

Table 1 Suppl. Selected differently expressed genes (DEGs) of *Haloxylon ammodendron* and their DNA primer sequences for real-time PCR. Genes with an adjusted *P*-value < 0.05 found by *DESeq* were assigned as differentially expressed.

Gene ID	Forward primer (5' - 3')	Reverse primer (5' - 3')
Unigene26705	GTCACCTTCACCAGCCAATT	GTCCATCCTCCCACCGTAA
CL2652.Contig1	GTCACCTTCACCAGCCAATT	GTCCATCCTCCCACCGTAA
Unigene4291	GTCACCTTCACCAGCCAATT	GTCCATCCTCCCACCGTAA
CL3635.Contig1	GTCACCTTCACCAGCCAATT	GTCCATCCTCCCACCGTAA
Unigene6318	GTGTTACAGACTCAAATACGCC	TACATGAAAACCTCAGATGCCC
CL5597.Contig2	GTGTTACAGACTCAAATACGCC	TACATGAAAACCTCAGATGCCC
CL4182.Contig4	TTCATTGGGTGAAACCGTGAA	TTCATTCCGGCAGCTTCCT
Unigene19507	CTGCTGCCACATCCTTGCTA	GCTCGCGAGATCATGAAAAC
Unigene25191	GTGAAGGGTTGCCTCCACTA	AAGCATTTGACCACCGACAA
Unigene26726	AAATCGAGGTACCCATTCTATGAC	AAATAAAGAAGCCATTGCAATTG
Unigene18640	GGATTGGCCAAAAGAGTTGGT	TGTGGAAGCAAAGGAAAATGG
Unigene3675	AGCCCTCATTCATCACCCCTACA	GATGCTTCGGATTGCAACGT
Unigene10944	CAGCACTTGAAAGGCTACATGATC	CCCCATCAATTGGAGCTACCT

Table 2 Suppl. Pathways and gene expressions of *Haloxylon ammodendron* in response to salinity stress.

Pathway	Gene ID	Gene Name	LSS	MSS	SSS
Transcription changes in ABA and other hormone-related genes	Unigene165	cytochrome P450	2.11	3.17	3.38
	Unigene20778	cytochrome P450	2.23	1.30	1.91
	Unigene15178	cytochrome P450 86B1-like	1.65	1.19	1.25
	Unigene20780	cytochrome P45082C4-like	1.29	1.15	1.18
	Unigene13446	gulonolactone	2.58	2.89	1.34
	CL943 .Contig1	mitogen activated protein kinase(KKK3)	5.04	4.37	5.05
	CL2936.Contig1	auxin response factor 8-like	5.00	4.95	8.06
	CL6842.Contig1	auxin-responsive protein	1.46	1.09	2.67
Changes in the expression of transcription factors	CL6644.Contig2	gibberellin receptor GID	0.71	0.00	1.08
	Unigene13909	hypothetical protein PRUPE_ppa023152mg	1.19	1.14	1.70
	Unigene9944	ethylene-responsive transcription factor	2.83	1.83	1.49
	Unigene24130	bZIP	1.22	1.33	1.28
	Unigene13635	bZIP	0.25	1.70	1.23
	Unigene3675	ERTF012	-2.23	-3.98	-4.75
	CL4042.Contig2	ERF034-like	1.51	1.10	1.10
	CL350.Contig2	bHLH74	2.62	1.72	1.94
	CL3500.Contig1	predicted protein	2.36	1.25	-1.12
	CL213.Contig1	predicted protein	1.31	1.72	1.68
	CL2305.Contig2	transcription elongation factor SPT5	2.17	2.02	1.93
	CL6074.Contig2	predicted: uncharacterized protein	1.00	1.27	1.60
	Unigene14210	predicted protein	1.41	1.03	1.58
	Unigene10242	Myb-related protein 330-like	2.03	1.83	1.83
	Unigene11417	transcription factor TCP19	1.03	1.26	1.09
	Unigene17144	ethylene-responsive transcription factor ERF003	1.80	1.63	-1.01
	CL4042.Contig2	ethylene-responsive transcription factor ERF034-like	1.51	1.10	1.10
	CL2384.Contig2	transcription factor MYB59-myb proto-oncogene protein	-0.13	0.31	1.65
	CL4495.Contig1	nucleic acid binding protein, putative	0.68	1.38	1.18
Carbon metabolism	Unigene7883	1 sugar-transport protein	1.55	1.64	1.72
	CL4049.Contig2	UDP-glycosyltransferase 85A2-like	13.52	14.56	14.54
	Unigene23953	UDP-glycosyltransferase 85A3-like	4.13	5.55	5.81
	CL1406.Contig1	UDP-glycosyltransferase 89A2-like	1.12	1.13	1.52
	Unigene35723	unnamed protein product	13.02	2.77	12.41
	CL2149.Contig1	amino acid permease 2-like	1.76	1.21	1.61
Osmotic regulation	CL4680.Contig2	proline iminopeptidase	12.07	11.86	12.12
	CL5895.Contig2	solute carrier family 25	3.66	2.48	2.11
	CL5828.Contig1	solute carrier family 13	2.76	2.81	4.10
	CL2892.Contig1	solute carrier family 40	0.29	0.15	0.45
	CL602.Contig1	solute carrier family 15	0.75	1.55	0.98
	CL2997.Contig3	solute carrier family 2	1.07	1.07	2.21
	CL801.Contig2	hypothetical protein ZEAMMB73_095591	6.91	4.99	5.55
	CL2574.Contig13	heat shock cognate 70 kDa protein isoform 1	2.28	2.70	2.70
	Unigene11667	small heat shock protein 17.4 kDa	2.67	2.41	2.76
	Unigene8639	small heat shock protein, chloroplastic	3.42	2.06	1.83
	CL4411.Contig1	heat shock protein 83-like	1.81	1.59	1.37
Protein kinases	CL2870.Contig1	heat shock protein, putative	1.80	1.64	1.12
	Unigene22252	serine-threonine kinase	1.08	1.17	1.03
	Unigene18472	serine/threonine-protein kinase sx32	-1.29	-1.98	-1.21
	CL1544.Contig2	serine/threonine-protein kinase AtPK2/AtPK19-like	2.30	2.13	2.11
Ubiquitin-proteasome system (UPS)	CL4751.Contig1	CBL-interacting serine/threonine-protein Kinase 6	4.75	3.58	3.06
	CL7928.Contig2	ubiquitin extension protein	1.52	1.65	1.61
	CL4959.Contig2	ubiquitin-conjugating enzyme E2 20	11.75	10.70	11.01
	CL5816.Contig3	ubiquitin-conjugating enzyme m, putative	2.44	1.96	2.05
	Unigene10144	E3 ubiquitin-protein ligase AIP2-like	2.93	2.75	3.51
Resistance	CL448.Contig1	E3 ubiquitin-protein ligase UPL1-like	2.35	1.67	2.28
	Unigene2395	disease resistance RPP13-like protein	-12.88	-12.93	-12.91

protein	Unigene5608	disease resistance protein RGA3-like	-2.82	-4.01	-3.73
	Unigene25823	disease resistance protein RGA4-like	-3.87	-13.15	-13.26
	Unigene2076	disease resistance protein RGA1	-4.79	-1.21	-1.90
	CL8031.Contig1	disease resistance protein RPM1	-6.69	-15.62	-5.79
	Unigene527	disease resistance protein RPS2	-4.51	-14.69	-14.78
