

Amjad E, Sokouti B, Asnaashari S, Dastmalchi S. Screening of salt stress in the overexpressed type of *Arabidopsis thaliana* (L.) Heynh. for the identification of significant hub genes using a systems biology approach. Plant Science Today. 2022;9(4):773–784.
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Supplementary Tables

Supplementary Table 1. Top upregulated and downregulated genes for four groups.

	Gene symbol	FC	P value
over-mock-salt	Upregulated		
	GLN1;4	2.39	0.000104
	ARR6	2.41	0.000843
	BP	2.54	0.000293
	AtGuLO5	2.61	0.0002014
	SIM	2.68	0.00013
	CRF2	2.68	0.000247
	ATSYTC	2.69	0.000102
	SNRK2-5	2.77	1.56E-05
	ATPRP3	2.82	0.00082
	ATLP-3	2.83	8.03E-05
	Downregulated		
	LTP4	0.0021	< 1e-07
	AtNPF7.2	0.0036	< 1e-07
	NATA1	0.0036	< 1e-07
	AOX1D	0.007	< 1e-07
	COR15	0.0085	< 1e-07
	BGLU30	0.0095	< 1e-07
	UGT74E2	0.01	< 1e-07
	ATJRG21	0.011	< 1e-07
	TAT	0.011	< 1e-07
	GES	0.011	< 1e-07
wild-over-mock	Upregulated		
	CYP97B3	6.1	< 1e-07
	ASN1	8.11	0.000296
	Downregulated		
	AtPPPsPase1	0.14	9.00E-07
	ATSDI1	0.14	4.60E-05
	AtPNP-A	0.17	3.00E-06
	LSU1	0.18	0.000608
	ATSPX1	0.21	6.00E-07
	UF3GT	0.22	1.26E-05
	LSU2	0.23	0.000275
	ATMGD3	0.27	7.50E-06
	ATGSTF12	0.27	2.11E-05
	BGLU28	0.27	0.000202
wild-over-salt	Upregulated		
	CYP97B3	3.98	9.53E+02
wild-mock-salt	Upregulated		
	ATHY2	2.26	0.000926
	AtKAT1	2.4	0.000806
	SPT42	2.42	0.000344
	ATMSH2	2.42	0.00044

	ACYB-2	2.42	0.000518
	SCM	2.44	0.000983
	ZFP6	2.45	0.00038
	PDE340	2.5	0.000471
	ATCRSH	2.51	0.00046
	MEE9	2.53	0.000463
	Downregulated		
	AOX1D	0.0084	1.40E-06
	AtNPF7.2	0.0085	7.40E-06
	GES	0.0097	< 1e-07
	LTP4	0.013	7.09E-05
	TAT	0.014	1.00E-06
	ACS2	0.0084	2.60E-06
	BGLU30	0.0085	1.38E-05
	JAZ7	0.0097	< 1e-07
	CRK36	0.013	< 1e-07
	BCS1	0.014	4.00E-07

Supplementary Table 2. List of potential gene biomarkers using ClusterOne module analysis.

	Item	Gene Symbol	Up- / Downregulated	Connectivity Degree
over-mock-salt	Module1	ATFKBP13	Upregulated	35
		PPL1	Upregulated	35
		AtTic62	Upregulated	35
	Module2	PPL1	Upregulated	35
		AtTic62	Upregulated	35
	Module3	3xHMG-box2	Upregulated	26
	Module4	RHS13	Upregulated	26
		RHS19	Upregulated	26
	Module5	RPS9	Upregulated	26
	Module6	MYB28	Upregulated	14
	Module7	AtNPF7.3	Upregulated	13
wild-mock-salt	Module8	ATMTP3	Upregulated	7
		NRAMP3	Downregulated	7
	Module-9	GPDHP	Upregulated	3
	Module-10	AtJAZ1	Downregulated	54
	Module-11	BEE2	Upregulated	5
		SAUR67	Upregulated	5
	Module-1	ATCYP38	Upregulated	36
	Module-2	ATCYP38	Upregulated	30
	Module-3	ATIRT1	Upregulated	11
		ATMTP3	Upregulated	11
wild-over-mock	Module-4	AtAUR2	Upregulated	9
		CYCB2;4	Upregulated	9
	Module-5	ATWRKY33	Downregulated	29
	Module-6	AtJAZ1	Downregulated	50
	Module-7	ATMTM1	Downregulated	3
		ATPLC	Downregulated	3
		5PTASE2	Downregulated	3
	Module-8	AtMTM2	Downregulated	3
		ATWRKY33	Downregulated	30
		ATWRKY40	Downregulated	30
	Module-9	AGP8	Upregulated	6
wild-over-mock	Module-1	ATSDI1	Downregulated	5
	Module-2	At1g73010	Downregulated	4
		ATRNS1	Downregulated	4
		ATSPX1	Downregulated	4
	Module-3	LURP1	Downregulated	2
	Module-4	DFR	Downregulated	2
		ATGSTF12	Downregulated	2
		UF3GT	Downregulated	2

Supplementary Table 3. Overlapping genes between current and Song et al. study along with their properties.

Compared groups	TAIR ID	Gene symbol	FC		Up- / Downregulated		P value	
			Current	Song et al	Current	Song et al	Current	Song et al
over-mock-salt	AT1G09340	CRB	4.71	4.87	Up	Down	< 1e-07	6.12E-05
	AT1G32470	unknown	3.55	3.74	Up	Down	1.00E-07	0.001146679
	AT3G16250	NDF4	3.56	3.46	Up	Down	4.00E-07	1.93E-04
	AT3G48420	unknown	3.66	3.61	Up	Down	6.00E-07	3.23E-04
	AT3G55330	PPL1	3.59	3.54	Up	Down	1.20E-06	0.006436502
	AT3G55800	SBPASE	5.32	5.54	Up	Down	< 1e-07	2.53E-05
	AT3G63140	CSP41A	6.07	6.13	Up	Down	< 1e-07	4.04E-04
	AT5G45680	ATFKBP13	4.45	4.43	Up	Down	< 1e-07	4.92E-05
wild-over-mock	AT1G73010	AtPPsPase1(PS2)	0.14	6.84	Down	Down	9.00E-07	0.003509145
	AT2G11810	MGD3	0.27	3.65	Down	Down	7.50E-06	0.001252212
	AT3G17790	ACP5(PAP17)	0.28	3.58	Down	Down	9.00E-07	3.36E-04
	AT4G14090	unknown	0.25	3.91	Down	Down	4.56E-05	0.00401191
	AT5G17220	GSTF12	0.27	3.64	Down	Down	2.11E-05	0.00284403
	AT5G20150	SPX1	0.21	4.82	Down	Down	6.00E-07	0.001750883
	AT5G20790	unknown	0.2	5.007	Down	Down	< 1e-07	1.30E-04
	AT5G42800	DFR	0.31	3.17	Down	Down	0.0002126	0.011159079
wild-mock-salt	AT5G54060	UF3GT	0.22	4.44	Down	Down	1.26E-05	0.001692526
	AT1G01560	MPK11	0.11	9.51	Down	Up	2.51E-05	0.00268814
	AT1G80840	WRKY40	0.1	9.49	Down	Up	3.36E-05	0.00210761
	AT2G18660	AtPNP-A(EXLB3)	0.13	7.87	Down	Up	2.10E-06	0.002122402
	AT3G01830	unknown	0.049	20.96	Down	Up	< 1e-07	0.008897668
	AT3G50930	BCS1	0.019	48.36	Down	Up	4.00E-07	0.00022964
	AT5G26920	CBP60G	0.11	8.55	Down	Up	2.30E-06	0.000542461
	AT5G59820	RHL41	0.062	15.30	Down	Up	8.68E-05	0.003849361
wild-over-salt	AT4G15110	CYP97B3	3.98	N/A	Up	N/A	0.0000953	N/A
	AT1G15010	N/A	3.89	N/A	Up	N/A	0.0005753	N/A
	AT4G19430	N/A	3.99	N/A	Up	N/A	0.0007749	N/A

Supplementary Table 4. Overlapping genes, chromosome location, and literature functional mechanisms.

	TAIR ID	Gene Symbol	Chromosome	Function	References
over-mock-salt	AT1G09340	CRB	1	• proper functioning of the chloroplast	(29)
	AT1G32470	unknown	1	• Growth	(30)
	AT3G16250	NDF4	3	• involved in cyclic electron flow around photosystem I to produce ATP	(31, 32)
	AT3G48420	unknown	3	• chloroplast • photosynthesis	(33, 34)
	AT3G55330	PPL1	3	• involved in biotic stress	(35)
	AT3G55800	SBPASE	3	• Encodes the chloroplast enzyme sedoheptulose-1,7-bisphosphatase (SBPase) • involved in the carbon reduction of the Calvin cycle	(36, 37)
	AT3G63140	CSP41A	3	• Encodes a protein with ribonuclease activity that is involved in plastid rRNA maturation	(38)
	AT5G45680	ATFKBP13	5	• involved in biotic stress	(35)
wild-over-mock	AT1G73010	AtPPsPase1(PS2)	1	• involved in salt stress	(39)
	AT2G11810	MGD3	2	• involved in chloroplast • chloroplast envelope	(40, 41)
	AT3G17790	ACP5(PAP17)	3	• chloroplast • response to oxidative stress	(42)
	AT4G14090	unknown	4	• combined light and drought stress.	(43)
	AT5G17220	GSTF12	5	• response to salt stress • chloroplast • response to oxidative stress	(43-45)
	AT5G20150	SPX1	5	• responsive to dehydration stress • chloroplast	(46)
	AT5G20790	unknown	5	• chloroplast • response to oxidative stress	(42)
	AT5G42800	DFR	5	• High Sucrose • Oxidative and Abiotic Stresses	(47, 48)

				<ul style="list-style-type: none"> • salt stress 	
	AT5G54060	UF3GT	5	<ul style="list-style-type: none"> • combined light and drought stress • chloroplast 	(43)
wild-mock-salt	AT1G01560	MPK11	1	<ul style="list-style-type: none"> • response to salt stress • growth and ribosome biogenesis 	(49)
	AT1G80840	WRKY40	2	<ul style="list-style-type: none"> • Tolerance to abiotic stress • brassinosteroid-mediated stress tolerance 	(50, 51)
	AT2G18660	AtPNP-A(EXLB3)	2	<ul style="list-style-type: none"> • Leaf mesophyll cell • Cell Death • Signaling 	(52, 53)
	AT3G01830	unknown	3	<ul style="list-style-type: none"> • Growth • Detoxification • Cell cycle 	(54, 55)
	AT3G50930	BCS1	3	<ul style="list-style-type: none"> • chloroplast • Cell Death 	(56)
	AT5G26920	CBP60G	5	<ul style="list-style-type: none"> • Defence response • salicylic acid signaling pathway 	(57, 58)
	AT5G59820	RHL41	5	<ul style="list-style-type: none"> • Transient Stress 	(59)
	AT4G15110	CYP97B3	4	<ul style="list-style-type: none"> • chloroplast • carotenoid hydroxylases 	(60, 61)
wild-over-salt	AT1G15010	N/A	1	<ul style="list-style-type: none"> • Transient stress • Drought tolerance 	(59, 62)
	AT4G19430	N/A	4	<ul style="list-style-type: none"> • Inactivation of chloroplast 	(63)

Supplementary Table 5. Overlapping genes, chromosome location, and literature functional mechanisms.

Accession No.	Gene Symbol	Chromosome	Function	References
AT3G01480	ATCYP38	3	<ul style="list-style-type: none"> • Promotes the plant tolerance to high light stress • Effective in plant growth by chloroplast involvement 	(64, 65)
AT4G19690	ATIRT1	4	<ul style="list-style-type: none"> • High sensitivity to Cd stress • Involved in salt stress 	(66, 67)
AT3G58810	ATMTP3	3	<ul style="list-style-type: none"> • Tolerance to Cd stress • genotoxic resistance 	(68, 69)
AT2G25880	AtAUR2	2	<ul style="list-style-type: none"> • Drought Tolerance Improvement 	(70)
AT1G76310	CYCB2;4	1	<ul style="list-style-type: none"> • Cell cycle regulation 	(71)
AT2G38470	ATWRKY33	2	<ul style="list-style-type: none"> • Contributed in abiotic stresses such as salt stress 	(50)
AT1G19180	AtJAZ1	1	<ul style="list-style-type: none"> • Defective under high light stress 	(72)
AT3G10550	ATMTM1	3	<ul style="list-style-type: none"> • Involved in dehydration stress 	(73)
AT5G58670	ATPLC	5	<ul style="list-style-type: none"> • Involved in salt stress 	(74)
AT4G18010	5PTASE2	4	<ul style="list-style-type: none"> • Involved in salt tolerance 	(75, 76)
AT5G04540	AtMTM2	5	<ul style="list-style-type: none"> • Involved in biotic stresses 	(35)
AT2G38470	ATWRKY33	1	<ul style="list-style-type: none"> • Mitochondrial and chloroplast stress • Involved in biotic stresses 	(77, 78)
AT1G80840	ATWRKY40	2	<ul style="list-style-type: none"> • Tolerance to abiotic stress • Brassinosteroid-mediated stress tolerance 	(50, 51)

Supplementary Table 6. The details of fifteen significant genes determined from the over-mock-salt type.

Accession No.	Gene Symbol	Chromosome	Function	References
AT5G45680	ATFKBP13	5	• Involved in biotic stress	(35)
AT3G55330	PPL1	3	• Involved in biotic stress	(35)
AT3G18890	AtTic62	3	• Involved in biotic stress	(35)
AT4G23800	3xHMG-box2	4	• Involved in biotic stress	(35)
AT4G02270	RHS13	4	• Involved in salt stress	(79)
AT5G67400	RHS19	5	• Tolerance to cold stress • Involved in oxidative stress	(80, 81)
AT1G74970	RPS9	1	• Tolerance to cold stress	(82)
AT5G61420	MYB28	5	• Involved in salt stress • Involved in dehydration stress	(83, 84)
AT1G32450	AtNPF7.3	1	• Involved in salt stress	(85)
AT3G58810	ATMTP3	3	• Tolerance to Cd stress • Genotoxic stress	(68, 69)
AT2G23150	NRAMP3	2	• Involved in salt stress	(79)
AT5G40610	GPDHp	5	• Involved in biotic stress	(35)
AT1G19180	AtJAZ1	1	• Involved in high light stress	(72)
AT4G36540	BEE2	4	• Involved in abiotic stress	(86)
AT1G29510	SAUR67	1	• Involved in high external calcium stress	(87)