

Table S1 Reads quality and mapping ratio of the transcriptomes

Sample	Clean reads number	Clean reads quality		Mapping ratio (%)		Mapped genes
		Q20 (%)	Q30 (%)	Total	Unique	
SS0-1	23960080	98.35	91.81	97.98	92.76	14682
SS0-2	23636340	97.72	90.13	97.07	91.07	14697
SS0-3	23677786	97.83	90.63	96.88	90.97	14684
SS6-1	23666259	97.97	90.98	97.12	91.22	14233
SS6-2	23778798	98.01	91.04	96.82	91.50	14327
SS6-3	24067181	98.03	90.46	98.26	92.98	14433

SS0 and SS6: 0 h and 6 h upon salinity stress (200 mM NaCl)

Clean Reads Q20(%): The ratio of bases with high quality (Quality value> 20) to the total bases in the clean reads

Clean Reads Q30(%): The ratio of bases with high quality (Quality value > 30) to the total bases in the clean reads

Total Mapping Ratio: The percentage of mapped reads

Uniquely Mapping Ratio: The percentage of reads that map to only one location of reference

Table S2 The primer sequences of selected genes used in qPCR experiments

Gene name	Gene ID	Forward primer (5'-3')	Reverse primer (5'-3')
<i>BC</i>	Cz13g10110	CGTGGCAGCTACGGCTTAAC	TGCACCAACTCCTGGAATGA
<i>KAS3</i>	Cz18g03070	CTGCGGTGCCATAGTGATGA	CCCCCTTCACCGCTGTATTT
<i>KAR</i>	Cz01g34370	TTCATTGCGTCCGACATGAC	AGCTAGGAAGCGCACCAAAC
<i>FAT</i>	Cz04g05080	GAGGGACGGCATGAAATAGC	CAAGTGTGCGGGCATCAC
<i>SAD</i>	Cz04g09090	GATGAGGGACGGCATGAAAT	GTGTGCGGGCATCACAATC
<i>LACS</i>	Cz11g20120	TGGATGACATTGGTGCTCTGA	GCGGGCAAAAGCATAGTTGA
<i>GPAT1</i>	Cz11g03260	GGAGTCTTTGCCCACATGCT	CAGGTTGCGACCCATGCT
<i>GPAT2</i>	Cz09g31330	GCCTTTGCTGTTCATCATGCA	GGCAACAATGTGACGATCCTT
<i>LPAAT1</i>	Cz16g02090	GTTCTCTACTGGCCATGTCA	CGTGTGCCTTCTGGGAAGAA
<i>LPAAT2</i>	Cz04g14150	CGTGTGGGATGCAAAATGG	AGCCAGCAAATACCGTCCAA
<i>LPAAT3</i>	Cz10g20070	GGGAACAGCTGCGACTCCTA	CAGTGATGGGCAGGATTGTG
<i>PAP1</i>	Cz05g23060	CACACGCCTGGTCATTTCTG	GCAGGTAGTCGCGAGTGATG
<i>PAP2</i>	Cz10g16040	TGACATCATCGGTGGGTTTG	GTGACAGGCAGGCCAGATCT
<i>PAP3</i>	Cz16g11240	TGGCAGAAGAACCCGAGAAT	CGTGGTGATGCTGTGACGTT
<i>DGAT1A</i>	Cz06g05010	GGCATCCGAATGAACCTCAT	AACTCCTCGTCCTGCTTCATG
<i>DGAT1B</i>	Cz09g08290	TGCCTTGCTTCATCGTCCTT	CCCTTCCCTCCTGGCTACAC
<i>DGTT5</i>	Cz09g27290	CCAGCAGCGTGTTCTCCATT	GCAATACCCCCACAATCAC
<i>MLDP</i>	Cz04g29220	GCTCCTTCGTTTCCTGCATTT	CGCAGCACCTTCTCGTAGT
<i>LCYe</i>	Cz09g18310	CAGTGTTTCGCGGTCTTTGA	ACGCGTTGGTAGCTGACAGA
<i>LCYb</i>	Cz12g10170	TTCCACTGGCATGGCTTCTT	CTGCCGAGCTCACCATCTG
<i>CHYb</i>	Cz12g16080	CGTTACGCACACAAGGCATT	CACAGGCTGAAGGCAGGTACA
<i>BKT1</i>	Cz13g13100	ACCTCAAGCCGCACTCAAAT	GCCAGCAGCCATGGTAAAAG
<i>bHLH</i>	UNPLg00160	GCTGAGCAACGCAGAAGGA	GAGTTGCGGTGCCTCAATG
<i>MYB</i>	Cz10g24240	CCGCCTGTACCCATGGTAGT	AGCAGTGCAGCAACCAGTTG
<i>Beta-actin</i>	Cz05g19150	GCTGGCATTACGACACAAC	TGCCACCACCTTGATCTTCA