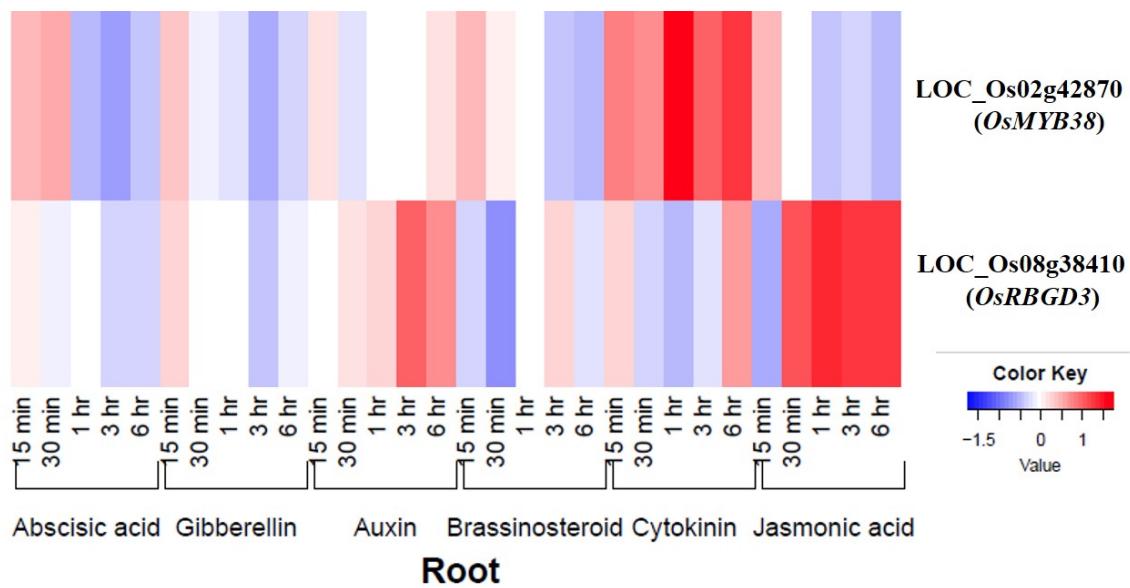
Ser151-Phe159 A

Glu183-Ala187 A

(a)



(b)



**Fig. S4.** The global expression profiles of *OsMYB38* (*LOC\_Os02g42870*) and *OsRGBD3* (*LOC\_Os08g38410*) genes in response to six plant hormones were derived: abscisic acid (ABA), gibberellic acid (GA3), indole-3-acetic acid (IAA), brassinolide (BL), Cytokinin (trans-zeatin (tZ)), and jasmonic acid (JA) (for details of methods, please check RiceXpro [http://ricexpro.dna.affrc.go.jp/RXP\\_1000/details-of-methods.html](http://ricexpro.dna.affrc.go.jp/RXP_1000/details-of-methods.html)). (a) Shoot. (b) Root.

**Table S1.** List of various primers used in this study

<b>Primers used for cloning CaMV35S:OsRGD3:sGFP into pUC18 vector</b>
OsRGD3GFP F: G <u>C</u> T <u>C</u> A <u>G</u> A TGG GGA AGG CGG AGG CGA GGT C OsRGD3GFP R: G <u>C</u> T <u>C</u> A <u>G</u> ACTG CTT TCT TGA TCT CCA CGT TTG CAC CAG
<b>Primers used for cloning <i>OsRGD3</i> into modified pCAMBIA1200 vector</b>
OsRGD3 BamH1 F: CG <u>G</u> <u>G</u> <u>A</u> <u>T</u> CC AAG ATG ATT CAA GCA TTC TTC CAG Os RGD3 Sac1R: CCG <u>A</u> <u>G</u> <u>C</u> <u>T</u> <u>C</u> CTA CTG CTT TCT TGA TCT CCA CGT TTG CAC
<b>Primers used for RT-qPCR of <i>OsRGD3</i> and <i>OsMYB38</i></b>
QRT <i>OsRGD3</i> F: TTGATCTTGCTGGTGC <u>A</u> <u>A</u> <u>AG</u> <u>G</u> TGG QRT <i>OsRGD3</i> R: TTGGCCAGTCCACC <u>A</u> <u>T</u> <u>G</u> T <u>C</u> ATTG MYB38QRTF: ACAAGCTCCTCGTC <u>G</u> <u>A</u> <u>C</u> <u>T</u> <u>A</u> <u>C</u> ATCCA MYB38QRTR: ATCATGGACC <u>A</u> <u>C</u> <u>T</u> <u>G</u> <u>T</u> <u>G</u> CCGAC
OsActin F: TCCGGTGGATCTTCATGCTTACCT OsActin R: ATGGACCATTGCGACGAGTCTTCT
<b>Primers for cloning the bait sequence (minimal <i>OSMYB02</i>) into pHIS2.1 vector</b>
BaitF-C <u>G</u> <u>G</u> <u>A</u> <u>A</u> <u>T</u> <u>T</u> <u>C</u> T AGG ACG GTA GGA GTA GG BaitR-C <u>G</u> <u>A</u> <u>G</u> <u>C</u> <u>T</u> <u>C</u> <u>G</u> GGC CAT CAG ATC AAG

**Table S2.** Putative *cis*-regulatory elements identified from Os02g42870 promoter (*OsMYB38*, -590 to -753 from ATG) in PLACE database and its corresponding interacting proteins isolated by Y1H screen

S. No.	Site Name	Sequence	Location(Strand) within the 164 bp bait sequence	Type of interacting protein isolated	Reference
1	MYBPZM	CCWACC	7 (-)	MYB	(Grotewold et al 1994)
2	EBOXBNNAPA	CANNTG	21 (+)	MYB	(Hartmann et al 2005)
3	RAV1AAT	CAACA	76 (+)	AP2	(Kagaya et al 1999)
4	IBOX	GATAAG	100 (-)	MYB	(Rose et al 1999)
5	EECCRCAH1	GANTTNC	129 (+)	MYB	(Yoshioka et al 2004)
6	MYCSENSUSAT	CANNTG	21 (+), 59 (+), 124 (+), 137 (+)	Not detected	(Chinnusamy et al 2003)

**Table S3. List of ORFs isolated by Y1H screen using minimal *MYB38* (Os02g42870) promoter**

NCBI Accession number	Maximum Similarity to MSU Loci	Annotation	Number of nucleotide in the ORF	Number of amino acid	Type of protein
FN556368	LOC_Os01g07120.1	<i>OsAP2-1</i>	711 nt	236 aa	AP2 domain containing protein
FN556369	LOC_Os01g07120.2	<i>OsAP2-2</i>	639 nt	212 aa	AP2 domain containing protein
FN556370	LOC_Os02g15640.1	<i>OsPYL3</i>	615 nt	204 aa	PYR/PYL/RCAR -like family protein
FN556371	LOC_Os04g49450.2	<i>OsMYB4</i>	1095 nt	364 aa	MYB family transcription factor, putative
FN556372	LOC_Os08g38410.3	<i>OsRBGD3</i>	567 nt	188 aa	RNA-binding glycine-rich (RBG) protein

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