

**Table S1.** 283 DEGs (178 up-regulated and 105 down-regulated) involved in cotyledons of castor under salt stress.

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
27504.t000004	2.654	1.408	0.00000	Up	<i>Cysteine-rich</i>	cysteine-rich receptor-like protein
					<i>RLK3</i>	kinase 3
27504.t000029	2.078	1.055	0.00018	Up	-	uncharacterized protein LOC8273499
27538.t000015	5.958	2.575	0.00000	Up	-	ubiquitin-like protein 5
27561.t000009	3.660	1.872	0.00121	Up	-	UDP-glucuronosyltransferase, putative
27766.t000007	4.678	2.226	0.00390	Up	-	pathogenesis-related protein PR-1
27789.t000001	2.414	1.271	0.00783	Up	-	aldehyde dehydrogenase family 7 member B4
27894.t000028	0.388	-1.368	0.00009	Down	<i>OsbZIP03</i>	conserved hypothetical protein
27940.t000006	4.909	2.296	0.03419	Up	<i>At-EXPR1</i>	expansin-like B1
27985.t000008	2.983	1.577	0.03568	Up	-	serine-threonine protein kinase, plant-type, putative
27985.t000009	3.521	1.816	0.00292	Up	-	serine-threonine protein kinase, plant-type, putative
28152.t000048	2.986	1.578	0.01622	Up	-	conserved hypothetical protein
28180.t000017	0.393	-1.349	0.00018	Down	<i>Gamma-TIP3</i>	aquaporin TIP1-3
28196.t000005	0.052	-4.262	0.00000	Down	-	flavonoid 3-hydroxylase, putative
28207.t000006	8.387	3.068	0.00000	Up	<i>AS2-like</i> <i>protein 38</i>	LOB domain-containing protein, putative
28219.t000002	2.846	1.509	0.00063	Up	<i>ANAC072</i>	NAC domain-containing protein 72
28327.t000015	0.238	-2.070	0.00125	Down	-	Tyrosine-specific transport protein, putative
						ribulose biphosphate
28345.t000005	4.800	2.263	0.00000	Up	<i>RA 1</i>	carboxylase/oxygenase activase 2, chloroplastic
28345.t000008	5.555	2.474	0.00009	Up	-	subtilisin inhibitor 1, putative
28401.t000005	2.294	1.198	0.00865	Up	<i>PPIase</i> <i>FKBP65</i>	peptidylprolyl isomerase, putative
28623.t000008	6.436	2.686	0.00000	Up	-	uncharacterized protein LOC8286660
28650.t000008	0.231	-2.117	0.02431	Down	-	conserved hypothetical protein
28663.t000002	2.592	1.374	0.00070	Up	<i>AtNSP2</i>	nitrile-specifier protein 5
28752.t000001	0.244	-2.035	0.00982	Down	-	serine-threonine protein kinase, plant-type, putative
28850.t000001	2.256	1.174	0.02475	Up	<i>CER2-like1</i>	protein ECERIFERUM 26
28872.t000005	15.467	3.951	0.00000	Up	-	putative glycine-rich cell wall structural protein 1
28927.t000001	3.674	1.878	0.00000	Up	ABC transporter <i>ABCG.25</i>	ATP-binding cassette transporter, putative
29044.t000010	11.760	3.556	0.00000	Up	<i>LTP</i>	non-specific lipid-transfer protein 1
29485.t000003	3.957	1.985	0.01632	Up	-	small heat shock protein

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29489.t000010	0.185	-2.436	0.01466	Down	-	serine-threonine protein kinase, plant-type, putative
29589.t000028	0.358	-1.481	0.02309	Down	-	protein NUCLEAR FUSION DEFECTIVE 4
29589.t000071	4.379	2.130	0.01748	Up	<i>PRCP</i>	lysosomal Pro-X carboxypeptidase
29596.t000001	9.338	3.223	0.00000	Up	-	uncharacterized protein At5g65660
29601.t000020	15.407	3.946	0.00000	Up	-	protein SLE1 [Ricinus communis]
29610.t000003	5.459	2.449	0.00002	Up	-	17.3 kDa class I heat shock protein [Ricinus communis]
29615.t000004	0.027	-5.197	0.00000	Down	-	conserved hypothetical protein [Ricinus communis]
29628.t000019	0.458	-1.128	0.00221	Down	-	pentatricopeptide repeat-containing protein, putative [Ricinus communis]
29633.t000030	19.629	4.295	0.00440	Up	-	class I heat shock protein [Ricinus communis]
29647.t000065	Inf	Inf	0.01187	Up	<i>LEA D-34</i>	late embryogenesis abundant protein D-34 [Ricinus communis]
29648.t000015	2.366	1.242	0.00002	Up	<i>AtFBL5</i>	F-box protein SKP2A [Ricinus communis]
29656.t000020	0.101	-3.303	0.00544	Down	-	protein NUCLEAR FUSION DEFECTIVE 4
29656.t000021	0.296	-1.758	0.01183	Down	<i>AtOPT7</i>	Oligopeptide transporter, putative
29661.t000036	3.547	1.827	0.00467	Up	-	conserved hypothetical protein
29665.t000004	3.872	1.953	0.00000	Up	-	secoisolaricresinol dehydrogenase
29666.t000042	0.195	-2.361	0.00066	Down	-	polygalacturonase, putative
29667.t000013	2.288	1.194	0.00003	Up	<i>AtOCT7</i>	sugar transporter, putative
29678.t000017	2.350	1.233	0.00965	Up	-	UDP-glycosyltransferase 74E2
29681.t000040	0.214	-2.221	0.00000	Down	-	ammonium transporter 1 member 3
29682.t000035	0.106	-3.239	0.04317	Down	-	uncharacterized protein LOC8288347
29684.t000002	0.087	-3.519	0.00000	Down	<i>PE 35</i>	pectinesterase
29692.t000006	3.061	1.614	0.00000	Up	<i>AtPCR2</i>	protein PLANT CADMIUM RESISTANCE 2
29693.t000012	3.086	1.626	0.00008	Up	-	ornithine aminotransferase, mitochondrial isoform X2
29693.t000021	8.962	3.164	0.00000	Up	-	uncharacterized protein LOC8264084
29693.t000022	35.148	5.135	0.00426	Up	-	serine-threonine protein kinase, plant-type, putative
29701.t000015	2.020	1.014	0.01148	Up	-	GDSL esterase/lipase CPRD49
29703.t000027	12.467	3.640	0.00000	Up	-	vicilin-like antimicrobial peptides 2-2
29703.t000080	7.700	2.945	0.00003	Up	-	uncharacterized protein LOC8285864
29724.t000016	0.194	-2.369	0.01589	Down	-	PREDICTED: 36.4 kDa proline-rich protein

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29724.t000024	3.896	1.962	0.02985	Up	<i>FaGT6</i>	anthocyanidin 3-O-glucosyltransferase 6
29726.t000070	0.315	-1.668	0.00131	Down	-	sugar transporter, putative
29726.t000131	3.179	1.669	0.00005	Up	<i>AtSRG1</i>	protein SRG1
29726.t000175	0.155	-2.688	0.00003	Down	-	phyloplanin
29726.t000176	5.901	2.561	0.00000	Up	-	late embryogenesis abundant protein Lea5 isoform X2
29726.t000183	3.530	1.819	0.00000	Up	-	uncharacterized protein LOC8278753
29727.t000025	0.136	-2.875	0.02270	Down	<i>AtGLO4</i>	peroxisomal (S)-2-hydroxy-acid oxidase GLO4
29729.t000023	0.087	-3.523	0.00000	Down	-	abscisic acid receptor PYL4
29729.t000037	2.585	1.370	0.00013	Up	-	prephenate dehydrogenase, putative
29738.t000053	2.815	1.493	0.00005	Up	-	plastid-lipid-associated protein, chloroplastic
29739.t000038	0.081	-3.618	0.00408	Down	<i>AtMSL10</i>	mechanosensitive ion channel protein 10
29739.t000074	2.537	1.343	0.00015	Up	-	uncharacterized protein LOC8258603
29739.t000120	2.071	1.051	0.00069	Up	<i>AtbHLH66</i>	DNA-directed RNA polymerase beta chain, putative
29739.t000172	6.389	2.675	0.00000	Up	-	protein LAZ1 homolog 2 isoform X1
29747.t000030	0.387	-1.369	0.00001	Down	-	conserved hypothetical protein
29747.t000058	2.408	1.268	0.01031	Up	-	calmodulin binding protein, putative
29751.t000050	0.416	-1.264	0.00403	Down	<i>AtGSTU7</i>	glutathione S-transferase U7
29751.t000055	0.221	-2.176	0.00000	Down	<i>AtGSTU7</i>	glutathione S-transferase U7
29751.t000085	2.344	1.229	0.00132	Up	<i>AtPP2C03</i>	protein phosphatase 2c, putative
29753.t000013	2.060	1.042	0.01827	Up	-	conserved hypothetical protein
29757.t000029	4.872	2.284	0.00024	Up	-	conserved hypothetical protein
29757.t000038	0.065	-3.953	0.00000	Down	-	conserved hypothetical protein
29761.t000013	4.586	2.197	0.00021	Up	-	hydrolase, hydrolyzing O-glycosyl compounds, putative
29780.t000063	10.454	3.386	0.00000	Up	-	non-specific lipid-transfer protein 4.1
29780.t000072	0.305	-1.711	0.00001	Down	-	aldo-keto reductase, putative
29783.t000016	2.176	1.122	0.00007	Up	-	uncharacterized protein DDB_G0282077
29785.t000013	2.418	1.274	0.00688	Up	<i>NC2-alpha</i>	dr1-associated corepressor
29788.t000008	2.049	1.035	0.03763	Up	-	12S seed storage globulin 1
29788.t000021	0.289	-1.789	0.00072	Down	<i>Gamma-TIP3</i>	aquaporin TIP1-3
29792.t000014	4.288	2.100	0.00001	Up	-	probable E3 ubiquitin-protein ligase XERICO
29792.t000018	0.426	-1.230	0.03445	Down	-	Alpha-L-fucosidase 2 precursor, putative
29792.t000019	0.407	-1.295	0.03394	Down	-	Alpha-L-fucosidase 2 precursor

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29794.t000038	0.454	-1.138	0.02290	Down	-	pollen-specific protein SF21
29794.t000071	3.776	1.917	0.00192	Up	<i>BnIII</i>	Oleosin, putative
29794.t000085	2.758	1.464	0.00000	Up	-	Protein pim1, putative
29794.t000108	4.003	2.001	0.00053	Up	-	Histidine-containing phosphotransfer protein, putative
29801.t000139	0.314	-1.671	0.00265	Down	-	protein PLANT CADMIUM RESISTANCE 2
29804.t000064	0.281	-1.829	0.00001	Down	<i>AtOPT4</i>	oligopeptide transporter 4
29806.t000002	0.475	-1.073	0.00703	Down	<i>DcPSKR1</i>	phytosulfokine receptor 1
29807.t000010	0.065	-3.951	0.00004	Down	-	conserved hypothetical protein
29810.t000003	19.803	4.308	0.00000	Up	-	E3 ubiquitin-protein ligase ATL31
29813.t000070	2.482	1.311	0.03695	Up	-	cytochrome P450 704B1
29815.t000004	15.568	3.961	0.00138	Up	-	GDSL esterase/lipase At5g03820
29815.t000032	78.393	6.293	0.04383	Up	-	cytochrome P450 76A1
29820.t000023	0.067	-3.906	0.00000	Down	-	abscisic acid receptor PYL4
29822.t000169	9.480	3.245	0.00001	Up	-	conserved hypothetical protein
29825.t000015	0.240	-2.060	0.00005	Down	-	DUF21 domain-containing protein At2g14520 isoform X2
29827.t000092	0.362	-1.467	0.04263	Down	-	transferase, putative
29827.t000113	14.793	3.887	0.00000	Up	-	conserved hypothetical protein
29830.t000067	3.418	1.773	0.00000	Up	-	conserved hypothetical protein
29836.t000002	50.598	5.661	0.00000	Up	-	conserved hypothetical protein
29836.t000015	6.108	2.611	0.00002	Up	<i>ATP-PFK 2</i>	phosphofructokinase, putative
29838.t000086	0.063	-3.994	0.03079	Down	-	conserved hypothetical protein
29841.t000023	0.005	-7.642	0.02768	Down	-	gibberellin 3-beta hydroxylase, putative
29841.t000070	Inf	Inf	0.00060	Up	-	late embryogenesis abundant protein D-7
29841.t000092	26.129	4.708	0.01215	Up	-	metallothiol transferase FosB
29841.t000117	10.106	3.337	0.00000	Up	-	aspartate, glycine, lysine and serine-rich protein
29841.t000174	0.295	-1.763	0.01900	Down	-	arsenite transport protein, putative
29842.t000053	2.638	1.399	0.00000	Up	-	aspartic proteinase
29842.t000126	0.396	-1.335	0.03470	Down	<i>AtBGLU47</i>	beta-glucosidase 46 isoform X1
29844.t000021	0.064	-3.969	0.00004	Down	-	auxin-responsive protein IAA4
29844.t000033	2.779	1.475	0.02277	Up	<i>KCS-20</i>	acyltransferase, putative
29844.t000045	5.027	2.330	0.00002	Up	-	vegetative cell wall protein gp1
29844.t000054	7.680	2.941	0.00000	Up	-	putative calcium-transporting ATPase 13, plasma membrane-type
29844.t000066	4.947	2.307	0.01358	Up	<i>ELIP</i>	early light-induced protein, chloroplastic
29851.t000069	3.972	1.990	0.00000	Up	-	uncharacterized protein LOC8279516 isoform X1

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29851.t000118	7.477	2.902	0.00000	Up	-	uncharacterized WD repeat-containing protein all2124
29851.t000125	2.689	1.427	0.00001	Up	-	conserved hypothetical protein
29851.t000145	0.482	-1.052	0.00066	Down	<i>AtCBP1</i>	conserved hypothetical protein
29863.t000015	0.306	-1.708	0.02585	Down	<i>AtCesA2</i>	cellulose synthase A catalytic subunit 5 [UDP-forming]
29864.t000073	0.193	-2.371	0.00000	Down	-	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1
29869.t000041	8.179	3.032	0.00000	Up	<i>AtHsp22.0</i>	22.7 kDa class IV heat shock protein
29877.t000013	7.894	2.981	0.00000	Up	<i>AtHIP23</i>	heavy metal-associated isoprenylated plant protein 26
29878.t000010	0.422	-1.245	0.04730	Down	-	conserved hypothetical protein
29883.t000047	0.307	-1.705	0.00000	Down	-	auxin-induced protein 22E
29889.t000030	0.120	-3.056	0.00000	Down	-	uncharacterized protein LOC8258783
29889.t000044	3.510	1.811	0.00036	Up	<i>AtbZIP1</i>	Ocs element-binding factor, putative
29889.t000095	10.129	3.340	0.02483	Up	-	enzyme inhibitor, putative
29889.t000096	5.694	2.510	0.00085	Up	<i>AtC/VIF1</i>	cell wall / vacuolar inhibitor of fructosidase 1
29889.t000116	2.428	1.280	0.00064	Up	-	transcription factor MYB108
29895.t000004	3.542	1.825	0.00000	Up	<i>ADF</i>	actin-depolymerizing factor
29895.t000011	5.121	2.356	0.00309	Up	-	conserved hypothetical protein
29898.t000003	0.241	-2.055	0.00000	Down	-	probable pectate lyase 13
29900.t000034	0.454	-1.139	0.00800	Down	<i>OsNCL2</i>	calmodulin, putative
29900.t000061	0.105	-3.249	0.00219	Down	-	protein CHUP1, chloroplastic
29900.t000076	4.933	2.302	0.03385	Up	-	uncharacterized protein LOC8259230
29900.t000079	0.380	-1.396	0.00003	Down	<i>AtHIP28</i>	copper ion binding protein, putative
29901.t000011	0.191	-2.387	0.00144	Down	-	cytochrome P450, putative
29904.t000112	4.609	2.205	0.01069	Up	-	uncharacterized PE-PGRS family protein PE_PGRS46
29907.t000020	0.392	-1.352	0.00726	Down	-	conserved hypothetical protein
29907.t000033	0.202	-2.310	0.00313	Down	<i>AtOPR1</i>	12-oxophytodienoate reductase opr, putative
29908.t000032	14.080	3.816	0.00001	Up	<i>AtHIP24</i>	metal ion binding protein, putative
29908.t000100	0.310	-1.692	0.00373	Down	<i>GjUGT2</i>	7-deoxyloganetin glucosyltransferase
29908.t000108	4.244	2.086	0.00001	Up	-	protein EXORDIUM
29908.t000110	4.250	2.087	0.00000	Up	-	protein EXORDIUM-like 2
29912.t000073	0.217	-2.201	0.03547	Down	<i>AtMIOX4</i>	PREDICTED: inositol oxygenase 4
29912.t000151	0.145	-2.782	0.00924	Down	-	dipeptidase, putative
29912.t000165	0.212	-2.240	0.00398	Down	<i>AtDTX51</i>	protein DETOXIFICATION 52
29912.t000219	2.366	1.242	0.00001	Up	-	sugar transporter, putative
29915.t000001	3.432	1.779	0.00000	Up	<i>LTP</i>	non-specific lipid-transfer protein 1
29916.t000019	2.883	1.528	0.00000	Up	<i>AtHsp23.6</i>	small heat shock protein, chloroplastic

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29924.t000001	0.412	-1.281	0.00071	Down	<i>AtBGLU44</i>	beta-glucosidase 44
29929.t000114	0.237	-2.074	0.00000	Down	-	ACT domain-containing protein ACR4
29929.t000135	37.381	5.224	0.00000	Up	-	uncharacterized protein LOC8286778
29933.t000025	0.421	-1.249	0.00071	Down	<i>atDjC76</i>	heat shock protein binding protein, putative
29933.t000061	2.550	1.351	0.00009	Up	<i>AtMYB102</i>	r2r3-myb transcription factor, putative
29933.t000062	28.415	4.829	0.00000	Up	-	phosphatidylethanolamine-binding protein, putative
29933.t000068	0.206	-2.276	0.00000	Down	<i>AtENT3</i>	equilibrative nucleotide transporter 3
29933.t000069	0.343	-1.542	0.00000	Down	-	uncharacterized protein LOC8275382
29948.t000018	0.356	-1.491	0.01327	Down	-	endoglucanase 11
29983.t000020	2.235	1.160	0.01417	Up	-	nucleic acid binding protein, putative
<i>Arabidopsis</i>						
29983.t000080	0.410	-1.286	0.00726	Down	<i>thaliana</i>	probable L-type lectin-domain
					<i>lectin-recepto</i>	containing receptor kinase VII.2
					<i>r kinase d</i>	
29983.t000126	2.265	1.179	0.00011	Up	<i>AtERF53</i>	ethylene-responsive transcription factor ERF054
29983.t000156	0.189	-2.404	0.00001	Down	-	formimidoyltransferase-cyclodeaminase isoform X3
29993.t000017	0.413	-1.277	0.00510	Down	-	probable galacturonosyltransferase 15
29993.t000024	5.415	2.437	0.00000	Up	<i>At-XTH15</i>	xyloglucan
						endotransglucosylase/hydrolase 2
30003.t000020	56.989	5.833	0.00001	Up	<i>(1-&gt;3)-beta-g</i>	Glucan endo-1,3-beta-glucosidase
					<i>lucanase</i>	precursor, putative
30003.t000021	3.394	1.763	0.00086	Up	<i>(1-&gt;3)-beta-g</i> <i>lucanase</i>	glucan endo-1,3-beta-glucosidase
30027.t000020	2.291	1.196	0.00366	Up	-	uncharacterized protein LOC8282436
30027.t000022	7.619	2.930	0.01649	Up	-	uncharacterized protein LOC8282438
30032.t000010	0.301	-1.731	0.01711	Down	<i>PRCP</i>	lysosomal Pro-X carboxypeptidase isoform X1
30060.t000022	0.185	-2.434	0.00107	Down	-	protein EXORDIUM-like 7
30064.t000028	3.401	1.766	0.00001	Up	<i>AtWRKY6</i>	probable WRKY transcription factor 31
30068.t000007	0.188	-2.414	0.00004	Down	<i>AtCslG3</i>	transferase, putative
30068.t000048	0.298	-1.747	0.00000	Down	<i>AtOPT7</i>	oligopeptide transporter 7
30068.t000068	0.024	-5.352	0.00000	Down	-	cytochrome P450 78A9
30073.t000078	12.282	3.618	0.04996	Up	-	PREDICTED: bark storage protein A
30074.t000080	3.074	1.620	0.00023	Up	-	conserved hypothetical protein
30076.t000001	0.353	-1.504	0.00650	Down	-	uncharacterized protein LOC8265172
30076.t000026	49.423	5.627	0.00001	Up	<i>S3H DLO1</i>	1-aminocyclopropane-1-carboxylate oxidase 5

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
30076.t000077	64.896	6.020	0.04481	Up	-	mannan endo-1,4-beta-mannosidase 4
30076.t000087	0.344	-1.537	0.00089	Down	-	hypothetical protein RCOM_1342140
30076.t000171	2.044	1.031	0.00042	Up	<i>AtMYB78</i>	transcription factor MYB108
30076.t000182	3.578	1.839	0.00000	Up	<i>AtGPAT3</i>	Glycerol-3-phosphate acyltransferase, putative
30076.t000239	0.482	-1.054	0.03086	Down	<i>AtBXL2</i>	probable beta-D-xylosidase 2
30076.t000266	5.029	2.330	0.00000	Up	-	uncharacterized protein LOC8265165
30078.t000023	0.275	-1.863	0.00947	Down	-	retinoid-inducible serine carboxypeptidase, putative
30091.t000001	0.222	-2.172	0.04931	Down	<i>Ps6OMT</i>	3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase 2
30099.t000062	0.298	-1.746	0.00275	Down	-	uncharacterized protein LOC8268907
30099.t000076	3.075	1.621	0.00001	Up	<i>AtEGY3</i>	probable zinc metallopeptidase EGY3, chloroplastic
30099.t000103	0.450	-1.151	0.00092	Down	-	serine carboxypeptidase, putative
30114.t000003	0.356	-1.489	0.00499	Down	-	putative glutamine amidotransferase YLR126C
30115.t000049	0.000	#NAM E?	0.03013	Down	-	uncharacterized protein LOC8270745
30116.t000010	4.257	2.090	0.00000	Up	-	Basic blue protein, putative
30116.t000011	5.736	2.520	0.00005	Up	-	conserved hypothetical protein
30128.t000001	0.316	-1.662	0.01695	Down	<i>AtDUF7</i>	uncharacterized protein LOC8285676 isoform X2
30128.t000039	3.655	1.870	0.00030	Up	<i>AtHAK1</i>	Potassium transporter, putative
30128.t000040	4.162	2.057	0.00003	Up	<i>AtHAK1</i>	Potassium transporter, putative
30128.t000181	0.471	-1.087	0.01821	Down	-	uncharacterized protein LOC8285509
30128.t000370	2.264	1.179	0.00002	Up	-	nicotianamine synthase
30128.t000417	8.139	3.025	0.00000	Up	-	histone chaperone ASF1
30128.t000505	8.849	3.146	0.00000	Up	-	GEM-like protein 5
30129.t000022	13.699	3.776	0.00011	Up	<i>AtTSPO</i>	translocator protein homolog
30130.t000009	0.215	-2.220	0.00065	Down	-	phototropin-1
30131.t000021	0.165	-2.601	0.00001	Down	-	conserved hypothetical protein
30131.t000022	0.187	-2.416	0.00009	Down	-	serine-threonine protein kinase, plant-type, putative
30131.t000160	2.136	1.095	0.00253	Up	<i>RcCASPLIF2</i>	RecName: Full=CASP-like protein 1F2,Short=RcCASPL1F2
30131.t000411	0.324	-1.626	0.00497	Down	-	GEM-like protein 4
30136.t000020	7.718	2.948	0.00003	Up	-	uncharacterized protein LOC8259126
30136.t000048	107.578	6.749	0.00065	Up	-	uncharacterized protein LOC8259154
30138.t000158	31.541	4.979	0.00000	Up	-	chaperone protein ClpB1
30138.t000195	0.414	-1.273	0.00001	Down	<i>AtbHLH72</i>	DNA binding protein, putative
30138.t000233	5.504	2.460	0.00073	Up	<i>AtEXPA15</i>	expansin-A15

Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
30143.t000033	2.877	1.525	0.00000	Up	<i>P5CS</i>	delta-1-pyrroline-5-carboxylate synthase
30143.t000059	4.841	2.275	0.00452	Up	-	uncharacterized protein LOC8287504
30146.t000007	7.238	2.856	0.00006	Up	-	conserved hypothetical protein
30146.t000011	2.894	1.533	0.00000	Up	-	hypothetical protein RCOM_1485780
30146.t000085	2.264	1.179	0.00052	Up	-	histidine-containing phosphotransfer protein 4
30147.t000015	78.866	6.301	0.02086	Up	-	hypothetical protein RCOM_1496000
30147.t000045	6.764	2.758	0.00000	Up	-	uncharacterized protein LOC8266341
30147.t000145	4.551	2.186	0.00000	Up	-	C2 and GRAM domain-containing protein At5g50170 isoform X1
30147.t000391	0.341	-1.554	0.02536	Down	-	Phytochrome kinase substrate, putative
30147.t000507	5.679	2.506	0.00000	Up	-	conserved hypothetical protein
30147.t000584	7.645	2.934	0.00000	Up	<i>Protein DREB1A</i>	dehydration-responsive element-binding protein 1A
30147.t000595	2.866	1.519	0.03395	Up	-	conserved hypothetical protein
30147.t000657	7.673	2.940	0.02132	Up	-	uncharacterized protein LOC8277423
30147.t000725	5.773	2.529	0.00002	Up	-	calmodulin binding protein, putative
30147.t000754	12.387	3.631	0.00000	Up	-	MADS-box transcription factor, putative
30147.t000803	0.352	-1.505	0.00368	Down	-	leucine-rich repeat protein, putative
30156.t000039	4.572	2.193	0.00000	Up	<i>AtBBX30</i>	DNA binding protein, putative
30169.t000292	17.880	4.160	0.00000	Up	<i>OsPP2C08</i>	probable protein phosphatase 2C 51
30169.t000342	5.003	2.323	0.00000	Up	-	G-type lectin S-receptor-like serine/threonine-protein kinase At5g24080
30169.t000349	9.391	3.231	0.03464	Up	-	late embryogenesis abundant protein At1g64065
30170.t000054	3.219	1.687	0.00196	Up	<i>EPF-like protein 2</i>	EPIDERMAL PATTERNING FACTOR-like protein 2
30170.t000064	3.202	1.679	0.00252	Up	<i>HlBCAT1</i>	branched-chain amino acid aminotransferase, putative
30170.t000232	3.524	1.817	0.00000	Up	-	uncharacterized protein LOC8288554
30170.t000289	3.326	1.734	0.00013	Up	-	alpha-amylase
30170.t000298	0.215	-2.220	0.00000	Down	-	conserved hypothetical protein
30170.t000370	Inf	Inf	0.03232	Up	-	cytochrome P450 CYP82D47
30170.t000474	0.222	-2.172	0.00013	Down	-	uncharacterized protein LOC8288949
30170.t000484	2.508	1.326	0.02754	Up	<i>DFR</i>	dihydroflavonol-4-reductase
30170.t000491	0.091	-3.452	0.00561	Down	-	jasmonate O-methyltransferase
30170.t000565	10.639	3.411	0.01098	Up	-	cytochrome P450 83B1
30170.t000594	3.217	1.686	0.00000	Up	-	conserved hypothetical protein
30170.t000619	0.409	-1.290	0.00000	Down	-	cytochrome P450 81E8



Table S1 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
30170.t000624	0.212	-2.238	0.00449	Down	-	putative receptor protein kinase ZmPK1
30170.t000692	3.010	1.590	0.00045	Up	-	E3 ubiquitin-protein ligase ATL23
30170.t000693	4.203	2.072	0.00000	Up	<i>OsNrx2</i>	probable nucleoredoxin 2 isoform X4
30170.t000710	12.610	3.656	0.00833	Up	<i>ODC</i>	ornithine decarboxylase
30170.t000711	3.179	1.669	0.02341	Up	<i>ODC</i>	ornithine decarboxylase isoform X1
30170.t000771	2.389	1.257	0.00001	Up	-	starch branching enzyme II, putative
30170.t000790	0.230	-2.122	0.00016	Down	-	calcium lipid binding protein, putative
					<i>Sphingoid</i>	
30174.t000076	0.162	-2.629	0.00000	Down	<i>LCB</i>	delta(8)-fatty-acid desaturase 2
					<i>desaturase 2</i>	
30174.t000082	8.883	3.151	0.00000	Up	-	BAG family molecular chaperone regulator 6
30174.t000125	4.161	2.057	0.00000	Up	<i>BnIII</i>	oleosin 1
30174.t000270	3.381	1.758	0.00012	Up	-	leucine rich repeat receptor kinase, putative
30174.t000472	3.936	1.977	0.04577	Up	-	conserved hypothetical protein
30174.t000495	3.254	1.702	0.00000	Up	<i>ABIS-binding protein 2</i>	ninja-family protein AFP2 isoform X1
30174.t000550	17.454	4.126	0.00021	Up	<i>POMGnT2</i>	glycosyltransferase, putative
30179.t000016	0.283	-1.820	0.00003	Down	-	serine-threonine protein kinase, plant-type, putative
						xyloglucan
30179.t000018	Inf	Inf	0.02919	Up	<i>At-XTH22</i>	endotransglucosylase/hydrolase protein 22
30179.t000025	20.590	4.364	0.00007	Up	<i>At-XTH25</i>	xyloglucan:xyloglucosyl transferase, putative
30183.t000014	14.374	3.845	0.00000	Up	<i>OC-X</i>	cysteine proteinase inhibitor 5
30190.t000051	0.344	-1.539	0.00830	Down	-	hypothetical protein RCOM_1691440
30190.t000145	0.343	-1.544	0.00069	Down	-	anthocyanidin 3-O-glucosyltransferase
30190.t000196	0.490	-1.029	0.01162	Down	-	uncharacterized protein LOC8271767
30190.t000213	18.712	4.226	0.00000	Up	-	uncharacterized protein LOC8271784
30190.t000497	3.496	1.806	0.00000	Up	-	conserved hypothetical protein
30190.t000498	4.593	2.199	0.00000	Up	<i>GenCHYB</i>	beta-carotene 3-hydroxylase, chloroplastic isoform X1
30190.t000545	4.516	2.175	0.00000	Up	<i>DROJ1</i>	dnaJ homolog subfamily B member 13
30190.t000559	0.368	-1.444	0.00614	Down	<i>AtERF12</i>	ethylene-responsive transcription factor 12
30204.t000008	4.299	2.104	0.00002	Up	-	uncharacterized protein LOC8264934 isoform X1
30226.t000067	3.423	1.775	0.00117	Up	<i>AtXYLP9</i>	lipid binding protein, putative
33363.t000001	2.180	1.125	0.00928	Up	-	aldehyde dehydrogenase family 7

**Table S1 (continued)**

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
38153.t000001	3.814	1.931	0.00001	Up	-	conserved hypothetical protein, partial
49862.t000001	0.178	-2.487	0.02084	Down	<i>S3H DLO1</i>	Flavonol synthase/flavanone 3-hydroxylase, putative, partial

**Table S2.** 283 DEGs (176 up-regulated and 107 down-regulated) involved in roots of castor under salt stress.

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
27504.t000004	2.332	1.221	0.00332	Up	<i>Cysteine-rich</i> <i>RLK3</i>	cysteine-rich receptor-like protein kinase 3
27504.t000029	2.001	1.001	0.01008	Up	-	uncharacterized protein LOC8273499
27538.t000015	2.812	1.492	0.00058	Up	-	ubiquitin-like protein 5
27561.t000009	0.115	-3.126	0.01318	Down	-	UDP-glucuronosyltransferase, putative
27766.t000007	3.245	1.698	0.00000	Up	-	pathogenesis-related protein PR-1
27789.t000001	2.197	1.136	0.00000	Up	-	aldehyde dehydrogenase family 7 member B4
27894.t000028	0.395	-1.339	0.00020	Down	<i>OsbZIP03</i>	conserved hypothetical protein
27940.t000006	2.386	1.255	0.00000	Up	<i>At-EXPR1</i>	expansin-like B1
27985.t000008	0.449	-1.156	0.00350	Down	-	serine-threonine protein kinase, plant-type, putative
27985.t000009	3.120	1.642	0.01621	Up	-	serine-threonine protein kinase, plant-type, putative
28152.t000048	6.927	2.792	0.00000	Up	-	conserved hypothetical protein
28180.t000017	0.294	-1.764	0.00760	Down	<i>Gamma-TIP3</i>	aquaporin TIP1-3
28196.t000005	0.122	-3.033	0.02904	Down	-	flavonoid 3-hydroxylase, putative
28207.t000006	2.451	1.293	0.00091	Up	<i>AS2-like</i> <i>protein 38</i>	LOB domain-containing protein, putative
28219.t000002	3.983	1.994	0.00000	Up	<i>ANAC072</i>	NAC domain-containing protein 72
28327.t000015	0.132	-2.919	0.00770	Down	-	Tyrosine-specific transport protein, putative
28345.t000005	2.505	1.325	0.00816	Up	<i>RA 1</i>	ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic
28345.t000008	3.390	1.761	0.00143	Up	-	subtilisin inhibitor 1, putative
28401.t000005	0.259	-1.948	0.02279	Down	<i>PPIase</i> <i>FKBP65</i>	peptidylprolyl isomerase, putative
28623.t000008	0.498	-1.006	0.00000	Down	-	uncharacterized protein LOC8286660
28650.t000008	0.159	-2.653	0.00000	Down	-	conserved hypothetical protein
28663.t000002	2.047	1.034	0.00000	Up	<i>AtNSP2</i>	nitrile-specifier protein 5
28752.t000001	0.383	-1.383	0.00045	Down	-	serine-threonine protein kinase, plant-type, putative
28850.t000001	4.008	2.003	0.00000	Up	<i>CER2-like1</i>	protein ECERIFERUM 26
28872.t000005	23.303	4.542	0.00000	Up	-	putative glycine-rich cell wall structural protein 1
28927.t000001	2.545	1.348	0.00000	Up	<i>ABC</i> <i>transporter</i> <i>ABCG.25</i>	ATP-binding cassette transporter, putative
29044.t000010	2.428	1.280	0.02319	Up	<i>LTP</i>	non-specific lipid-transfer protein 1
29485.t000003	3.688	1.883	0.03180	Up	-	small heat shock protein, chloroplastic isoform X1

Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29489.t000010	0.491	-1.026	0.00132	Down	-	serine-threonine protein kinase, plant-type, putative
29589.t000028	0.494	-1.019	0.00002	Down	-	protein NUCLEAR FUSION DEFECTIVE 4
29589.t000071	3.273	1.711	0.01582	Up	<i>PRCP</i>	lysosomal Pro-X carboxypeptidase
29596.t000001	5.824	2.542	0.00000	Up	-	uncharacterized protein At5g65660
29601.t000020	4.012	2.004	0.00000	Up	-	protein SLE1
29610.t000003	5.156	2.366	0.01197	Up	-	17.3 kDa class I heat shock protein
29615.t000004	0.293	-1.773	0.03231	Down	-	conserved hypothetical protein
29628.t000019	2.359	1.238	0.02768	Up	-	pentatricopeptide repeat-containing protein, putative
29633.t000030	24.705	4.627	0.00652	Up	-	class I heat shock protein
29647.t000065	Inf	Inf	0.04849	Up	<i>LEA D-34</i>	late embryogenesis abundant protein D-34
29648.t000015	2.974	1.572	0.00000	Up	<i>AtFBL5</i>	F-box protein SKP2A
29656.t000020	3.588	1.843	0.00721	Up	-	protein NUCLEAR FUSION DEFECTIVE 4
29656.t000021	0.326	-1.617	0.00068	Down	<i>AtOPT7</i>	Oligopeptide transporter, putative
29661.t000036	2.034	1.024	0.00001	Up	-	conserved hypothetical protein
29665.t000004	4.782	2.258	0.00000	Up	-	secoisolariciresinol dehydrogenase
29666.t000042	2.156	1.108	0.00474	Up	-	polygalacturonase, putative
29667.t000013	2.583	1.369	0.00000	Up	<i>AtOCT7</i>	sugar transporter, putative
29678.t000017	2.496	1.320	0.00636	Up	-	UDP-glycosyltransferase 74E2
29681.t000040	0.484	-1.048	0.01924	Down	-	ammonium transporter 1 member 3
29682.t000035	0.287	-1.801	0.00000	Down	-	uncharacterized protein LOC8288347
29684.t000002	0.404	-1.308	0.00158	Down	<i>PE 35</i>	pectinesterase
29692.t000006	2.125	1.087	0.00000	Up	<i>AtPCR2</i>	protein PLANT CADMIUM RESISTANCE 2
29693.t000012	2.518	1.332	0.00000	Up	-	ornithine aminotransferase, mitochondrial isoform X2
29693.t000021	Inf	Inf	0.00001	Up	-	uncharacterized protein LOC8264084
29693.t000022	13.366	3.741	0.01486	Up	-	serine-threonine protein kinase, plant-type, putative
29701.t000015	3.641	1.864	0.00000	Up	-	GDSL esterase/lipase CPRD49
29703.t000027	2.353	1.235	0.02389	Up	-	vicilin-like antimicrobial peptides 2-2
29703.t000080	4.571	2.193	0.00000	Up	-	uncharacterized protein LOC8285864
29724.t000016	0.424	-1.238	0.00000	Down	-	36.4 kDa proline-rich protein
29724.t000024	2.172	1.119	0.03313	Up	<i>FaGT6</i>	anthocyanidin 3-O-glucosyltransferase 6
29726.t000070	0.332	-1.589	0.00046	Down	-	sugar transporter, putative
29726.t000131	0.370	-1.436	0.01937	Down	<i>AtSRG1</i>	protein SRG1
29726.t000175	0.045	-4.487	0.00212	Down	-	phylloplanin
29726.t000176	4.783	2.258	0.00000	Up	-	late embryogenesis abundant protein Lea5 isoform X2

Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29726.t000183	2.897	1.535	0.00000	Up	-	uncharacterized protein LOC8278753
29727.t000025	0.066	-3.920	0.00000	Down	<i>AtGLO4</i>	peroxisomal (S)-2-hydroxy-acid oxidase GLO4
29729.t000023	0.194	-2.364	0.00000	Down	-	abscisic acid receptor PYL4
29729.t000037	2.059	1.042	0.00141	Up	-	prephenate dehydrogenase, putative
29738.t000053	2.142	1.099	0.00000	Up	-	plastid-lipid-associated protein, chloroplastic
29739.t000038	0.440	-1.186	0.00000	Down	<i>AtMSL10</i>	mechanosensitive ion channel protein 10
29739.t000074	2.238	1.162	0.00408	Up	-	uncharacterized protein LOC8258603
29739.t000120	2.074	1.052	0.00000	Up	<i>AtbHLH66</i>	DNA-directed RNA polymerase beta chain, putative
29739.t000172	6.347	2.666	0.00708	Up	-	protein LAZ1 homolog 2 isoform X1
29747.t000030	2.200	1.137	0.00016	Up	-	conserved hypothetical protein
29747.t000058	0.343	-1.544	0.00307	Down	-	calmodulin binding protein, putative
29751.t000050	2.185	1.128	0.00000	Up	<i>AtGSTU7</i>	glutathione S-transferase U7
29751.t000055	0.404	-1.306	0.00000	Down	<i>AtGSTU7</i>	glutathione S-transferase U7
29751.t000085	6.076	2.603	0.00000	Up	<i>AtPP2C03</i>	protein phosphatase 2c, putative
29753.t000013	2.320	1.214	0.01654	Up	-	conserved hypothetical protein
29757.t000029	88.062	6.460	0.00000	Up	-	conserved hypothetical protein
29757.t000038	0.230	-2.121	0.00000	Down	-	conserved hypothetical protein
29761.t000013	2.189	1.130	0.00000	Up	-	hydrolase, hydrolyzing O-glycosyl compounds, putative
29780.t000063	3.204	1.680	0.00000	Up	-	non-specific lipid-transfer protein 4.1
29780.t000072	0.229	-2.124	0.00000	Down	-	aldo-keto reductase, putative
29783.t000016	5.127	2.358	0.00000	Up	-	uncharacterized protein DDB_G0282077
29785.t000013	2.268	1.181	0.00111	Up	<i>NC2-alpha</i>	dr1-associated corepressor
29788.t000008	2.702	1.434	0.00000	Up	-	12S seed storage globulin 1
29788.t000021	0.331	-1.595	0.00372	Down	<i>Gamma-TIP3</i>	aquaporin TIP1-3
29792.t000014	2.351	1.234	0.00000	Up	-	probable E3 ubiquitin-protein ligase XERICO
29792.t000018	0.421	-1.249	0.00000	Down	-	Alpha-L-fucosidase 2 precursor, putative
29792.t000019	0.223	-2.168	0.00000	Down	-	Alpha-L-fucosidase 2 precursor, putative
29794.t000038	0.347	-1.528	0.00000	Down	-	pollen-specific protein SF21
29794.t000071	5.449	2.446	0.04160	Up	<i>BnIII</i>	Oleosin, putative
29794.t000085	2.786	1.478	0.00000	Up	-	Protein pim1, putative
29794.t000108	2.885	1.528	0.02552	Up	-	Histidine-containing phosphotransfer protein, putative
29801.t000139	0.474	-1.076	0.01712	Down	-	protein PLANT CADMIUM RESISTANCE 2
29804.t000064	0.178	-2.487	0.00000	Down	<i>AtOPT4</i>	oligopeptide transporter 4
29806.t000002	0.198	-2.335	0.01478	Down	<i>DcPSKRI</i>	phytosulfokine receptor 1
29807.t000010	0.310	-1.692	0.00000	Down	-	conserved hypothetical protein

Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29810.t000003	3.822	1.934	0.00003	Up	-	E3 ubiquitin-protein ligase ATL31
29813.t000070	6.783	2.762	0.00001	Up	-	cytochrome P450 704B1
29815.t000004	3.902	1.964	0.00000	Up	-	GDSL esterase/lipase At5g03820
29815.t000032	6.390	2.676	0.00000	Up	-	cytochrome P450 76A1
29820.t000023	0.222	-2.170	0.00000	Down	-	abscisic acid receptor PYL4
29822.t000169	5.139	2.362	0.00000	Up	-	conserved hypothetical protein
29825.t000015	2.753	1.461	0.00001	Up	-	DUF21 domain-containing protein
29827.t000092	0.007	-7.096	0.00000	Down	-	At2g14520 isoform X2
29827.t000113	3.388	1.761	0.00011	Up	-	transferase, putative
29830.t000067	2.447	1.291	0.00000	Up	-	conserved hypothetical protein
29836.t000002	5.811	2.539	0.00000	Up	-	conserved hypothetical protein
29836.t000015	2.714	1.440	0.00153	Up	<i>ATP-PFK 2</i>	phosphofructokinase, putative
29838.t000086	0.000	#NAME?	0.00860	Down	-	conserved hypothetical protein
29841.t000023	0.384	-1.381	0.00000	Down	-	gibberellin 3-beta hydroxylase, putative
29841.t000070	8.410	3.072	0.00576	Up	-	late embryogenesis abundant protein D-7
29841.t000092	2.314	1.211	0.00000	Up	-	metallothiol transferase FosB
29841.t000117	29.047	4.860	0.00005	Up	-	aspartate, glycine, lysine and serine-rich protein
29841.t000174	0.203	-2.302	0.00000	Down	-	arsenite transport protein, putative
29842.t000053	0.475	-1.074	0.00000	Down	-	aspartic proteinase
29842.t000126	0.462	-1.113	0.00481	Down	<i>AtBGLU47</i>	beta-glucosidase 46 isoform X1
29844.t000021	0.409	-1.290	0.00000	Down	-	auxin-responsive protein IAA4
29844.t000033	0.210	-2.249	0.03291	Down	<i>KCS-20</i>	acyltransferase, putative
29844.t000045	2.482	1.311	0.00333	Up	-	vegetative cell wall protein gp1
29844.t000054	3.068	1.617	0.01518	Up	-	putative calcium-transporting ATPase 13, plasma membrane-type
29844.t000066	2.514	1.330	0.03051	Up	<i>ELIP</i>	early light-induced protein, chloroplastic
29851.t000069	2.270	1.183	0.00000	Up	-	uncharacterized protein LOC8279516 isoform X1
29851.t000118	2.298	1.200	0.02720	Up	-	uncharacterized WD repeat-containing protein all2124
29851.t000125	2.800	1.486	0.00000	Up	-	conserved hypothetical protein
29851.t000145	2.029	1.021	0.02130	Up	<i>AtCBP1</i>	conserved hypothetical protein
29863.t000015	0.270	-1.888	0.00000	Down	<i>AtCesA2</i>	cellulose synthase A catalytic subunit 5 [UDP-forming]
29864.t000073	0.391	-1.356	0.00048	Down	-	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1
29869.t000041	6.955	2.798	0.00000	Up	<i>AtHsp22.0</i>	22.7 kDa class IV heat shock protein
29877.t000013	2.545	1.348	0.00000	Up	<i>AtHIP23</i>	heavy metal-associated isoprenylated plant protein 26

Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29878.t000010	0.401	-1.319	0.02477	Down	-	conserved hypothetical protein
29883.t000047	0.403	-1.311	0.00011	Down	-	auxin-induced protein 22E
29889.t000030	0.273	-1.871	0.00000	Down	-	uncharacterized protein LOC8258783
29889.t000044	3.588	1.843	0.00367	Up	<i>AtbZIP1</i>	Ocs element-binding factor, putative
29889.t000095	2.327	1.219	0.00616	Up	-	enzyme inhibitor, putative
29889.t000096	2.045	1.032	0.00011	Up	<i>AtC/NIF1</i>	cell wall / vacuolar inhibitor of fructosidase 1
29889.t000116	2.098	1.069	0.00025	Up	-	transcription factor MYB108
29895.t000004	2.908	1.540	0.00000	Up	<i>ADF</i>	actin-depolymerizing factor
29895.t000011	8.364	3.064	0.00000	Up	-	conserved hypothetical protein
29898.t000003	0.346	-1.533	0.00000	Down	-	probable pectate lyase 13
29900.t000034	0.457	-1.131	0.00001	Down	<i>OsNCL2</i>	calmodulin, putative
29900.t000061	0.424	-1.237	0.00001	Down	-	protein CHUP1, chloroplastic
29900.t000076	16.084	4.008	0.00033	Up	-	uncharacterized protein LOC8259230
29900.t000079	0.357	-1.484	0.00342	Down	<i>AtHIP28</i>	copper ion binding protein, putative
29901.t000011	0.274	-1.868	0.01938	Down	-	cytochrome P450, putative
29904.t000112	10.680	3.417	0.01047	Up	-	uncharacterized PE-PGRS family protein PE_PGRS46
29907.t000020	0.343	-1.543	0.01288	Down	-	conserved hypothetical protein
29907.t000033	0.458	-1.126	0.00091	Down	<i>AtOPR1</i>	12-oxophytodienoate reductase opr, putative
29908.t000032	3.366	1.751	0.00000	Up	<i>AtHIP24</i>	metal ion binding protein, putative
29908.t000100	0.268	-1.900	0.01608	Down	<i>GjUGT2</i>	7-deoxyloganetin glucosyltransferase
29908.t000108	2.297	1.200	0.00617	Up	-	protein EXORDIUM
29908.t000110	3.587	1.843	0.00000	Up	-	protein EXORDIUM-like 2
29912.t000073	0.118	-3.079	0.00002	Down	<i>AtMIOX4</i>	inositol oxygenase 4
29912.t000151	0.379	-1.401	0.00001	Down	-	dipeptidase, putative
29912.t000165	0.445	-1.167	0.04070	Down	<i>AtDTX51</i>	protein DETOXIFICATION 52
29912.t000219	3.140	1.651	0.00000	Up	-	sugar transporter, putative
29915.t000001	2.220	1.151	0.03361	Up	<i>LTP</i>	non-specific lipid-transfer protein 1
29916.t000019	2.001	1.001	0.00001	Up	<i>AtHsp23.6</i>	small heat shock protein, chloroplastic
29924.t000001	0.354	-1.497	0.00000	Down	<i>AtBGLU44</i>	beta-glucosidase 44
29929.t000114	0.482	-1.054	0.01660	Down	-	ACT domain-containing protein ACR4
29929.t000135	2.349	1.232	0.00000	Up	-	uncharacterized protein LOC8286778
29933.t000025	0.145	-2.782	0.00330	Down	<i>atDjC76</i>	heat shock protein binding protein, putative
29933.t000061	2.499	1.322	0.00000	Up	<i>AtMYB102</i>	r2r3-myb transcription factor, putative
29933.t000062	21.513	4.427	0.00000	Up	-	phosphatidylethanolamine-binding protein, putative
29933.t000068	0.351	-1.512	0.00000	Down	<i>AtENT3</i>	equilibrative nucleotide transporter 3
29933.t000069	0.438	-1.190	0.00000	Down	-	uncharacterized protein LOC8275382
29948.t000018	0.440	-1.184	0.00002	Down	-	endoglucanase 11

Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
29983.t000020	2.010	1.007	0.00000	Up	-	nucleic acid binding protein, putative
					<i>Arabidopsis</i>	
29983.t000080	0.338	-1.565	0.00000	Down	<i>thaliana</i> <i>lectin-receptor</i> <i>kinase d</i>	probable L-type lectin-domain containing receptor kinase VII.2
29983.t000126	2.003	1.002	0.03009	Up	<i>AtERF53</i>	ethylene-responsive transcription factor ERF054
29983.t000156	0.472	-1.084	0.00600	Down	-	formimidoyltransferase-cyclodeaminase isoform X3
29993.t000017	0.411	-1.284	0.00000	Down	-	probable galacturonosyltransferase 15
29993.t000024	2.178	1.123	0.01104	Up	<i>At-XTH15</i>	xyloglucan endotransglucosylase/hydrolase 2
30003.t000020	6.008	2.587	0.00000	Up	<i>(1-&gt;3)-beta-gl</i> <i>ucanase</i>	Glucan endo-1,3-beta-glucosidase precursor, putative
30003.t000021	2.318	1.213	0.00253	Up	<i>(1-&gt;3)-beta-gl</i> <i>ucanase</i>	glucan endo-1,3-beta-glucosidase
30027.t000020	2.138	1.096	0.00091	Up	-	uncharacterized protein LOC8282436
30027.t000022	2.877	1.524	0.03241	Up	-	uncharacterized protein LOC8282438
30032.t000010	0.359	-1.476	0.00000	Down	<i>PRCP</i>	lysosomal Pro-X carboxypeptidase isoform X1
30060.t000022	0.290	-1.787	0.00000	Down	-	protein EXORDIUM-like 7
30064.t000028	2.100	1.070	0.00000	Up	<i>AtWRKY6</i>	probable WRKY transcription factor 31
30068.t000007	0.331	-1.597	0.00000	Down	<i>AtCslG3</i>	transferase, putative
30068.t000048	0.493	-1.021	0.00076	Down	<i>AtOPT7</i>	oligopeptide transporter 7
30068.t000068	0.111	-3.172	0.01149	Down	-	cytochrome P450 78A9
30073.t000078	7.280	2.864	0.00006	Up	-	bark storage protein A
30074.t000080	5.420	2.438	0.00000	Up	-	conserved hypothetical protein
30076.t000001	0.474	-1.077	0.00000	Down	-	uncharacterized protein LOC8265172
30076.t000026	7.705	2.946	0.00980	Up	<i>S3H DLO1</i>	1-aminocyclopropane-1-carboxylate oxidase 5
30076.t000077	11.430	3.515	0.00000	Up	-	mannan endo-1,4-beta-mannosidase 4
30076.t000087	0.490	-1.029	0.00000	Down	-	hypothetical protein RCOM_1342140
30076.t000171	2.088	1.062	0.02722	Up	<i>AtMYB78</i>	transcription factor MYB108
30076.t000182	2.279	1.188	0.02186	Up	<i>AtGPAT3</i>	Glycerol-3-phosphate acyltransferase, putative
30076.t000239	0.361	-1.469	0.00023	Down	<i>AtBXL2</i>	probable beta-D-xylosidase 2
30076.t000266	6.246	2.643	0.00000	Up	-	uncharacterized protein LOC8265165
30078.t000023	0.301	-1.732	0.00306	Down	-	retinoid-inducible serine carboxypeptidase, putative
30091.t000001	0.416	-1.267	0.00000	Down	<i>Ps6OMT</i>	3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase 2
30099.t000062	2.094	1.066	0.00045	Up	-	uncharacterized protein LOC8268907



Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
30099.t000076	Inf	Inf	0.04929	Up	<i>AtEGY3</i>	probable zinc metallopeptidase EGY3, chloroplastic
30099.t000103	0.487	-1.038	0.00000	Down	-	serine carboxypeptidase, putative
30114.t000003	0.433	-1.208	0.00002	Down	-	putative glutamine amidotransferase YLR126C
30115.t000049	0.218	-2.196	0.00032	Down	-	uncharacterized protein LOC8270745
30116.t000010	2.729	1.449	0.00001	Up	-	Basic blue protein, putative
30116.t000011	2.892	1.532	0.00231	Up	-	conserved hypothetical protein
30128.t000001	0.381	-1.393	0.02673	Down	<i>AtDUF7</i>	uncharacterized protein LOC8285676 isoform X2
30128.t000039	0.309	-1.696	0.00037	Down	<i>AtHAK1</i>	Potassium transporter, putative
30128.t000040	0.327	-1.611	0.00002	Down	<i>AtHAK1</i>	Potassium transporter, putative
30128.t000181	0.498	-1.006	0.00002	Down	-	uncharacterized protein LOC8285509
30128.t000370	5.131	2.359	0.00000	Up	-	nicotianamine synthase
30128.t000417	3.330	1.736	0.00000	Up	-	histone chaperone ASF1
30128.t000505	2.831	1.501	0.00000	Up	-	GEM-like protein 5
30129.t000022	9.428	3.237	0.00000	Up	<i>AtTSPO</i>	translocator protein homolog
30130.t000009	0.369	-1.437	0.00867	Down	-	phototropin-1
30131.t000021	0.309	-1.693	0.03718	Down	-	conserved hypothetical protein
30131.t000022	0.485	-1.042	0.04533	Down	-	serine-threonine protein kinase, plant-type, putative
30131.t000160	0.326	-1.617	0.00009	Down	<i>RcCASPL1F2</i>	RecName: Full=CASP-like protein 1F2,Short=RcCASPL1F2
30131.t000411	0.233	-2.099	0.00320	Down	-	GEM-like protein 4
30136.t000020	6.605	2.724	0.00292	Up	-	uncharacterized protein LOC8259126
30136.t000048	Inf	Inf	0.00810	Up	-	uncharacterized protein LOC8259154
30138.t000158	3.384	1.759	0.00750	Up	-	chaperone protein ClpB1
30138.t000195	0.463	-1.112	0.00377	Down	<i>AtbHLH72</i>	DNA binding protein, putative
30138.t000233	2.582	1.369	0.00220	Up	<i>AtEXPA15</i>	expansin-A15
30143.t000033	2.511	1.328	0.00000	Up	<i>P5CS</i>	delta-1-pyrroline-5-carboxylate synthase
30143.t000059	2.056	1.040	0.00000	Up	-	uncharacterized protein LOC8287504
30146.t000007	2.043	1.031	0.01385	Up	-	conserved hypothetical protein
30146.t000011	2.539	1.345	0.00000	Up	-	hypothetical protein RCOM_1485780
30146.t000085	2.284	1.192	0.02022	Up	-	histidine-containing phosphotransfer protein 4
30147.t000015	21.781	4.445	0.00000	Up	-	hypothetical protein RCOM_1496000
30147.t000045	4.806	2.265	0.00017	Up	-	uncharacterized protein LOC8266341
30147.t000145	2.618	1.388	0.03757	Up	-	C2 and GRAM domain-containing protein At5g50170 isoform X1
30147.t000391	2.420	1.275	0.00244	Up	-	Phytochrome kinase substrate, putative
30147.t000507	2.542	1.346	0.00090	Up	-	conserved hypothetical protein
30147.t000584	3.753	1.908	0.00052	Up	<i>DREB1A</i>	dehydration-responsive element

Table S2 (continued)

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
30147.t000595	2.421	1.276	0.00000	Up	-	conserved hypothetical protein
30147.t000657	8.314	3.056	0.00000	Up	-	uncharacterized protein LOC8277423
30147.t000725	2.281	1.190	0.00047	Up	-	calmodulin binding protein, putative
30147.t000754	Inf	Inf	0.00132	Up	-	MADS-box transcription factor, putative
30147.t000803	0.411	-1.282	0.00000	Down	-	leucine-rich repeat protein, putative
30156.t000039	3.055	1.611	0.00000	Up	<i>AtBBX30</i>	DNA binding protein, putative
30169.t000292	47.248	5.562	0.00000	Up	<i>OsPP2C08</i>	probable protein phosphatase 2C 51
30169.t000342	2.803	1.487	0.00005	Up	-	G-type lectin S-receptor-like serine/threonine-protein kinase At5g24080
30169.t000349	2.021	1.015	0.00002	Up	-	late embryogenesis abundant protein At1g64065
30170.t000054	2.406	1.267	0.01750	Up	<i>EPF-like protein 2</i>	EPIDERMAL PATTERNING FACTOR-like protein 2
30170.t000064	5.827	2.543	0.00000	Up	<i>HlBCAT1</i>	branched-chain amino acid aminotransferase, putative
30170.t000232	4.456	2.156	0.00000	Up	-	uncharacterized protein LOC8288554
30170.t000289	2.370	1.245	0.00000	Up	-	alpha-amylase
30170.t000298	0.338	-1.567	0.00036	Down	-	conserved hypothetical protein
30170.t000370	3.692	1.884	0.00000	Up	-	cytochrome P450 CYP82D47
30170.t000474	2.770	1.470	0.00166	Up	-	uncharacterized protein LOC8288949
30170.t000484	0.324	-1.625	0.02904	Down	<i>DFR</i>	dihydroflavonol-4-reductase
30170.t000491	0.074	-3.761	0.04889	Down	-	jasmonate O-methyltransferase
30170.t000565	3.397	1.764	0.01131	Up	-	cytochrome P450 83B1
30170.t000594	2.233	1.159	0.00055	Up	-	conserved hypothetical protein
30170.t000619	0.381	-1.392	0.00000	Down	-	cytochrome P450 81E8
30170.t000624	0.321	-1.639	0.02480	Down	-	putative receptor protein kinase ZmPK1
30170.t000692	3.095	1.630	0.00000	Up	-	E3 ubiquitin-protein ligase ATL23
30170.t000693	6.670	2.738	0.00000	Up	<i>OsNrx2</i>	probable nucleoredoxin 2 isoform X4
30170.t000710	0.282	-1.829	0.02288	Down	<i>ODC</i>	ornithine decarboxylase
30170.t000711	0.343	-1.543	0.00035	Down	<i>ODC</i>	ornithine decarboxylase isoform X1
30170.t000771	2.674	1.419	0.00000	Up	-	starch branching enzyme II, putative
30170.t000790	0.494	-1.016	0.00000	Down	-	calcium lipid binding protein, putative
30174.t000076	0.471	-1.086	0.00000	Down	<i>Sphingoid LCB desaturase 2</i>	delta(8)-fatty-acid desaturase 2
30174.t000082	3.735	1.901	0.00281	Up	-	BAG family molecular chaperone regulator 6
30174.t000125	3.543	1.825	0.00000	Up	<i>BnIII</i>	oleosin 1
30174.t000270	2.068	1.048	0.00000	Up	-	leucine rich repeat receptor kinase, putative
30174.t000472	5.050	2.336	0.00000	Up	-	conserved hypothetical protein

**Table S2 (continued)**

Gene ID	FC	log2FC	pValue	Regulation	Gene_symbol	Description
30174.t000550	2.452	1.294	0.00000	Up	<i>POMGnT2</i>	glycosyltransferase, putative
30179.t000016	0.116	-3.112	0.00000	Down	-	serine-threonine protein kinase, plant-type, putative xyloglucan
30179.t000018	4.175	2.062	0.00001	Up	<i>At-XTH22</i>	endotransglucosylase/hydrolase protein 22
30179.t000025	2.891	1.532	0.01446	Up	<i>At-XTH25</i>	xyloglucan:xyloglucosyl transferase, putative
30183.t000014	2.890	1.531	0.00001	Up	<i>OC-X</i>	cysteine proteinase inhibitor 5
30190.t000051	2.045	1.032	0.01712	Up	-	hypothetical protein RCOM_1691440
30190.t000145	0.436	-1.199	0.02524	Down	-	anthocyanidin 3-O-glucosyltransferase
30190.t000196	0.472	-1.082	0.00000	Down	-	uncharacterized protein LOC8271767
30190.t000213	45.219	5.499	0.00000	Up	-	uncharacterized protein LOC8271784
30190.t000497	2.899	1.536	0.00000	Up	-	conserved hypothetical protein
30190.t000498	4.045	2.016	0.00000	Up	<i>GenCHYB</i>	beta-carotene 3-hydroxylase, chloroplastic isoform X1
30190.t000545	2.349	1.232	0.00009	Up	<i>DROJ1</i>	dnaJ homolog subfamily B member 13
30190.t000559	0.486	-1.041	0.00000	Down	<i>AtERF12</i>	ethylene-responsive transcription factor 12
30204.t000008	2.273	1.184	0.00148	Up	-	uncharacterized protein LOC8264934 isoform X1
30226.t000067	2.130	1.091	0.00013	Up	<i>AtXYLP9</i>	lipid binding protein, putative
33363.t000001	2.013	1.010	0.00000	Up	-	aldehyde dehydrogenase family 7 member B4
38153.t000001	2.058	1.042	0.02153	Up	-	conserved hypothetical protein, partial
49862.t000001	6.757	2.756	0.00000	Up	<i>S3H DLO1</i>	Flavonol synthase/flavanone 3-hydroxylase, putative, partial
30174.t000495	3.896	1.962	0.00000	Up	<i>ABI5</i>	ninja-family protein AFP2 isoform X1

**Table S3.** Up-regulated DEGs involved in starch and sucrose metabolism pathway in the cotyledons of castor under salt stress.

Gene ID	FC	log <sub>2</sub> FoldChange	pValue	Gene_symbol	Description
29585.t000006	2.122	1.085	0.0001	<i>UGD</i>	UDP-glucuronic acid decarboxylase 6
29630.t000018	3.538	1.823	0.0001	-	alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic isoform X1 (2.4.1.1)
29692.t000011	2.811	1.491	5.58E-07	<i>PE 6</i>	pectinesterase
29692.t000012	2.099	1.069	0.0001	<i>PGM</i>	phosphoglucomutase, cytoplasmic (5.4.2.2)
29783.t000019	2.299	1.201	7.48E-06	<i>AtUGlAE3</i>	UDP-glucuronate 4-epimerase 1
29908.t000058	2.858	1.515	0.002	<i>AtTPPD</i>	probable trehalose-phosphate phosphatase D (3.1.3.12)
29951.t000003	15.644	3.967	0.0006	<i>AtSUS6</i>	sucrose synthase, putative (2.4.1.13)
29986.t000065	Inf	Inf	0.036	<i>ExoPG</i>	Exopolygalacturonase clone GBGE184 precursor, putative
30147.t000809	4.788	2.259	0.013	CsF26G	beta-glucosidase, putative (3.2.1.21)
30170.t000289	3.325	1.733	0.0001	-	alpha-amylase (3.2.1.1)
30170.t000721	2.747	1.458	2.29E-07	<i>AtAMY2</i>	alpha-amylase, putative (3.2.1.1)
30170.t000771	2.389	1.256	5.89E-06	-	starch branching enzyme II, putative (2.4.1.18)

**Table S4.** Down-regulated DEGs involved in starch and sucrose metabolism pathway in the cotyledons of castor under salt stress.

Gene ID	FC	log <sub>2</sub> FoldChange	pValue	Gene_symbol	Description
28629.t000019	0.124	-3.007	0.048	-	beta-fructofuranosidase, insoluble isoenzyme 3 (3.2.1.26)
29308.t000001	0.261	-1.934	0.003	<i>PE 3</i>	pectinesterase 3
29607.t000001	0.490	-1.028	0.0004	<i>AtTPSI</i>	alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1 (2.4.1.15) (3.1.3.12)
29822.t000192	0.052	-4.264	2.37E-37	<i>CT-BMY</i>	Beta-amylase, putative (3.2.1.2)
29842.t000126	0.396	-1.335	0.034	<i>AtBGLU47</i>	beta-glucosidase 46 isoform X1 (3.2.1.22)
29924.t000001	0.411	-1.280	0.0007	<i>AtBGLU44</i>	beta-glucosidase 44 (3.2.1.22)
29993.t000017	0.412	-1.277	0.005	-	probable galacturonosyltransferase 15
30026.t000074	0.337	-1.566	0.039	<i>AtTPSI</i>	trehalose-6-phosphate synthase, putative (2.4.1.15) (3.1.3.12)
30147.t000485	0.391	-1.352	1.58E-06	<i>AtTPPA</i>	trehalose-phosphate phosphatase A (3.1.3.12)
30169.t000162	0.219	-2.186	0.0004	-	uncharacterized protein LOC8272657 (3.2.1.22)

**Table S5.** Up-regulated DEGs involved in starch and sucrose metabolism pathway in the roots of castor under salt stress.

Gene ID	FC	log <sub>2</sub> FoldChange	pValue	Gene_symbol	Description
29864.t000076	4.120	2.042	2.51E-10	<i>AtQRT2</i>	polygalacturonase QRT2
29904.t000160	2.400	1.263	5.53E-09	<i>TR-BAMY</i>	beta-amylase 1, chloroplastic (3.2.1.2)
29986.t000062	4.157	2.055	3.04E-09	-	sucrose synthase, putative (2.4.1.13)
30042.t000008	3.258	1.704	6.67E-12	<i>PG</i>	polygalacturonase
30042.t000010	2.879	1.525	2.29E-05	<i>PG</i>	polygalacturonase
30147.t000249	2.536	1.342	0.0009	<i>AtTPS9</i>	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 (2.4.1.15) (3.1.3.12)
30147.t000480	2.039	1.028	0.029	<i>PE 2</i>	Pectinesterase-2 precursor, putative
30169.t000163	2.526	1.336	2.00E-05	-	beta-glucosidase 12 (3.2.1.21)
30170.t000289	2.370	1.245	4.19E-06	-	alpha-amylase (3.2.1.1)
30170.t000771	2.674	1.419	4.37E-17	-	starch branching enzyme II, putative (2.4.1.18)
30174.t000244	18.42	4.203	5.83E-05	<i>PE 36</i>	Pectinesterase-2 precursor, putative
4					

**Table S6.** Down-regulated DEGs involved in starch and sucrose metabolism pathway in the roots of castor under salt stress.

Gene ID	FC	log <sub>2</sub> FoldChange	pValue	Gene_symbol	Description
28865.t000001	0.485	-1.043	1.06E-09	<i>AtCEL3</i>	endo-1,4-beta-glucanase, putative (3.2.1.4)
29005.t000011	0.384	-1.377	1.66E-11	-	glucan endo-1,3-beta-glucosidase 2 (3.2.1.39)
29629.t000093	0.399	-1.323	6.42E-10	<i>AtUGlcAE2</i>	UDP-glucuronate 5-epimerase, putative
29739.t000105	0.449	-1.152	1.51E-09	<i>PE U1</i>	pectinesterase
29739.t000107	0.097	-3.354	5.13E-06	<i>PE U1</i>	Pectinesterase-3 precursor, putative
29739.t000111	0.187	-2.411	5.74E-13	<i>PE 12</i>	probable pectinesterase/pectinesterase inhibitor 12
29739.t000115	0.406	-1.300	8.47E-08	<i>PE 54</i>	pectinesterase
29808.t000003	0.373	-1.421	0.004	-	beta-glucosidase, putative (3.2.1.21)
29808.t000016	0.362	-1.465	3.20E-13	<i>AtBGLU17</i>	beta-glucosidase, putative (3.2.1.21)
29842.t000126	0.462	-1.112	0.004	<i>AtBGLU47</i>	beta-glucosidase 46 isoform X1 (3.2.1.21)
29924.t000001	0.354	-1.497	1.55E-13	<i>AtBGLU44</i>	beta-glucosidase 44 (3.2.1.21)
29986.t000060	0.243	-2.039	0.015	<i>PE 40</i>	pectinesterase
29993.t000017	0.410	-1.283	4.70E-13	-	probable galacturonosyltransferase 15
30147.t000484	0.496	-1.009	0.012	-	Beta-fructofuranosidase, soluble isoenzyme I precursor, putative (3.2.1.26)
30155.t000027	0.246	-2.020	0.007	<i>PE 25</i>	probable pectinesterase/pectinesterase inhibitor 25
30221.t000012	0.304	-1.714	5.45E-23	<i>MsXyl2</i>	beta-xylosidase/alpha-L-arabinofuranosidase 2
30226.t000001	0.363	-1.458	8.48E-17	<i>AtBGLU17</i>	beta-glucosidase, putative, partial (3.2.1.21)
30226.t000006	0.474	-1.076	3.84E-12	<i>VH</i>	vicianin hydrolase (3.2.1.21)

**Table S7.** DEGs involved in protein processing in endoplasmic reticulum pathway in the cotyledons of castor under salt stress.

Gene ID	FC	log <sub>2</sub> FoldChange	pValue	Gene_symbol	Description
27699.t000007	2.118	1.082	0.004	<i>AtHsp15.7</i>	conserved hypothetical protein
28659.t000004	12.109	3.598	0.0006	-	class I heat shock protein
29520.t000005	20.122	4.330	0.003	<i>AtHsp18.1</i>	18.1 kDa class I heat shock protein
29520.t000006	8.006	3.001	0.040	<i>AtHsp18.1</i>	18.1 kDa class I heat shock protein
29585.t000002	3.143	1.652	2.50E-09	<i>AtHsc70-4</i>	heat shock cognate 70 kDa protein 2
29610.t000003	5.459	2.448	2.12E-05	-	17.3 kDa class I heat shock protein
29610.t000006	9.655	3.271	1.09E-10	<i>OsHsp17.4</i>	18.1 kDa class I heat shock protein
29633.t000030	19.629	4.294	0.004	-	class I heat shock protein
29727.t000002	4.697	2.231	2.42E-06	<i>AtHsp17.4B</i>	17.4 kDa class III heat shock protein
29739.t000024	10.476	3.389	4.54E-07	-	17.3 kDa class II heat shock protein
29751.t000039	8.852	3.146	2.69E-09	-	heat-shock protein, putative
29751.t000040	2.166	1.115	0.0002	-	18.1 kDa class I heat shock protein
29751.t000059	5.767	2.528	0.048	-	17.3 kDa class I heat shock protein
29854.t000032	3.162	1.661	3.88E-09	-	dnaJ protein homolog
29869.t000041	8.178	3.031	4.26E-06	<i>AtHsp22.0</i>	22.7 kDa class IV heat shock protein
30131.t000031	2.582	1.368	5.52E-06	-	heat shock 70 kDa protein 5
30147.t000492	6.046	2.596	2.19E-14	<i>AtHsp23.6</i>	heat shock 22 kDa protein, mitochondrial
30174.t000429	3.313	1.728	1.09E-06	-	18.1 kDa class I heat shock protein