

Accessory Publication

Table S1. Changes in gene expression intensities after 1 h and 24 h of 150 mM NaCl in rice seedlings measured as \log_{10} ratio of stress/unstressed

Genes used as probes	NCBI GI no	Log ratio		Homologous gene in rice	Blastx values		
		1 h	24 h		Q. C.	e value	max id
Signaling molecules							
^A MKK1	2196703:117-1181	0.4172		OmMKK1-2; induced by brown plant hopper	92%	5.00E-71	45%
^A MAP3Kq1	20197220:72418	0.3513	0.8562	Protein tyrosine kinase	83%	4.00E-108	78%
^A MPK1	30681599	-0.483	0.6604	MAP kinase 3	68%	4.00E-180	78%
^A Phosphatidylinositol-specific phospholipase	18424131:50-1735		0.6738	Phospholipase C (Fragment)	98%	2.00E-152	48%
^A ABI (ABA induced protein phosphatase 2C)	499300		-0.5	Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C)	46%	4.00E-99	58%
Transcription factors							
^A Salt-tolerance zinc finger protein	18402298:120-941	0.46		Zinc finger protein ZFP252	70%	9.00E-31	40%
^A DREB2A-specific	30680919:189-1196	0.3597		Dehydration responsive element binding protein 2A	99%	4.00E-138	74%
^A AP2 domain DNA-binding protein		-0.3			94%	3.00E-32	40%
^A DREB1B-specific	30686903:164-805	-0.991	-0.471	Dehydration-responsive element-binding protein	88%	3.00E-30	40%
^A WRKY family transcription factor	186522487		0.66	WRKY transcription factor 72	35%	2.00E-41	86%
^A Similar to putative RING zinc finger protein	30687041		0.54	RING type Zn finger containing protein	54%	2.00E-26	39%
^A DREB2-conserved	79327025:189-1097		-0.314	Dehydration responsive element binding protein 2A	99%	4.00E-138	74%
^A Putative CCCH-type zinc finger protein	145360824		0.4842	Zn-finger, C-x8-C-x5-C-x3-H type domain containing	69%	2.00E-105	40%
^A DREB1C-specific	18416556:135-785		-0.985	CRT/DRE binding factor 1	99%	4.00E-38	40%
^A Salt-tolerance zinc finger protein	30690059		-0.3	C2H2 zinc finger	62%	6.00E-32	39%
^A Glycine-rich RNA-binding protein	186502097:78-608		-0.5	Glycine-rich RNA-binding protein 1	48%	2.00E-35	80%
Cellular growth related							
^A Beta-actin	48927617	0.3768		OsRac1	77%	3.00E-167	96%
^A IPT	14278983	0.3663	0.4683	UDP-glucuronosyl transferase	82%	4.00E-54	41%
^G 4CL	4038970	-0.6		4- Coumarate co A ligase	35%	1.00E-97	82%
^{GA} Beta-actin	211236	-0.505		OsRac1, Actin1	64%	0	90%

^A Nodulin-like gene	30699520	-0.4		Nodulin like gene	81%	5.00E-111	41%
^A Nitrilase 2	30692061	0.82	-0.5	Nitrilase like protein	69%	8.00E-123	63%
^A Galactinole Synthase	18391011		0.5679	WSI76 protein induced by water stress	77%	5.00E-132	66%

Photosynthesis related genes

^A Rubisco activase,	23397138	0.6741		Rubisco activase large	83%	0	82%
^A PsaB	5881673	0.5885	0.8486	PSI 700 chlorophyl a apoprotein A2	99%	0	96%
^A PsbA	5881673	0.5474	0.8036	Photosystem II protein D1	99%	0	98%
^A PPDK	186511834		0.3186	Orthophosphate dikinase precursor	98%	0	80%

Mineral partitioning

^A V-type-H ⁺ ATPase-A subunit	186496306	0.6876	0.9196	Vacuolar ATP synthase catalytic subunit A	77%	0	89%
^A V-ATPase c subunit	30692112:120-614	0.4987	1.7645	V-ATPase subunit c	21%	2.00E-35	76%
^A H ⁺ -ATPase a subunit	42569217:84-2549	0.44		Vacuolar proton-ATPase subunit-like protei	55%	1.00E-98	80%
^A Phosphate transporter-PHO1;H3	30678049	0.5631		PHO1-like protein	93%	2.00E-107	30%
^M Na-Pi-Transporter Pht2;1	24079960	-0.33		Putative phosphate transporter 2-1	66%	3.00E-134	56%
^A G subunit	186509658:82-414		2.4869	Vacuolar ATP synthase subunit G 1 (EC 3.6.3.14)	99%	4.00E-30	62%
^A Phosphate transporter-Pht1;4	145360776:175-1779		0.4421	Phosphate transporter 6	95%	0	70%

Osmotic adjustment related gene

^A SAMDC	238479623:595-1695	0.42	1.31	SAMDC family protein	93%	2.00E-89	51%
^A ACC Synthase	1254989	-0.3	1.04	Oryza ACC synthase	39%	2.00E-91	64%
^A ACL (Spermine synthase)	145334518:176-1174	0.4913		Spermine synthase family protein	66%	3.00E-66	56%
^A ADC (Arginine decarboxylase)	30794010		3.385	Oryza sativa Japonica Group arginine decarboxylase mRNA, complete CDS	74%	0	59%
^A Late embryogenesis abundant protein	145334949:123-578	0.3412		Late Embryogenesis Abundant protein Lea14-A	87%	7.00E-20	36%
^A Dehydrin	30693387:49-630	-0.446		Have hsp 70 binding site / Dehydrin RAB 16B	67%	0.002	81%
^A Dehydrin	42570555:500-1282		0.76	Dehydrin COR410 (Cold-induced COR410 protein)	93%	6.00E-16	40%
^A Late embryogenesis abundant protein	27808633		1.7232	Late embryogenesis abundant protein Lea14-A	60%	5.00E-07	43%
^A BADH	31711909		0.3945	Betaine Aldehyde Dehydrogenase (BADH2)	99%	0	74%

ROS (Reactive oxygen species) removal

^A P450(82C2)	18417918	0.5147		Cytochrome P450 family protein	99%	2.00E-93	38%
^A P450(77A4)	30680588:55-1593	0.5083	1.0144	Cytochrome P450 77A2	88%	1.00E-147	54%
^A P450(704A)	186508160:19-1536	0.48		E-class P450, group I family protein	98%	3.00E-99	42%
^A P450(94B1)	30697847:55-1587	-0.435		Cytochrome P450-like protein	90%	3.00E-145	53%
^A Peroxidase,	30690653	0.5114		Peroxidase	75%	4.00E-120	67%
^M COX2	223941909	-0.477		Alpha dioxygenase, animal haem like peroxidase family protein	19%	2.00E-11	21%
COX1(cytochrome C oxidase1)			-0.532	Cytochrome C oxidase subunit 3	99%	0	91%

^A Glutathione transferase	22326539	-0.5	2.17	Glutathione transferase	61%	4.00E-45	47%
^{MG} ABC-type transporter	2625137		0.6309	pdr11 gene for PDR-like ABC transporter	52%	1.00E-99	32%
^A CYP	19310551:10-1116	0.4285	0.5862	Cysteine proteinase 1 precursor (EC 3.4.22.-)	76%	9.00E-137	70%
^A Copper/zinc superoxide dismutase	145335438:27-989		0.4808	Copper/Zinc superoxide dismutase family protein	87%	5.00E-63	55%
^{MG} Metallothionein	46254400		1.45	Oryza sativa (indica cultivar-group) clone OSE-289-384-B5 metallothionein	26%	4.7	1

Defense related gene

^A Avr9 elicitor response protein, putative	145336355	1.1254		avr9 elicitor response-like protein	68%	3.00E-142	61%
^A Thionin Thi2.2	30692991		0.5929	Putative thionin Osth1	43%	6.00E-13	39%
^A Gamma Thionin family			0.5265	Gama-thionin	73%	5.00E-11	56%
^A Chitinase	186507783		0.8247	Chitinase class IVa	67%	2.00E-89	58%
^A IFR	6573168		-0.411	Isoflavone reductase homolog	75%	8.00E-107	61%

Others stress specific and metabolism related gene

^A sHSP c p 2	166759	0.4976	0.9192	Heat shock protein 26	24%	6.00E-41	53%
^A Unknown protein	186523647:929-1858	0.5367		Conserved hypothetical protein	85%	1.00E-92	62%
^G UFGT	148878502	0.4493	0.8558	UDP-glucosyltransferase family protein	96%	3.00E-50	52%
^A Cpn 60-β			2.4188	RuBisCo subunit binding-protein beta subunit	93%	0	84%
^A GDH	1336083		0.5762	Glutamate dehydrogenase ,	76%	0	82%
^A Unknown protein	145340200:35-907	-0.413	-0.754	Conserved hypothetical protein	82%	4.00E-76	57%
^A Tyrosine trans-aminase	30686249:39-1307	-0.426	1.0577	Tyrosine amino transferase	86%	6.00E-83	43%
^H RalA	33946328	0.9909	-0.678	Ras GTPase family protein	79%	2.00E-26	38%
^A ANP1	2342420:1-1987	0.8144		Serine threonine protein kinase	82%	5.00E-145	49%

Probe sources: A, *Arabidopsis thaliana*; H, *Homo sapiens*; G, *Glycine max*; GA, *Gallus gallus*; M, *Medicago truncatula*; MG, *Magnaporthe grisea*

Q.C: query coverage

Fig. S1. Cluster analysis of all genes expressed in Horkuch after 1 h and 24 h of salt stress

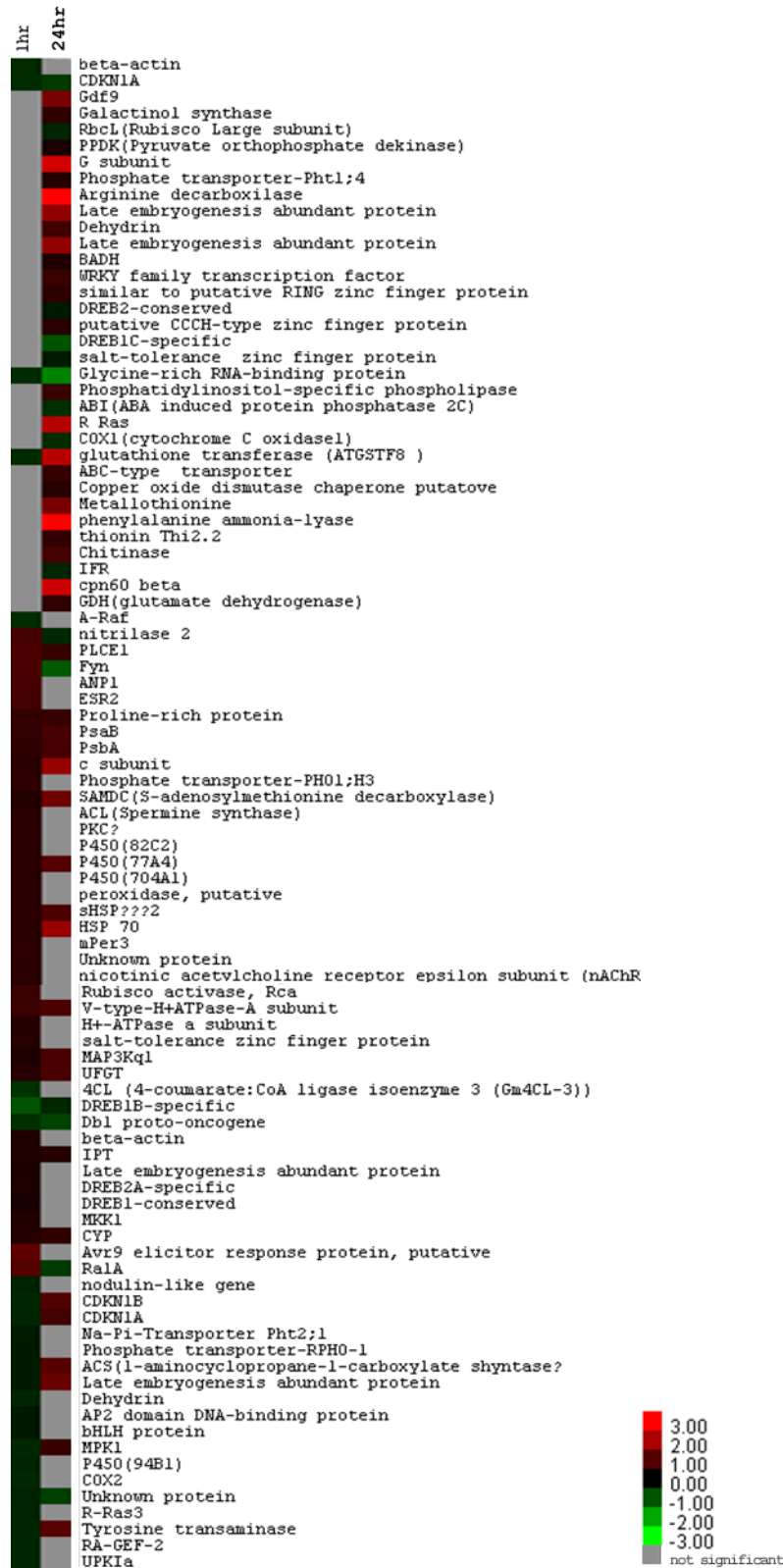


Fig. S2. Comparison of GO terms (biological process and molecular function) associated with differentially expressed genes in Horkuch under 1 h and 24 h of salt stress

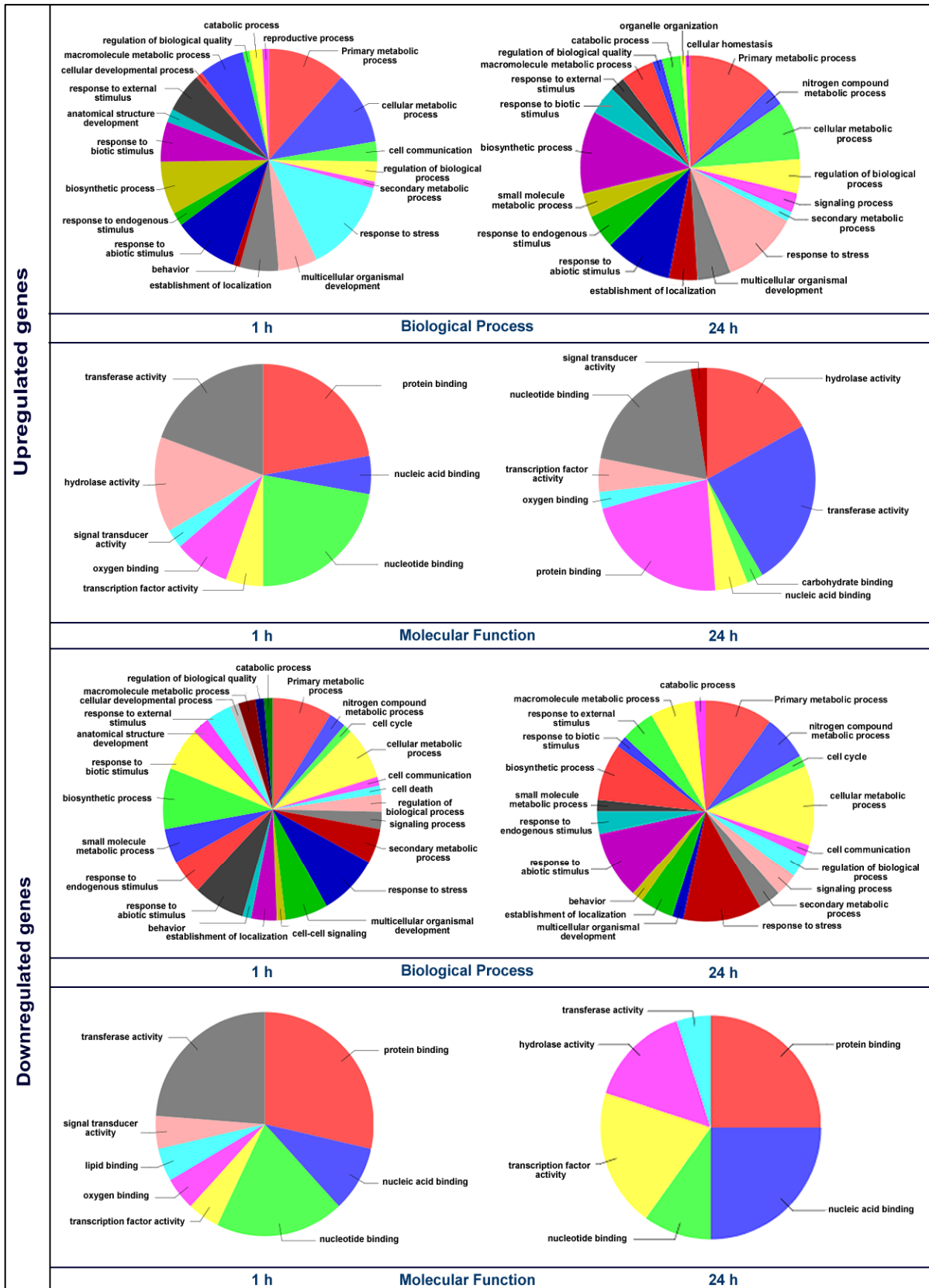


Fig S3. Standard curve for selection of control genes in the microarray experiment

