

Supplementary Table S1. Sequences of specific primers

Primer name	Primer sequence (5'-3')
<i>Unigene0002140</i>	F: CCGTGGCACAAGGAGAAGGAGTA R: GGAGGTACTTGTCAATGAGCGTCTG
<i>Unigene0105480</i>	F: TCCTAGCACTCGTTAGAGCAACAGA R: AAGATCCTGATGCTTGAAGGCGATT
<i>Unigene0007112</i>	F: CATCAAGGCATCGGACGCATACC R: AACGCCATCTGCTCCACTTCCT
<i>Unigene0032727</i>	F: GATGAATCCGTCGTTACCACAAGT R: GAACAGTGCTGCCGAAGGTAAGG
<i>Unigene0068803</i>	F: TCGCTCTTGGAGTCCTTGGAGTAAT R: GCTCGGTCGTCAATTCGGTAGTC
<i>Unigene0056095</i>	F: ACAACTCTTCCTCCTGCTGCTCTC R: ACCCTGACTTTGCTCTTGCTGTAAA
<i>Unigene0105238</i>	F: GCGATGGAGGTTGGAAGTTGGAG R: AGACTTGGATGCTGTATCTGCTCAC
<i>Unigene0102888</i>	F: TCAGCCTCATCCTATCCACAAGCA R: GCAGCATAAGCCTCAGCAACAGT
<i>Unigene0066846</i>	F: CAAGCCCTACAGCGATCAAGCAAT R: GCCACATCCACAACATTCCTACCAT
<i>Unigene0037768</i>	F: TCCGACTACGACATCACGAAACCT R: TTGCGTTCAGACCATTAGCGTTCT
<i>Tubulin</i>	F: GCTGAGATTACAACCGCTG R: CTGTTCGTTTGGTCTTGATT

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

Supplementary Table S2. Pfam A protein domain analysis of *Myo*-inositol oxygenase-related genes

ID	envelope start	envelope end	hmm acc	hmm name	type	hmm length	bit score	clan	PfamA_definition
<i>Unigene0002140</i>	21	278	PF05153.15	MIOX	Family	249	339.4	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0095980</i>	69	317	PF05153.15	MIOX	Family	249	411.9	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0032727</i>	68	318	PF05153.15	MIOX	Family	249	405.6	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0095469</i>	70	318	PF05153.15	MIOX	Family	249	417.2	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0006164</i>	1	108	PF05153.15	MIOX	Family	249	146.5	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0006165</i>	62	110	PF05153.15	MIOX	Family	249	34.5	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0017638</i>	1	170	PF05153.15	MIOX	Family	249	289.7	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0056095</i>	69	319	PF05153.15	MIOX	Family	249	417.7	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0006163</i>	1	88	PF05153.15	MIOX	Family	249	132.5	CL0237	<i>Myo</i> -inositol oxygenase
<i>Unigene0067118</i>	1	55	PF05153.15	MIOX	Family	249	61.7	CL0237	<i>Myo</i> -inositol oxygenase

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 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, PfamA\_definition: the name of the structure corresponding to the query sequence in PfamA.

Supplementary Table S3. Log<sub>2</sub> fold-change of DEGs in the ascorbate and aldarate metabolism pathway.

ID	Description	Log <sub>2</sub> fold- change		
		CK-0 h vs. N-48 h	N-48 h vs. N-168 h	CK-0 h vs. N-168 h
<i>Unigene0000210</i>	UDP-glucose 6-dehydrogenase	11.24	-11.24	0.00
<i>Unigene0090218</i>	UDP-glucose 6-dehydrogenase 4	2.53	-2.59	-0.06
<i>Unigene0066845</i>	UDP-glucose 6-dehydrogenase 3-like	1.39	-1.14	0.25
<i>Unigene0066846</i>	UDP-glucose 6-dehydrogenase 4-like	-1.84	2.26	0.41
<i>Unigene0068803</i>	L-gulonolactone oxidase like	1.54	-2.19	-0.65
<i>Unigene0007112</i>	Predicted: L-gulonolactone oxidase 3	1.82	-2.34	-0.52
<i>Unigene0033490</i>	Aldehyde dehydrogenase	10.49	-10.49	0.00
<i>Unigene0081717</i>	Aldehyde dehydrogenase 2F1	-12.24	0.00	-12.24
<i>Unigene0068112</i>	Predicted: aldehyde dehydrogenase family 2 member B7, mitochondrial isoform X1	1.64	-0.81	0.83
<i>Unigene0015725</i>	Aldehyde dehydrogenase family 2 member B4, mitochondrial-like	-1.03	-1.93	-2.95
<i>Unigene0033491</i>	Aldehyde dehydrogenase, partial	10.10	-10.10	0.00
<i>Unigene0081716</i>	Aldehyde dehydrogenase 2F1	-12.15	5.74	-6.41
<i>Unigene0063029</i>	Aldehyde dehydrogenase family 2 member B7, mitochondrial-like	-10.49	0.00	-10.49
<i>Unigene0011551</i>	Predicted: aldehyde dehydrogenase family 2 member B7, mitochondrial isoform X1	1.37	-2.57	-1.20
<i>Unigene0010709</i>	L-galactono-1,4-lactone dehydrogenase, mitochondrial	1.07	-1.03	0.04
<i>Unigene0037768</i>	Predicted: L-ascorbate oxidase-like	-2.46	2.95	0.49
<i>Unigene0105617</i>	L-ascorbate oxidase	-9.79	10.27	0.48
<i>Unigene0105238</i>	Predicted: L-ascorbate oxidase homolog	-5.45	6.30	0.85
<i>Unigene0048033</i>	Cytosolic ascorbate peroxidase	1.24	-0.57	0.67
<i>Unigene0008513</i>	Peroxidase domain-containing protein	2.67	-3.21	-0.53
<i>Unigene0016921</i>	L-ascorbate peroxidase	9.55	-9.55	0.00
<i>Unigene0002140</i>	Inositol oxygenase	-3.61	4.95	1.34

<i>Unigene0006164</i>	inositol oxygenase	11.13	-11.13	0.00
<i>Unigene0095469</i>	Inositol oxygenase-like	12.33	-12.33	0.00
<i>Unigene0032727</i>	Inositol oxygenase 1-like	-2.36	1.68	-0.68
<i>Unigene0056095</i>	Inositol oxygenase 1-like	-1.41	0.36	-1.06
	Predicted:			
<i>Unigene0008076</i>	monodehydroascorbate reductase 5, mitochondrial	-1.22	-0.49	-1.72
<i>Unigene0023134</i>	GDP-mannose 3,5-epimerase 2-like isoform X1	1.06	-1.47	-0.42
<i>Unigene0077411</i>	dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	10.70	-3.92	6.78
<i>Unigene0062175</i>	Predicted: UDP-glucose 6-dehydrogenase 1	0.81	-1.14	-0.33
<i>Unigene0044406</i>	DHAR class glutathione transferase DHAR2	9.57	-9.57	0.00
<i>Unigene0007113</i>	L-gulonolactone oxidase 3	2.81	-10.61	-7.80
<i>Unigene0105480</i>	Probable L-gulonolactone oxidase 6 isoform X1	0.18	1.17	1.35
	Low quality protein: aldehyde			
<i>Unigene0090252</i>	dehydrogenase family 3 member F1-like	2.21	-7.64	-5.44
<i>Unigene0021103</i>	Aldehyde dehydrogenase	1.20	1.53	2.73
<i>Unigene0021104</i>	Aldehyde dehydrogenase	4.06	4.46	8.52
<i>Unigene0051554</i>	Aldehyde dehydrogenase family 3 member H1-like isoform X1	0.13	-1.34	-1.21
<i>Unigene0017008</i>	L-ascorbate oxidase-like	1.47	2.42	3.90
<i>Unigene0102888</i>	Predicted: L-ascorbate oxidase-like	-0.37	2.54	2.17
<i>Unigene0095980</i>	Inositol oxygenase-like	0.00	9.36	9.36
<i>Unigene0064911</i>	Calcium-dependent phosphotriesterase	-6.06	7.69	1.63
<i>Unigene0095536</i>	Aldehyde dehydrogenase	6.98	2.51	9.49
<i>Unigene0105664</i>	Thylakoid ascorbate peroxidase precursor, partial	1.09	0.37	1.46

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

Supplementary Table S4. Analysis of differentially expressed metabolites in the ascorbate and aldarate metabolism pathway

Name	Formula	Molecular Weight	RT [min]	m/z	Control group-0 h		200 mM NaCl-48 h		200 mM NaCl-168 h	
					mean	standard deviation	mean	standard deviation	mean	standard deviation
L-Gulono-1,4-lactone	C <sub>6</sub> H <sub>10</sub> O <sub>6</sub>	178.05	1.43	177.04	22860058.95	2519752.71	17020878.88	5334321.57	80986301.93	6757170.04
L-Threonate	C <sub>4</sub> H <sub>8</sub> O <sub>5</sub>	136.04	1.24	135.03	69731801.43	6649592.84	28800647.13	4158393.35	42449178.55	1452156.77
<i>Myo</i> -inositol	C <sub>6</sub> H <sub>12</sub> O <sub>6</sub>	180.06	1.26	181.07	635191705.93	125601062.62	523967880.43	52545829.76	1286750168.00	70684525.76
2-Oxoglutarate	C <sub>5</sub> H <sub>6</sub> O <sub>5</sub>	146.02	2.07	147.03	128909411.37	12784530.72	72075325.06	39448745.87	25744148.90	6275817.99

Note: The metabolite content is relative quantification and has no units.

Supplementary Table S5. Log<sub>2</sub> fold-change of DEGs in the inositol phosphate metabolism pathway.

ID	Description	Log <sub>2</sub> fold- change		
		CK-0 h vs. N-48 h	Na-48 h vs. N-168 h	CK-0 h vs. N-168 h
<i>Unigene0076706</i>	<i>Myo</i> -inositol - pentakisphosphate 2-kinase-like	1.26	-0.35	0.91
<i>Unigene0066145</i>	<i>Myo</i> -inositol 2 - dehydrogenase oxidoreductase, NAD-binding,	10.49	-10.49	0.00
<i>Unigene0041348</i>	<i>Myo</i> -inositol 2 - dehydrogenase	2.57	-10.31	-7.74
<i>Unigene0032727</i>	<i>Myo</i> -inositol oxygenase 1-like	-2.36	1.68	-0.68
<i>Unigene0006164</i>	<i>Myo</i> -inositol oxygenase	11.13	-11.13	0.00
<i>Unigene0002140</i>	<i>Myo</i> -inositol oxygenase	-3.61	4.95	1.34
<i>Unigene0095469</i>	<i>Myo</i> -inositol oxygenase-like	12.33	-12.33	0.00
<i>Unigene0012913</i>	phosphatidylinositol 4-phosphate 5-kinase 1-like	1.59	-1.35	0.23
<i>Unigene0021143</i>	Inositol 1,3,4-trisphosphate 5/6-kinase family protein	10.11	-10.11	0.00
<i>Unigene0024466</i>	Predicted: phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN2A-like	1.35	-1.30	0.05
<i>Unigene0077650</i>	phosphatidylinositol 3,4,5-Trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN1 isoform X2	0.27	-1.09	-0.82
<i>Unigene0079063</i>	Non-specific phospholipase C2	1.59	-1.45	0.14
<i>Unigene0095938</i>	Phosphoesterase	1.49	-1.25	0.25
<i>Unigene0022055</i>	Inositol 1,3,4-trisphosphate 5/6-kinase 4-like isoform X2	1.45	-1.42	0.04
<i>Unigene0015803</i>	Triosephosphate isomerase	10.31	-10.31	0.00
<i>Unigene0101660</i>	Triosephosphate isomerase-like	10.78	-10.78	0.00
<i>Unigene0031578</i>	Triosephosphate isomerase	10.98	-10.98	0.00
<i>Unigene0090825</i>	Inositol-3-phosphate synthase-like	14.00	-10.27	3.74
<i>Unigene0037080</i>	Inositol-3-phosphate synthase-like	-5.91	7.64	1.74
<i>Unigene0038696</i>	Inositol-3-phosphate synthase A	10.65	-10.65	0.00
<i>Unigene0077925</i>	Predicted: multiple inositol polyphosphate phosphatase 1	-2.99	3.22	0.22
<i>Unigene0077924</i>	Multiple inositol polyphosphate phosphatase 1-like isoform X1	1.10	-1.44	-0.34

<i>Unigene0068974</i>	Phosphoinositide phospholipase C 6-like isoform X2	-3.75	4.24	0.49
<i>Unigene0044077</i>	Inositol monophosphatase family protein	1.56	-1.36	0.20
<i>Unigene0026986</i>	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	0.00	9.03	9.03
<i>Unigene0075107</i>	Aldehyde dehydrogenase	-3.83	-5.98	-9.82
<i>Unigene0097436</i>	Methylmalonate-semialdehyde dehydrogenase	-9.98	6.44	-3.54
<i>Unigene0095980</i>	<i>Myo</i> -inositol oxygenase-like	0.00	9.36	9.36
<i>Unigene0056095</i>	<i>Myo</i> -inositol oxygenase 1-like	-1.41	0.36	-1.06
<i>Unigene0090036</i>	Phosphatidylinositol 4-phosphate 5-kinase 2	-4.26	-0.42	-4.68
<i>Unigene0005364</i>	Non-specific phospholipase C4-like	-1.21	-0.01	-1.22
<i>Unigene0101311</i>	Triosephosphate isomerase-like	0.78	3.52	4.30
<i>Unigene0023711</i>	<i>Myo</i> -inositol-1-phosphate synthase, partial	-11.37	7.49	-3.88
<i>Unigene0104656</i>	Predicted: inositol-3-phosphate synthase	0.09	0.91	1.00
<i>Unigene0069542</i>	<i>Myo</i> -inositol-1-phosphate synthase	-9.07	6.32	-2.75
<i>Unigene0077431</i>	Predicted: phosphoinositide phosphatase SAC2 isoform X2	-9.80	0.00	-9.80

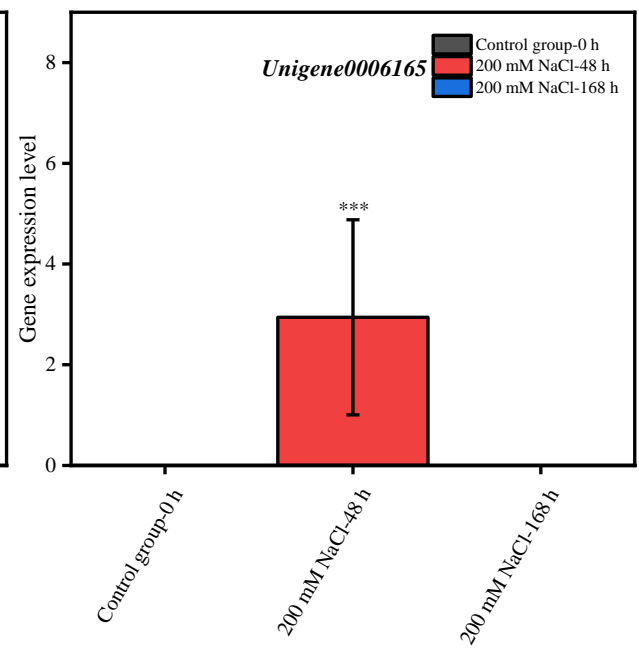
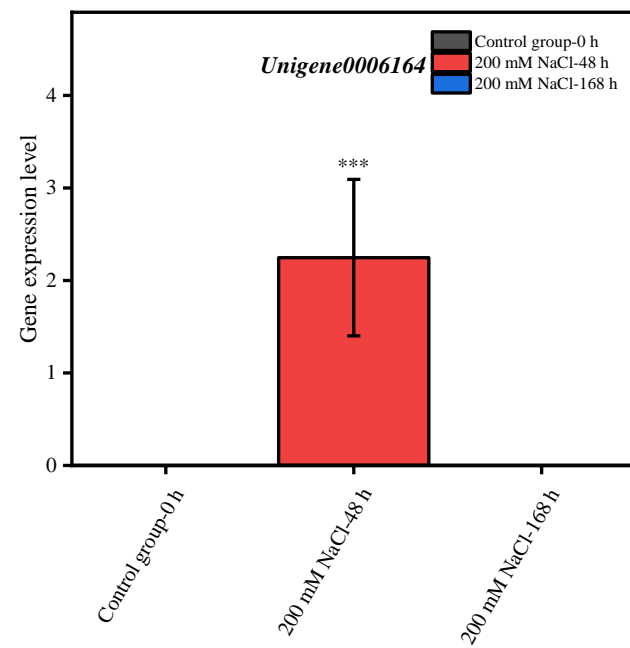
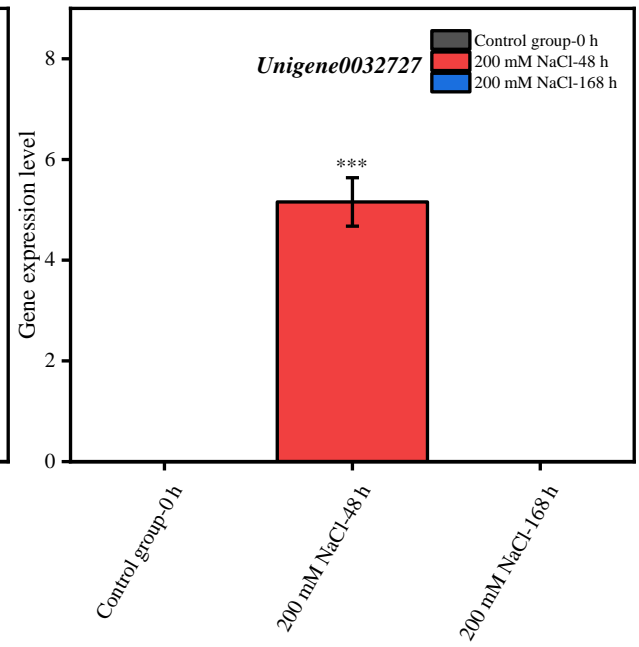
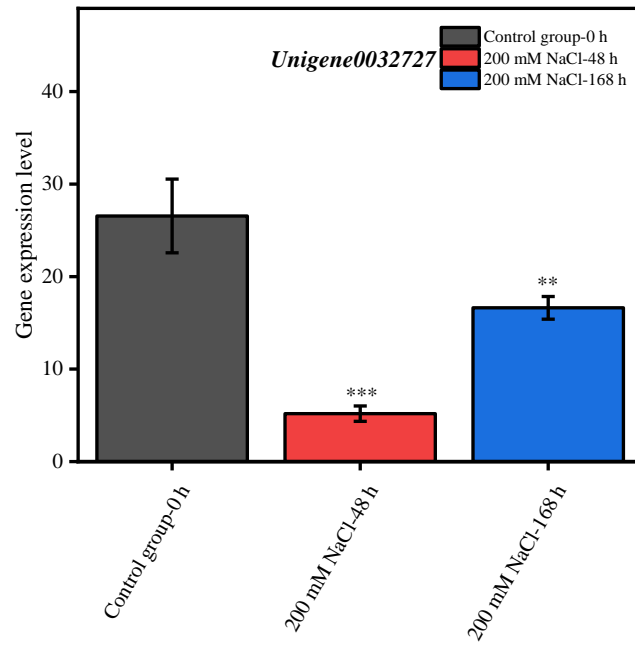
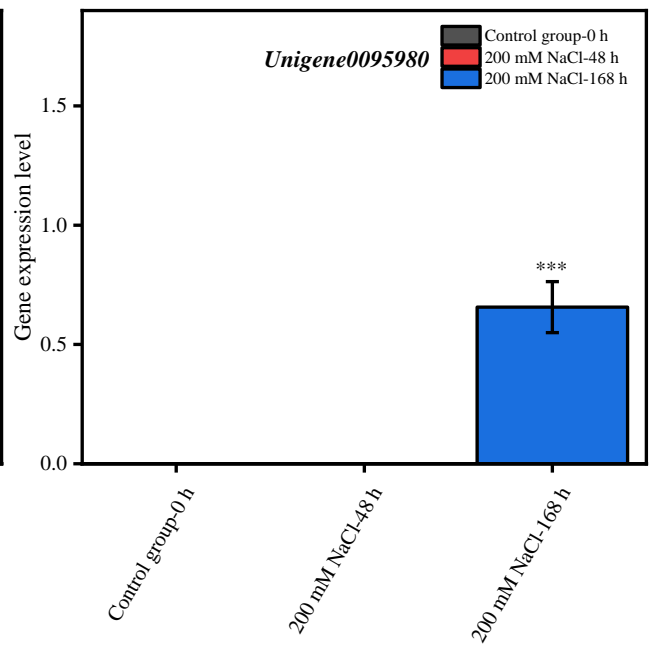
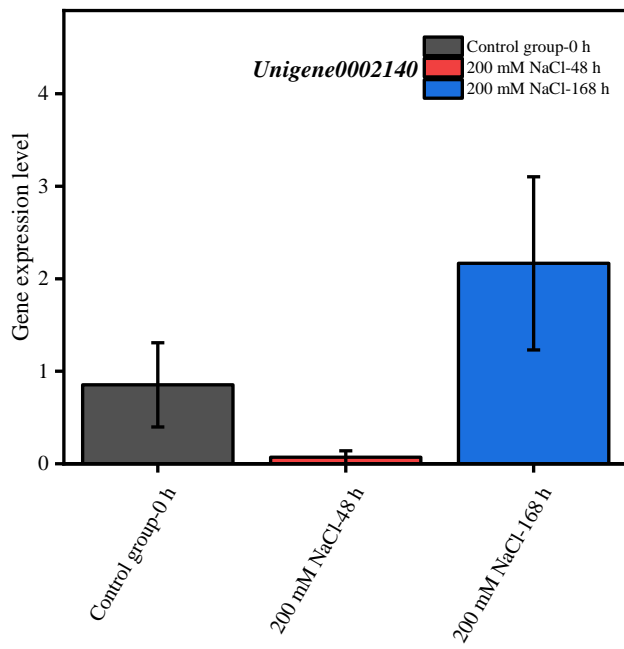
Note: Control group-0 h:CK-0 h; 200 mM NaCl-48 h: N-48 h; 200 mM NaCl-168 h: N-168 h.

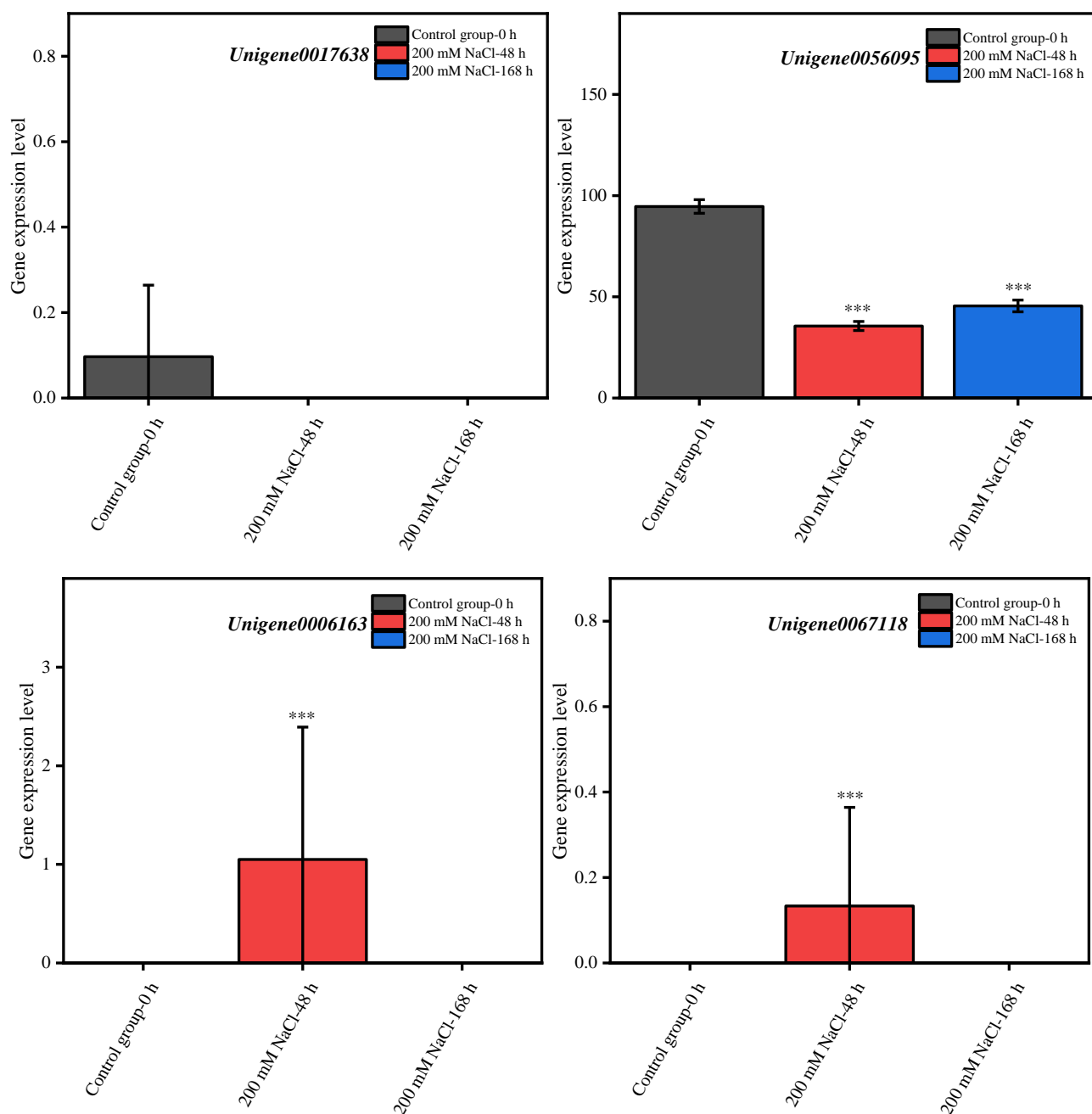
Supplementary Table S6. Analysis of differentially expressed metabolites in the inositol phosphate metabolism pathway

Name	Formula	Molecular Weight	RT [min]	m/z	Control group-0 h		200 mM NaCl-48 h		200 mM NaCl-168 h	
					mean	standard deviation	mean	standard deviation	mean	standard deviation
<i>Myo</i> -inositol	C <sub>6</sub> H <sub>12</sub> O <sub>6</sub>	180.06	1.26	181.07	635191705.93	125601062.62	523967880.43	52545829.76	1286750168.00	70684525.76
D-Glucose 6-phosphate	C <sub>6</sub> H <sub>13</sub> O <sub>9</sub>	260.03	1.36	261.04	61549313.40	37970566.00	47304845.90	2811083.71	13564200.00	460504.60

Note: The metabolite content is relative quantification and has no units.

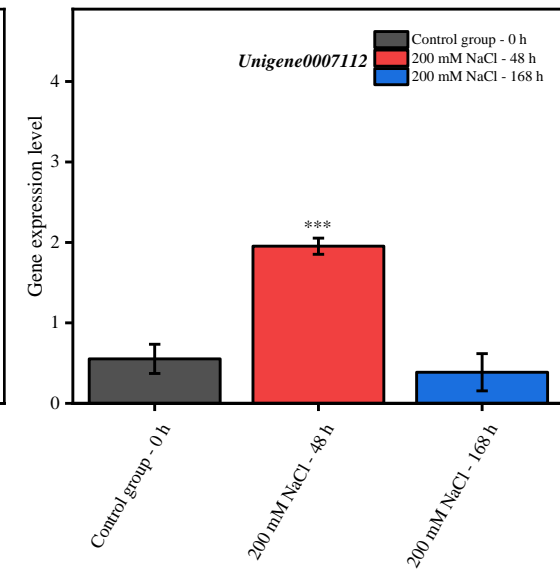
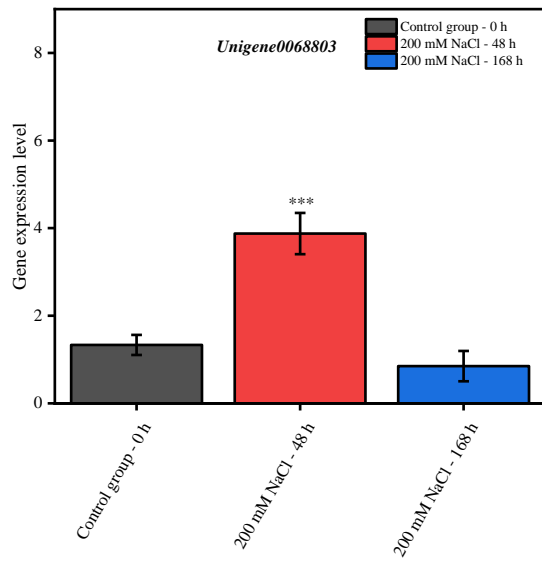
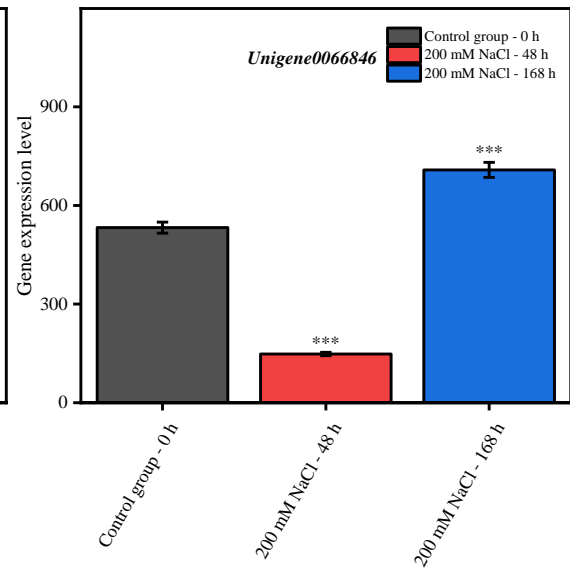
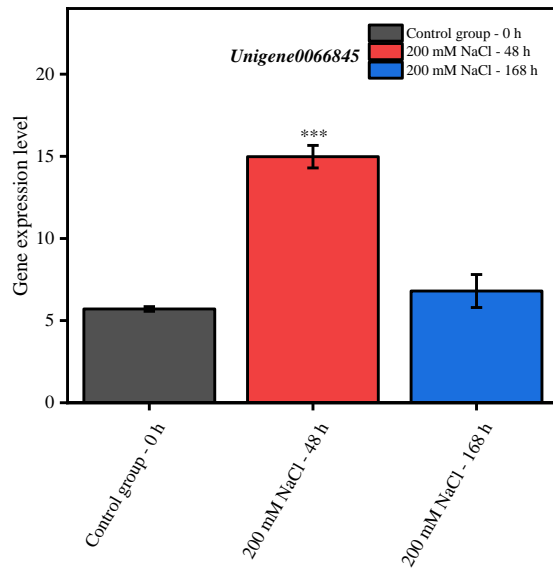
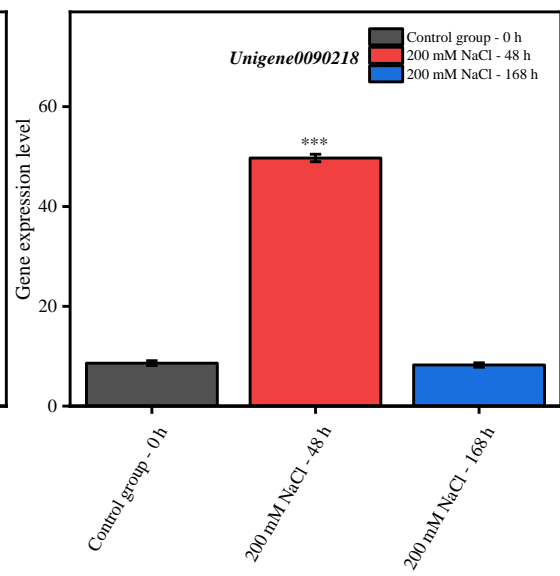
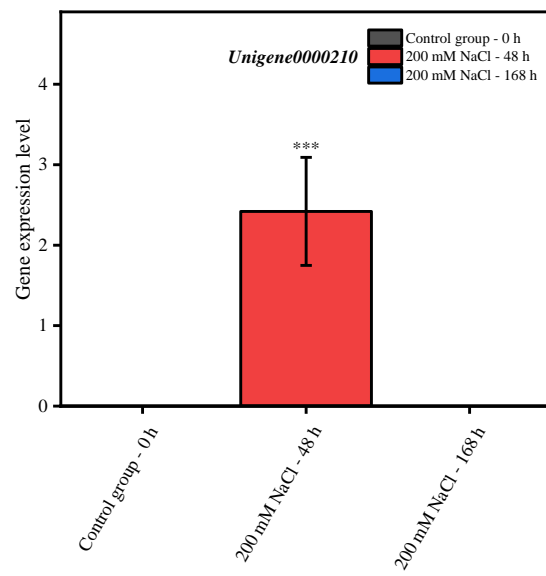


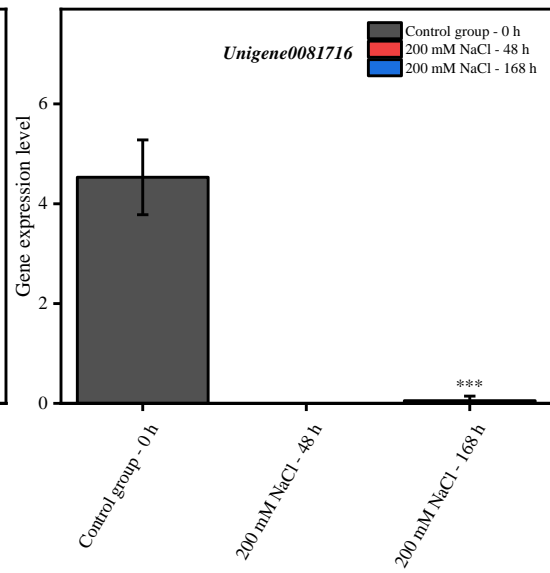
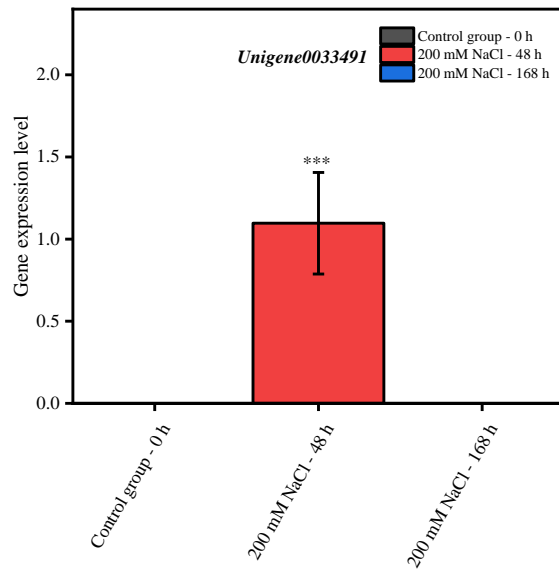
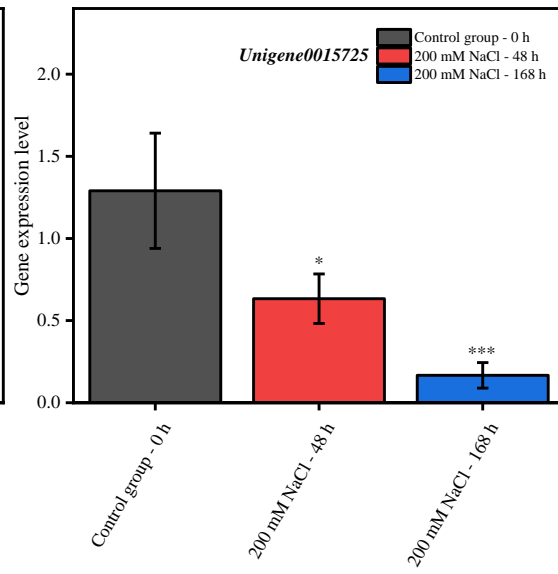
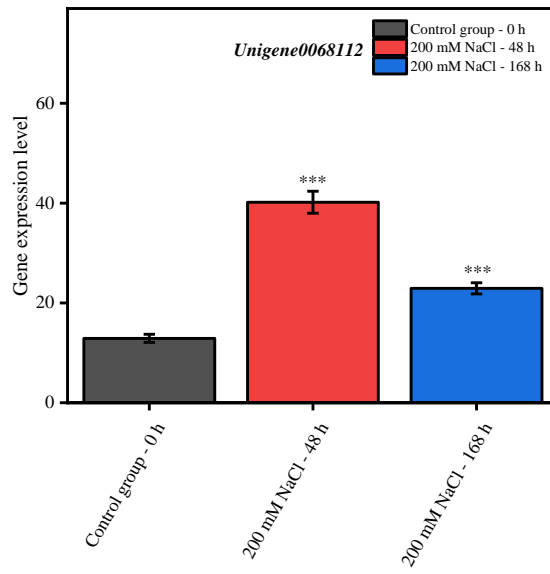
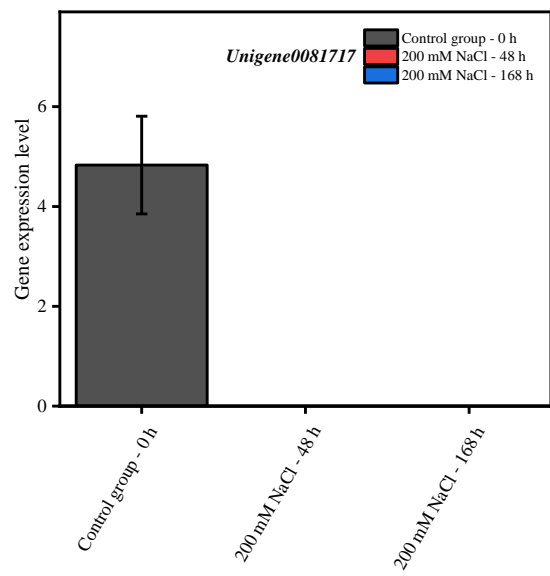
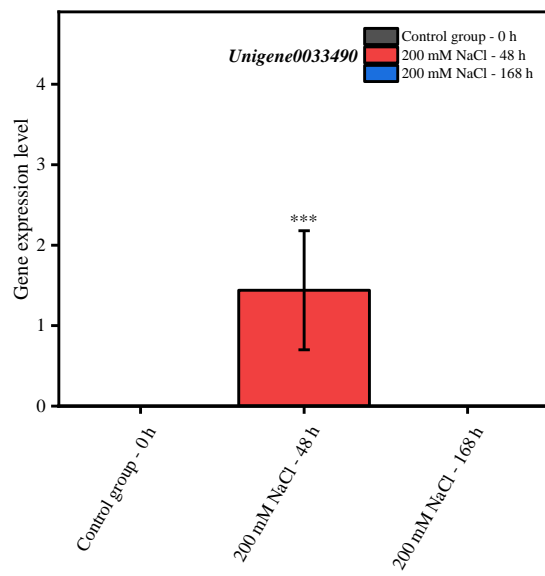


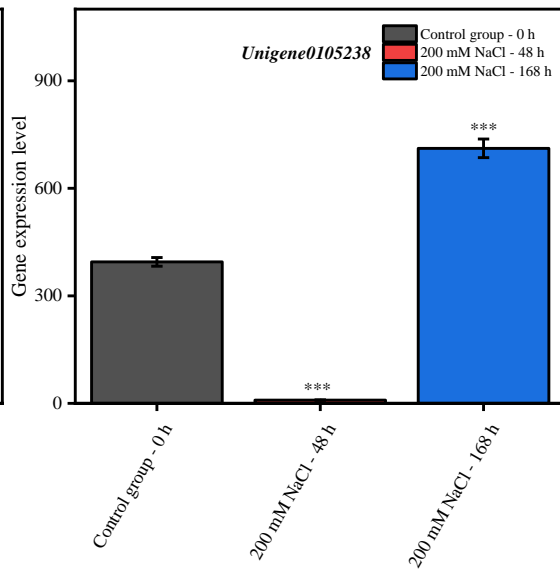
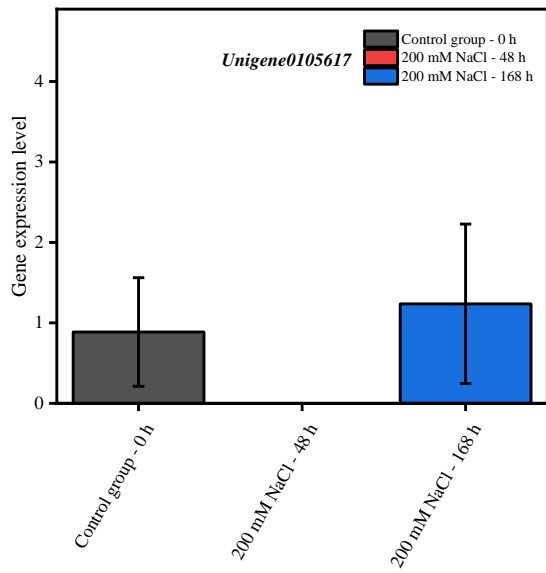
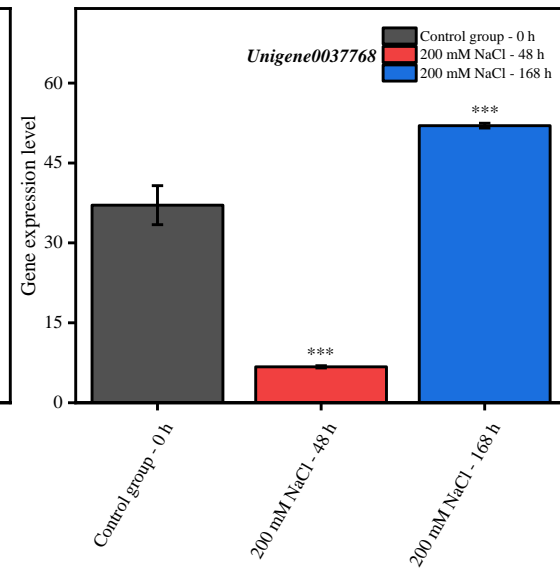
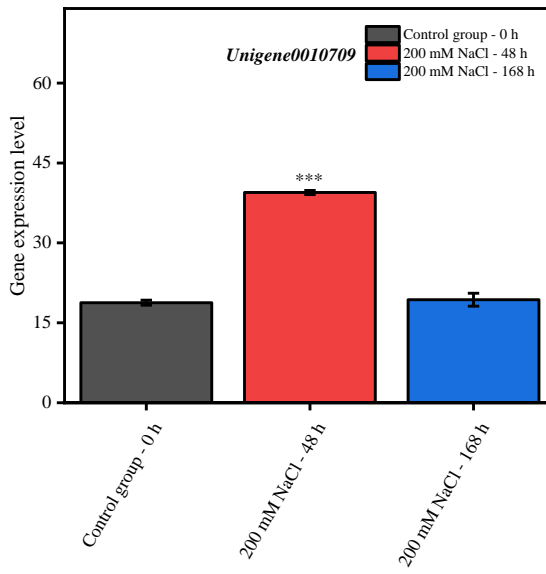
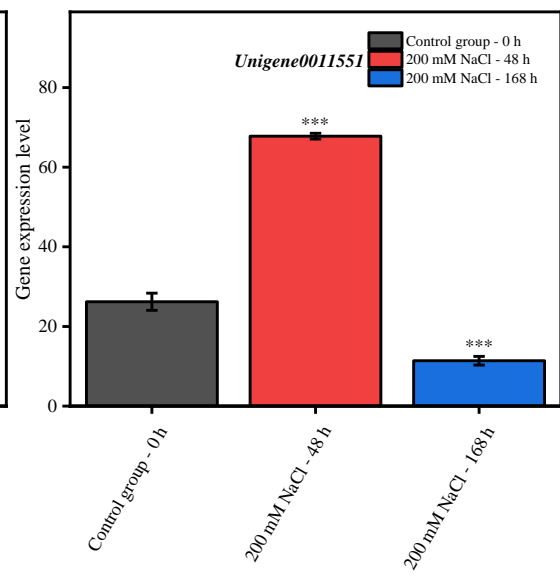
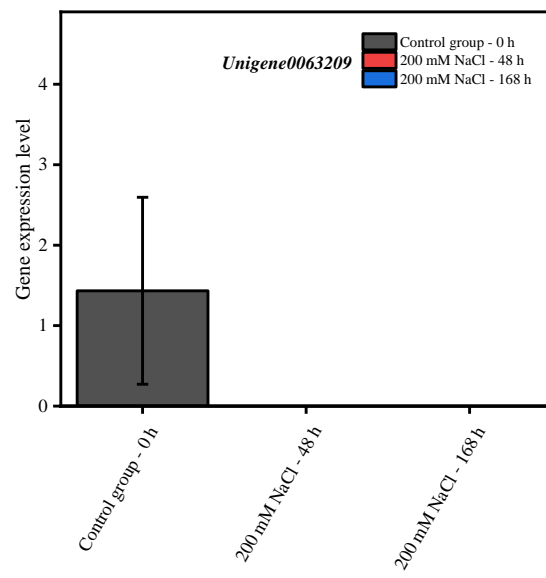


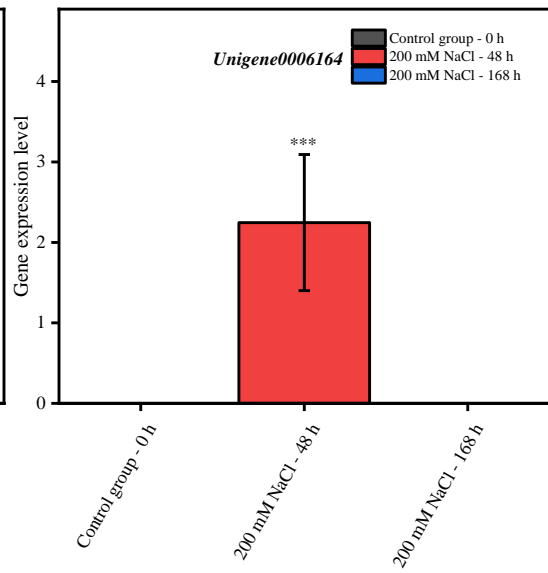
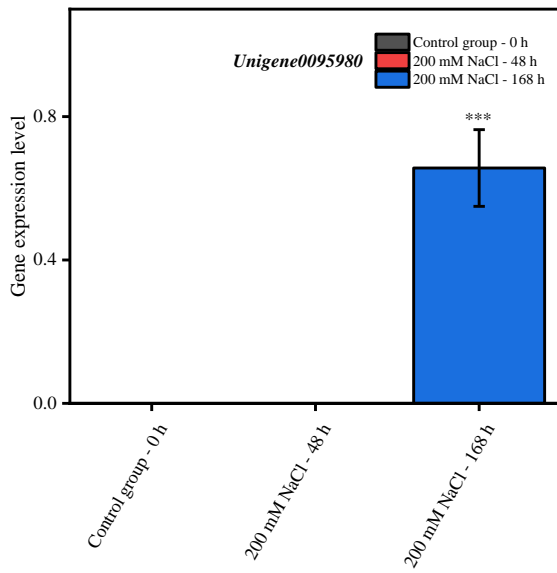
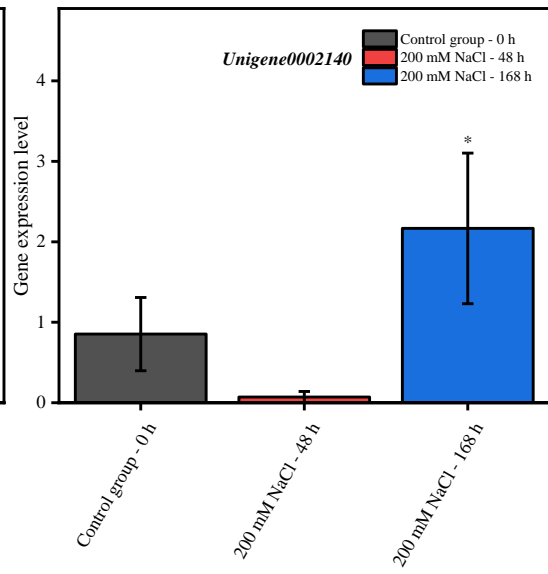
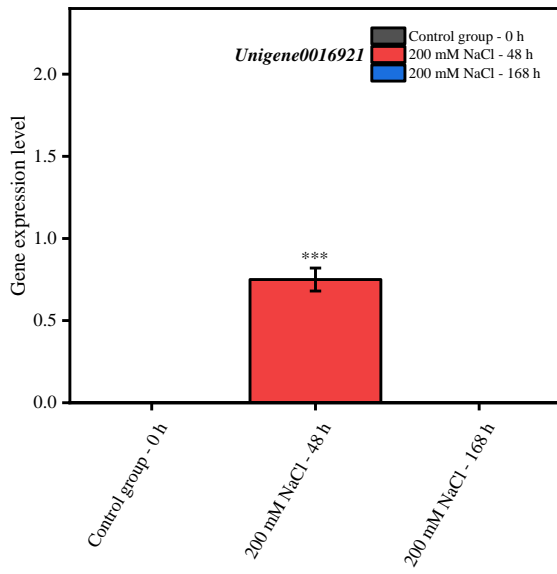
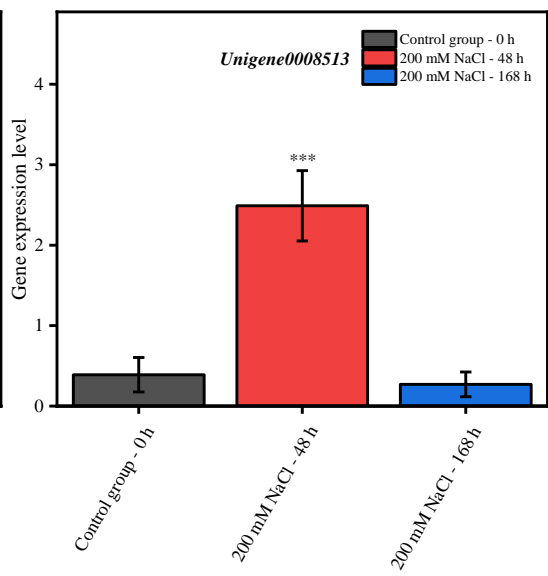
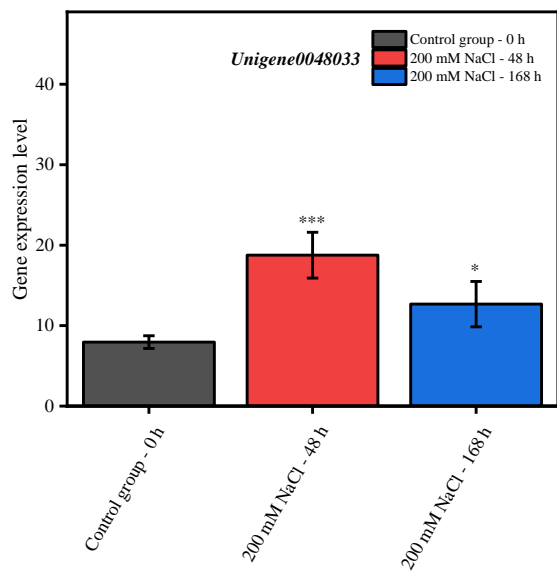
Supplementary Figure S1. Expression levels of *Myo*-inositol oxygenase-related genes

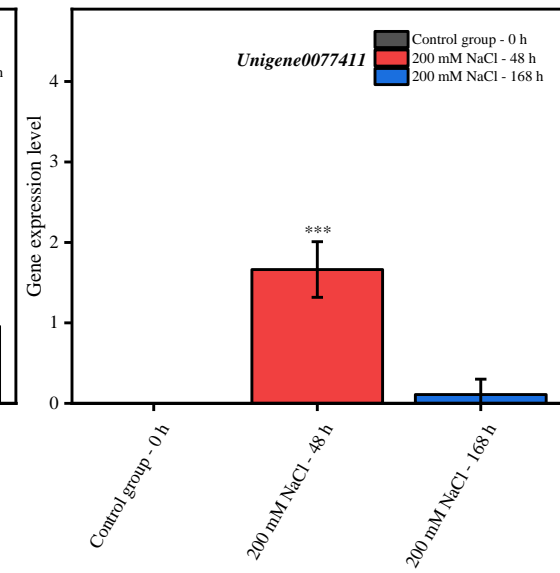
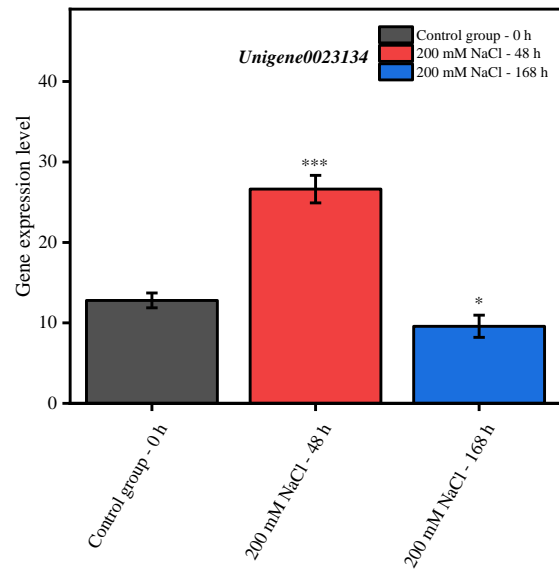
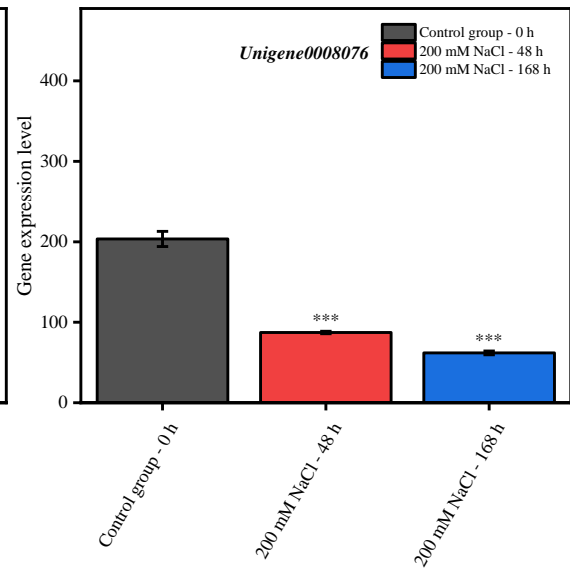
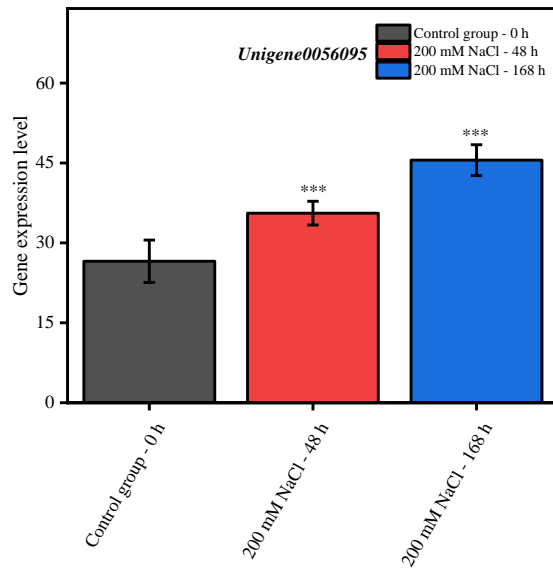
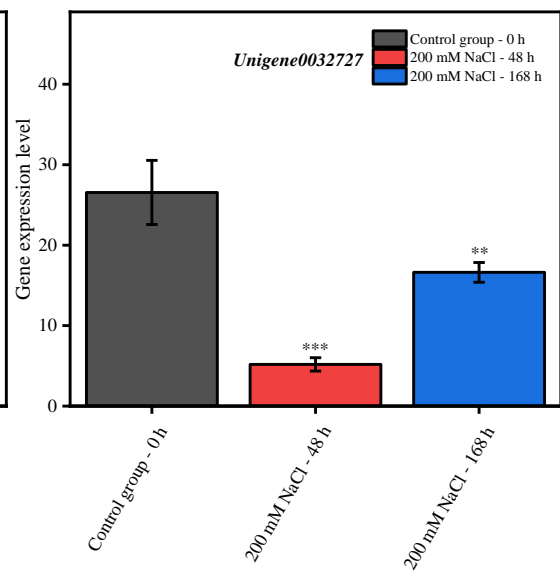
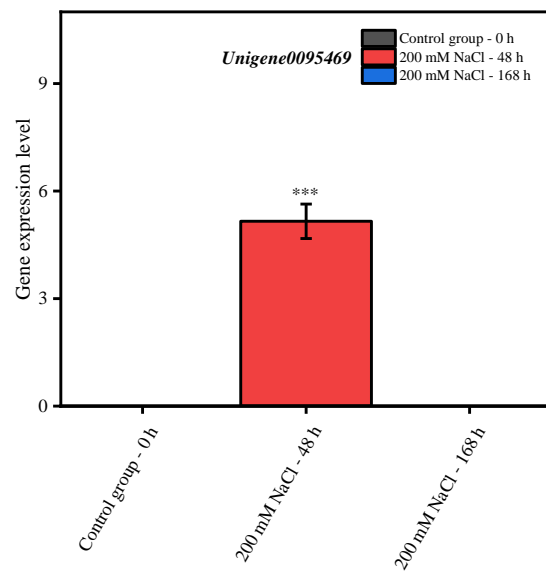
(The changes in the expression levels of 10 *Myo*-inositol oxygenase-related genes in the roots of *T. ramosissima* under NaCl stress at 0 h, 48 h, and 168 h. Note:  $p \geq 0.05$  is not marked;  $0.01 < p < 0.05$  is marked as \*;  $0.001 < p < 0.01$  is marked as \*\*,  $p \leq 0.001$  is marked as \*\*\*).

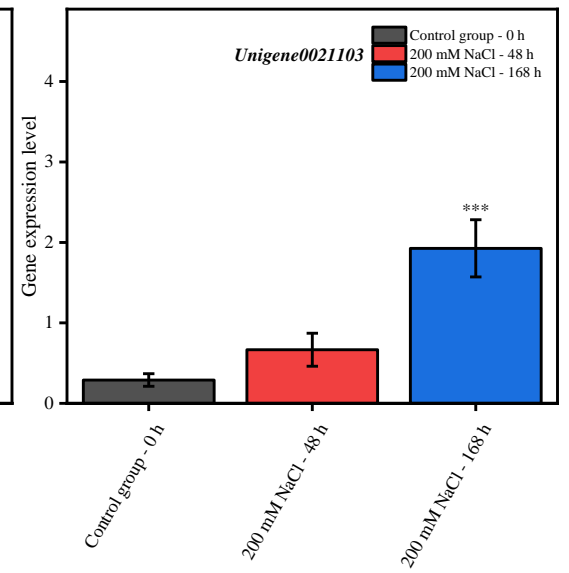
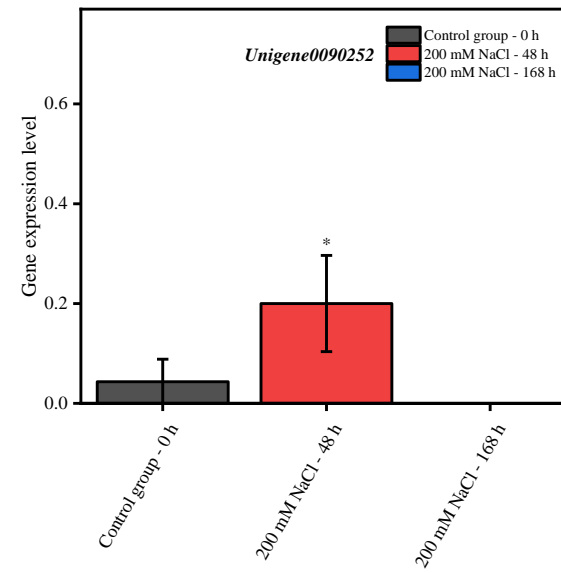
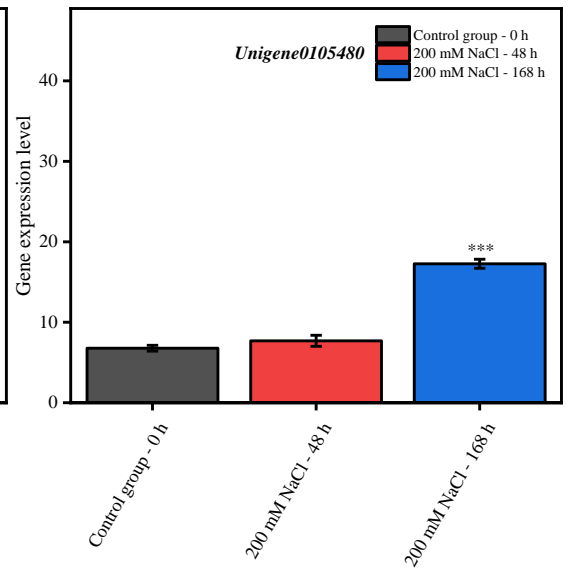
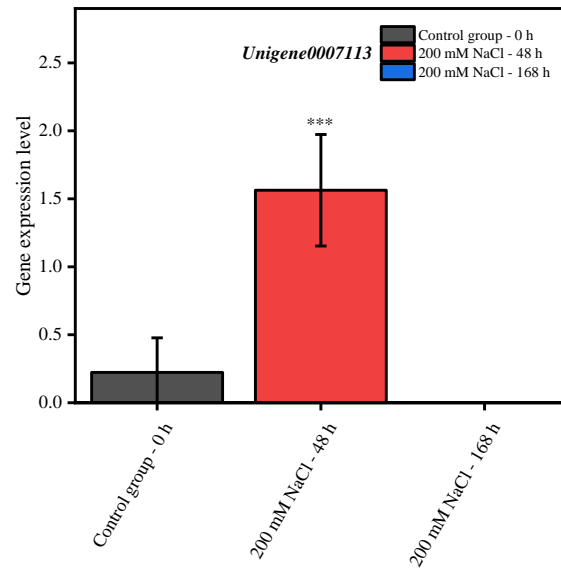
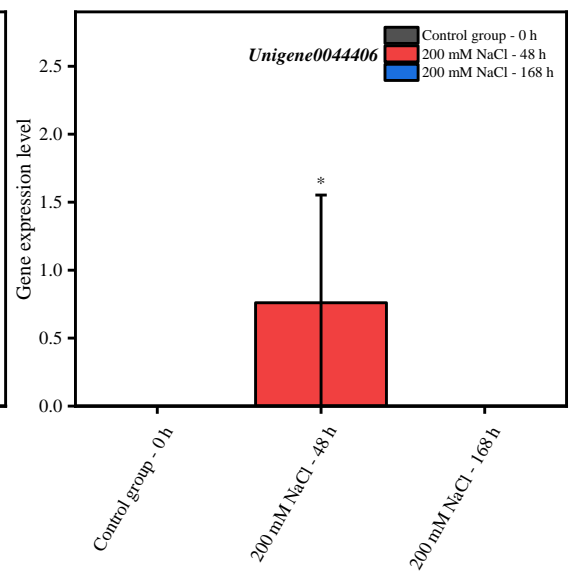
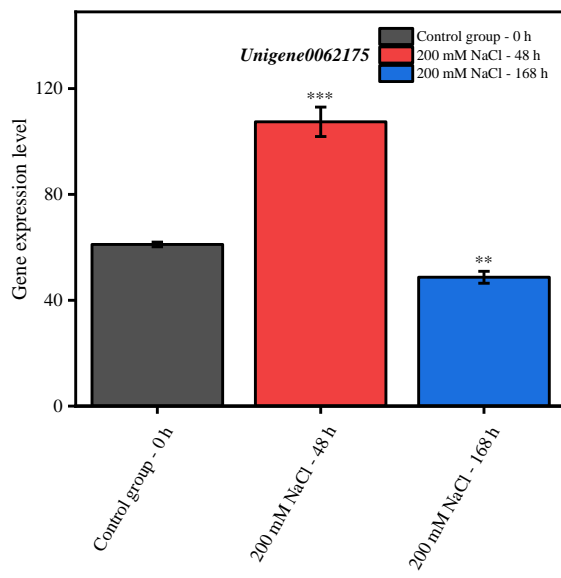




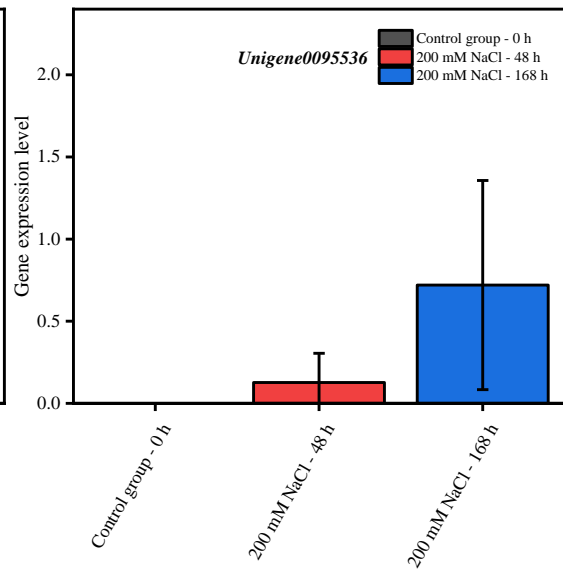
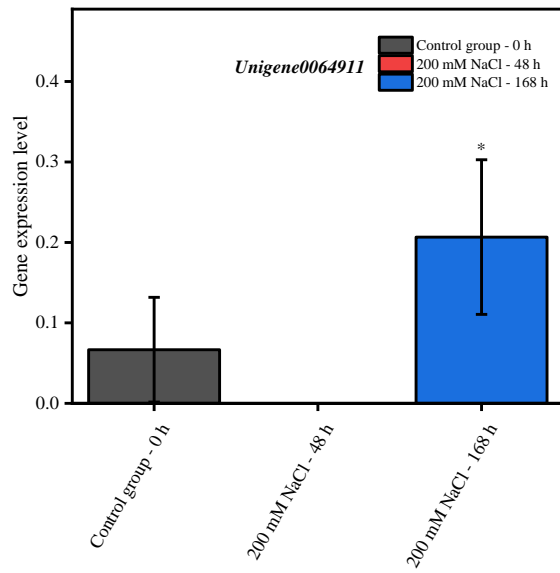
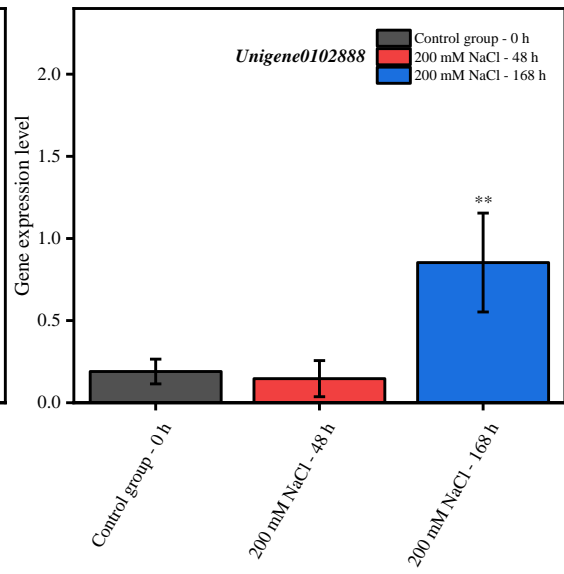
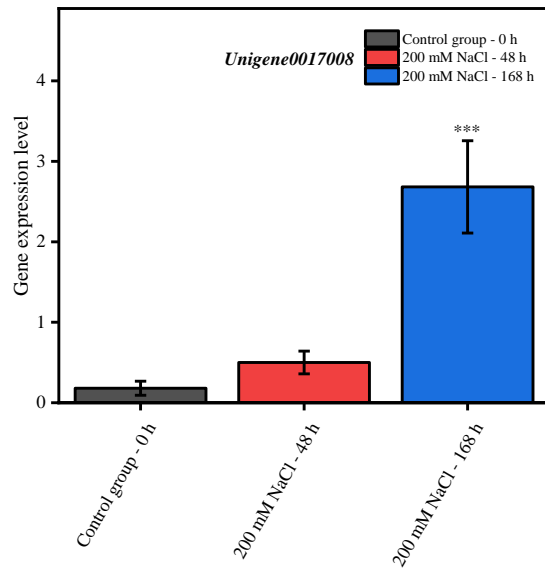
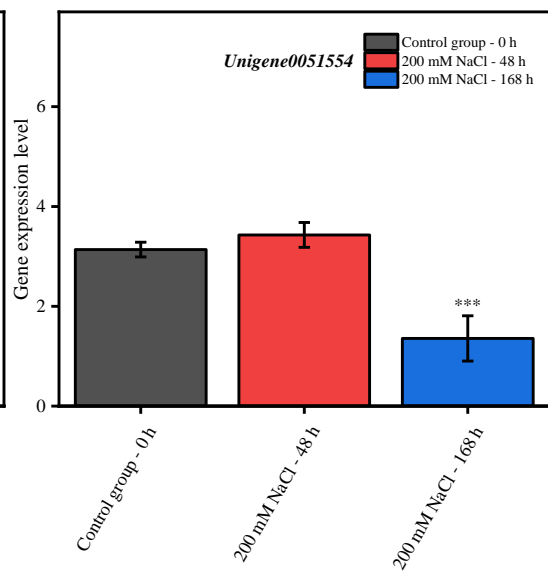
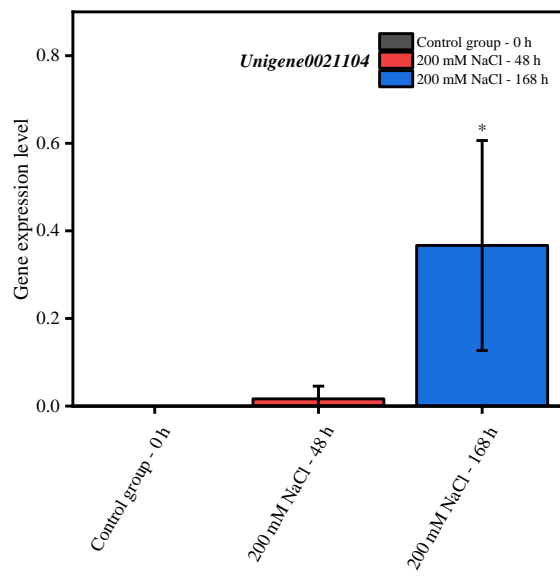


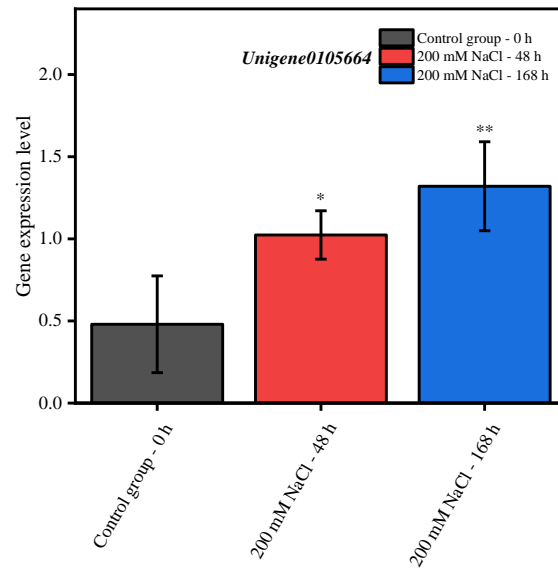




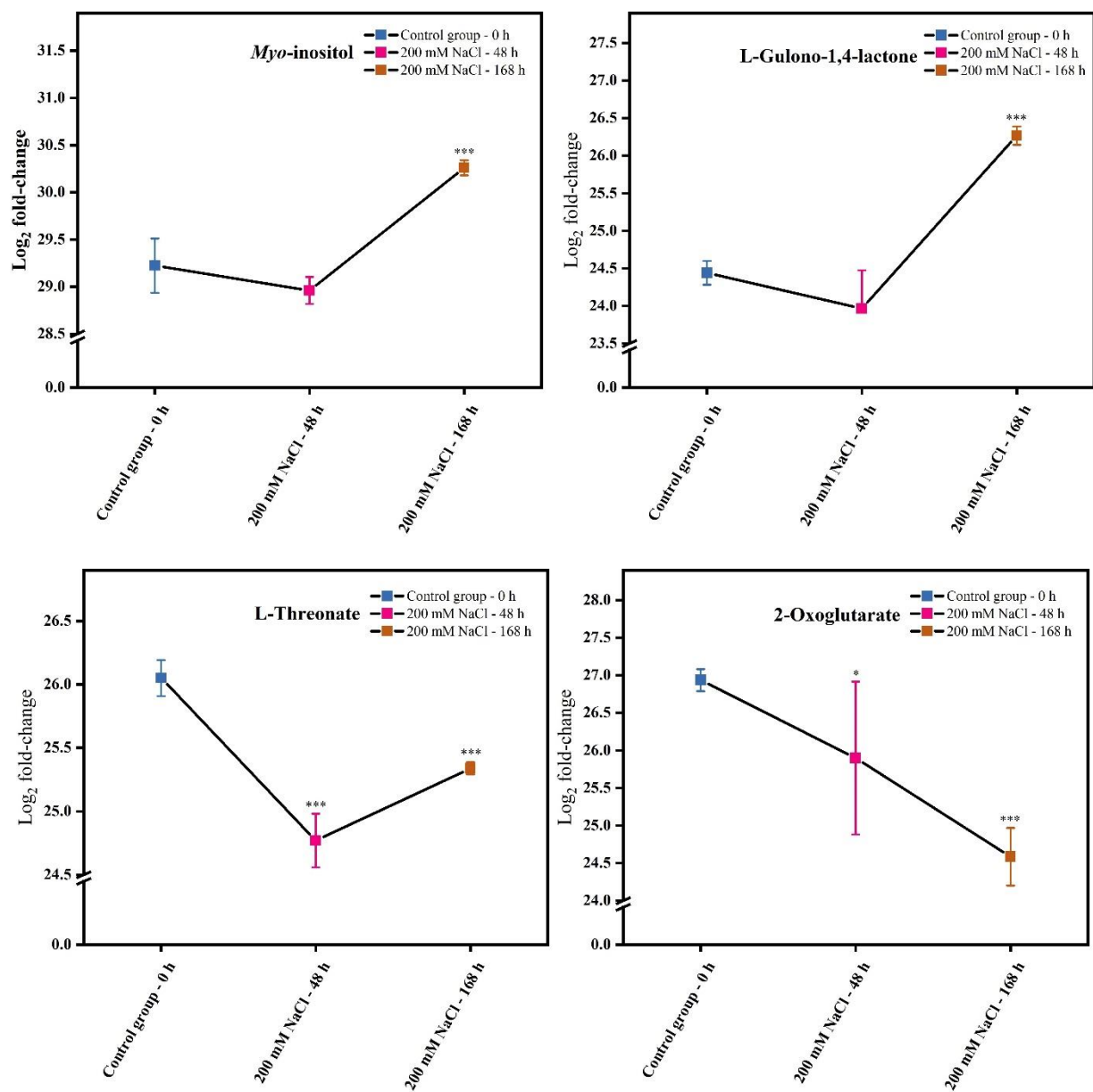






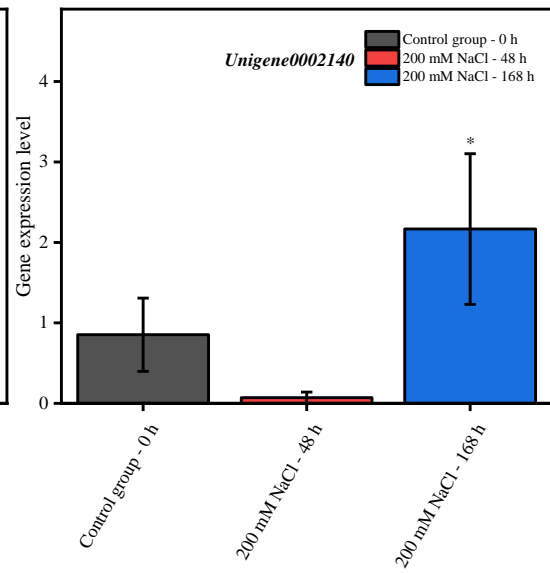
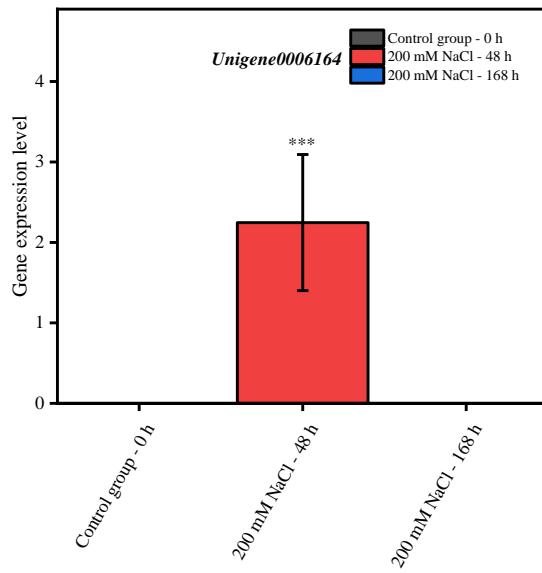
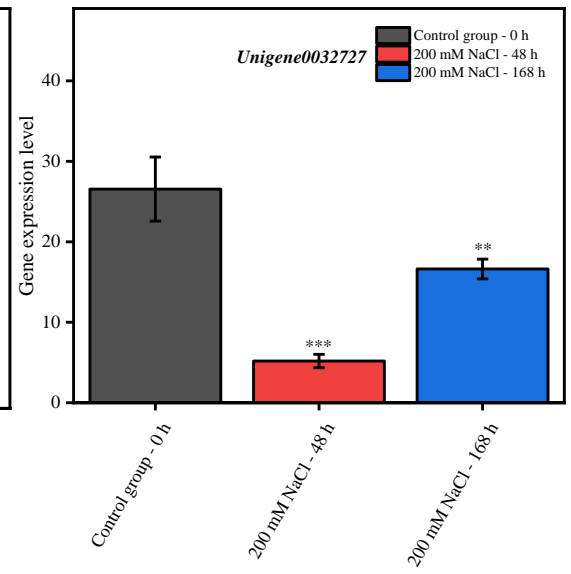
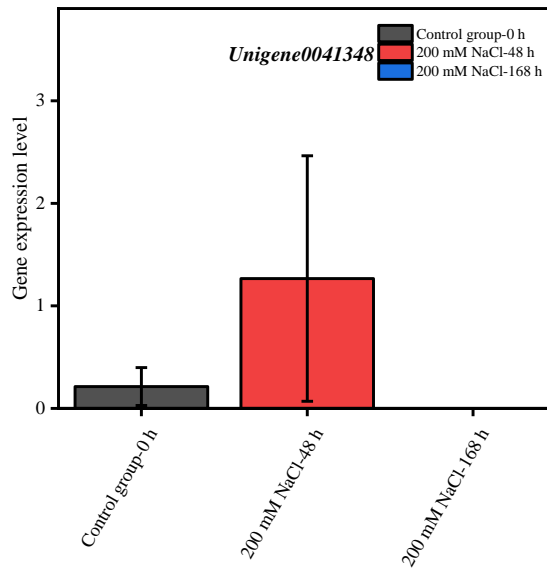
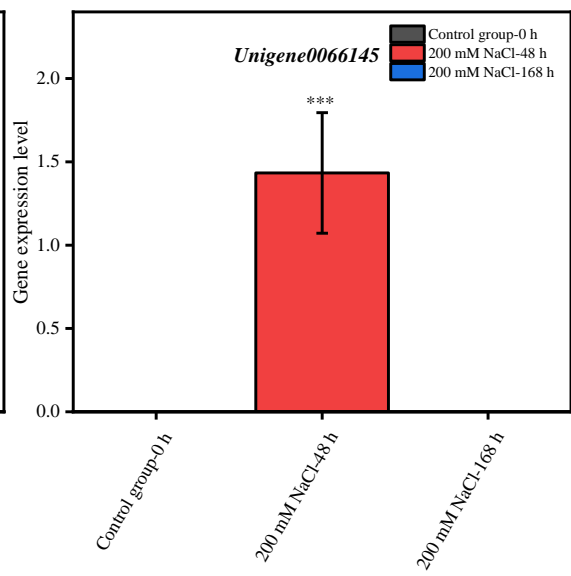
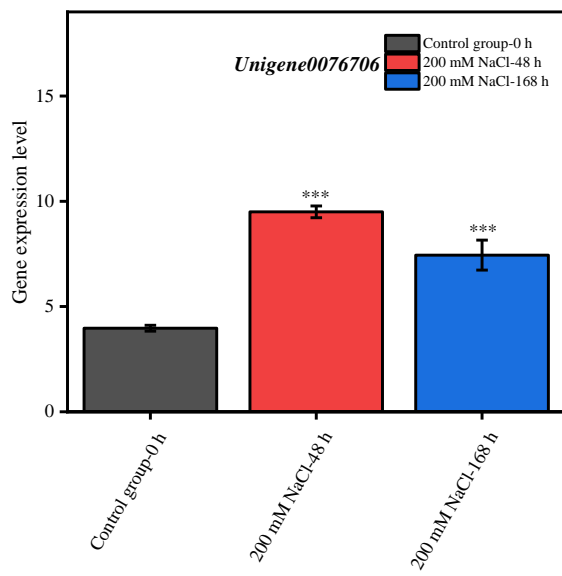


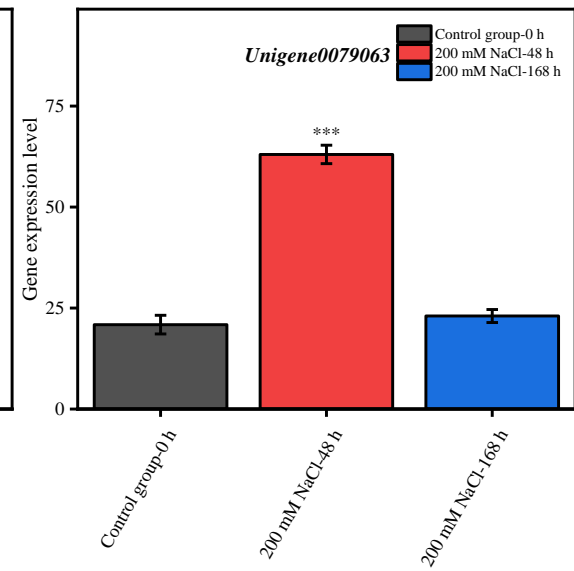
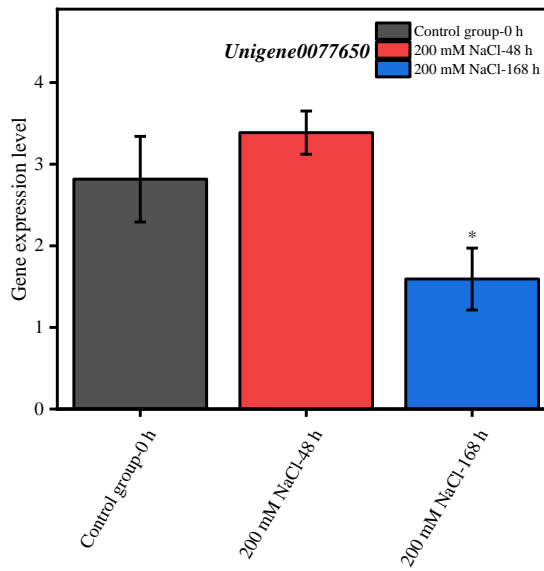
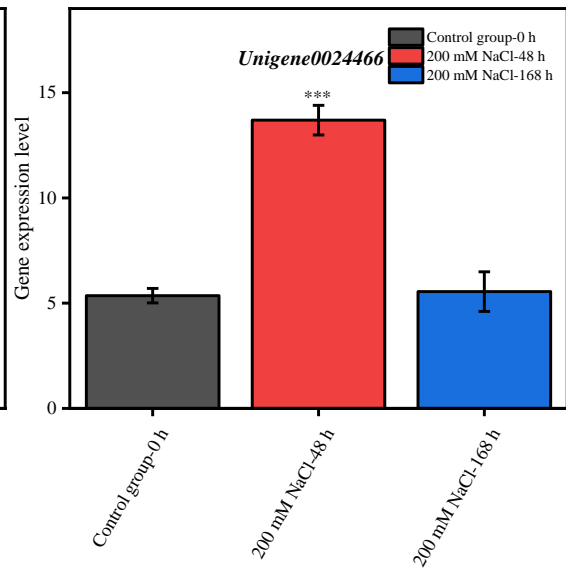
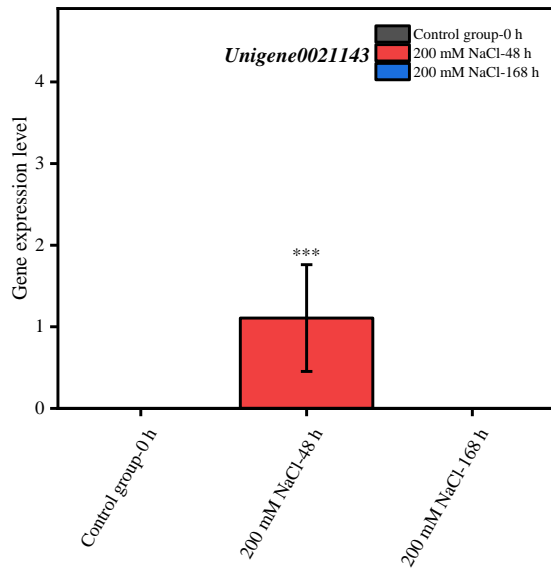
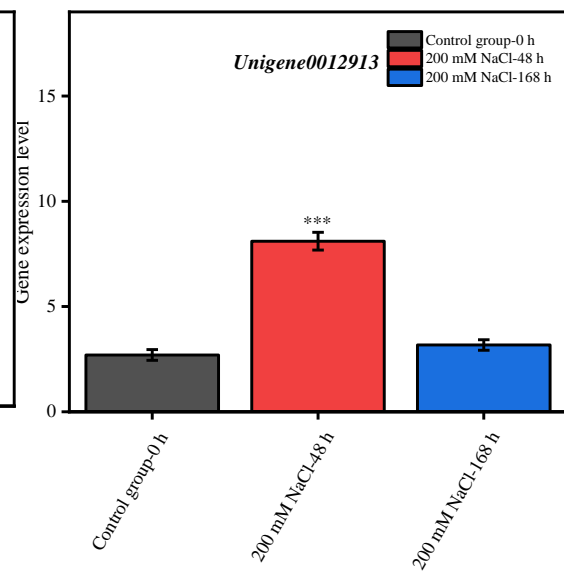
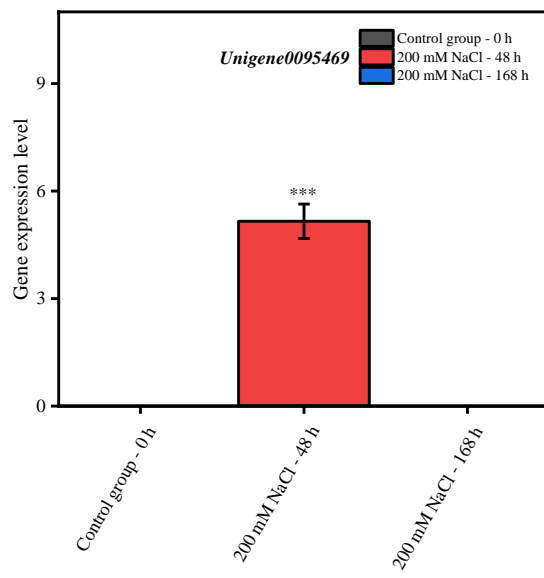
Supplementary Figure S2. Changes in expression levels of DEGs in the ascorbate and aldarate metabolism pathway (Changes in expression levels of 43 DEGs annotated to the ascorbate and aldarate metabolism pathway in the root system of *T. ramosissima* under NaCl stress at 0 h, 48 h, and 168 h. Note:  $p \geq 0.05$  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 \*\*\*).

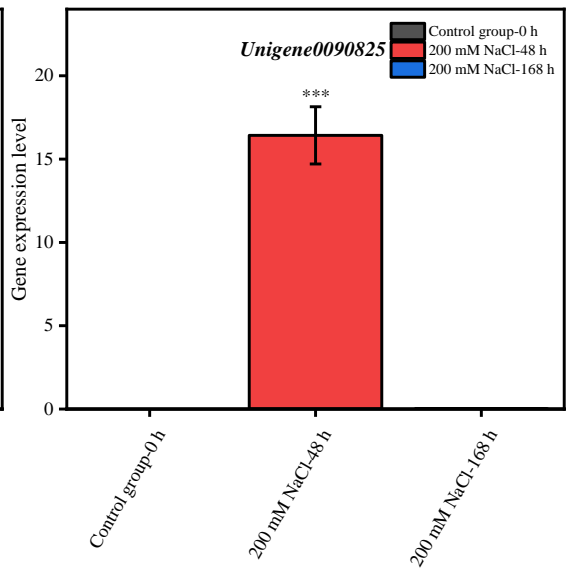
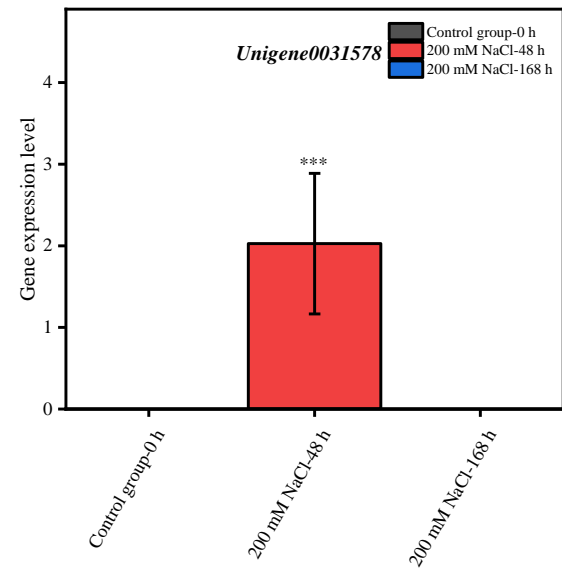
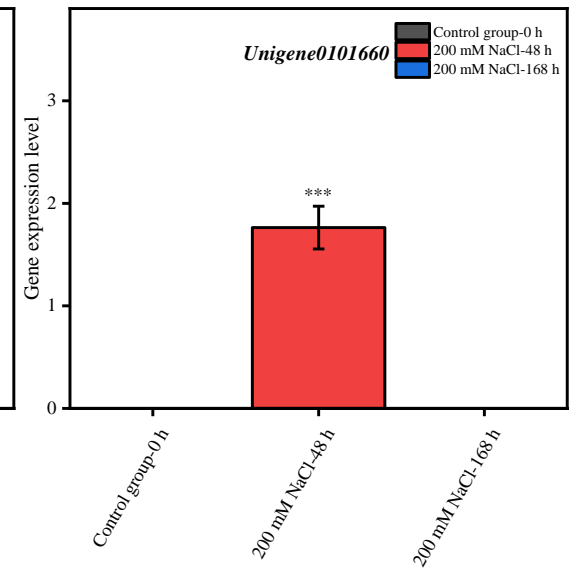
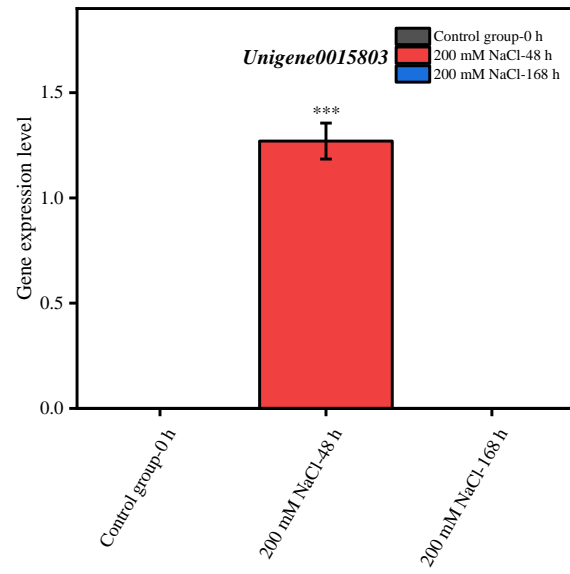
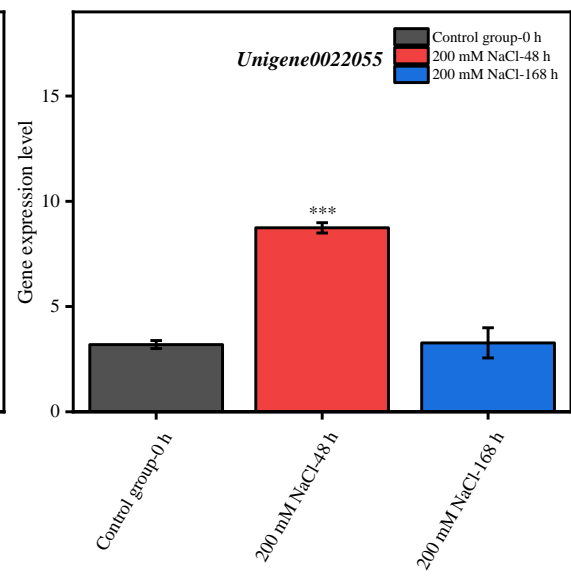
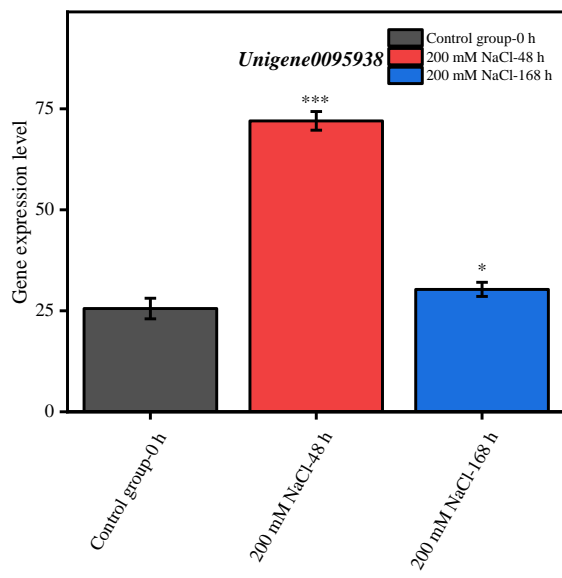


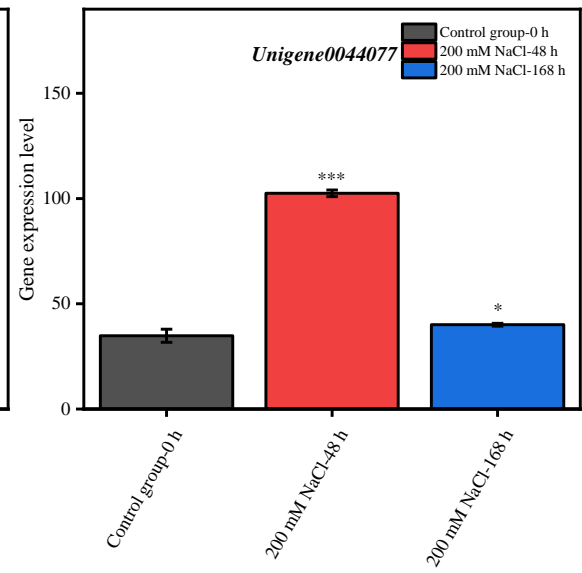
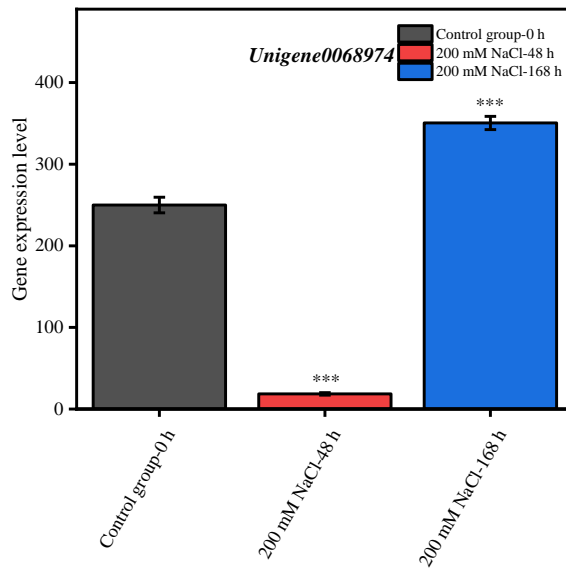
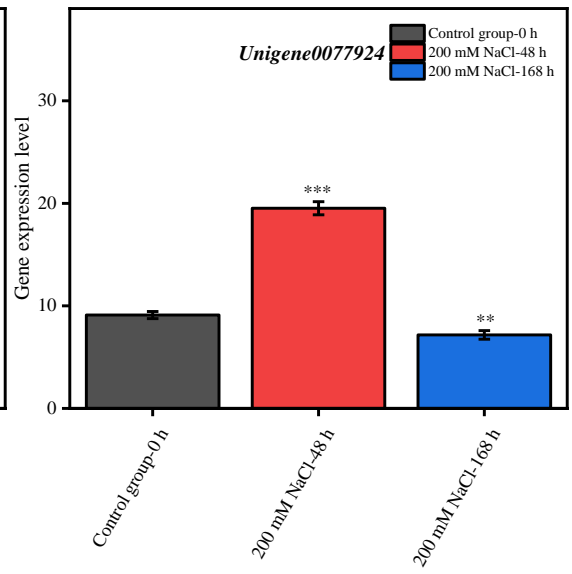
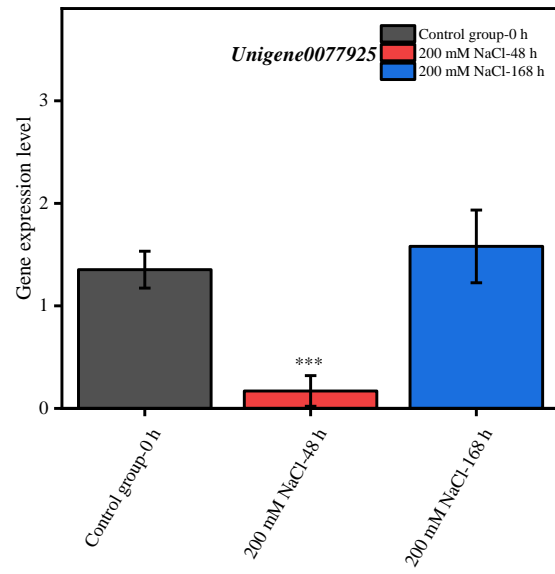
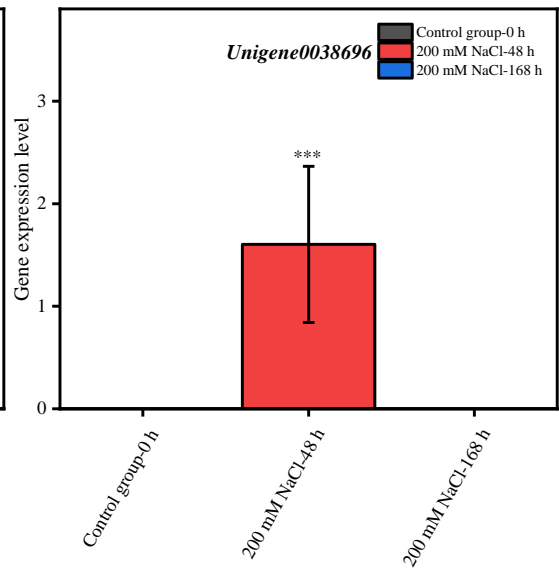
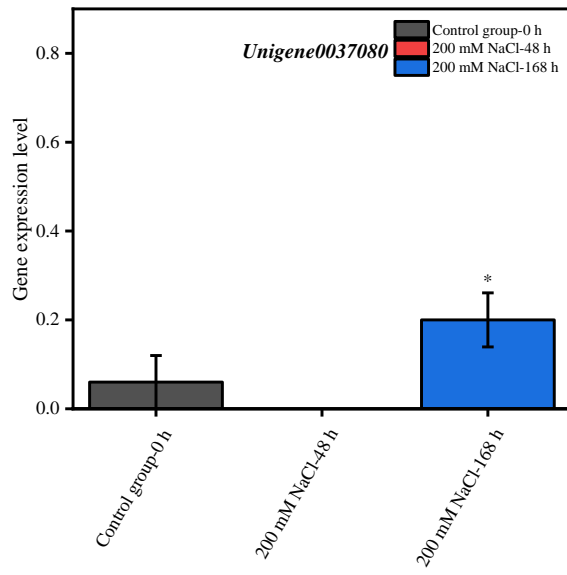
Supplementary Figure S3. Log<sub>2</sub> fold-change of differentially expressed metabolite content in the ascorbate and aldarate metabolism pathway

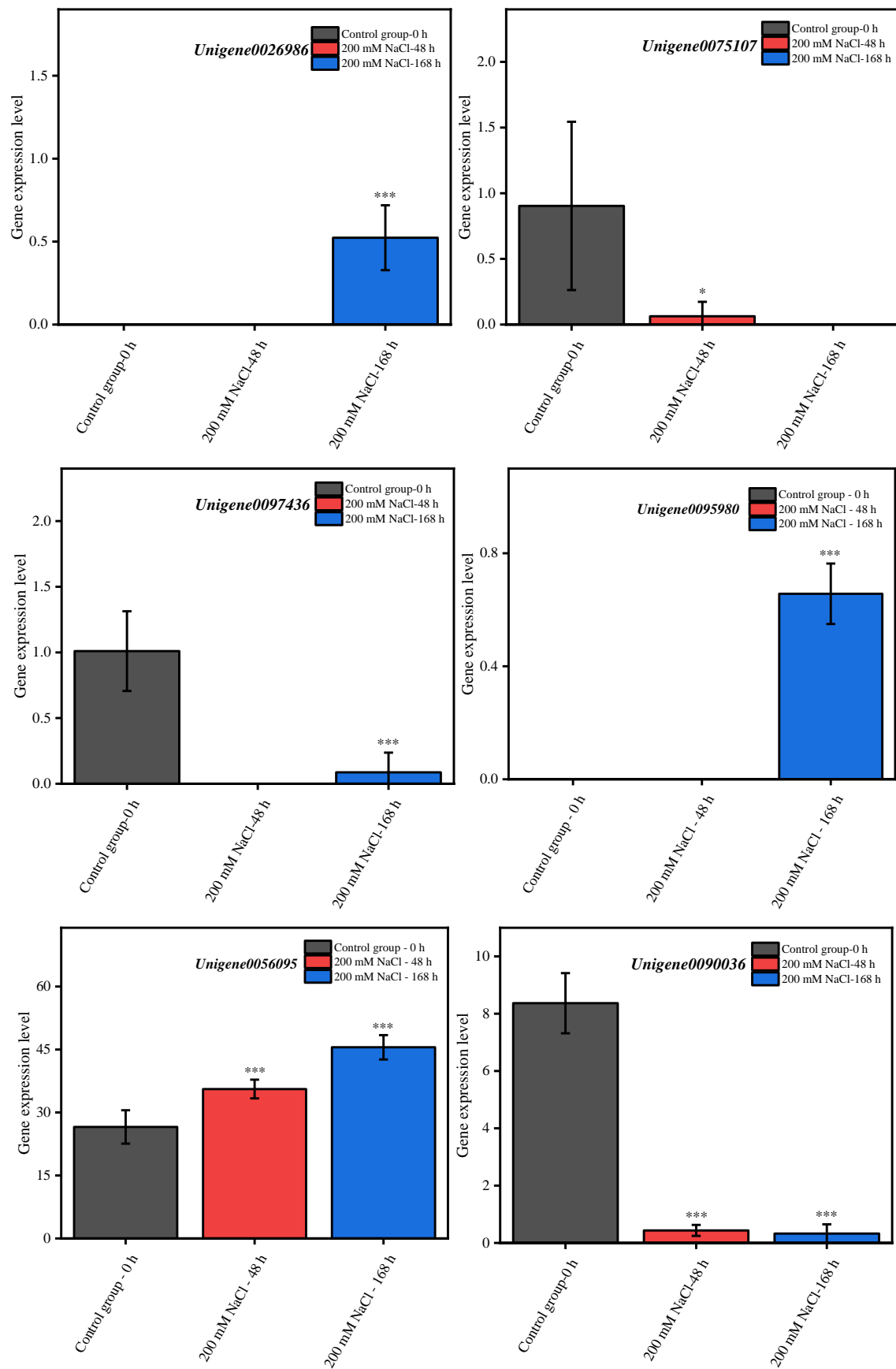
(The Log<sub>2</sub> fold-change of differentially expressed metabolite content annotated to the ascorbate and aldarate metabolism pathway in the roots of *T. ramosissima* under NaCl stress at 0 h, 48 h, and 168 h. Note:  $p \geq 0.05$  is not marked;  $0.01 < p < 0.05$  is marked as \*;  $0.001 < p < 0.01$  is marked as \*\*;  $p \leq 0.001$  is marked as \*\*\*).



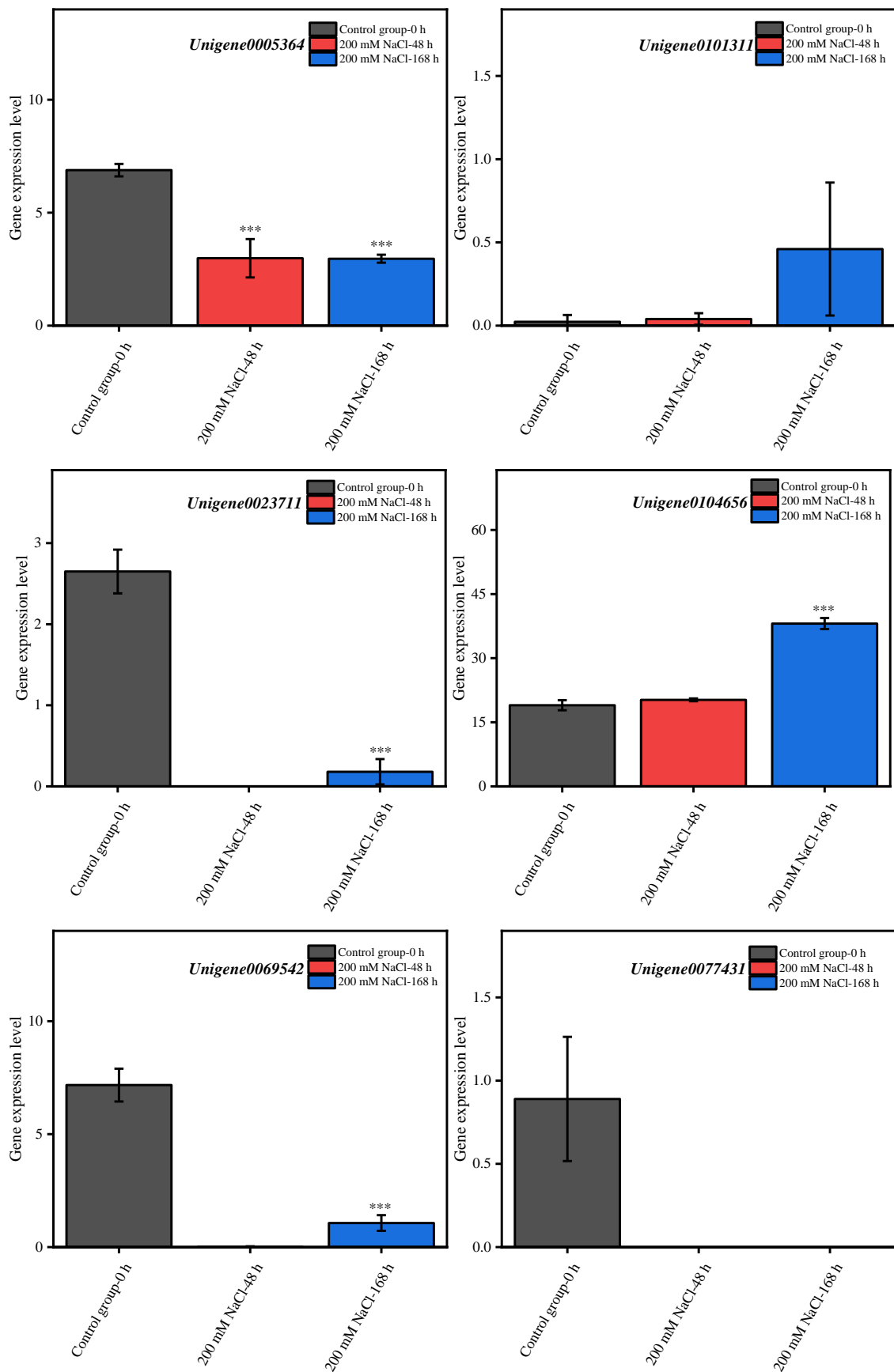




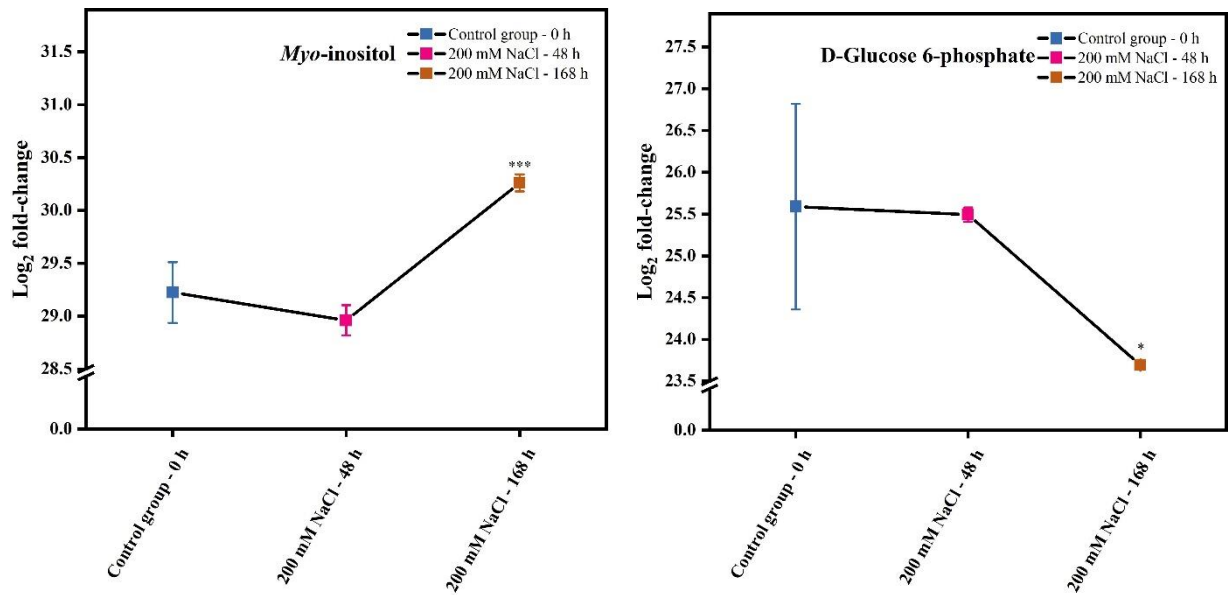






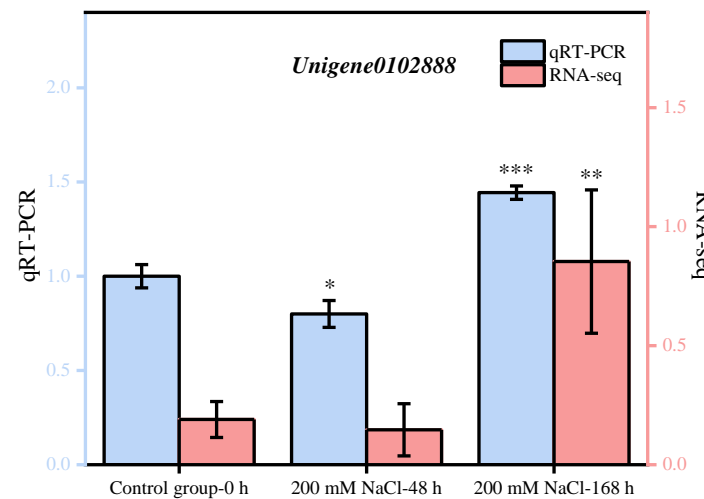
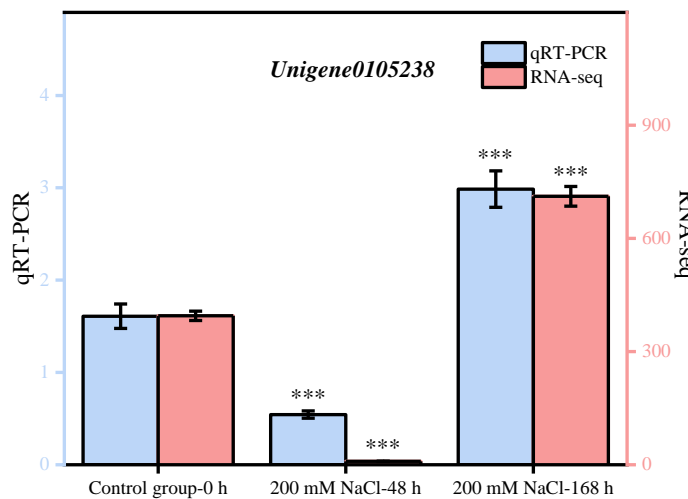
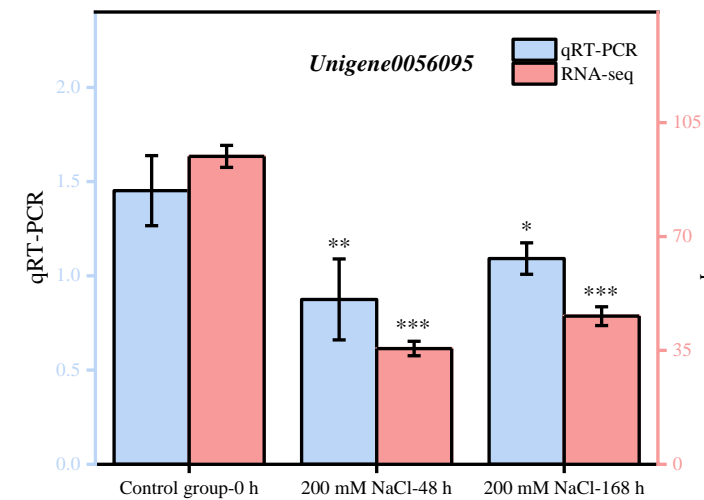
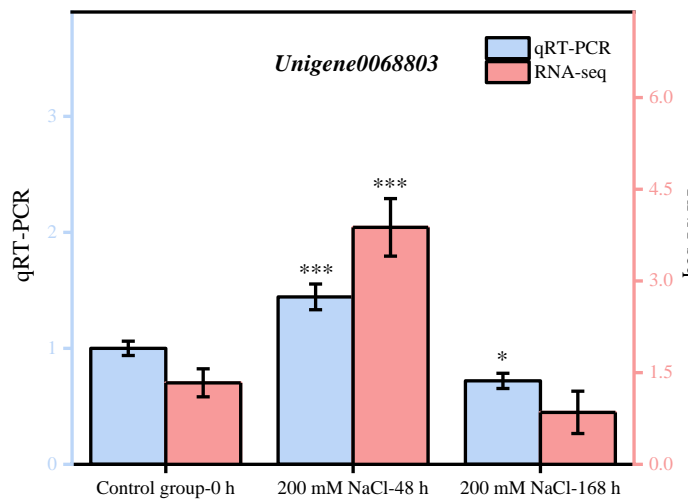
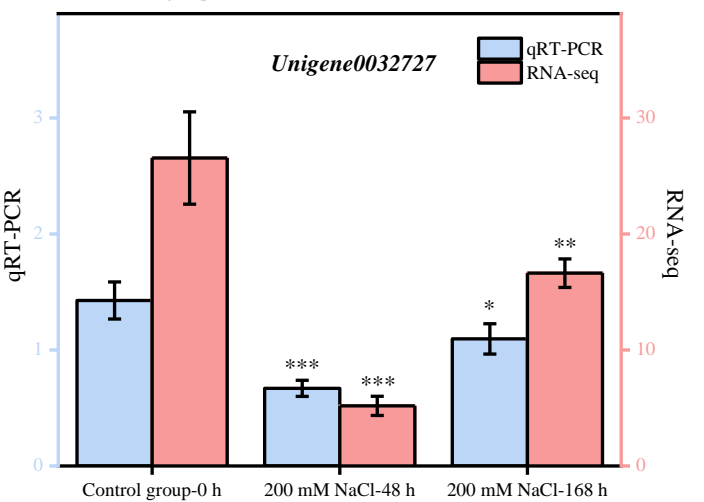
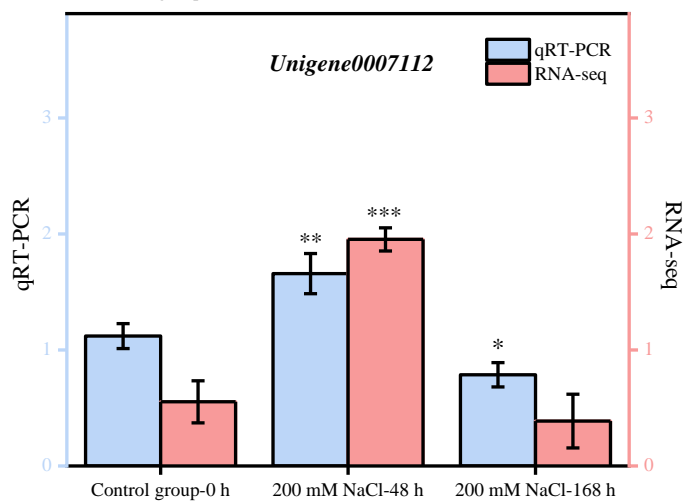
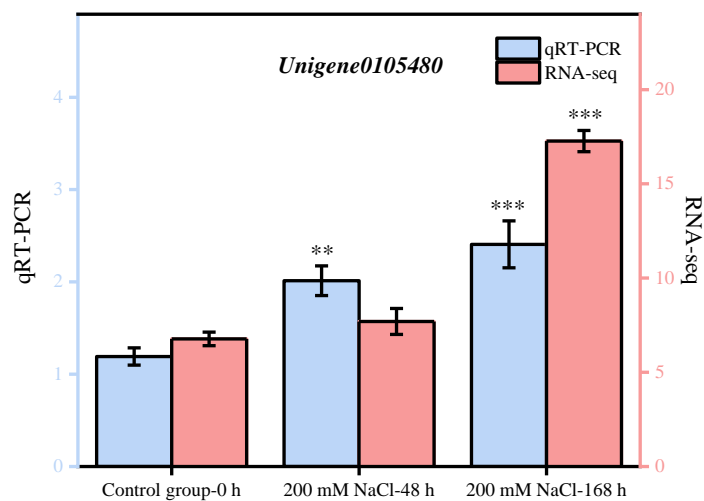
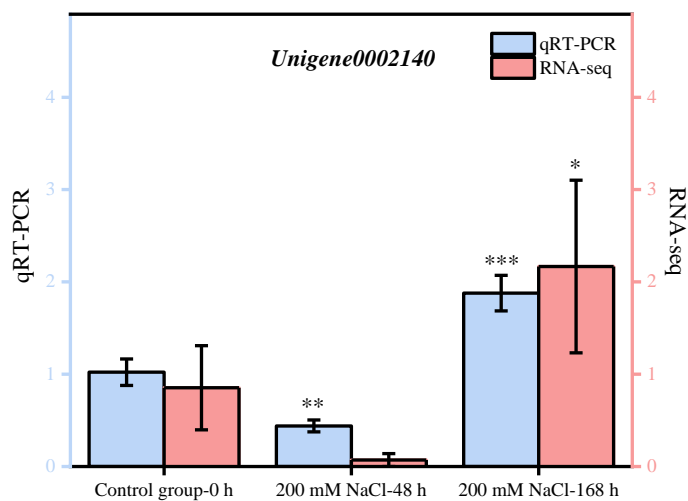


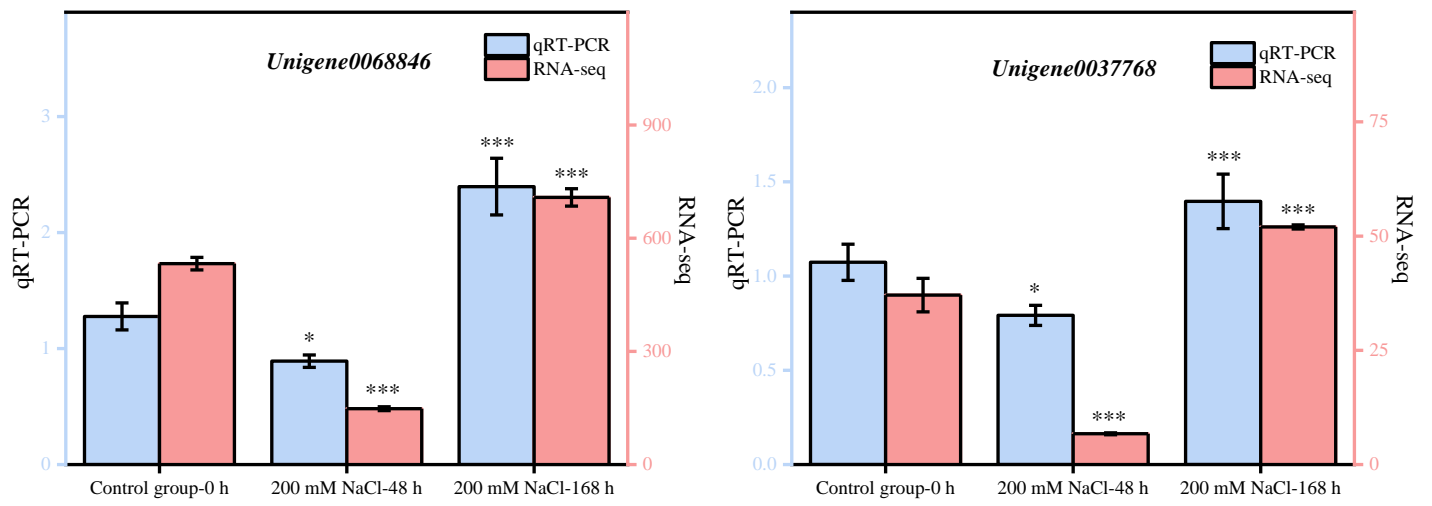
Supplementary Figure S4. Changes in expression levels of DEGs in the inositol phosphate metabolism pathway (Changes in expression levels of 36 DEGs annotated to the inositol phosphate metabolism pathway in the root system of *T. ramosissima* under NaCl stress at 0 h, 48 h, and 168 h. Note:  $p \geq 0.05$  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. Log<sub>2</sub> fold-change of differentially expressed metabolite content in the inositol phosphate metabolism pathway

(The Log<sub>2</sub> fold-change of differentially expressed metabolite content annotated to the inositol phosphate metabolism pathway in the roots of *T. ramosissima* under NaCl stress at 0h, 48 h, and 168 h. 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 S6. Validation of DEGs by qRT-PCR

(Ten DEGs were randomly selected for qRT-PCR validation, and the error bars were obtained from multiple replicates of qRT-PCR. 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).