Supplemental Table S1. Sequences of specific primers

Primer name	Primer sequence (5'-3')
Unigene0000288	F: GTCGCAGGTCCTCTTGGAAA
	R: TGGAAAAGCGGCCACAAATG
Unigene0001622	F: GAAGCAGTTGCGCCATGAAA
	R: CCAAGACCGAATCCCCAACA
Unigene0015746	F: GTTGATCGTCCTGTGCCTCT
	R: CGGAGTGATCCCCATTGCTT
Unigene0049771	F: AAGAAAGCGCATTGGTGTGG
	R: GACGCAAACACCTTCTCTGC
Unigene0091673	F: AGTGGAAGTGATACCGGTGC
	R: ACAGTGGGATCGTGGTGTTC
Unigene0042390	F: GGGGCGAGGAAAAGATGTCA
	R: CTAGGCAGCACTCAGCAACT
Unigene0008166	F: TGATCGTCCTGTTGCTCGTT
	R: TCTGACACCACCAGGGTACT
Unigene0021959	F: CGTGGATGACCCAGATCGAG
	R: AGGTTTTGTCGGGCCTTTGA
Unigene0095053	F: CTCGTCCTCTATCAACCGGC
	R: GTACCGATTTCACCGCTCCT
Tubulin	F: GCTGAGATTACAACCGCTG
	R: CTGTTCGTTTGGTCTTGATT

Note: F means Forward primer, R means Reversed primer.

Supplementary Table S2. Prediction data table of Pfam protein structure domains of *trehalose*-related genes

ID	envelope start	envelope end	hmm start	hmm end	hmm length	bit score	hmm acc	clan	PfamA_definition
Unigene0000288	594	753	1	160	233	170.8	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0001622	593	827	1	232	233	265.4	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0008166	593	826	1	233	233	260.4	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0008340	596	831	1	232	233	257.9	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0010526	121	364	1	233	233	247.1	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0010527	1	54	178	232	233	45.4	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0014917	125	370	1	233	233	246.1	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0015746	595	827	1	231	233	244.6	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0015747	595	829	1	231	233	268.7	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0021959	136	382	1	232	233	242.0	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0025943	97	355	1	232	233	187.5	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0042390	602	761	1	160	233	163.7	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0049766	593	662	1	70	233	72.7	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0049771	1	170	70	232	233	170.6	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0074391	115	357	1	232	233	230.4	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0078133	1	88	104	195	233	84.9	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0080946	123	353	1	216	233	238.1	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0091673	152	379	15	211	233	181.9	PF02358.16	CL0137	Trehalose-phosphatase
Unigene0095053	65	321	1	229	233	212.3	PF02358.16	CL0137	Trehalose-phosphatase

Note: **envelope start:** HMM model predicted structural domain start position of Unigene coding protein sequence; **envelope end:** HMM model predicted structural domain end position of Unigene coding protein sequence; **hmm start:** start position of matching sequence in the database; **hmm end:** end position of matching sequence in the database; **hmm length:** length of matching sequence in the database; **bit score:** score of Unigene coding protein sequence structure compared to HMM model; **clan:** classification of Unigene coding protein sequence by protein sequence, structure and HMM file in the Pfam database; **hmm acc:** The model ID of the gene/protein sequence corresponding structure in Pfam; **PfamA_definition:** the name of the structure corresponding to the query sequence in PfamA.

Supplementary Table S3. KEGG pathway annotations and Log_2 fold Change variations of *trehalose*-related genes

ID	Description	Pathway	Log_2 Fold Change	
			N-48 h vs. N + K-48 h	N-168 h vs. N + K-168 h
Unigene0000288	Trehalose-6-phosphate synthase	ko01100; ko01110; ko00500	1.57	−0.03
Unigene0001622	Predicted: probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	ko01100; ko01110; ko00500	0.82	1.21
Unigene0008166	Predicted: probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10 isoform X2	ko01100; ko01110; ko00500	0.40	0.81
Unigene0008340	Trehalose-6-phosphate synthase 3	ko01100; ko01110; ko00500	−2.00	−0.57
Unigene0010526	Predicted: trehalose-phosphate phosphatase A	ko01100; ko01110; ko00500	1.25	−2.03
Unigene0010527	Trehalose-phosphate phosphatase A	ko01100; ko01110; ko00500	−0.77	2.17
Unigene0014917	Probable trehalose-phosphate phosphatase F isoform X1	ko01100; ko01110; ko00500	−0.45	0.03
Unigene0015746	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 isoform X1	ko01100; ko01110; ko00500	1.61	1.23
Unigene0015747	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 isoform X1	ko01100; ko01110; ko00500	0.44	1.53
Unigene0021959	Trehalose-6-phosphate phosphatase A	ko01100; ko01110; ko00500	1.37	2.56
Unigene0025943	Predicted: probable trehalose-phosphate phosphatase 2	ko01100; ko01110; ko00500	−1.20	0.31
Unigene0042390	Trehalose-6-phosphate synthase 2	ko01100; ko01110; ko00500	0.46	0.70
Unigene0049766	Predicted: probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7	ko01100; ko01110; ko00500	2.80	−1.11
Unigene0049771	Trehalose-6-phosphate synthase	ko01100; ko01110; ko00500	1.50	−0.84
Unigene0074391	Probable trehalose-phosphate phosphatase J isoform X2	ko01100; ko01110; ko00500	−0.37	1.16
Unigene0078133	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	ko01100; ko01110; ko00500	0.00	2.64
Unigene0080946	Predicted: trehalose-phosphate phosphatase A	ko01100; ko01110; ko00500	−0.86	1.13
Unigene0091673	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1-like	ko01100; ko01110; ko00500	-0.55	-1.23
Unigene0095053	Predicted: probable trehalose-phosphate phosphatase C isoform X2	ko01100; ko01110; ko00500	-0.34	0.48

Note: ko01100: Metabolic pathways; ko01110: Biosynthesis of secondary metabolites; ko00500: Starch and sucrose metabolism; 200 mM NaCl-48 h vs. 200 mM NaCl+10 mM KCl-48 h: N-48 h vs. N+K-48 h; 200 mM NaCl-168 h vs. 200 mM NaCl+10 mM KCl-168 h: N-168 h vs. N+K-168 h.

Supplementary Table S4. Starch and sucrose metabolism pathway analysis

Pathway	Candidate genes with pathway annotation	Gene (Up)	Gene (Down)	*P*-value (Gene)	Candidate Metabolites with pathway annotation	*P*-value (Metabolite)
N-48 h vs. N + K-48 h						
Starch and sucrose metabolism	71	22	49	0.395663	2	0.369721
N-168 h vs. N + K-168 h						
Starch and sucrose metabolism	59	13	46	0.41911	2	0.451439

Note: N-48 h vs. N + K-48 h: 200 mM NaCl-48 h vs. 200 mM NaCl + 10 mM KCl-48 h; N-168 h vs. N + K-168 h: 200 mM NaCl-168 h vs. 200 mM NaCl + 10 mM KCl-168 h.

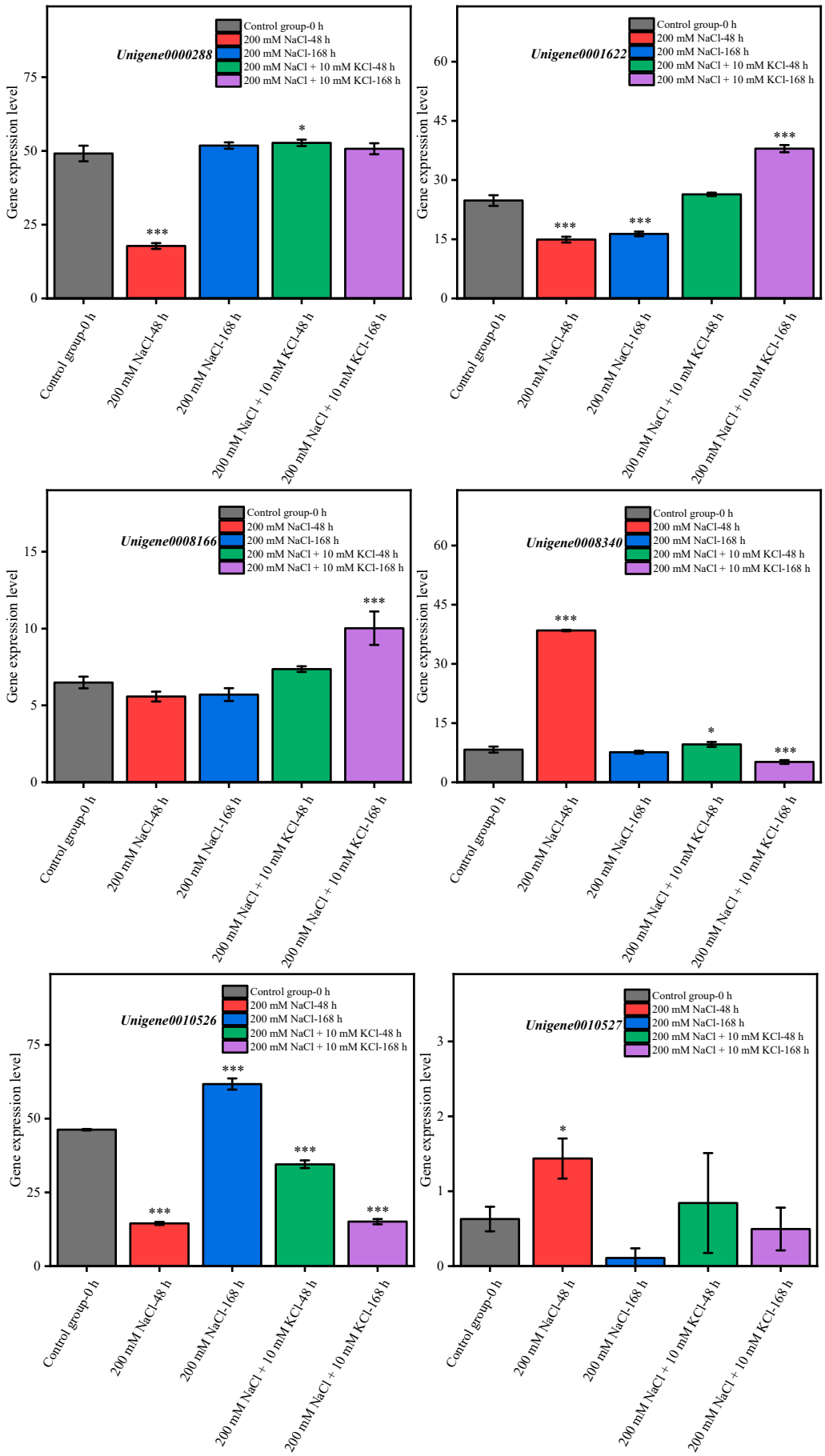
Supplementary Table S5. Analysis of differential metabolites in the starch and sucrose metabolism pathway

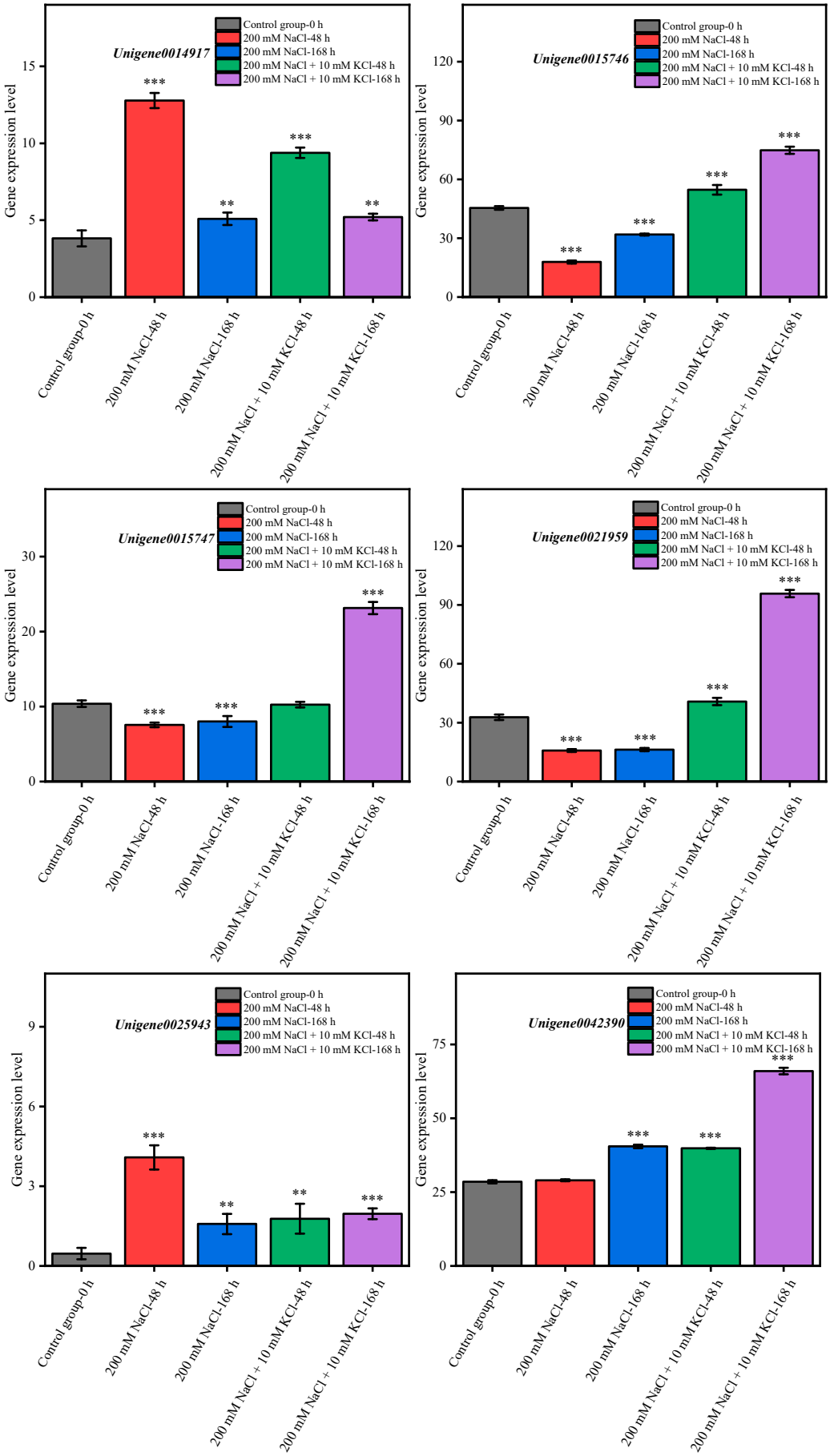
Name	Formula	Molecular Weight	PPM	RT [min]	m/z	Control group-0 h		N-48 h		N+K-48 h		N-168 h		N+K-168 h	
						Mean	Standard deviation	Mean	Standard deviation	Mean	Standard deviation	Mean	Standard deviation	Mean	Standard deviation
D-Glucose 6P	$C_6H_{13}O_9P$	214.02	176921.23	1.37	213.02	70026834.33	54905390.16	65265476.36	8248891.54	74732554.71	27849331.92	14494720 7.97	7532566.27	10675124 8.90	71696899.84
α D-Glucose 1P	$C_6H_{13}O_9P$	260.03	1.20	1.22	259.02	74820764.65	55721889.39	62572017.94	8059405.36	45193168.03	19896525.48	13241019 3.53	5673444.22	15976637 5.07	10511643.61

Note: Control group-0 h: CK-0 h; 200 mM NaCl-48 h: N-48 h; 200 mM NaCl+10 mM KCl-48 h: N+K-48 h; 200 mM NaCl-168 h: N-168 h; 200 mM NaCl+10 mM KCl-168 h: N+K-168 h.

Supplementary Table S6. Information table of 20 species

Family	Species	Description	Protein ID	CDS (bp)	ORF length (aa)
Amaranthaceae	*Chenopodium quinoa*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 isoform X1	XP_021733646.1	2628	875
Juglandaceae	*Juglans regia*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_018831647.1	2634	877
Juglandaceae	*Carya illinoinensis*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 isoform X2	XP_042947363.1	2583	860
Euphorbiaceae	*Mercurialis annua*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_050223303.1	2586	861
Betulaceae	*Betula platyphylla*	Trehalose-6-phosphate synthase 4	ATE80675.1	2646	881
Euphorbiaceae	*Manihot esculenta*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10	XP_021591773.1	2586	861
Euphorbiaceae	*Ricinus communis*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_015579849.1	2586	861
Euphorbiaceae	*Hevea brasiliensis*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10	XP_021674483.1	2586	861
Rhamnaceae	*Ziziphus jujuba* var. *spinosa*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_015882649.1	2574	857
Rosaceae	*Rosa chinensis*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_024174983.1	2592	863
Vitaceae	*Vitis riparia*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10 isoform X1	XP_034682535.1	2574	857
Pedaliaceae	*Sesamum indicum*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10	XP_011086535.1	2577	858
Rosaceae	*Malus domestica*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_008340008.2	2583	860
Proteaceae	*Telopea speciosissima*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_043724508.1	2586	861
Salicaceae	*Populus alba*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_034908781.1	2574	857
Malvaceae	*Hibiscus syriacus*	Alpha,alpha-trehalose-phosphate synthase 6	KAE8730256.1	2613	870
Celastraceae	*Tripterygium wilfordii*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_038705255.1	2580	859
Fagaceae	*Quercus suber*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_023908486.1	2577	858
Malvaceae	*Durio zibethinus*	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 isoform X1	XP_022726963.1	2586	861
Malvaceae	*Theobroma cacao*	Predicted: probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	XP_017973680.1	2586	862


Unigene0000288
Unigene0001622
Unigene0008166
Unigene0008340
Unigene0010526
Unigene0010527
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level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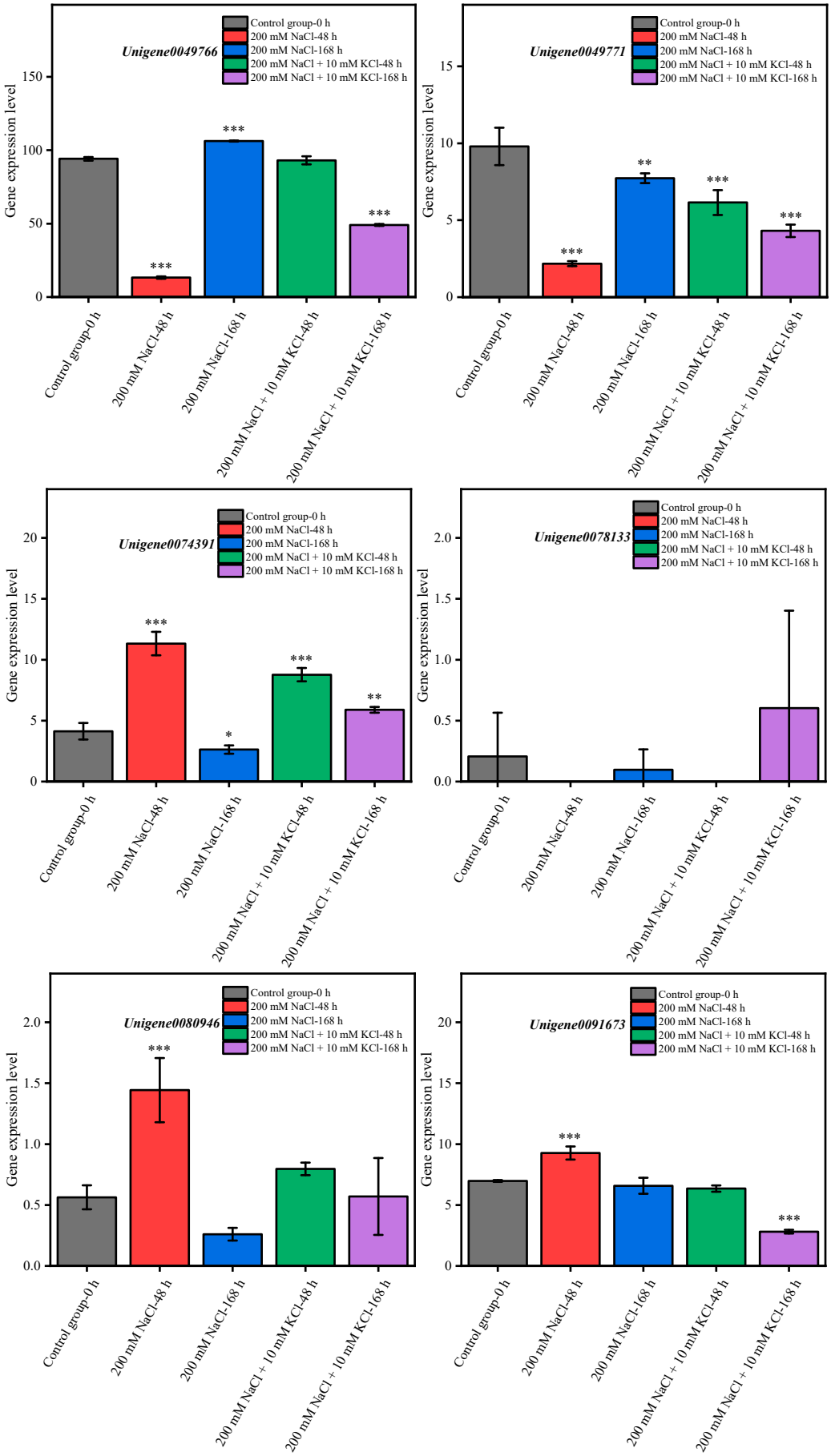
Unigene0015746
Unigene0015747
Unigene0021959
Unigene0025943
Unigene0042390
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
***
**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Unigene0049771
Unigene0074391
Unigene0078133
Unigene0080946
Unigene0091673
Control group-0 h
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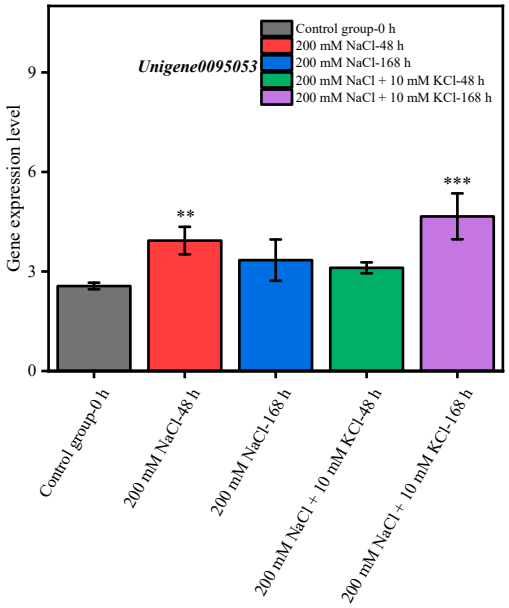
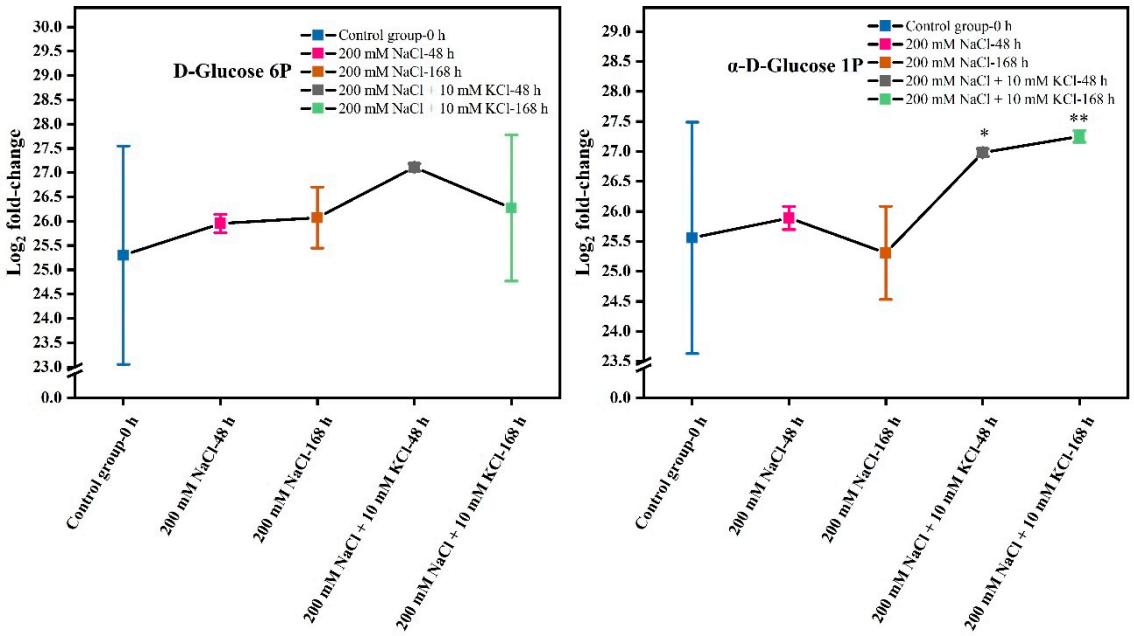
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
***
**
*



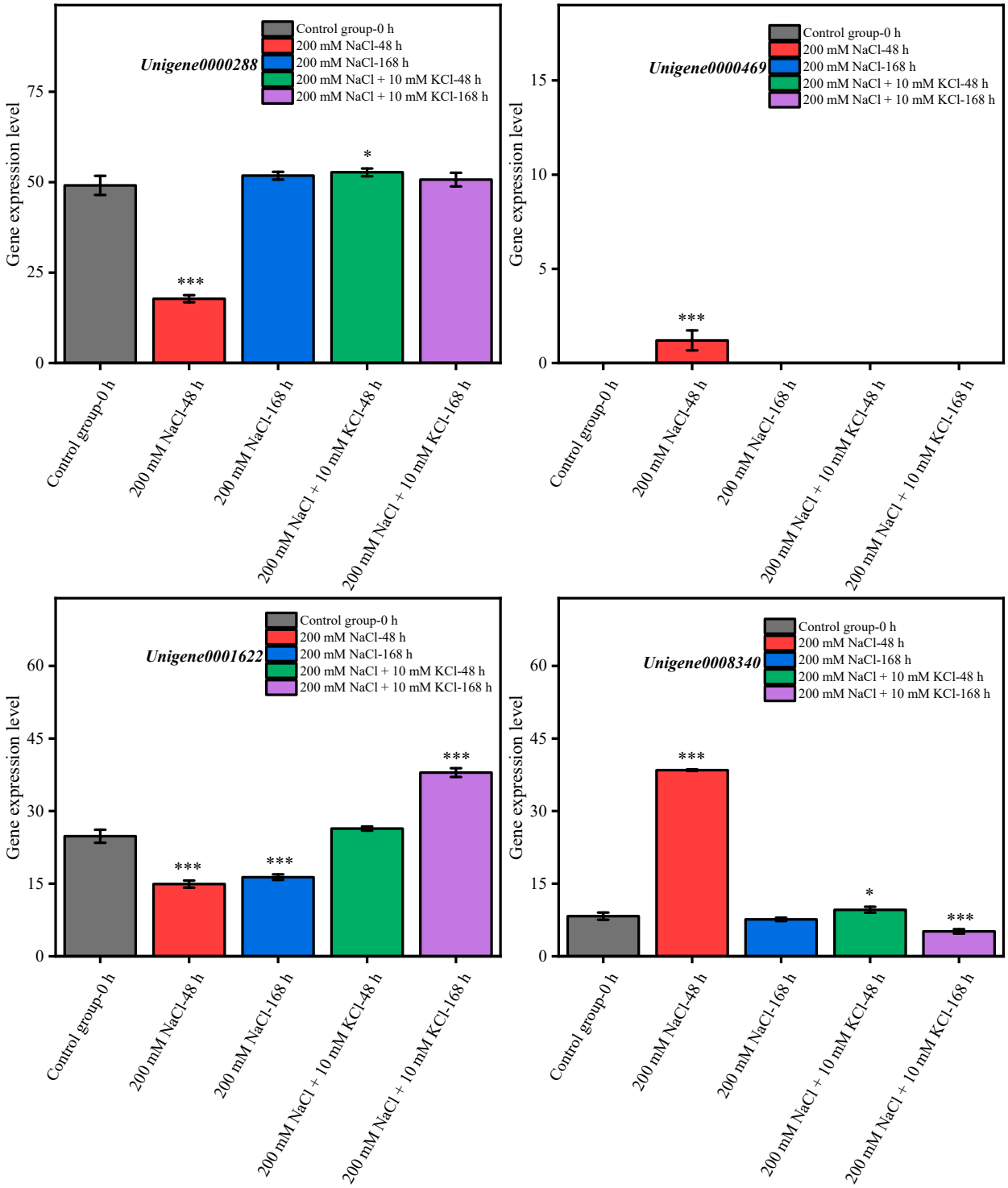
Supplementary Figure S1. Expression level changes of *trehalose*-related genes

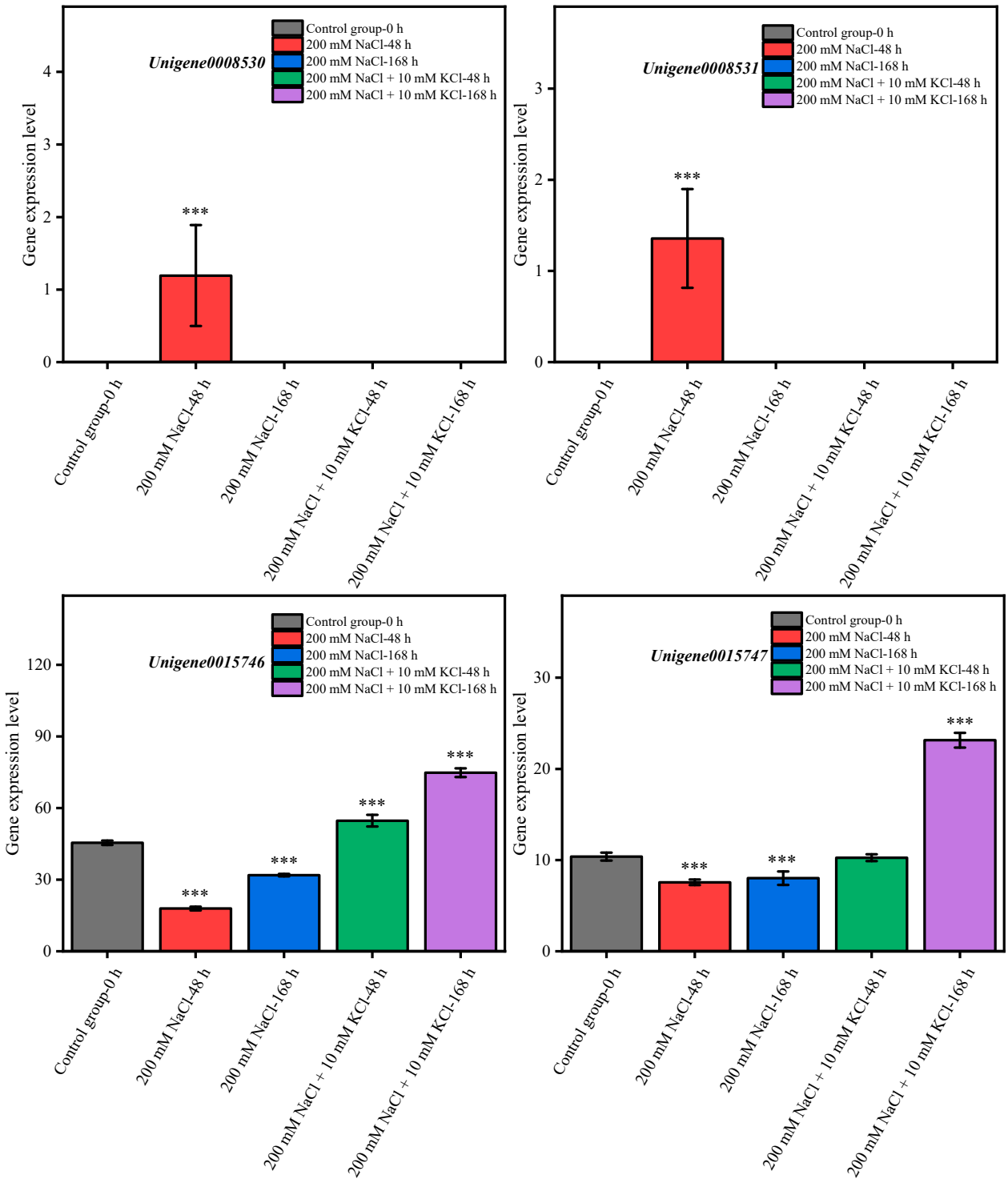
(The roots of *T.ramosissima* show changes in the expression levels of 19 *trehalose*-related genes in response to exogenous K^+ under NaCl stress. Note: $p \geq 0.05$ is not marked; $0.01 < p < 0.05$ is marked as *; $0.001 < p < 0.01$ is marked as **; $p \leq 0.001$ is marked as ***).

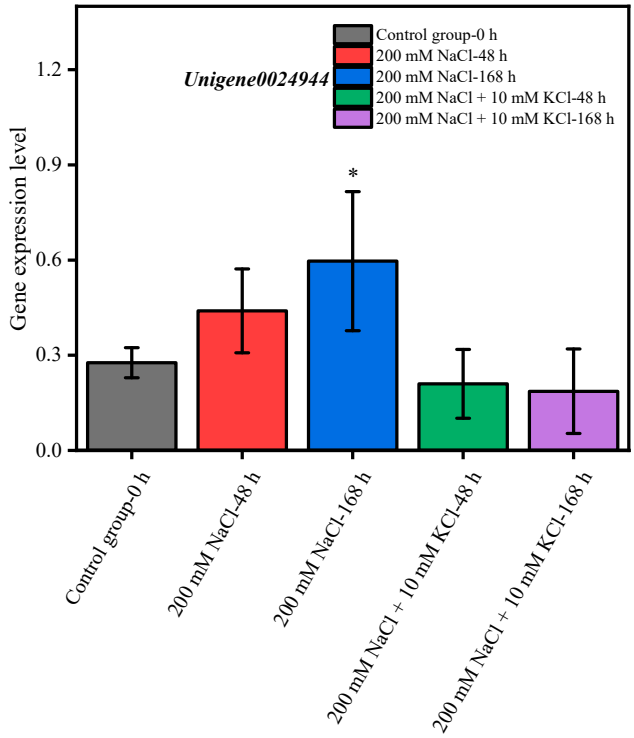


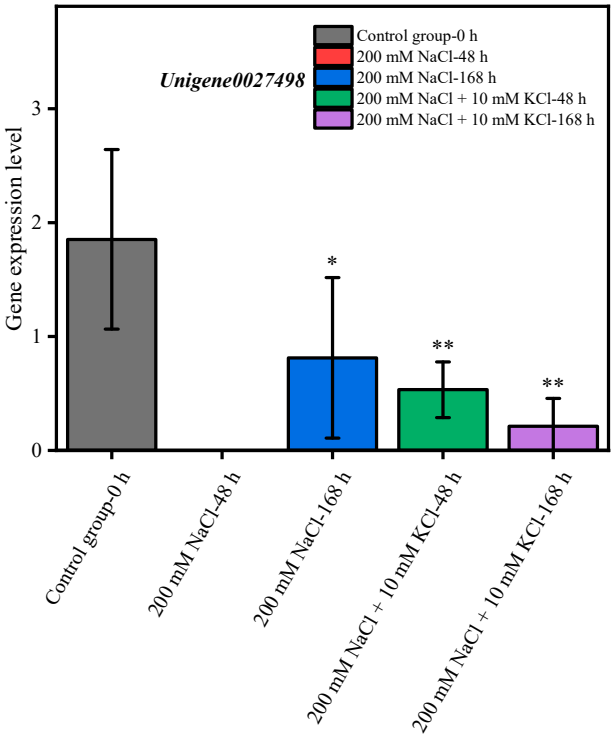
Supplementary Figure S2. Log_2 fold change of differential metabolites annotated in the starch and sucrose metabolism pathway

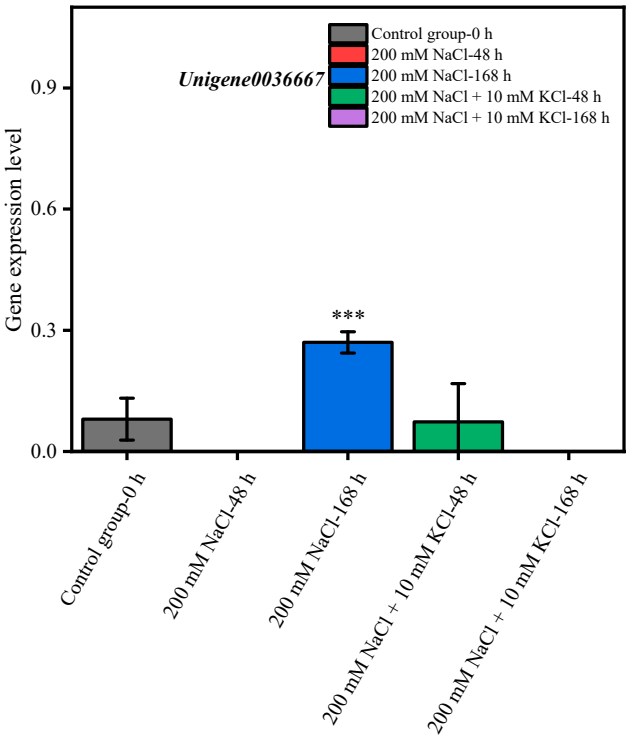
(The roots of *T.ramosissima* show log_2 fold changes in differential metabolites in response to exogenous K^+ under NaCl stress. Note: $p \geq 0.05$ is not marked; $0.01 < p < 0.05$ is marked as *; $0.001 < p < 0.01$ is marked as **; $p \leq 0.001$ is marked as ***).

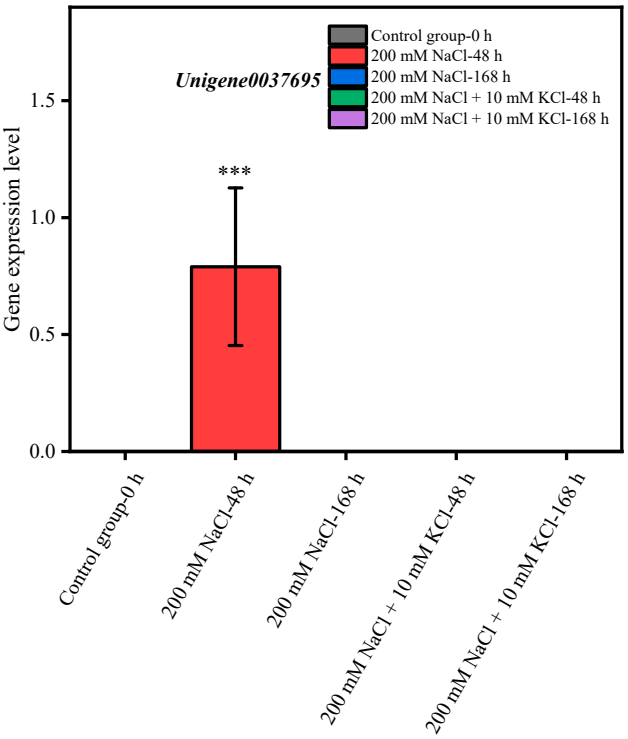

Unigene0000288
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0
25
50
75
***
*
Unigene0000469
0
5
10
15
***
Unigene0001622
0
15
30
45
60
***
***
***
Unigene0008340
0
15
30
45
60
***
*
***

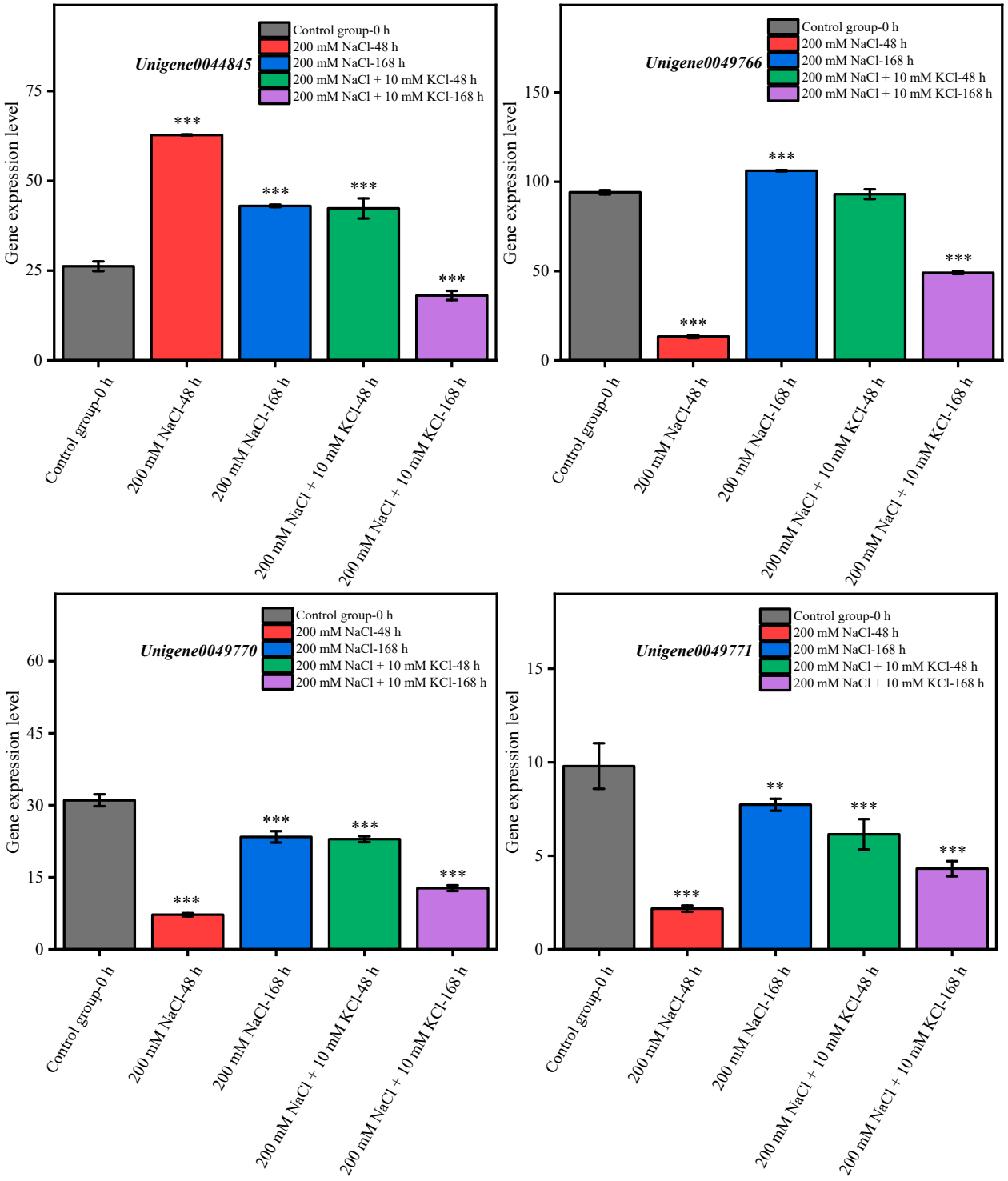

Unigene0008530
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
***
Unigene0008531
Unigene0015746
Unigene0015747

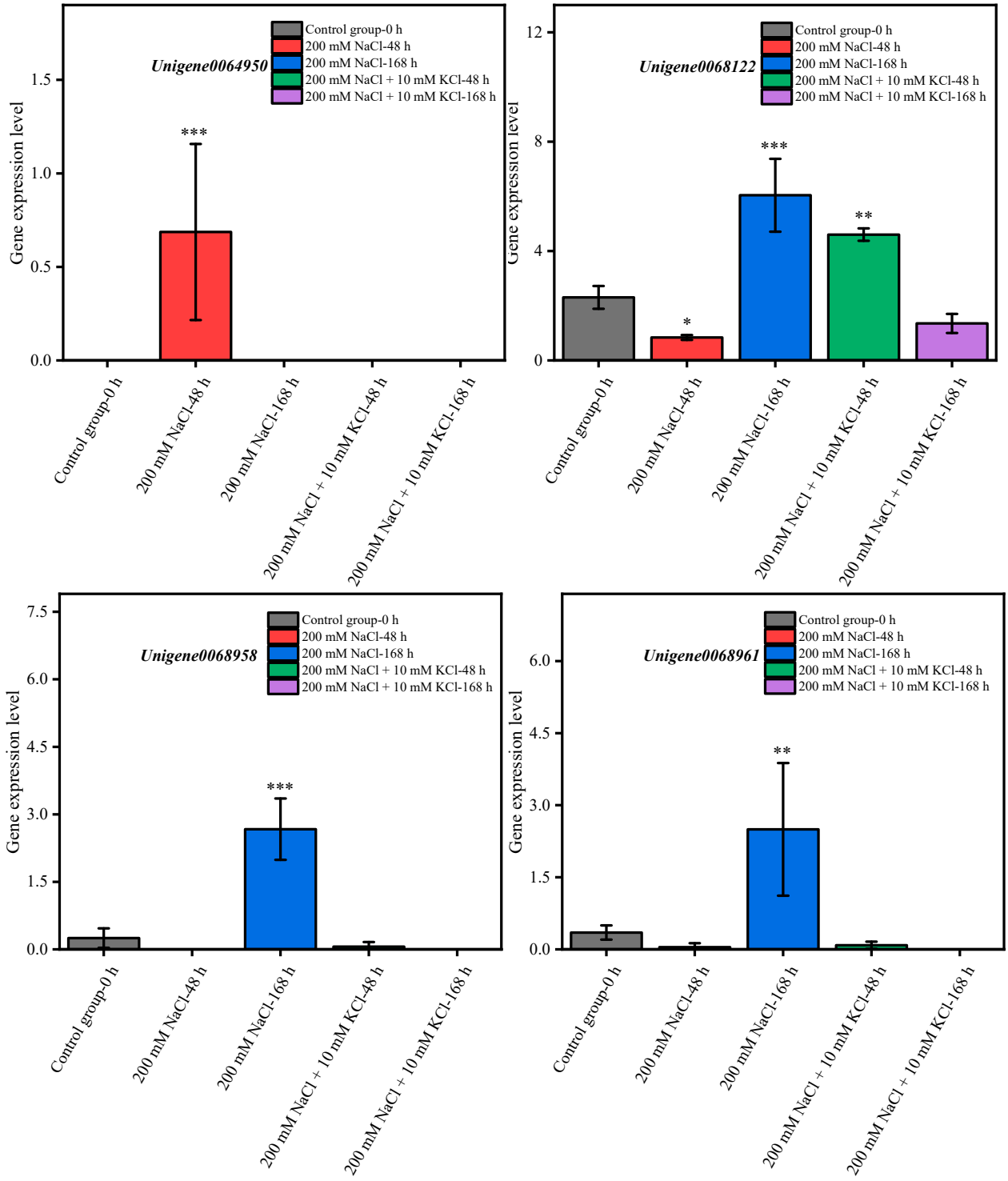

Unigene0024944
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0.0
0.3
0.6
0.9
1.2
*
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h

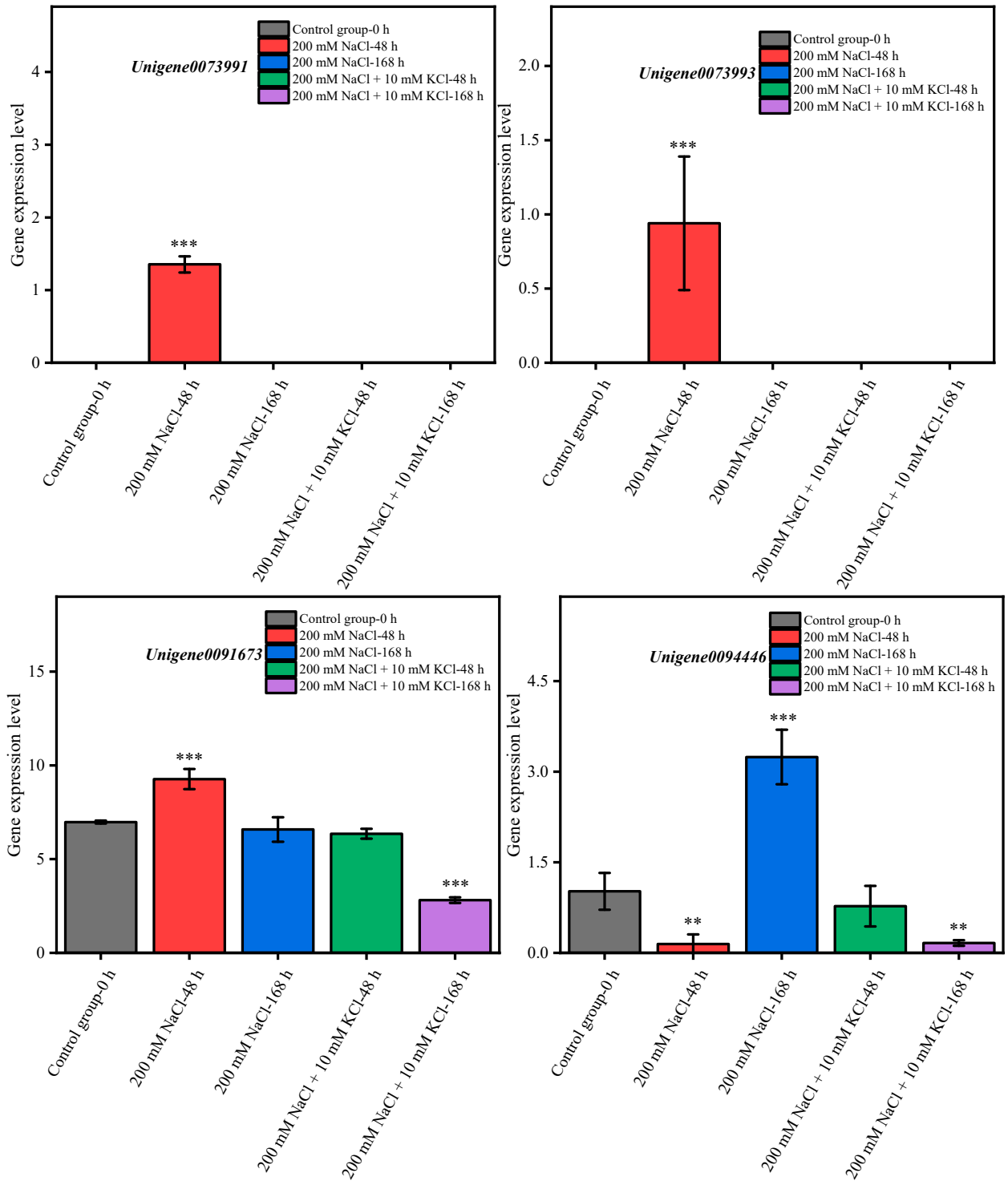

Unigene0027498
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0
1
2
3
*
**
**
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h

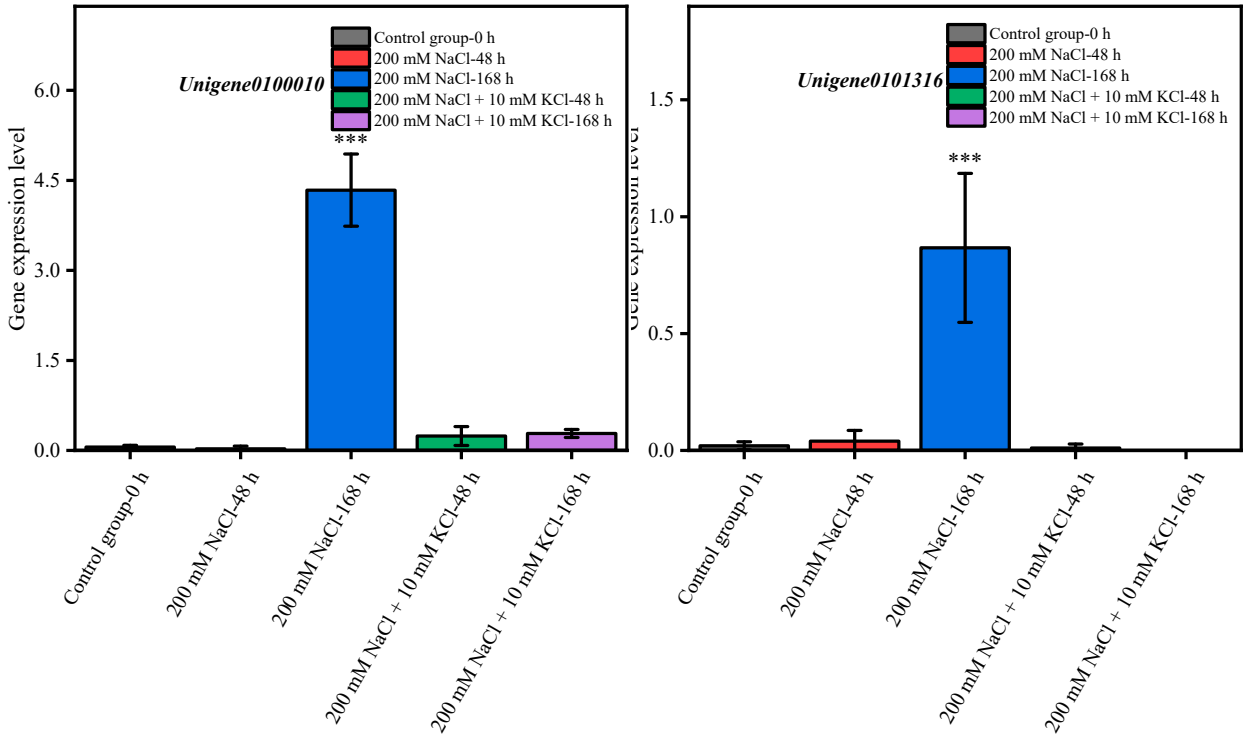

Unigene0036667
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0.0
0.3
0.6
0.9
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h


Unigene0037695
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0.0
0.5
1.0
1.5
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h


Unigene0044845
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0
25
50
75
***
***
***
***
Unigene0049766
0
50
100
150
***
***
***
Unigene0049770
0
15
30
45
60
***
***
***
***
Unigene0049771
0
5
10
15
***
**
***
***

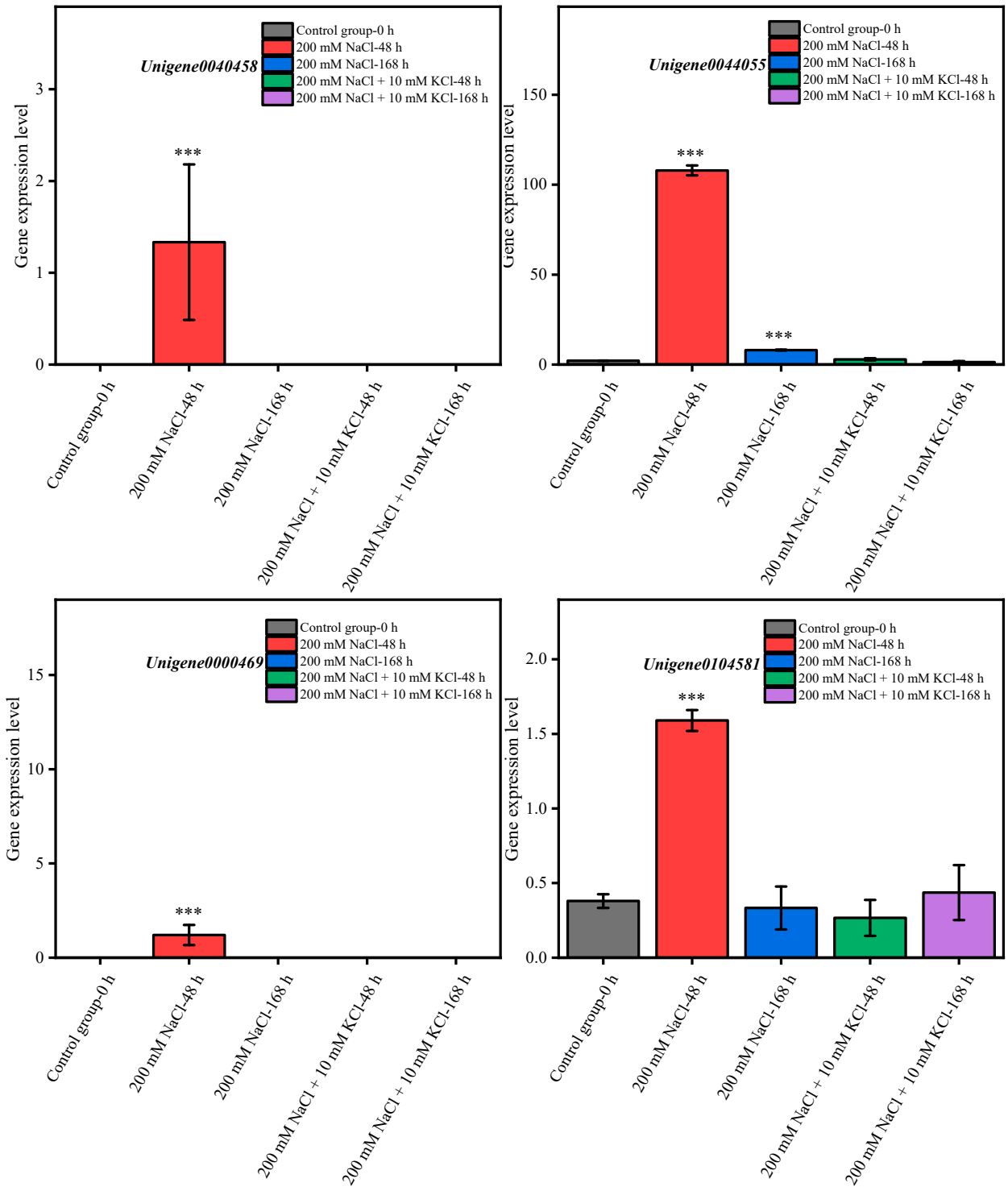

Unigene0064950
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0.0
0.5
1.0
1.5
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0068122
Gene expression level
0
4
8
12
*
***
**
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0068958
Gene expression level
0.0
1.5
3.0
4.5
6.0
7.5
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0068961
Gene expression level
0.0
1.5
3.0
4.5
6.0
**

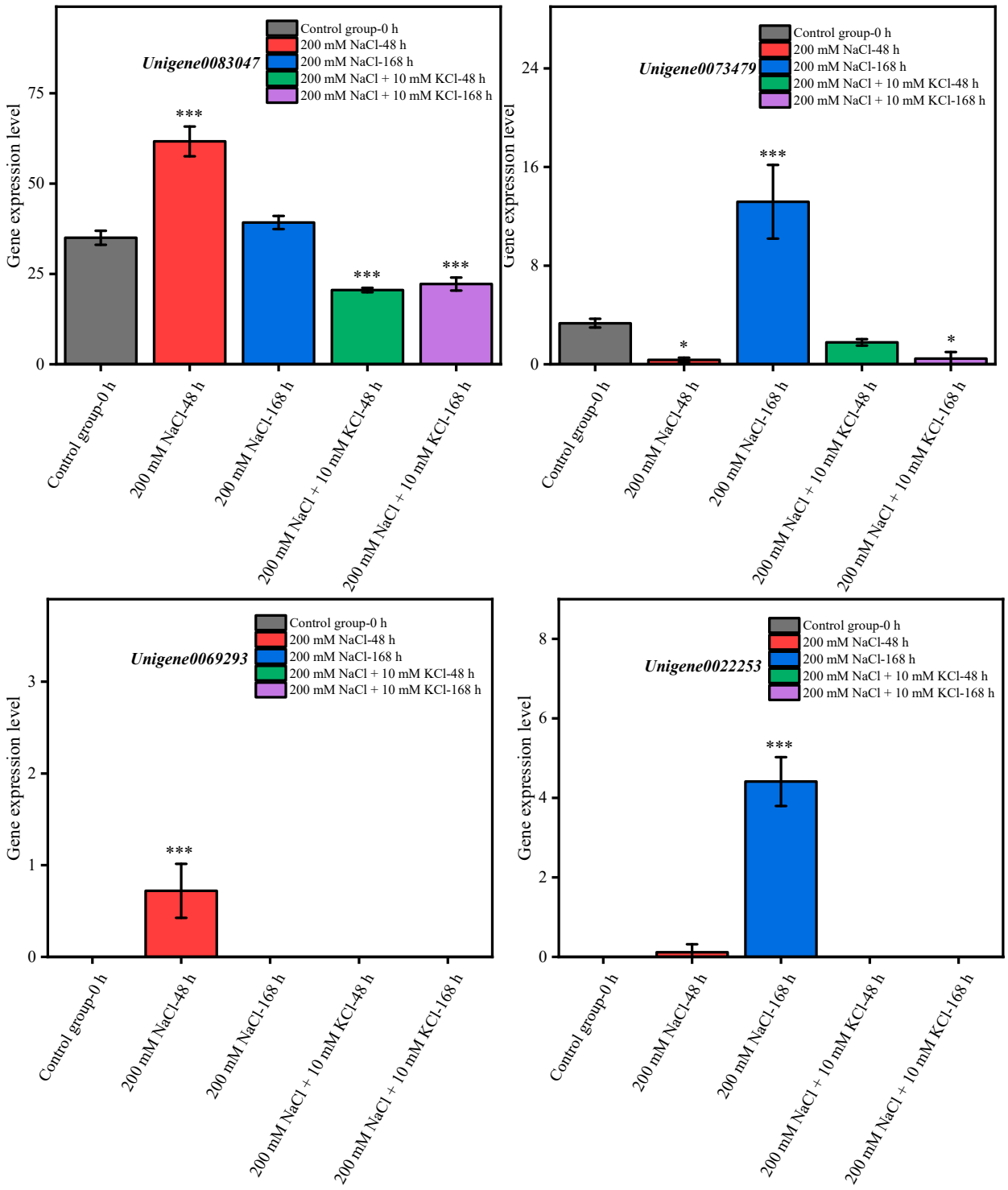

Unigene0073991
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
***
Unigene0073993
Unigene0091673
Unigene0094446
**

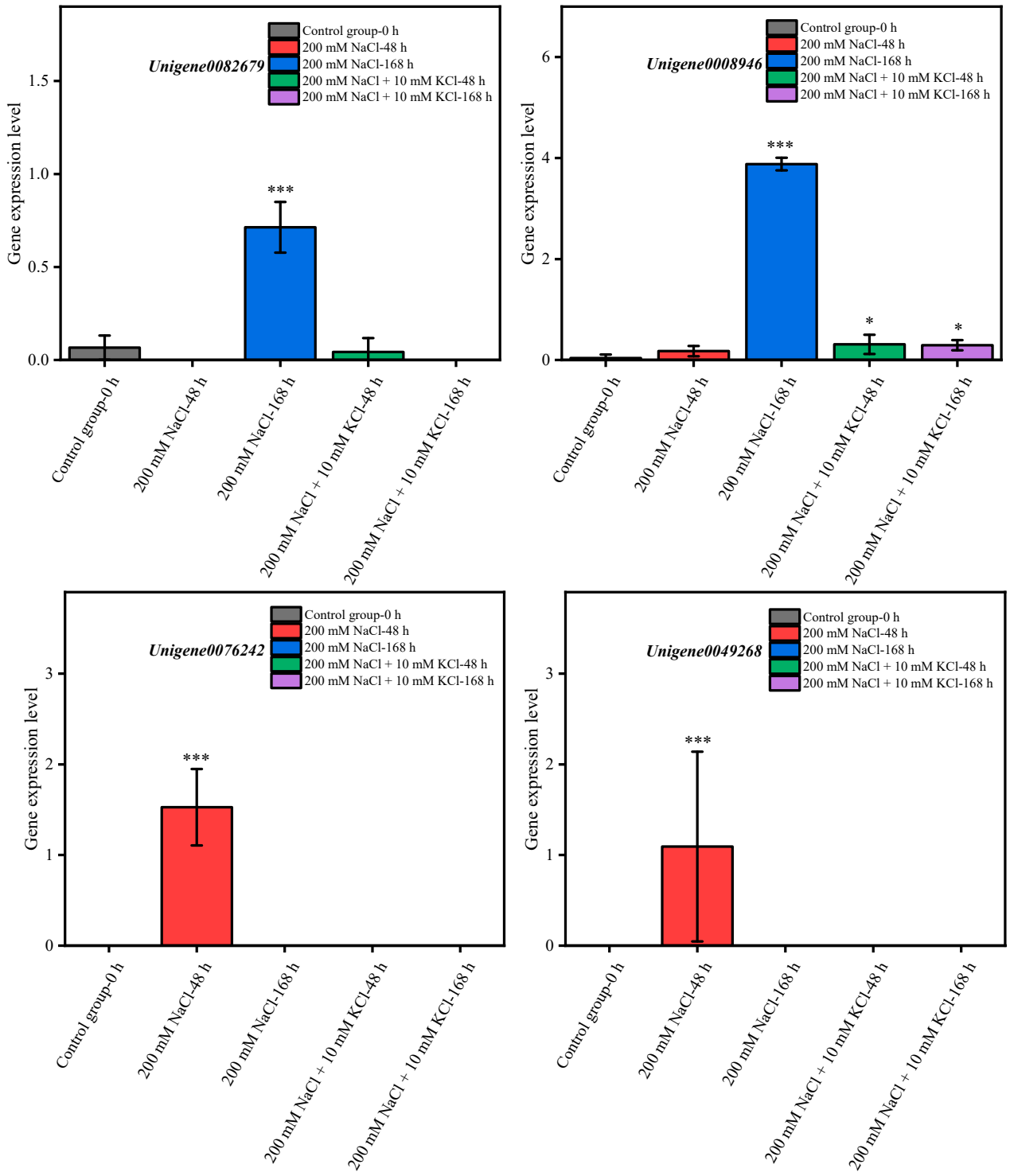


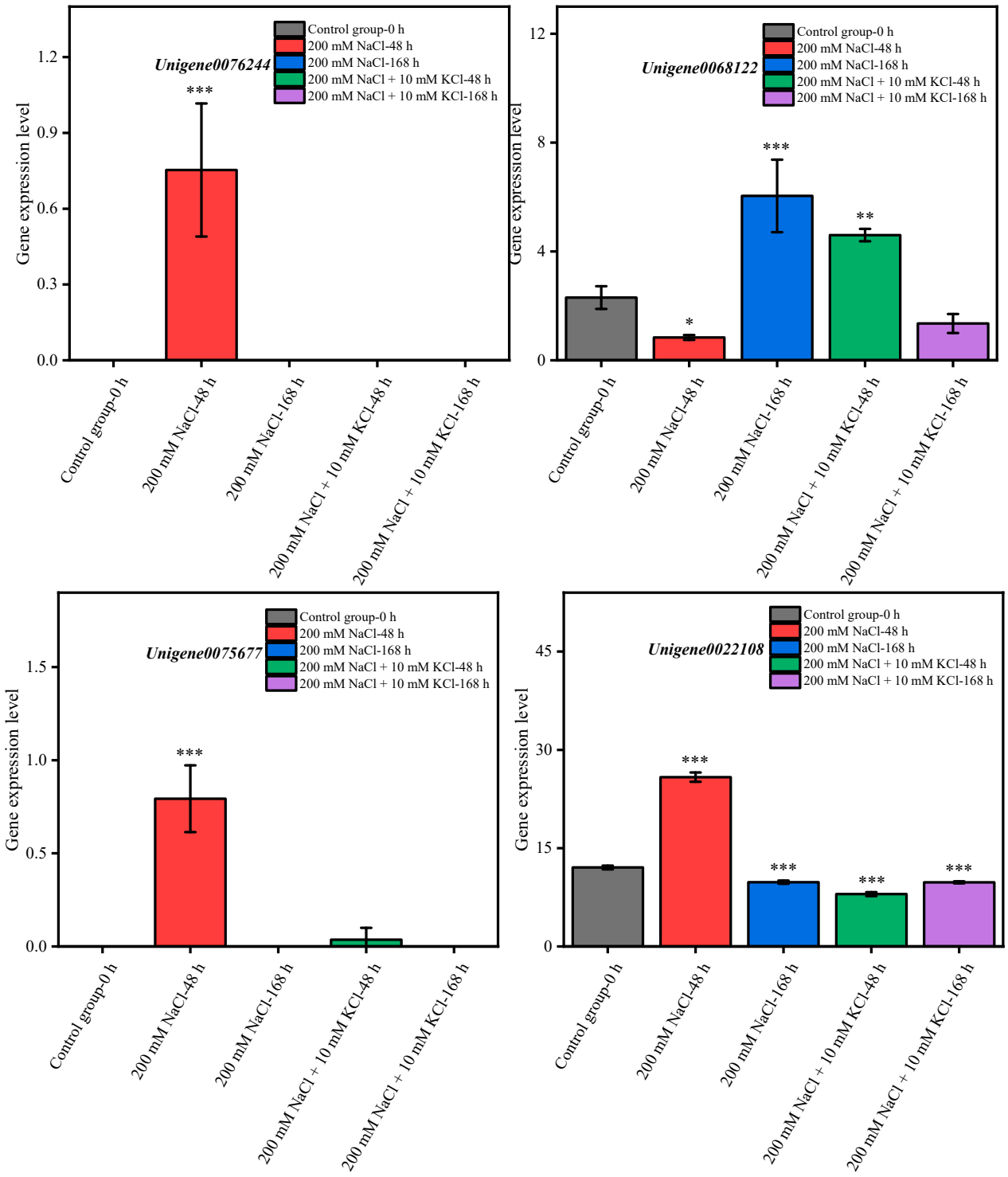
Supplementary Figure S3. Differential expression of genes in the starch and sucrose metabolism pathway involved in regulating D-Glucose 6-phosphate

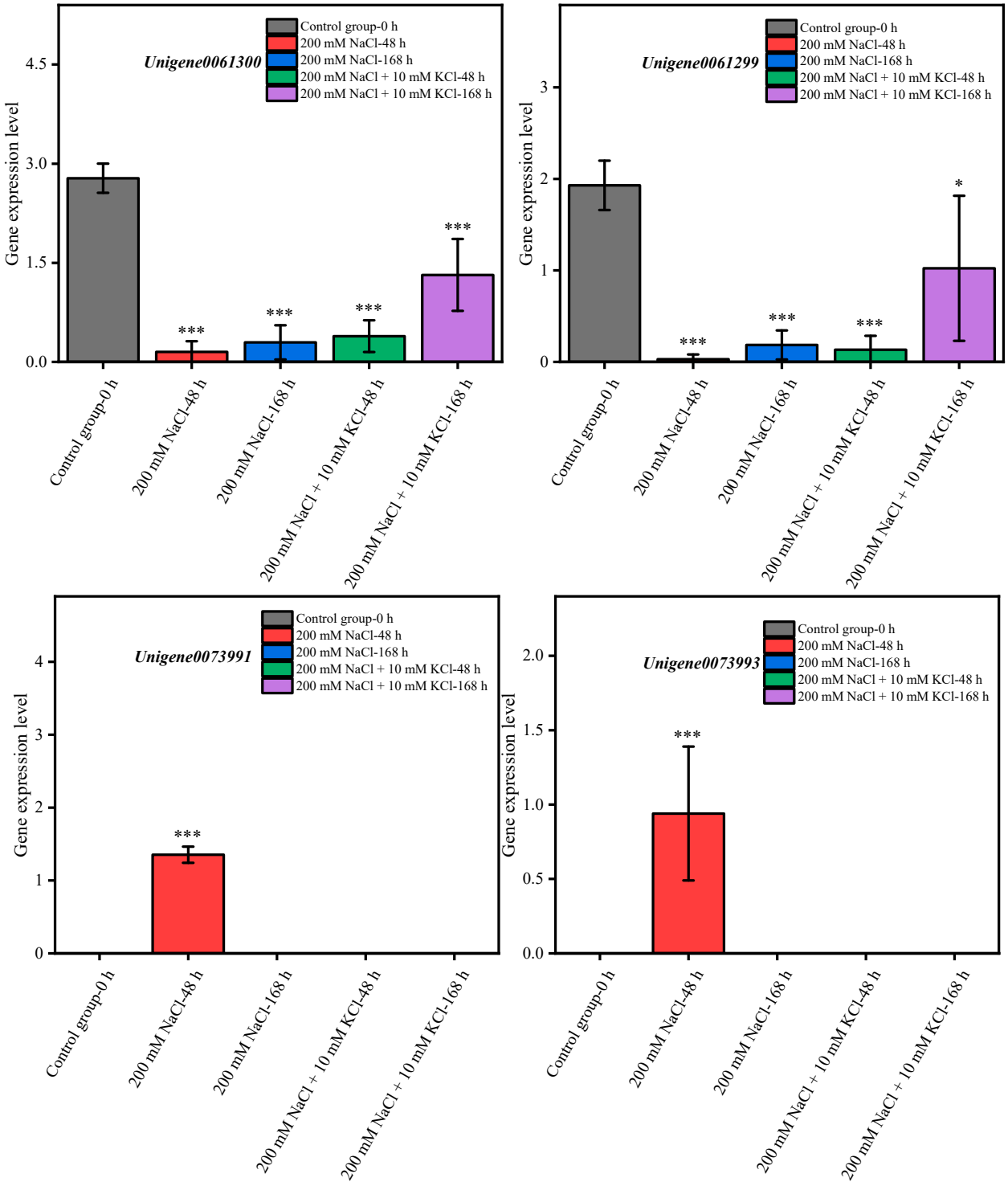
(The roots of *T. ramosissima* under NaCl stress with exogenous K^+ applied for 48h and 168h show expression level changes of 26 differentially expressed genes in the starch and sucrose metabolism pathway that regulate D-Glucose 6-phosphate. Note: $p \geq 0.05$ is not marked; $0.01 < p < 0.05$ is marked as *; $0.001 < p < 0.01$ is marked as **; $p \leq 0.001$ is marked as ***).

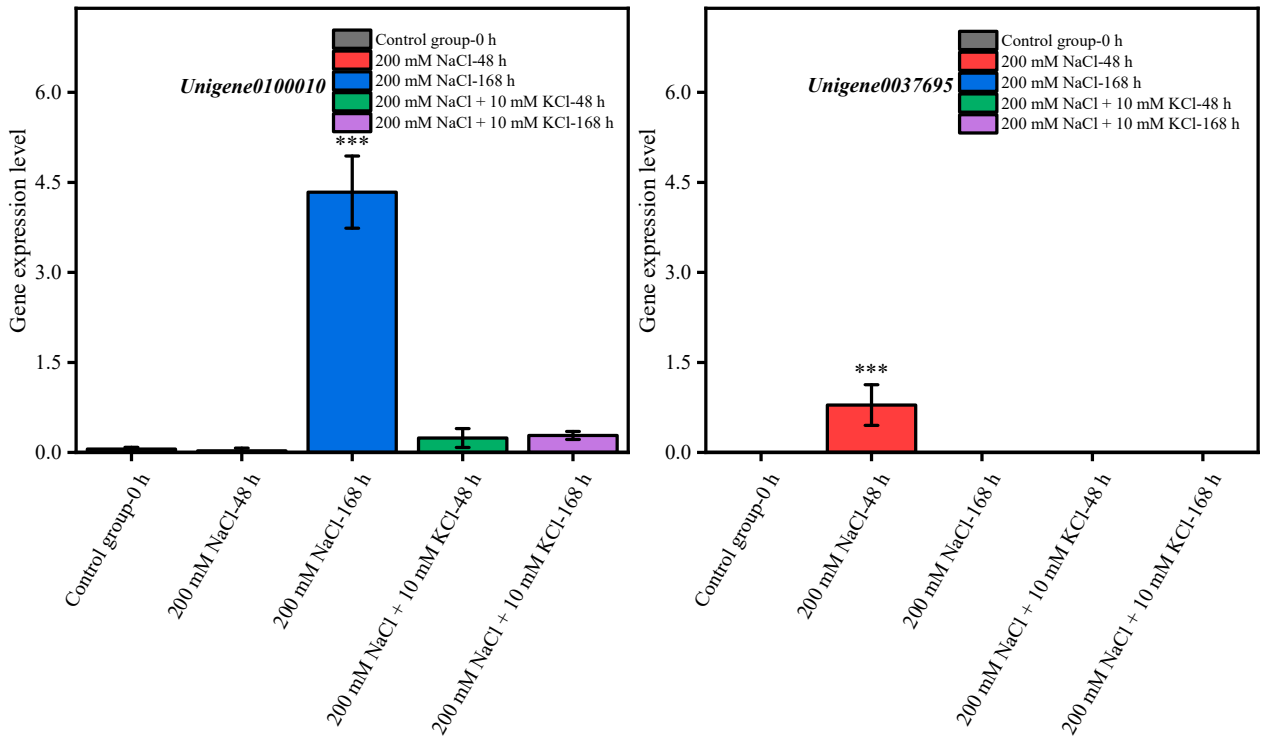

Unigene0040458
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
***
Unigene0044055
Unigene0000469
Unigene0104581


Unigene0083047
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0
25
50
75
***
***
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0073479
Gene expression level
0
8
16
24
*
***
*
Unigene0069293
Gene expression level
0
1
2
3
***
Unigene0022253
Gene expression level
0
2
4
6
8
***


Unigene0082679
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
0.0
0.5
1.0
1.5
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0008946
Gene expression level
0
2
4
6
***
*
*
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0076242
Gene expression level
0
1
2
3
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0049268
Gene expression level
0
1
2
3
***

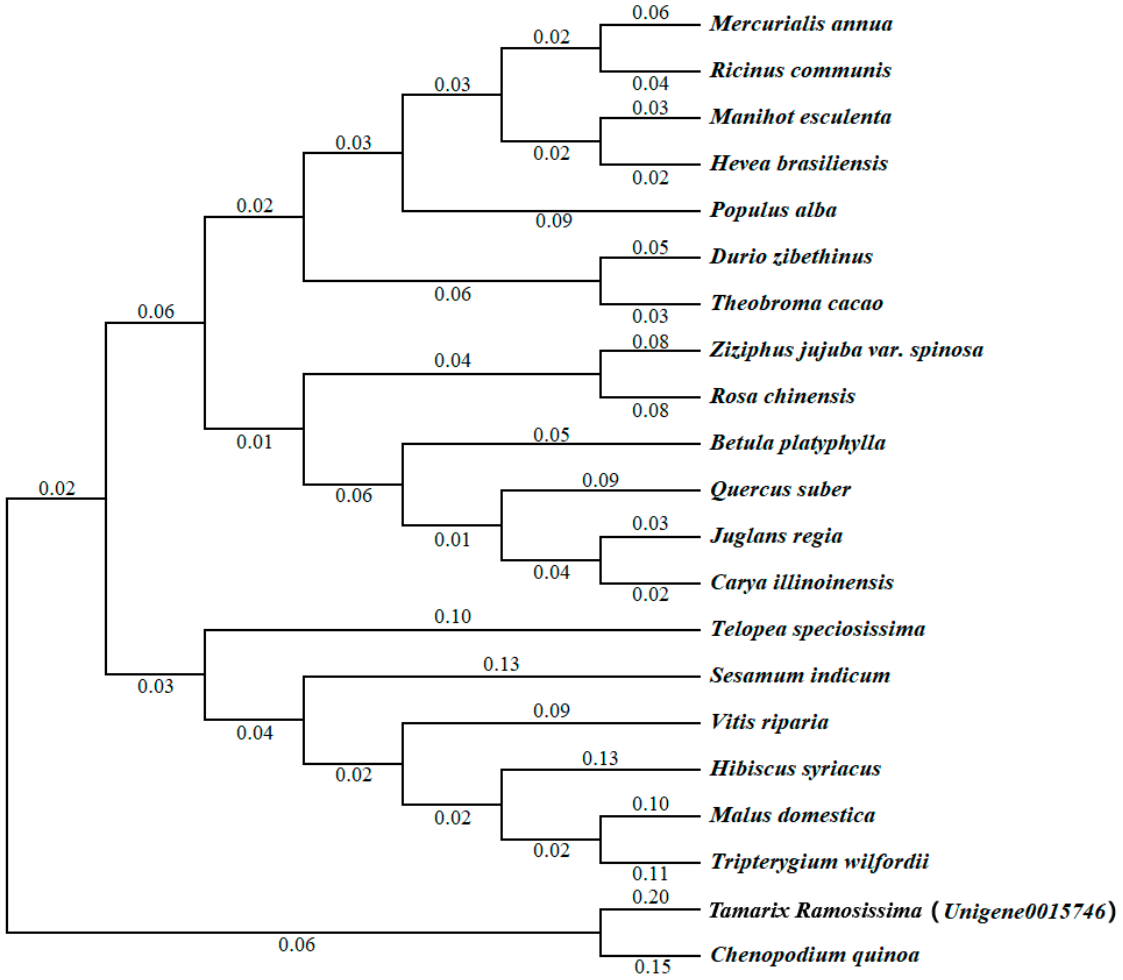

Unigene0076244
Unigene0068122
Unigene0075677
Unigene0022108
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
***
**
*


Unigene0061300
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Gene expression level
4.5
3.0
1.5
0.0
***
***
***
***
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0061299
Gene expression level
3
2
1
0
***
***
***
*
Unigene0073991
Gene expression level
4
3
2
1
0
***
Unigene0073993
Gene expression level
2.0
1.5
1.0
0.5
0.0
***

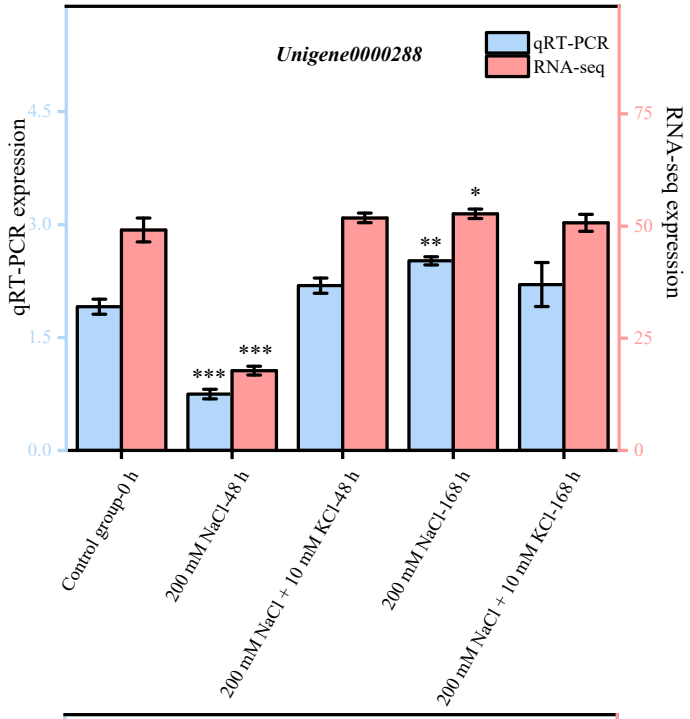


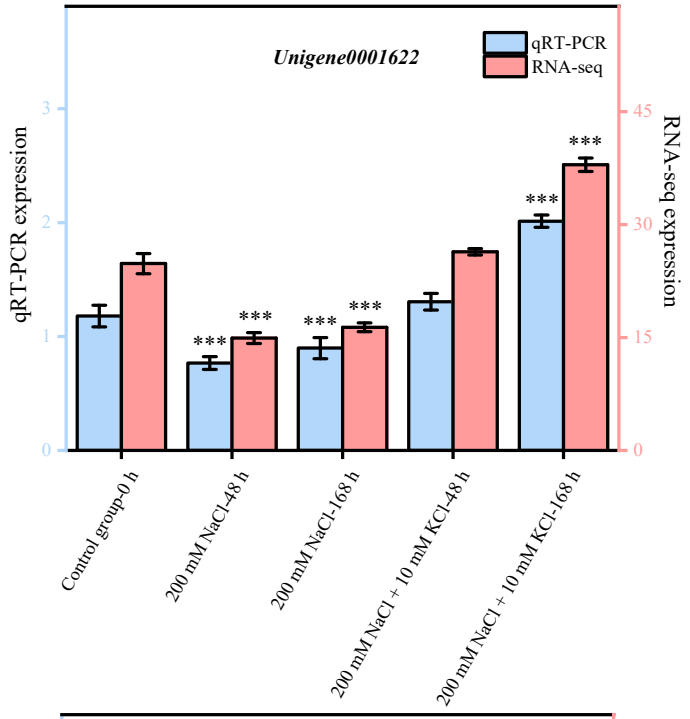
Supplementary Figure S4. Differential expression genes in the Starch and Sucrose Metabolism Pathway involved in regulating alpha-D-Glucose 1-phosphate

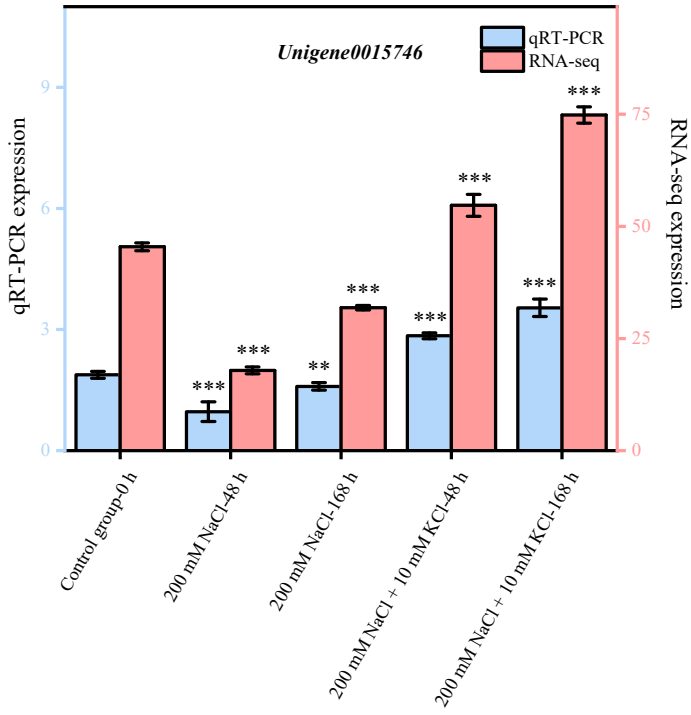
(The roots of *T.ramosissima* under NaCl stress with exogenous K^+ applied for 48h and 168h show expression level changes of 22 differentially expressed genes in the starch and sucrose metabolism pathway that regulate alpha-D-Glucose 1-phosphate. Note: $p \geq 0.05$ is not marked; $0.01 < p < 0.05$ is marked as *; $0.001 < p < 0.01$ is marked as **; $p \leq 0.001$ is marked as ***).

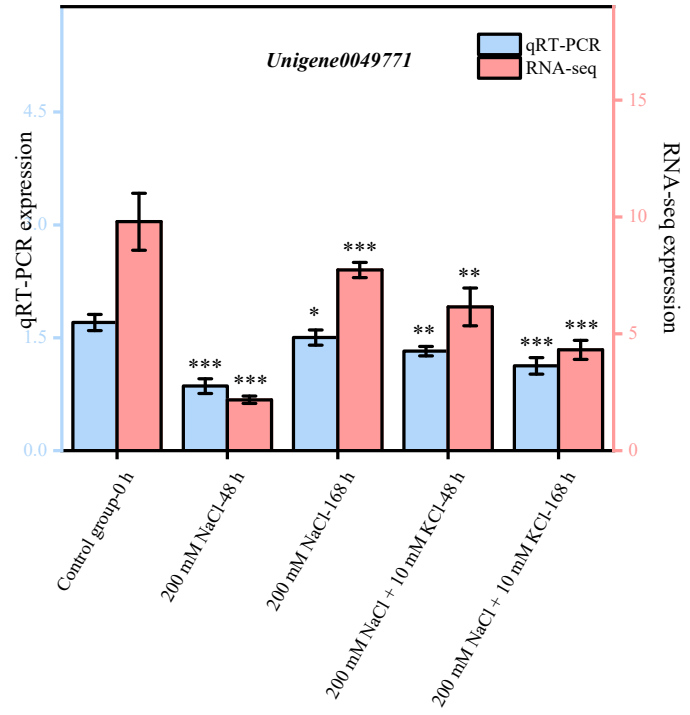


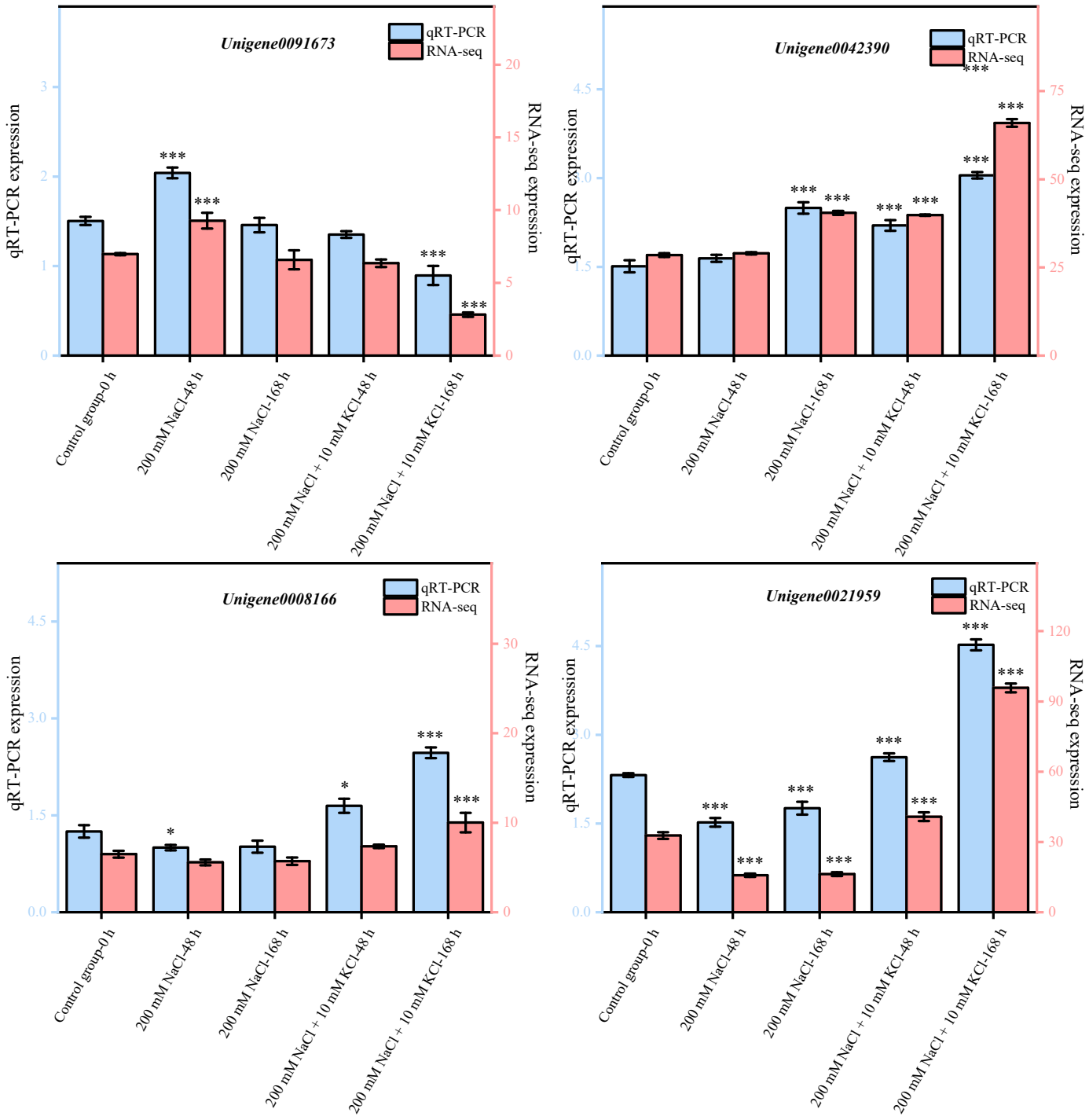
Supplementary Figure S5. Phylogenetic tree analysis of the key candidate genes related to trehalose in *T.ramosissima* (A phylogenetic tree was constructed for analysis of the protein amino acid sequences of Unigene0015746 from *T. ramosissima* roots and the protein amino acid sequences of other 20 species)

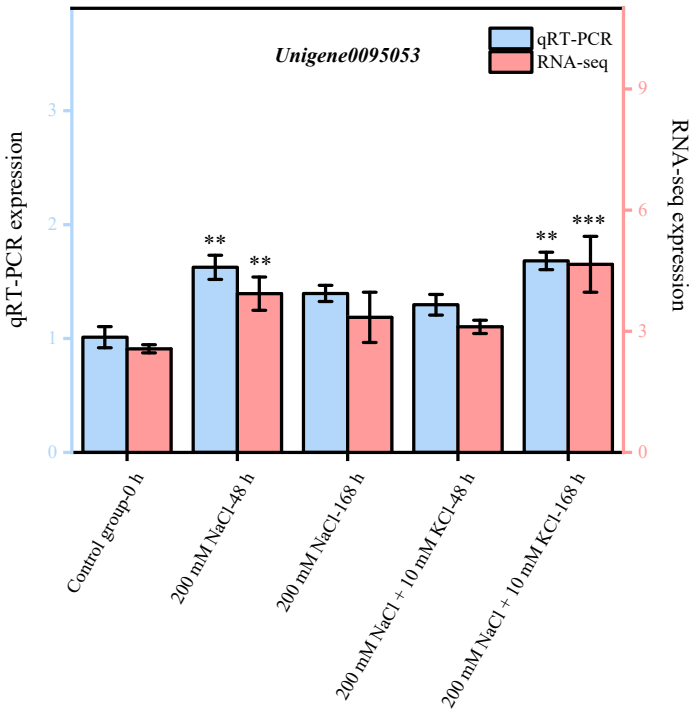

Unigene0000288
qRT-PCR
RNA-seq
qRT-PCR expression
RNA-seq expression
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-168 h


Unigene0001622
qRT-PCR
RNA-seq
qRT-PCR expression
RNA-seq expression
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h


Unigene0015746
qRT-PCR
RNA-seq
qRT-PCR expression
RNA-seq expression
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h


Unigene0049771
qRT-PCR
RNA-seq
qRT-PCR expression
RNA-seq expression
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h


Unigene0091673
qRT-PCR
RNA-seq
qRT-PCR expression
RNA-seq expression
Control group-0 h
200 mM NaCl-48 h
200 mM NaCl-168 h
200 mM NaCl + 10 mM KCl-48 h
200 mM NaCl + 10 mM KCl-168 h
Unigene0042390
Unigene0008166
Unigene0021959



Supplementary Figure S6. Validation of candidate key *trehalose*-related genes by qRT-PCR

(Nine *trehalose*-related candidate genes were randomly selected for qRT-PCR validation, and the error bars were obtained from multiple replicates of qRT-PCR. The trends of qRT-PCR value and the RNA-seq value for each gene were consistent and the transcription sequencing results were reliable. Note: $p \geq 0.05$ is not marked; $0.01 < p < 0.05$ is marked as *; $0.001 < p < 0.01$ is marked as **; $p \leq 0.001$ is marked as ***; : Numerical value has been shown on the left side of the *Y* axis; : Numerical value has been shown on the right side of the *Y* axis; qRT-PCR value is the relative quantitative value, and RNA-seq value is the fpkm value).