

Table 1 Suppl. Unigene specific primers (19 pairs) used in the real-time qPCR.

Gene	Acc. No. (RNA-seq)	Gene names	Classification	Primer sequence (from 5' to 3')
<i>Actin</i>	AY305733	Actin		ATCCTCCGTCTTGACCTTG TGTCCGTCAGGCAACTCAT
L1	comp74030_C0	MPK3 (Mitogen-activated protein kinase 3)	L-NaCl/CK-up and L-BL+NaCl/NaCl-down	TCGTGAGATTAAGCTCCTTCG GAAATACTGGCAATGCTCCTC
L2	comp75935_C0	PP2C (protein phosphatase 2C)	L-NaCl/CK-up and L-BL+NaCl/NaCl-down	CTATGGACAACGGGATCGGAAAT CAGATACGACTGGCGGGAACA
L3	comp71518_C0	Xyloglucosyl transferase TCH4	L-NaCl/CK-up and L-BL+NaCl/NaCl-down	CCTTTGTTGGCTCGTTAT ATGTTCTCCACCTCACC
L4	comp44264_C1	Hsp70 protein 1	L-NaCl/CK-up and L-BL+NaCl/NaCl-down	TGAAGGAAAGGCGATTGGGATT GCCGCTCGGTGTCTAGTAAAGG
L5	comp44264_C0	Heat shock protein	L-NaCl/CK-up and L-BL+NaCl/NaCl-down	TGATTGGTCGTCGGTTCACCTG CTCCGCAACCTCCTTCATCTT
L6	comp74110_C0	PsbE (photosystem II cytochrome b559 subunit alpha)	L-NaCl/CK-down and L-BL+NaCl/NaCl-up	GCGAATCAGACAAAGAAAGAG TGGAATAATGGATAATGGGAC
L7	comp58258_C1	PsaG (photosystem I subunit V)	L-NaCl/CK-down and L-BL+NaCl/NaCl-up	CCCTTCAGCATCTCATTCAC CGCTTATCACAACCTGGGTGG
L8	comp65435_C0	LHCA2 (light-harvesting complex I chlorophyll a/b)	L-NaCl/CK-down and L-BL+NaCl/NaCl-up	CCAACAAACGCCAACATAGC ACCCAACCTTCCCAACAAGA
L9	comp75192_C0	LHCB2 (light-harvesting complex II chlorophyll a/b binding protein 2)	L-NaCl/CK-down and R-BL+NaCl/NaCl-up	CGGCAAAACAAACCAAGTCAA GTCCCACCCATAGTCACCAG
R1	comp68500_C0	CDC42 (cell division control protein 42)	R-NaCl/CK-down and R-BL+NaCl/NaCl-up	ACTCTTTCCCTTCCTCCTTG TTTCCGACAGCACCATCTCC
R2	comp74823_C0	PBS2 (mitogen-activated protein kinase kinase)	R-NaCl/CK-down and R-BL+NaCl/NaCl-up	AGGGTAAAGGCCACTGGGTGA GGAATGGAAGCAAGCAAGGGT
R3	comp43578_C0	RP-S20e (small subunit ribosomal protein S20e)	R-NaCl/CK-down and R-BL+NaCl/NaCl-up	CGCAAGGAGTCTTACGGG ATTCTCCGCCGATTGTAT
R4	comp67123_C0	RP-Sae (small subunit ribosomal protein SAe)	R-NaCl/CK-down and R-BL+NaCl/NaCl-up	CCCCATCCACCATCGCCAGTA GCTATCAATCCCGCCCTCGTT
R5	comp66348_C0	PAK1 (p21-activated kinase 1)	R-NaCl/CK-up and R-BL+NaCl/NaCl-down	ACCTCTTATGGGCGTTAGCA TTGGTCCATTGTTTCGGGTAG
R6	comp74838_C0	PSMD3 (26S proteasome regulatory subunit N3)	R-NaCl/CK-up and R-BL+NaCl/NaCl-down	TACTGTTCTCGTCCATCTCGC CATGTGCCAACCTACCAAG
R7	comp73557_C0	PSMD2 (26S proteasome regulatory subunit N1)	R-NaCl/CK-up and R-BL+NaCl/NaCl-down	CATCAAATGCTGGAAGTGTCTC GAAGCTCTACGTGCTGTCTCG
R8	comp78069_C0	PBS2 (mitogen-activated protein kinase kinase)	R-NaCl/CK-up and R-BL+NaCl/NaCl-down	GAAGCAGCGTTAGCAGTAGGC GGATGTTGGGATGTCTGAAGAAT
R9	comp59536_C0	P38 (p38 MAP kinase)	R-NaCl/CK-Up and R-BL+NaCl/NaCl-down	GACAACTTGGGTAGGAGCAGC ACGAGCCTATCGCATCAGAAC

Suppl. Table 2. Length distribution of the transcripts and unigenes.

Length [bp]	Transcript	Unigenes
200 - 500	71 959	54 247
500 - 1 000	39 886	18 667
1 001 - 2 000	43 208	13 752
> 2 000	23 950	6 690
Total	179 003	93 356
Mean	1 012	730
N50	1 619	1 216
Minimum length	201	201
Maximum length	11 470	11 470
Total length	181 126 444	68 107 751

Table 3. Suppl. Number and distribution rate of unigenes in the *NR*, *NT*, *KO*, *SWISS-PROT*, *PFAM*, *GO*, and *KOG* databases. *NR* - *NCBI* non-redundant protein sequences, *NT* - *NCBI* nucleotide sequences, *KO* - *KEGG* ortholog, *PFAM* - protein family, *KOG* - eukaryotic ortholog groups.

Database	Number of unigenes	Distribution rate [%]
NR	58 537	62.70
NT	20 586	22.05
KO	18 266	19.56
Swissprot	38 490	41.22
PFAM	38 592	41.33
GO	43 290	46.37
KOG	23 149	24.79
All databases	5 638	6.03
At least one database	64 118	68.68
Total number of unigenes	93 356	100.00

Table 4 Suppl. Five most enriched Gene Ontology (GO) categories of the brassinolide-responsive genes in NaCl-stressed cotton leaves and roots. BP - biological process, CC - cellular component, MF - molecular function.

Treatments	GO accession number	Description	Term type	Corrected <i>P</i> -value	Number of DEGs
L-BL+NaCl/L-NaCl-down and L-NaCl/L-CK-up	GO:0050896	response to stimulus	BP	0.0877	94
	GO:0006950	response to stress	BP	2.27E-06	60
	GO:0009628	response to abiotic stimulus	BP	0.0365	17
	GO:1901700	response to oxygen-containing compound	BP	0.0115	14
L-BL+NaCl/L-NaCl-up and L-NaCl/L-CK-down	GO:0010035	response to inorganic substance	BP	0.0192	13
	GO:0008152	metabolic process	BP	0.0010	121
	GO:0044436	thylakoid part	CC	1.38E-15	22
	GO:0009579	thylakoid	CC	4.80E-15	22
	GO:0034357	photosynthetic membrane	CC	1.34E-14	20
	GO:0015979	photosynthesis	BP	4.08E-09	19
R-BL+NaCl/R-NaCl-down and R-NaCl/CK-up	GO:0030529	ribonucleoprotein complex	CC	0.0019	164
	GO:0005198	structural molecule activity	MF	0.0373	159
	GO:0006412	translation	BP	0.0031	159
	GO:0005840	ribosome	CC	0.0046	129
	GO:0022613	ribonucleoprotein complex biogenesis	BP	0.0498	116
R-BL+NaCl/R-NaCl-up and R-NaCl/CK-down	GO:0044085	cellular component biogenesis	BP	4.46E-06	90
	GO:0030529	ribonucleoprotein complex	CC	1.83E-07	78
	GO:0005198	structural molecule activity	MF	9.15E-06	74
	GO:0006412	translation	BP	5.13E-06	72
	GO:0005840	ribosome	CC	4.44E-08	67

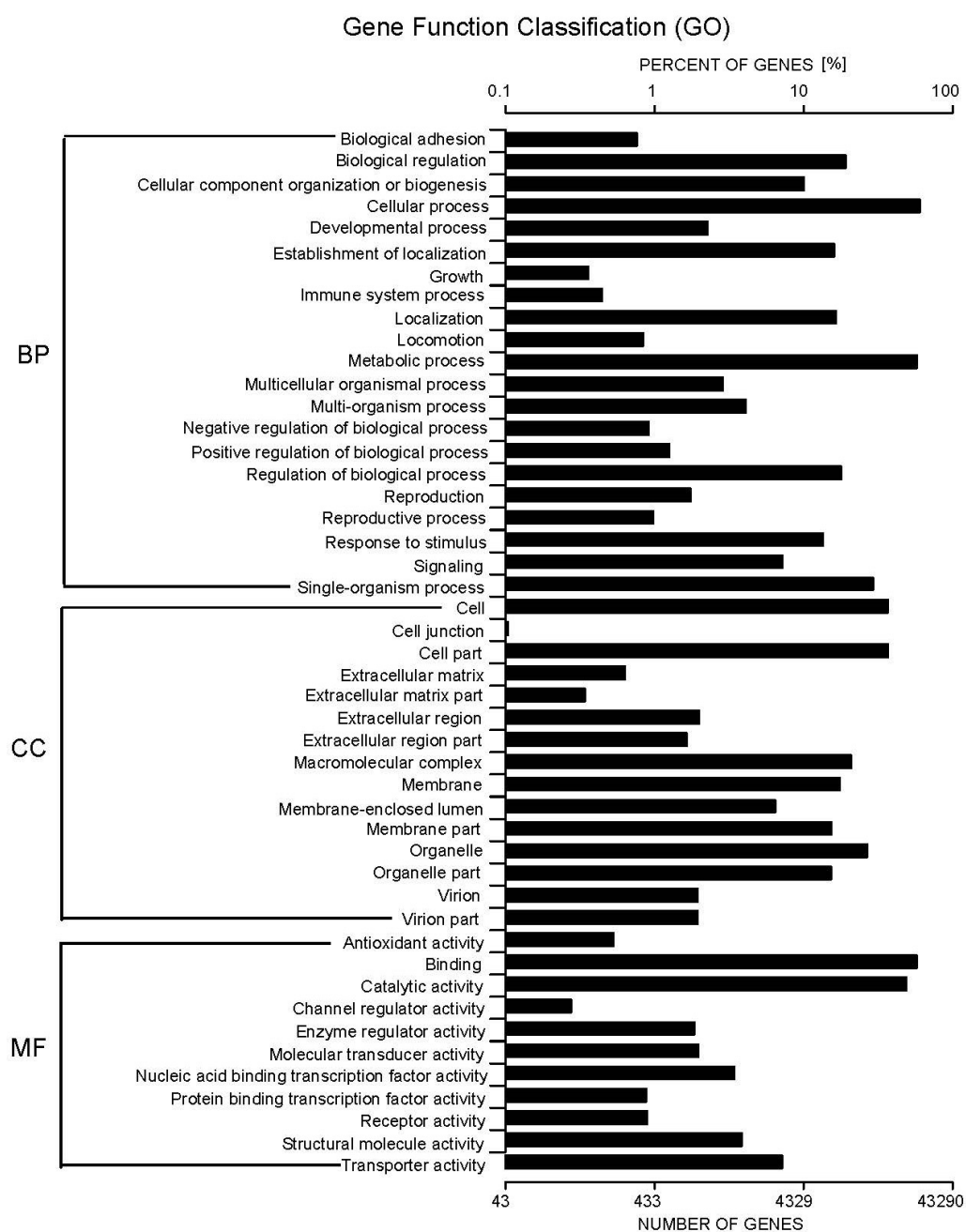


Fig. 1 Suppl. GO annotation of non-redundant consensus sequences. BP - biological process, CC - cellular component, MF - molecular function.

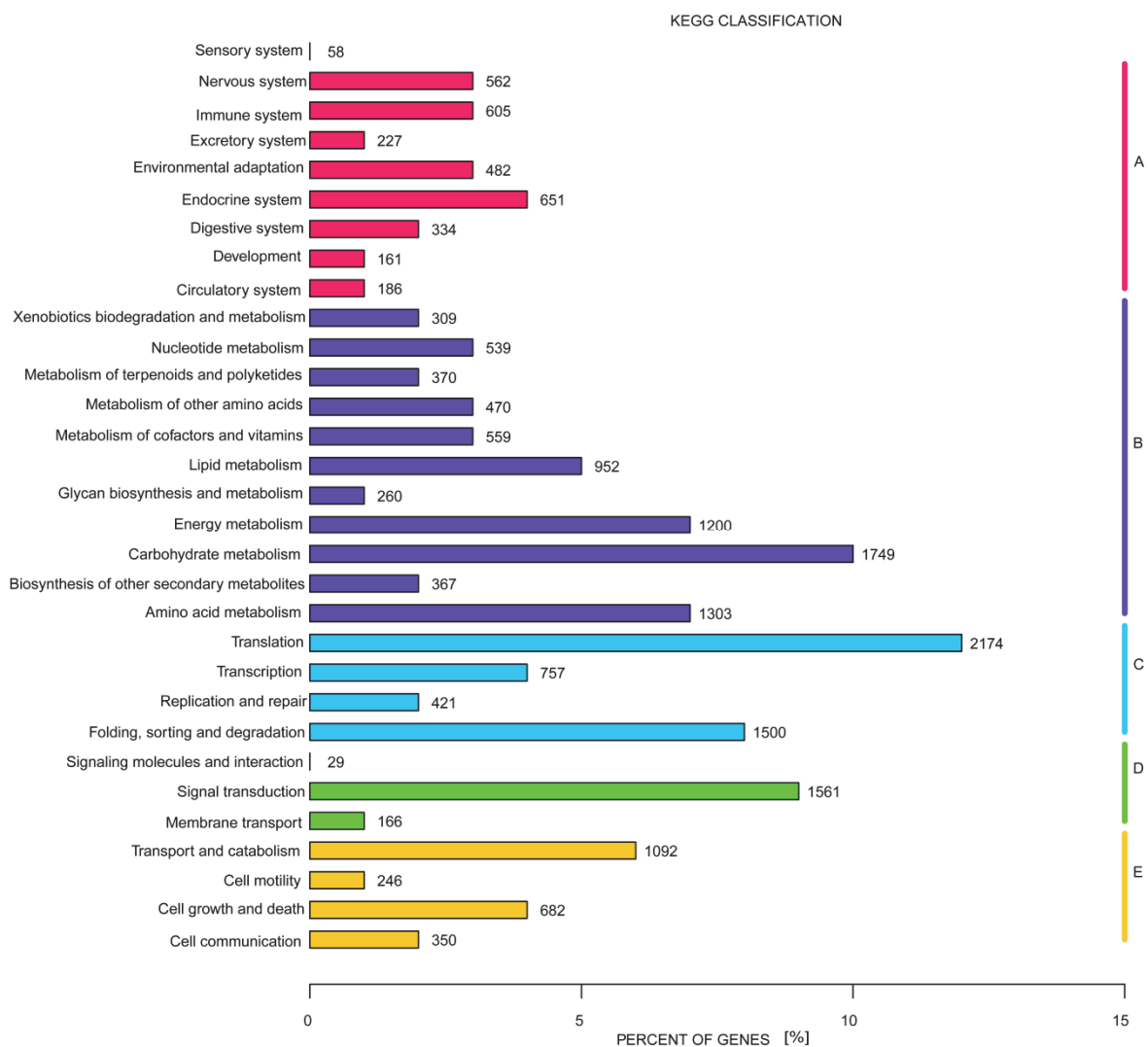


Fig. 2 Suppl. *KEGG* classification of unigenes. These genes were divided into 5 branches according to *KEGG* metabolic pathways: A - organismal systems, B - metabolism, C - genetic information processing, D - environmental information processing, and E - cellular processes.

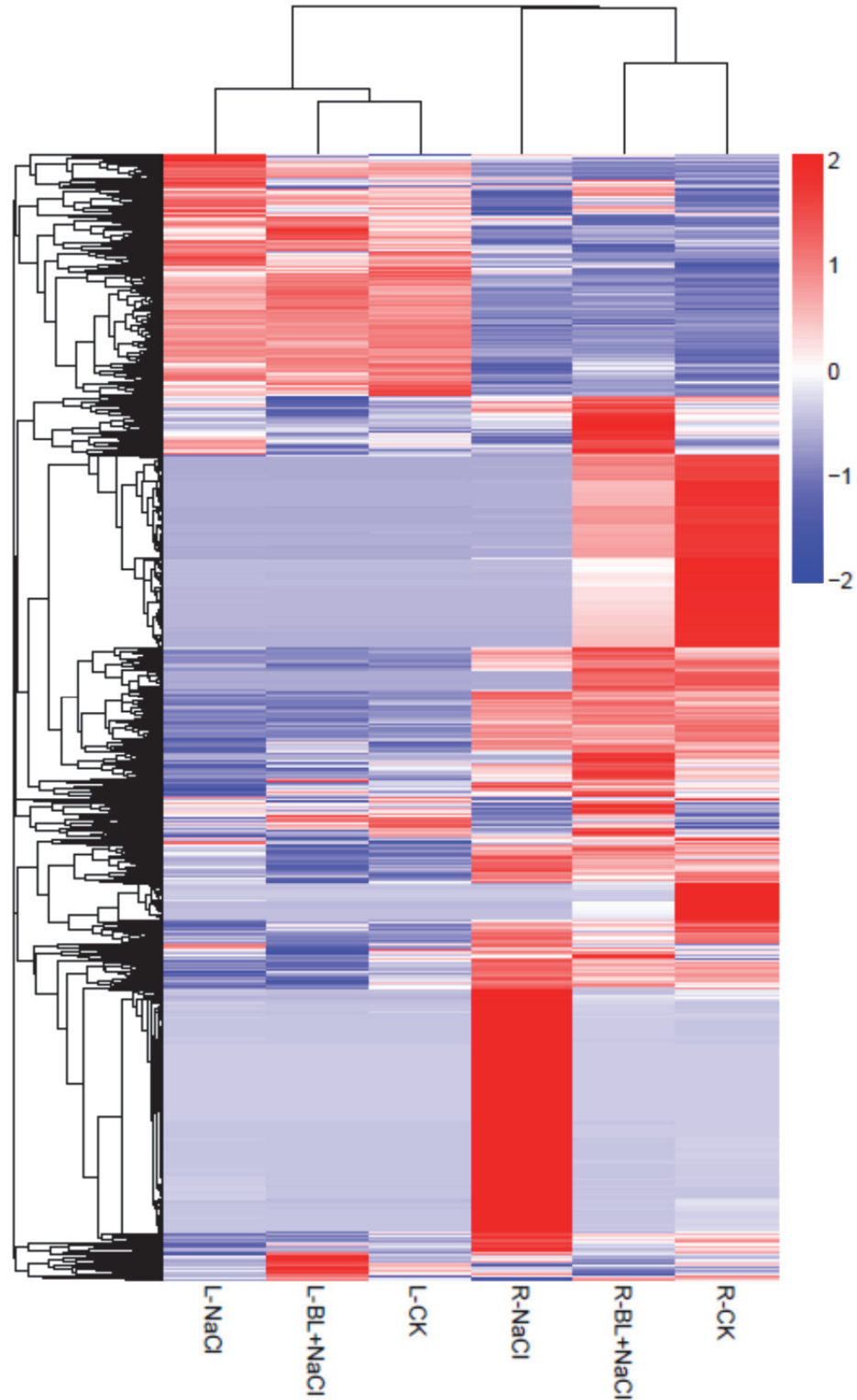


Fig. 3 Suppl. Hierarchical cluster analysis of differentially expressed genes (DEGs) in cotton leaves and roots among different treatments. Results are displayed as a $\log_{10}(\text{FPKM}+1)$ value on a colour scale from **magenta (high)** to **green (low)**?? to indicate the intensity of expression of each DEG. FPKM - fragments per kilobase of exon per million fragments mapped.

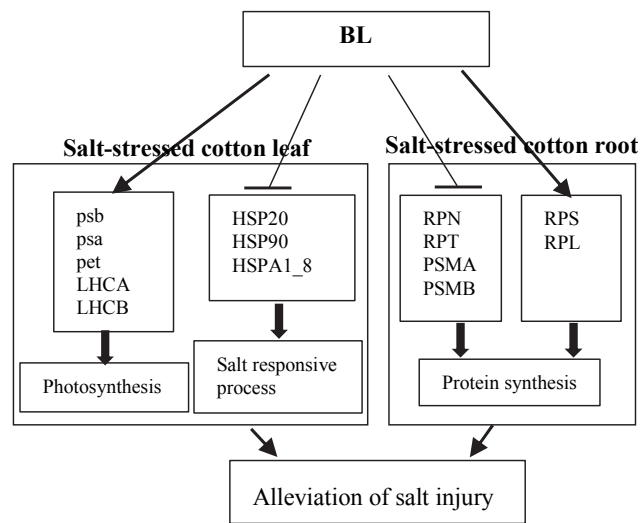


Fig. 4 Suppl. Overview of the BL-regulated pathways in salt-stressed cotton leaves and roots.