Supplemental Data

Table S1. Salt stress regulated rice root apoplastic proteins

Spot No*.	Accession No.	Protein name	Theoretical	Exprimental	Queries Matched	Sequence Coverage (%)	Mascot Score	Predicted location**
			pI/MW	pI/ MW				
1	gi|19387274	OsRMC	5.01/27916	4.59/43132	16	62%	192	s
2	gi|34393251	peroxidase precursor	5.77/33311	5.86/33990	12	52%	86	s
3	gi|2429292	Peroxidase 2 precursor	5.51/33042	6.02/32949	13	50%	97	s
4	gi|4884530	peroxidase precursor	5.77/33311	5.81/32420	14	44%	101	s
5	gi|4884530	beta-1,3-glucanase	7.01/35699	6.98/31781	16	60%	158	s
6	gi|19387274	OsRMC	5.01/27916	5.01/25859	9	43%	76	s
7	gi|5931625	rab5B	6.84/21748	6.65/191760	6	36%	65	-
8	gi|33440014	Prb1 (putative pathogenesis-related protein)	4.32/17452	4.32/15432	6	64%	75	s
9	gi|34394950	putative beta-1,3-glucanase	4.98/59363	4.98/16024	11	22%	71	s
10	gi|3915131	Thioredoxin H-type (TRX-H)	5.16/13319	5.4/15023	9	55%	79	-

* Spot numbers from the analyses shown in Figure 2

**Location of identified proteins was predicted by TargetP (http://ww.cbs.dtu.dk/services/TargetP). S: contained signal pepetide in secretory pathway. -: any other location

Table S2. Primers sequences used in gene construction and Q-PCR

Purpose	Sequence
35S::OsRMC-YFP	5’ CCATGGCGCGGTGCACTTTG 3’
	5’ CCATGGCCTCACGCAGCACCACCATC 3’
OsRMCpro::GUS	5’ AAGCTTGACATGCTGCCTGTCCAGAT 3’
	5’ TCTAGATGCAATGGCAGTGATCGTTA 3’
RNAi	5’ GGGGTACC ACTAGTCACTTTGCTCGTTCTCCTCGT 3’
	5’ CGGGATCC GAGCTCTGATGTTGGTGCTGCTCATGA 3’
Ubi-1pro::OsRMC-GUS	5’ CGGGATCCATGGCGCGGTGCACTTT 3’
	5’ CGGGATCCCCTCACGCAGCACCACCATC 3’
Q-PCR (*OsRMC*)	5’ TCGGAGGTGTACCCGTTCTACA 3’
	5’ ACTCTTAATTTGTGCCATTTTATTCTAGCT 3’
Q-PCR(*OsACTIN1*)	5’ ACCATTGGTGCTGAGCGTTT 3’
	5’ CGCAGCTTCCATTCCT ATGAA 3’
Q-PCR (*OsDREB2A*)	5’ AAAAGCGATGGCCCTGATTC 3’
	5’ TTGGCTGGCGCTTTCCT 3’
Q-PCR (*Rab16A*)	5’ CACACCACAGCAAGAGCTAAGTG 3’
	5’ TGGTGCTCCATCCTGCTTAAG 3’
Hygromycin B	5’ AAGTTCGACAGCGTCTCCGAC 3’
	5’ TCTACACAGCCATCGGTCCAG 3’
OsRMC purification	5’ CGGGATCCCGCGGTGCACTTTG 3’
	5’ CGGAATTCCCTCACGCAGCACCACCATC 3’

Figure S1 . MALDI-TOF mass fingerprint of OsRMC. **A,** The polypeptide that matched this peptide ion spectrum was identified as OsRMC. Signal peptide for extracellular secretion (bold italics) and the peptide coverage (underlined) are highlighted. **B,** MALDI-TOF ion spectrum generated from tryptic digest of spot 1 in Figure 2. The spectral peaks show the intensities for different peptides. The peaks of matched peptides in panel A were marked with arrows.

Figure S2 . LC-Mass/Mass result show spot 1 and spot 6 are identical protein. Mass spectrums of spot 1 (A) and spot 6 (B) obtained from a precursor ion with m/z value 753.30 (spot 1) and 753.64 (spot 6)

Figure S3 . Bioinformatic analysis for OsRMC. **A,** predicted signal pepteide sites using the SignalP 3.0 prediction program (http://www.cbs.dtu.dk/services/SignalP/). **B,** predicted Potential transmembrane domain using the TMHMM2.0 program (www.cbs.dtu.dk/services/ TMHMM2.0/). **C,** Structure of the OsRMC protein. The DUF26 domains and the putative N-terminal signal peptide are shown. **D,** Prediction of *cis*-acting elements distribution in the promoter region of OsRMC. ACGTG: ABRE; ACCGAGA: DRE; CCGAC: LTRE; TAACTG, AACGG: MYB recognition site; CANNTG: MYC recognition site.

Figure S1

A

1 ***MARCTLLVLL VAAAVAVVPL AAG***QPWATCG DGTYEQGSAY ENNLLNLALT

51 LR**DGASSQEI LFSTGSNGAA PNTVYGLLLC R**GDISR**AACY DCGTSVWRDA**

101 **GSACR**R**AKDV ALVYNECYAR LSDKDDFLAD K**VGPGQLTTL MSSTNISSGA

151 DVAAYDRAVT R**LLAATAEYA AGDIARKLFA TGQRVGADPG FPNLYATAQC**

201 **AFDITLEACR GCLEGLVARW WDTFPANVDG AR**IAGPRCLL R**SEVYPFYTG**

251 **APMVVLRE**

B

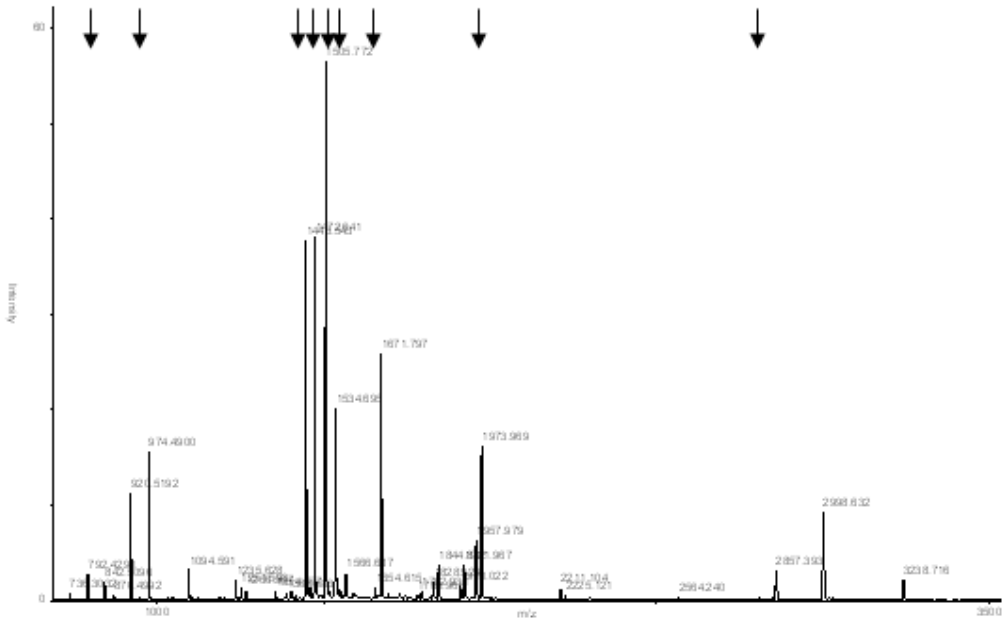
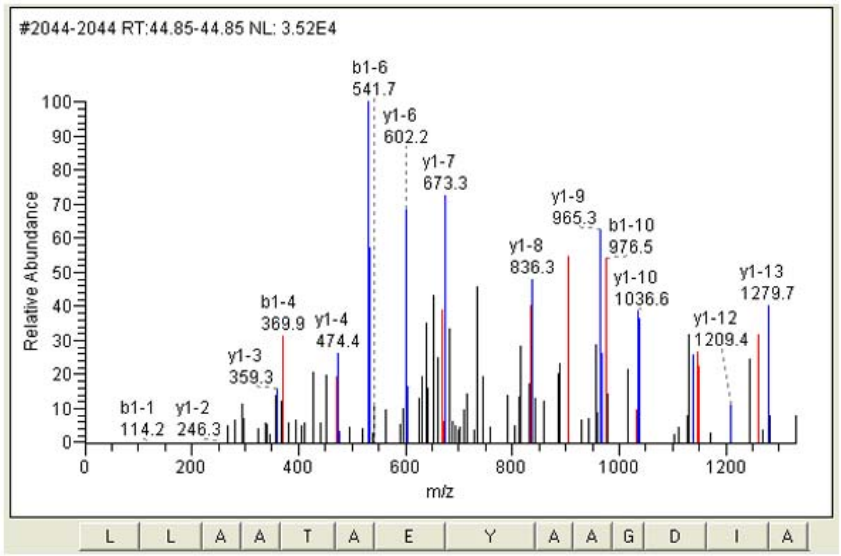


Figure S2

A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Relative Abundance
m/z
b1-6 541.7
y1-6 602.2
y1-7 673.3
y1-9 965.3
b1-10 976.5
y1-8 836.3
y1-10 1036.6
y1-13 1279.7
y1-12 1209.4
b1-4 369.9
y1-4 474.4
y1-3 359.3
b1-1 114.2
y1-2 246.3
L L A A T A E Y A A G D I A

B

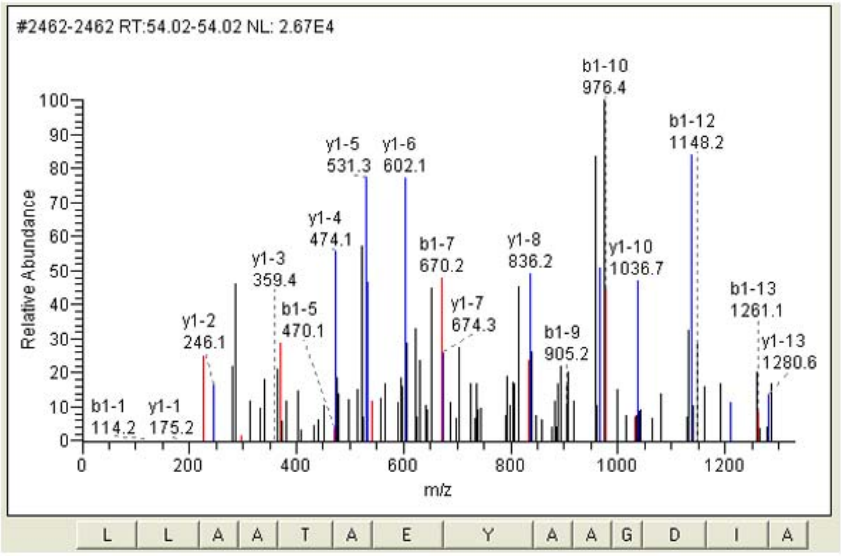
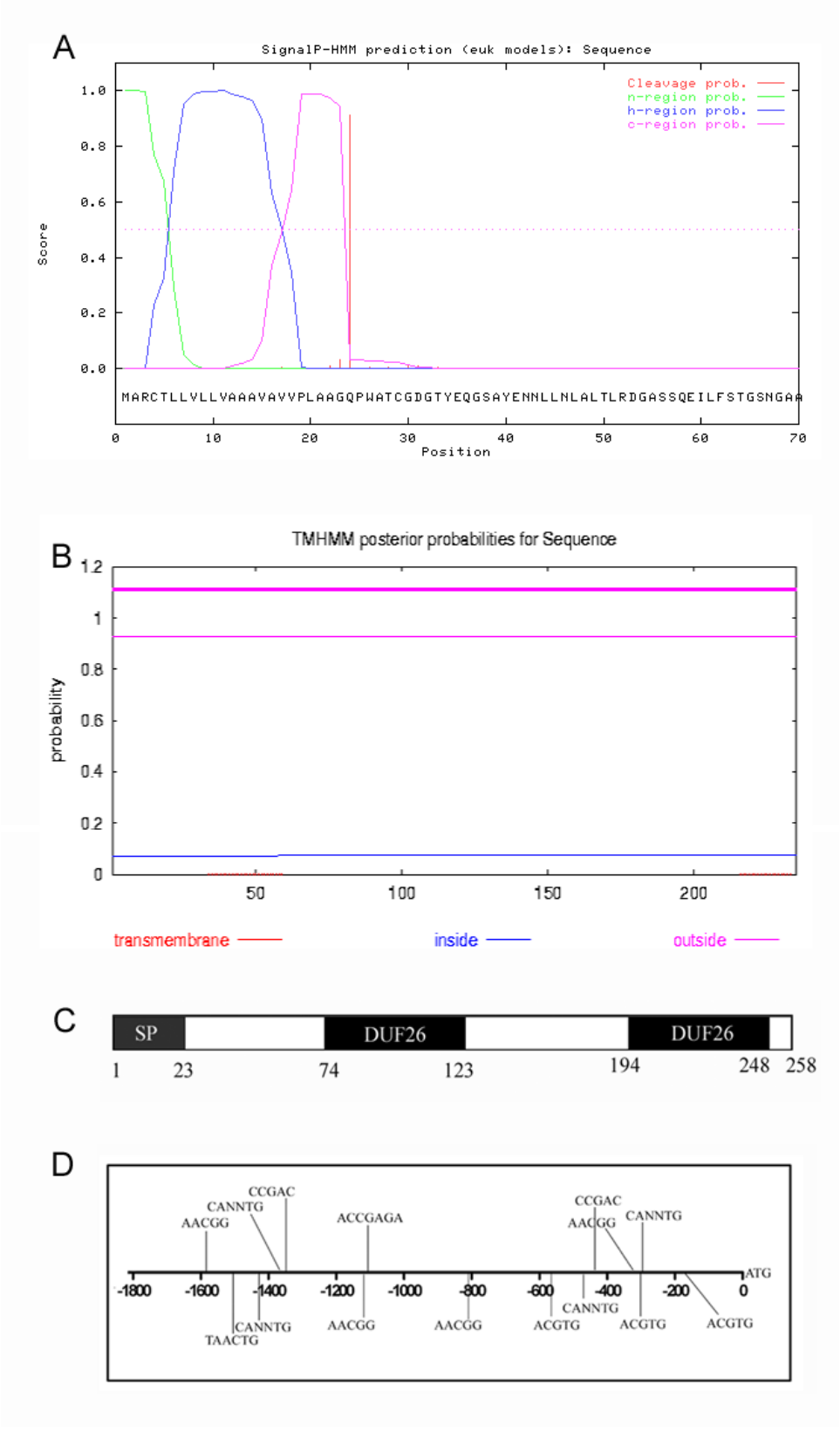

#2462-2462 RT:54.02-54.02 NL: 2.67E4
Relative Abundance
m/z
b1-10 976.4
b1-12 1148.2
y1-5 531.3
y1-6 602.1
y1-4 474.1
b1-7 670.2
y1-8 836.2
y1-10 1036.7
y1-3 359.4
b1-5 470.1
y1-7 674.3
b1-13 1261.1
y1-2 246.1
b1-9 905.2
y1-13 1280.6
b1-1 114.2
y1-1 175.2
L L A A T A E Y A A G D I A

Figure S3


A
SignalP-HMM prediction (euk models): Sequence
Cleavage prob.
n-region prob.
h-region prob.
c-region prob.
Score
Position
MARCTLLVLLVAAAVAVVPLAAGQPWATCGDGTYEQGSAYENNLLNLALTLRDGASSQEILFSTGSNGAA
B
TMHMM posterior probabilities for Sequence
probability
transmembrane
inside
outside
C
SP
DUF26
DUF26
1
23
74
123
194
248
258
D
CCGAC
CANNTG
AACGG
ACCGAGA
CCGAC
AACGG
CANNTG
ATG
-1800
-1600
-1400
-1200
-1000
-800
-600
-400
-200
0
CANNTG
TAACTG
AACGG
AACGG
CANNTG
ACGTG
ACGTG
ACGTG