

Supplementary files

Supplementary Table 1. Basic characteristics of the BZR1 predicted genes in rice responses to salt stress

Gene name	CDS length	Protein length aa	Chromosome	Molecular weight KDa	pI	Instability indices	Gravy values
<i>OsAM1</i>	3465	1154	4	12.38	4.76	41.23	0.087
<i>OsAOC</i>	723	240	3	2.61	9.53	50.08	-0.182
<i>OsBIP130</i>	795	264	5	2.83	8.99	56.52	-0.925
<i>OsBTBZ1</i>	1242	413	1	4.71	8.24	61.98	-0.255
<i>OsbHLH148</i>	900	299	3	3.29	5.29	71.31	-0.692
<i>OsbHLH38</i>	1038	345	8	3.60	6.28	54.94	-0.324
<i>OsCYP2</i>	519	172	2	1.84	8.49	21.79	-0.157
<i>OsCYP94C2b</i>	1530	509	12	5.52	8.64	40.36	0.154
<i>OsCBL1</i>	642	213	10	2.45	4.40	35.46	-0.259
<i>OsCSLD4</i>	3648	1215	12	13.22	7.90	47.46	-0.115
<i>OsDSG1</i>	963	320	9	3.58	4.92	48.4	-0.514
<i>OsDREB1C</i>	645	214	6	2.31	4.79	59.57	-0.542
<i>OsGRX20</i>	1026	341	8	3.72	7.29	45.9	-0.189
<i>OsGF14b</i>	789	262	4	2.98	4.45	52.54	-0.521
<i>OsGPX3</i>	717	238	2	2.58	9.89	41.45	-0.144
<i>OsGF14d</i>	798	265	11	2.93	4.55	50.15	-0.499
<i>OsGW5L</i>	1398	465	1	4.96	11.11	64.92	-0.479
<i>OsGF14c</i>	771	256	8	2.88	4.49	45.86	-0.446
<i>OsGF14f</i>	783	260	3	2.91	4.52	46.4	-0.467
<i>OsHAK15</i>	2604	867	4	9.55	5.37	40.49	0.383
<i>OsHSFC1b</i>	753	250	1	2.72	8.95	45.86	-0.368
<i>OsKOB1</i>	987	328	2	3.64	7.49	34.14	-0.27
<i>OsLEA3-2</i>	1035	344	3	3.68	6.80	15.28	-1.009
<i>OsNAC6</i>	912	303	1	3.29	9.06	55.68	-0.366
<i>OsNHX1</i>	1608	535	7	5.91	8.66	35.53	0.555
<i>OsNHX4</i>	1587	528	6	5.82	6.78	34.7	0.54
<i>OsORAP1</i>	1734	577	9	6.29	7.71	35.04	-0.156
<i>OsP5CS1</i>	2151	716	5	7.77	6.83	45.16	0.464
<i>OsRST1</i>	2103	700	6	7.59	7.57	45.04	-0.308
<i>OsTCP19</i>	1164	387	6	3.87	9.17	57.88	-0.399
<i>OsTIP1;1</i>	753	250	3	2.57	6.50	24.64	0.823
<i>OsTIFY1b</i>	816	271	3	2.90	6.51	52	-0.588
<i>OsVDE</i>	1407	468	4	5.29	6.11	43.73	-0.404

aa, amino acids; CDS, coding sequences; pI, isoelectric point; kDa, kilo dalton

7
8
9

Supplementary Table 2. The number and percentage of cDEGs associated with specific GO terms

GO Items	GO term ID	Number of cDEGs	% of cDEGs
Biological process (BP)			
Potassium ion (K ⁺) transport	0006813	5	15.15
Salt stress response	0009651	5	15.15
K ⁺ transmembrane transport	0071805	4	12.12
Osmotic stress response	0006970	5	15.15
Tolerance to stress	0006950	9	27.27
Sodium ion (Na ⁺) transmembrane transport	0035725	2	6.06
Na ⁺ import across plasma membrane	0098719	2	6.06
K ⁺ homeostasis	0055075	2	6.06
Na ⁺ transport	0006814	2	6.06
Positive regulation of salt stress response	1901002	2	6.06
Cellular component (CC)			
Vacuole	0005773	5	15.15
Vacuolar membrane	0005774	4	12.12
Bounding membrane of organelle	0098588	6	18.18
Chloroplast	0009507	6	18.18
Plastid	0009536	6	18.18
Chloroplast envelope	0009941	3	9.09
Organelle membrane	0031090	6	18.18
Plant-type vacuole	0000325	1	3.03
Cytoplasmic vesicle	0031410	1	3.03
Intracellular vesicle	0097708	1	3.03
Molecular function (MF)			
Protein domain-specific binding	0019904	5	15.15
Potassium (K ⁺): proton (H ⁺) antiporter activity	0015386	3	9.09
K ⁺ antiporter activity	0022821	3	9.09
DNA-binding transcription factor activity	0003700	3	9.09

K ⁺ transmembrane transporter activity	0015079	4	12.12
Transcription regulator activity	0140110	3	9.09
Transmembrane transporter activity	0022857	6	18.18
Transporter activity	0005215	6	18.18
Sodium (Na ⁺): proton (H ⁺) antiporter activity	0015385	2	6.06
Na ⁺ transmembrane transporter activity	0015081	2	6.06

Supplementary Table 3. Log2FC and *P*-value for shoot and root in rice

Gene name	Log2FC	P-value	Gene name	Log2FC	P-value
For shoot			For root		
<i>OsAM1</i>	-0.21124	0.430982	<i>OsAM1</i>	-5.46278	0.016636
<i>OsAOC</i>	0.409255	0.346311	<i>OsAOC</i>	2.36611	0.613886
<i>OsBIP130</i>	0.762222	0.059807	<i>OsBIP130</i>	6.209068	0.041752
<i>OsBTBZ1</i>	-0.99319	0.250094	<i>OsBTBZ1</i>	-2.09954	0.011664
<i>OsbHLH148</i>	1.073623	0.067973	<i>OsbHLH148</i>	5.759839	0.032108
<i>OsHLH38</i>	0.289507	0.741801	<i>OsHLH38</i>	-7.43244	2.01E-32
<i>OsCYP2</i>	-0.70109	0.406048	<i>OsCYP2</i>	-4.47216	0.004391
<i>OsCYP94C2b</i>	5.196397	0.092405	<i>OsCYP94C2b</i>	3.321413	0.028851
<i>OsCBL1</i>	0.28054	0.441312	<i>OsCBL1</i>	-7.78226	0.024112
<i>OsCSLD4</i>	-0.66742	0.474048	<i>OsCSLD4</i>	3.847997	0.371461
<i>OsDSG1</i>	0.198875	0.295533	<i>OsDSG1</i>	-2.81745	0.008452
<i>OsDREB1C</i>	3.098032	0.160269	<i>OsDREB1C</i>	-7.4201	0.008589
<i>OsGRX20</i>	0.697162	0.018896	<i>OsGRX20</i>	-5.11201	0.795225
<i>OsGF14b</i>	-1.28445	0.1738	<i>OsGF14b</i>	-2.25909	0.018761
<i>OsGPX3</i>	0.017426	0.942543	<i>OsGPX3</i>	6.276775	0.144996
<i>OsGF14d</i>	0.173912	0.213706	<i>OsGF14d</i>	5.139623	0.192496
<i>OsGW5L</i>	0.280108	0.753422	<i>OsGW5L</i>	-5.26679	0.501567
<i>OsGF14c</i>	-1.09955	0.20737	<i>OsGF14c</i>	-2.50186	0.015247
<i>OsGF14f</i>	-0.29794	0.501456	<i>OsGF14f</i>	-4.18954	0.425186
<i>OsHAK15</i>	0.025912	0.954521	<i>OsHAK15</i>	-4.61585	0.031764
<i>OsHSFC1b</i>	-1.22239	0.435654	<i>OsHSFC1b</i>	5.643665	8.98E-32
<i>OsKOB1</i>	0.108586	0.909681	<i>OsKOB1</i>	-3.62785	0.441093
<i>OsLEA3-2</i>	2.247928	0.42265	<i>OsLEA3-2</i>	-6.19004	0.533684
<i>OsNAC6</i>	1.848292	0.161716	<i>OsNAC6</i>	3.227315	0.069173
<i>OsNHX1</i>	1.491065	0.296314	<i>OsNHX1</i>	3.365027	0.088068
<i>OsNHX4</i>	0.304855	0.269703	<i>OsNHX4</i>	7.577468	0.351215
<i>OsORAP1</i>	1	0.07418	<i>OsORAP1</i>	5.653324	2.75E-65
<i>OsP5CS1</i>	0.440573	0.42265	<i>OsP5CS1</i>	-3.35225	3.09E-11

<i>OsRST1</i>	0.075376	0.737029	<i>OsRST1</i>	-7.29678	0.468025
<i>OsTCP19</i>	0.263034	0.82858	<i>OsTCP19</i>	6.291049	0.619635
<i>OsTIP1;1</i>	-0.09615	0.682662	<i>OsTIP1;1</i>	7.015993	7.49E-43
<i>OsTIFY1b</i>	-0.27349	0.597143	<i>OsTIFY1b</i>	-3.47957	0.040994
<i>OsVDE</i>	-0.04874	0.587521	<i>OsVDE</i>	-4.69617	0.066627

Log2FC, Fold Change

A

RiceTFtarget

A Rice Transcription Factor-Target Prediction Server Based on Gene Co-expression and Machine Learning

Regulation Prediction Results

total results: 745

co-expression library size: 20

cutoff of PCC: 0.6

Motif binding site Number: >= 1

Machine Learning Prediction Label: 0

Network

Download Result

Search

TF Gene id	TF Family	Target gene id	Target gene annotation	PCC	Graph	Bind Site Number	Machine Learning Prediction ②
LOC_Os07g39220	BES1	LOC_Os04g47170	ATROPGEF7/ROPGEF7, putative, expressed	0.904		num: 1 detail: 	probability: 0.18 label: 0 detail: 

B



PlantRegMap

Plant Transcriptional Regulatory Map

[Home](#) [PlantTFDB](#) [cis-Map](#) [Network](#) [ATRM](#) [Tools](#) [Download](#) [Help](#) [About](#)

Retrieve Results

844 regulations(721 unique regulations) are found.

You can download the 844 regulations [here](#).

Or download the 721 unique regulations with regulations between TF and target from different tissues or methods merged [here](#).

Only the network view with less than 50 nodes will be shown.

Show 10 entries

Search:

TF	Target	Organ	Method	Details
LOC_Os07g39220	LOC_Os04g58620	-	motif	details
LOC_Os07g39220	LOC_Os04g58620	-	motif_CE	details

19

Supplementary Fig. 2. Different consensus sequences of cDEGs.