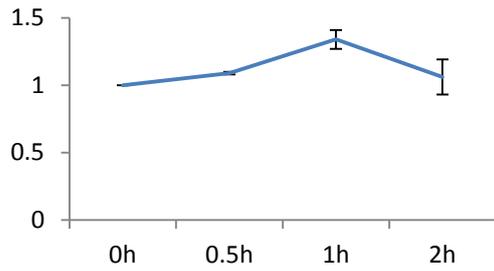
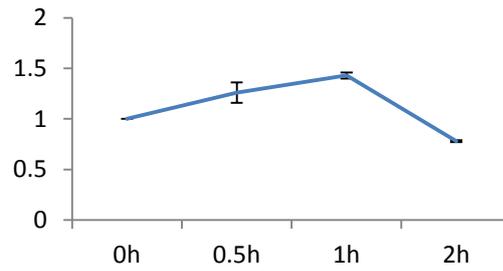


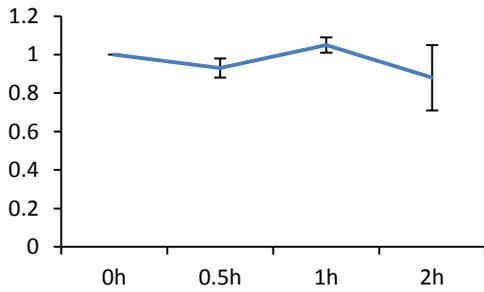
carbonic anhydrase



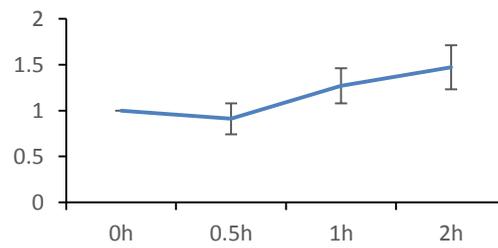
Rubisco activase



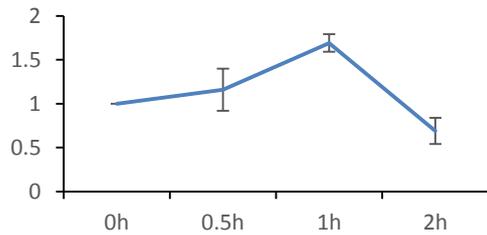
Catalase isozyme B



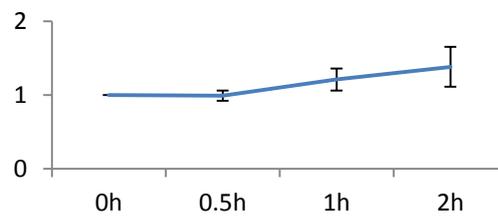
L-ascorbate peroxidase 8



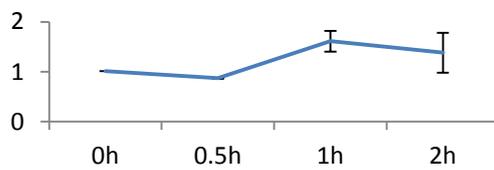
starch phosphorylase



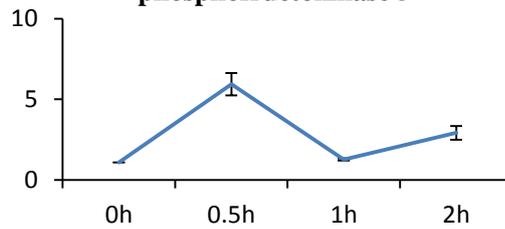
Phosphoglucomutase



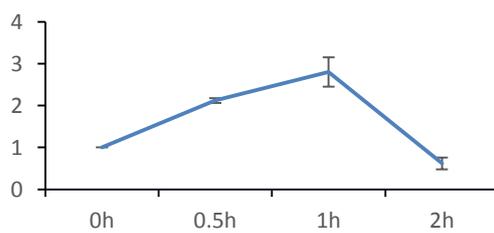
Glucose-6-phosphate isomerase



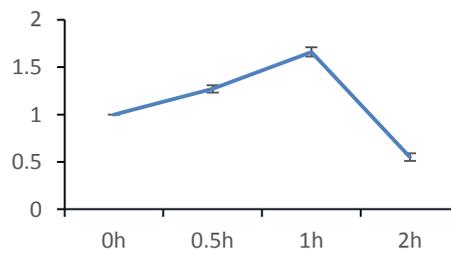
ATP-dependent 6-phosphofructokinase 5



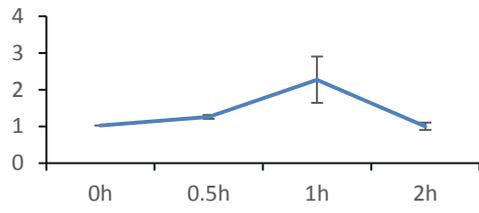
Triosephosphate isomerase



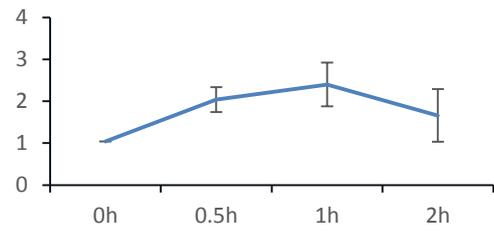
Pyruvate kinase



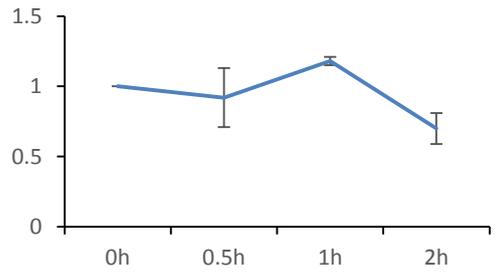
glycerol-3-phosphate dehydrogenase (DsGPDH2)



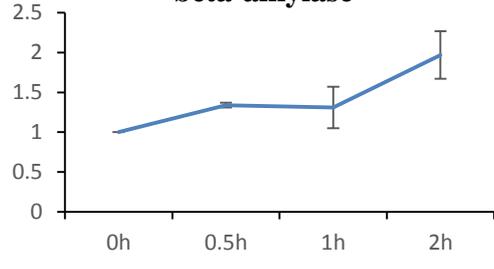
trehalose-6-phosphate OstA



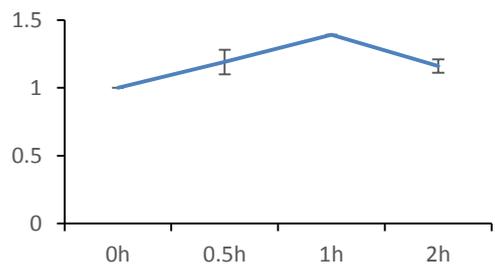
trehalose-6-phosphate OstB



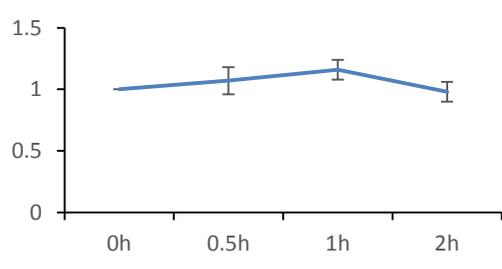
beta-amylase



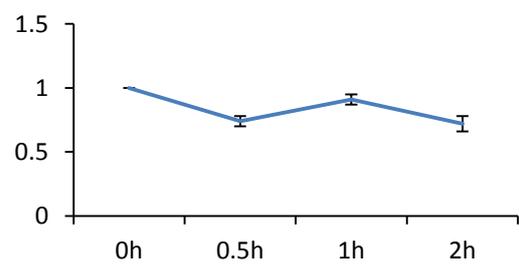
alpha-amylase-1



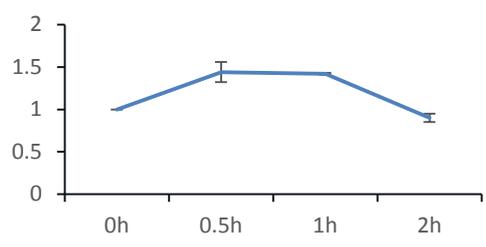
4-alpha-glucanotransferase-DPE2

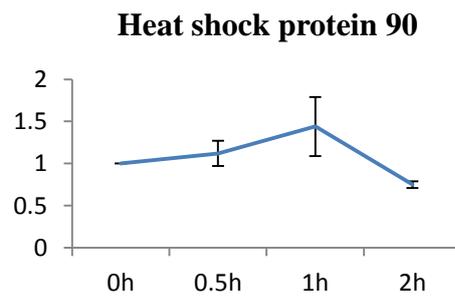
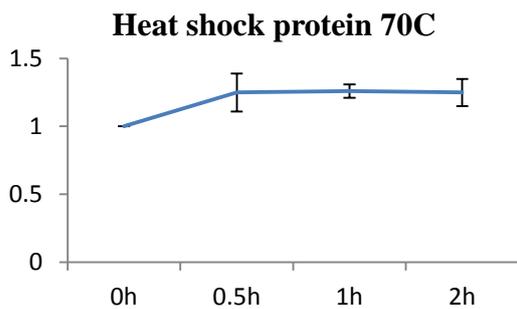
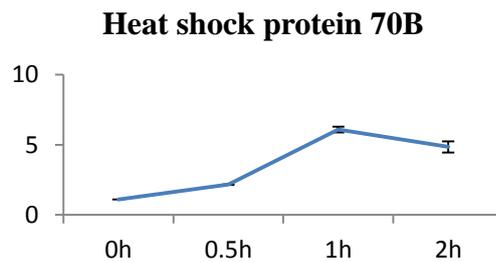
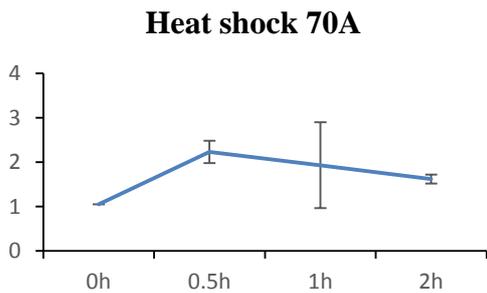
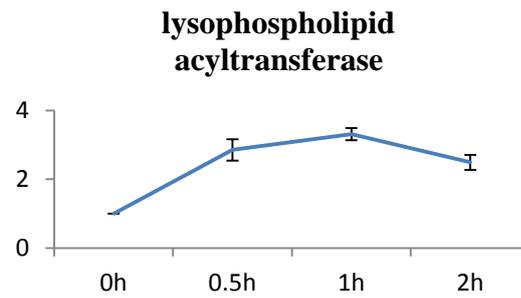
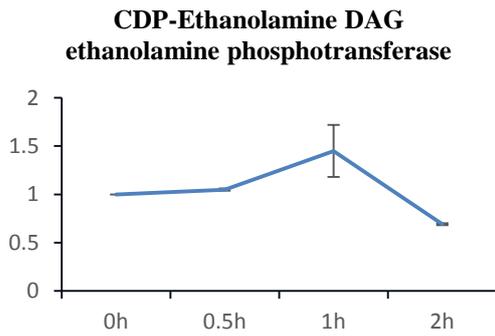
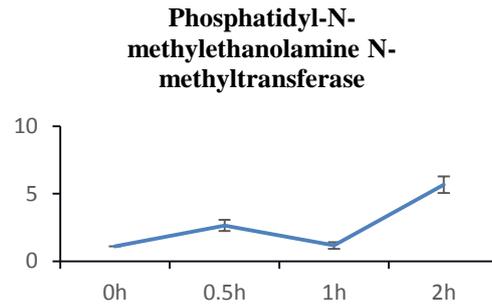
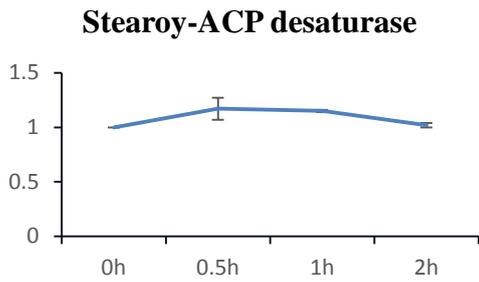
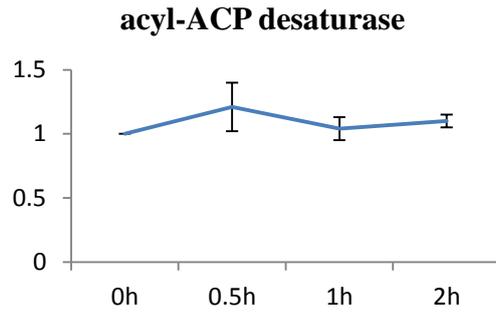
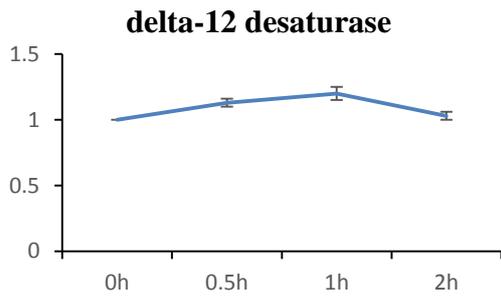


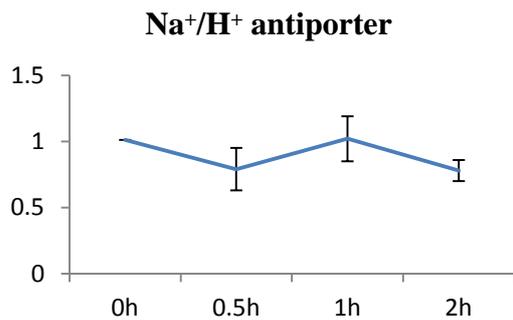
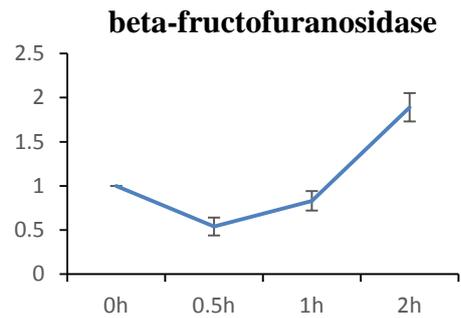
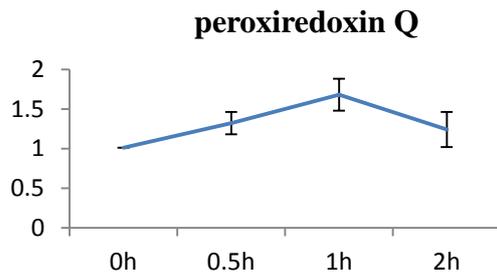
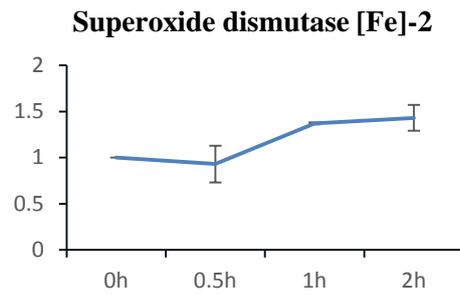
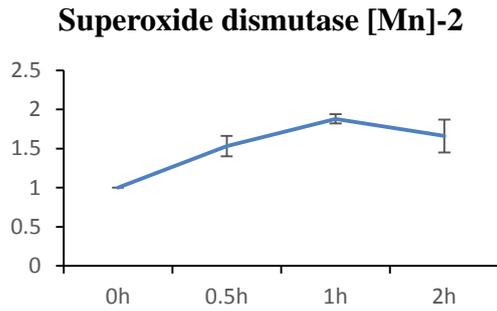
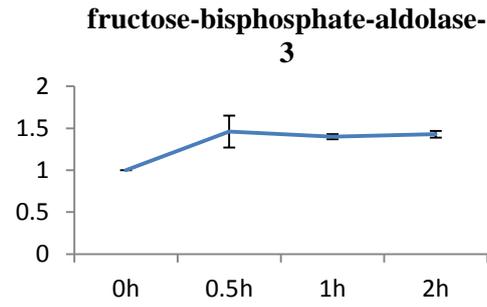
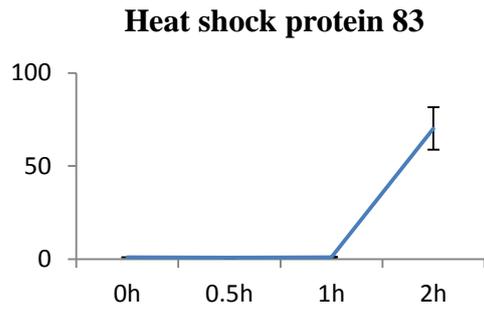
Acetyl-CoA carboxylase



Acetyl-coA carboxylase beta subunit







Additional file 3, confirmation of the expressions of the key genes by qPCR, the y axis represents the relative expression value; the x axis represents the salt stress time.

Primers used in qPCR

Gene name		Primer sequence
fructose-bisphosphate-aldolase-3	ps	AAGCGTTGGCCACTGGTTTAG
	pa	CACAGCACGCCATTTTGCA
Rubisco activase	ps	GGGCGCTGGAAGTCGATCGA
	pa	TTGTTGGTGCCCGCAGCTCC
carbonic anhydrase	ps	AAATTGCATCAGGTGCCATCA
	pa	AGCCAGCATATCCAAGCTCAGA
Phosphoglucomutase	ps	CCCTCAGACTCCGTTGCCA
	pa	CCGGTGGGGTCTCAAAGTA
delta-12 desaturase	ps	CTCTGCCGATGCCGGTACA
	pa	GATGAGCACGGAACGCCAG
Pyruvate kinase	ps	TCAGCAAGGTTGAGAACCAGGA
	pa	TCATCTTTTGGGCCAGGAAGA
Stearoy-ACP desaturase	ps	TACATCCCTTCCCAGAAGACGC
	pa	GCTTTGCACGGGTTTGAGGTAG
Acetyl-coA carboxylase beta subunit	ps	TGCTGCACGGGATCCCTGT
	pa	CCTCCTGCGTGGCGTACTCA
Catalase isozyme B	ps	CGCACCATGCCTGGCTTT
	pa	CCTCGTCGTCCAGCAGGTTG
Na-H antiporter	ps	CCACCCAGGCCAGAATCTGTG
	pa	TGTCTGCCCTCGCACTGATCA
acyl-ACP desaturase	ps	GCCCCATCATCCTCAACA
	pa	AGCACTTGTGCACAGGTGTCAG
Heat shock protein 83-1	ps	AGCGGAAATCAACCAACTGCT
	pa	ATGTGCATGTTGGGGTTGCT
Superoxide dismutase [Mn]-2	ps	GGGATGTTACCGCCAAACT
	pa	TGCTCCATTGCAGCGTTGTAG
beta-fructofuranosidase	ps	AAGCCCAGCTTCCACCTGC
	pa	TCGTGCGGTGGTGCTGATAG
Superoxide dismutase [Fe]-2	ps	CTCACCCCCCTCCTTATGGT
	pa	CGCCACCTTGACAAGCTTCAG
Acetyl-coA carboxylase beta subunit	ps	CATCCGGGCTATGGTTTCT
	pa	TCCCTGGCTGAGTTCTTGTCAC
Phosphatidyl-N-methylethanolamine N-methyltransferase	ps	TGCCAAAATCCAGTCCCATAACC
	pa	TGAACACGCTGGTCCACACTTC
ATP-dependent 6-phosphofructokinase 5	ps	CTGTGCTATTGCAGCGCGAA
	pa	TGAGGCAGGCCAAGATCTGAG
Heat shock protein 90-1	ps	CGTCATCCGCAGGCAGCTT
	pa	CGGCTGGAGAAGAAGCGCA
Heat shock protein 70C	ps	ATGTGAAGGACATCCTGCTGCT
	pa	TGTTGAGAAGACCTGGCCCTT
peroxiredoxin	ps	ATTAATCCACAGGGTGTGGTGC

	pa	GGCACACTTCTCCATGCTTCTC
peroxiredoxin Q	ps	GAACCCCTGGATGCACCAA
	pa	TTGCCCAGGCTGCATTCTC
lysophospholipid acyltransferase	ps	CGTGTCCGTGCCTCAGCTAC
	pa	GAAGGATGCCCGTGACCAG
Heat shock protein 70B	ps	GCACCATGTGCGGCAAGGAG
	pa	TGAGCTTGGTGGCCACACCG
Glucose-6-phosphate isomerase	ps	ACGGGCTCGACGTGACCAGA
	pa	TTCCACTCGCCACTGCGCA
starch phosphorylase	ps	CACCCCAACCAGTGGAACAA
	pa	GCTCGTCCTTGACGATCTCAGA
Heat shock 70A	ps	GAGACCGCTGGTGGTGTGATG
	pa	CGCTCACCTCGTACACCTGA
beta-amylase	ps	CCTGAGTGGGGCTTGAGTGG
	pa	GCAGCAGTGAGGATGCGCT
glycerol-3-phosphate dehydrogenase (DsGPDH2)	ps	ATGCCCAGCATGCCTCCA
	pa	AGGCGTAGTGGCAGCAGCA
trehalose-6-phosphate OstA	ps	GAGGGCCAGACATGGAACACC
	pa	CGTCTCGATGCTGCTCCCAT
L-ascorbate peroxidase 8	ps	GAGGTGCCAACGGTGCCAT
	pa	TGGGAGACGTCAGGGTACTTGG
Triosephosphate isomerase	ps	AAGTTCTTTGTGGGCGGGAAC
	pa	TTGCAGTTGGAGTCGCTGACA
CDP-Ethanolamine DAG ethanolamine phosphotransferase	ps	GCCCTGGAGGGCTGAAGGAGT
	pa	TACAACGCGGAGGCGAGGTAGG
alpha amylase-1	ps	AGGGAAGGCCTCCTGGTGTC
	pa	CCCTCAGGCAGGTTCTTCCA
trehalose-6-phosphate OstB	ps	CCACAGATGTGGATGGCACAC
	pa	GGTTGAGCTGCGAGAACACCT
4-alpha-glucanotransferase-DPE2	ps	ACAAGTGGTGGAGGAGAAGGCT
	pa	CGGCTGTCAAGCTCATGCTT