

Supplementary materials

(a)

<i>SaCLCa2</i>	1	MEASMQSPLSENNSSNAIDESARLNEGANTQNTPEVAANGEPDLESNFLHQPLLKRNRRLSASHLAMVGAKVSHIESLDYEINEN	86
<i>SfCLCa2</i>	1	MEASAESPLSENNSSNAIDESTRFNEGANTQNTMEAAANGEPDLESNFLQPLLKRNRRLSASHLAMVGAKVSHIESLDYEINEN	86
<i>SaCLCa2</i>	87	DLFKQDWRSRSKAQVLQYVFLKWKLAFLVGLLTGLIATAINLAIEIAGYKLLLVSGYVLEKRYIMGLITLTGANFLLTSSLLV	172
<i>SfCLCa2</i>	87	DLFKQDWRSRSKAQVLQYVFLKWKLAFLVGLLTGLIATAINLAIEIAGYKLLLVSGYVLEKRYMMGLITLTGANFLLTSSLLV	172
<i>SaCLCa2</i>	173	VFFAPTAAGPGIPEIKAYLNGIDTPNMYGAPTLLVKIFGSIQAVSAGLDLGEKGPLVHIGACIASLLGGGGTDKHRVKRWRYRIMN	258
<i>SfCLCa2</i>	173	VFFAPTAAGPGIPEIKAYLNGIDTPNMYGASTLLVKIFGSIQAVSAGLDLGEKGPLVHIGACVASLLGGGGTDKHRVRWRWYRIMN	258
<i>SaCLCa2</i>	259	NDRDRRDLITCGSSAGVCAAFRSPVGGVLFALLEEVATWWSALLWRTFFSTAVVVVVLRAFIEYCSSGKCGLFNGGGLIMFDVSNV	344
<i>SfCLCa2</i>	259	NDRDRRDLITCGSSAGVCAAFRSPVGGVLFALLEEVATWWSALLWRTFFSTAVVVVVLRAFIEYCSSGKCGLFNGGGLIMFDVSNV	344
<i>SaCLCa2</i>	345	TVSYRLMDIIPIALIGLIGGVLGSLNYTLHKVLRLYSLINERGLAKVLLSLTVSIFTSVCLYGLPFLVGCTKCDPSLTECSTTG	430
<i>SfCLCa2</i>	345	TVSYRLMDIIPIALIGLIGGALGSLNYTLHKVLRLYSLINERGLAKILLSLTVSVFTSVCLYGLPFLVGCTKCDPSLTECSTTG	430
<i>SaCLCa2</i>	431	RTGNYKRFCNDGYYNDLASLLFSTNDDAVRNIFSTNTPGEFHPLSLVIYFILYCIQLGLFTFGIAVPSGLFLPIILMGSAYGRLLG	516
<i>SfCLCa2</i>	431	RTGNYKRFCNDGYYNDLASLLFSTNDDAVRNIFSTNTPGEFHPLSLVIYFILYCIQLGLFTFGIAVPSGLFLPIILMGSAYGRLLG	516
<i>SaCLCa2</i>	517	IAMGSYTKIDRGLFAVLGAASLMAGSMRMTVSLGVIFLELTNNLLLPVTMLVLLIAKSVGGDFNLSIYEILELKGLPFLDANPE	602
<i>SfCLCa2</i>	517	IAMGSYTKIDRGLFAVLGAASLMAGSMRMTVSLGVIFLELTNNLLLPVTMLVLLIAKSVGGDFNLSIYEILELKGLPFLDANPE	602
<i>SaCLCa2</i>	603	PWMRNITVGLADVKPPVVTLRGIEKVSRIVDILKNTTHNAFPVIDDNVTVPEDGTAKELHGLILRAHLVAVLKRKWFLAGSR	688
<i>SfCLCa2</i>	603	PWMRNITVGLADVKPPVVTLRGIEKVSRIVDILKNTTHNAFPVIDDNVTVPEDGTAKELHGLILRAHLVAVLKRKWFLAGPR	688
<i>SaCLCa2</i>	689	TEEWVREKFTWVELAERDLNFEQVAITKQEMEMYDLHPFTNKPTPTVVEDMSAAKAMVLFQVALRHLLIVPKYQGAGIYPVIG	774
<i>SfCLCa2</i>	689	TEEWVREKFTWVELAERDLNFEQVAITKQEMEMYDLHPFTNKPTPTVVEDMSAAKAMVLFQVALRHLLIVPKYQGAGIYPVIG	774
<i>SaCLCa2</i>	775	VLTRQDLRAHNIQSVFPHVAKSKKQK	800
<i>SfCLCa2</i>	775	VLTRQDLRAHNIQSVFPHVAKSKKQK	800

(b)

<i>SaCLCc2</i>	1	MENELFKEDWRSRTKSEIFQYIFLKWTLSLLIGLFTGVVGFNNLGVENISGFKFLQITDYVRHEKHFKGFTFYAGCNLLLAAGA	86
<i>SfCLCc2</i>	1	MSMVLCLV.....TK...FLYIMLCSLMIGLIEIF.....	26
<i>SaCLCc2</i>	87	ALCAFIAPAAAGSGIPEVKAYLNGVDAHSILAPSTLFVKIIGSILGVAAGFVVGKEGPMVHTGACLASLLGQGGSRKYHLTWKWL	172
<i>SfCLCc2</i>	27D.....IIGSILGVAAGFVVGKEGPMVHTGACLASLLGQGGSRKYHLTWKWL	74
<i>SaCLCc2</i>	173	YFKNDRDRRDLITCGSAAGVAAAFRAPVGGVLFALLEEVASWWSALLWRTFFTTAVVAVVLRSLIGFERHGNCGLFEGGGLIMFDV	258
<i>SfCLCc2</i>	75	YFKNDRDRRDLITCGSAAGVAAAFRAPVGGVLFALLEEVASWWSALLWRTFFTTAVVAVVLRSLIGIERHGNCGLFEGGGLIMFDV	180
<i>SaCLCc2</i>	259	NHATSKWSVPDLILLILGIVGGVLSFYNYLVDKVLRITYSINEGGPVFKVLLVMTISLLTSCGSYGLPWLAPOCTPCPELQDEG	344
<i>SfCLCc2</i>	161	NHATSKWSAPDLMILLILGIVGGVLSFYNYLVDKVLRITYSINEGGPVFKVLLVMTISLLTSCGSYGLPWLAPOCTPCPELQDEG	246
<i>SaCLCc2</i>	345	PSIGRSGNYKNFNCPAGHYNDLASLMFTTNDDAIRNLFNNSVSKDFHVSTLYTYFGAMYCLGIITYGAIAPSGLFIPIVILAGASYG	430
<i>SfCLCc2</i>	247	PSIGRSGNYKNFNCPAGHYNDLASLMFTTNDDAIRNLFNNSVSKDFHVSTLYTYFGATYCLGIITYGAIAPSGLFIPIVILAGASYG	332
<i>SaCLCc2</i>	431	RLVGTIMGPFCSLDPLFAILGAASFLGGTMRMTVSLGVILLELTNDLLMLPLVMLVLLISKSVADNFNKGVDQIVKMKGLPFME	516
<i>SfCLCc2</i>	333	RLVGTIMGPFCSLDPLFAILGAASFLGGTMRMTVSLGVILLELTNDLLMLPLVMLVLLISKSVADNFNKGVDQIVKMKGLPFME	418
<i>SaCLCc2</i>	517	IHAEPYMRHLAASDVITGPLVVFSSVERVGTIMHALRATGHNGFPVIDEPPFTDAPELGGIVLRSHLLVLLKAKFTQHRELMRSN	602
<i>SfCLCc2</i>	419	IHAEPYMRHLAASDVITGPLVAFSSVERVGTIMHALRATGHNGFPVIDEPPFTDAPELGGIVLRSHLLVLLKAKFTQHRELMRSN	504
<i>SaCLCc2</i>	603	IKRSFQAFDFAKPGSGKGPKIDDLVITDEEMDMYVDLHPITNTCPYTVVETMSLAKAAVLFRELGLRHLCVVPKTEKPPIVGILT	688
<i>SfCLCc2</i>	505	IKKSFQAFDFAKPGSGKGPKIDDLVITDEEMDMYVDLHPITNTCPYTVVETMSLAKAAVLFRELGLRHLCVVPKTEKPPIVGILT	590
<i>SaCLCc2</i>	689	RHDFTPHEHILGLYPHLEVHK	708
<i>SfCLCc2</i>	591	RHDFTPHEHILGLYPHLKVHK	610

Figure S1. Alignment of the proteins from *Suaeda altissima*, SaCLCa2 (a) and SaCLCc2 (b), with their homologs from closely related species *Suaeda fruticosa*, SfCLCa2 (a) and SfCLCc2 (b), respectively. SaCLCc2, unlike to SaCLCa2, is shortened from N-terminus.

(a)



(b)

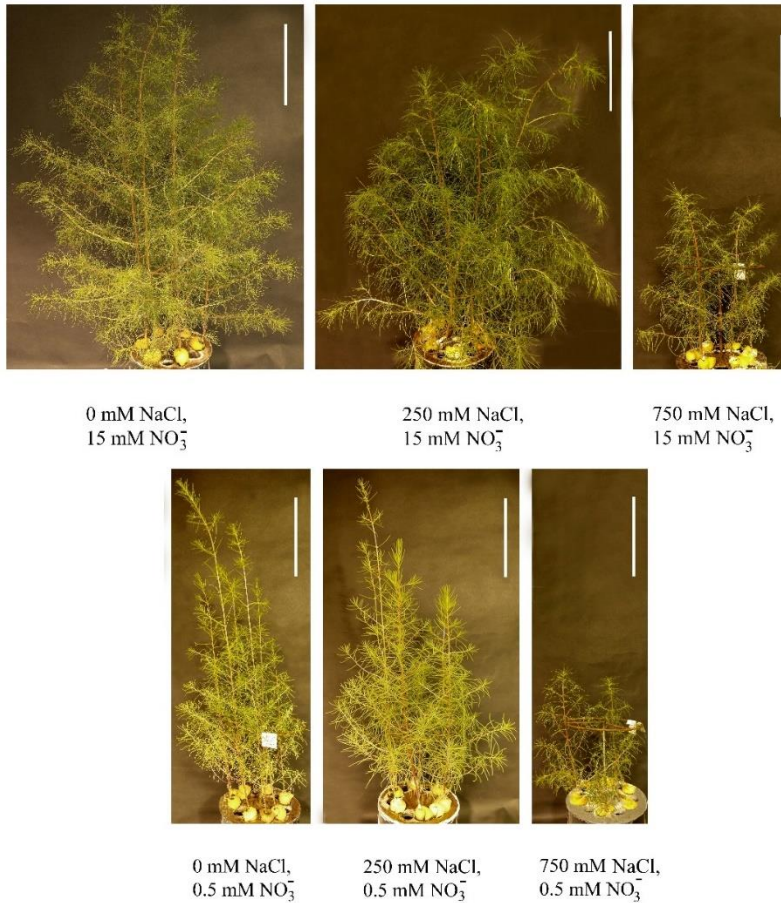


Figure S3. *Suaeda altissima* plants grown under different concentrations of NaCl and nitrate in the aerated nutrient medium. **(a)** General view of the plants in the growth chamber. **(b)** *S. altissima* 45-day-old plants grown under different concentrations of NaCl (0, 250, 750 mM) and nitrate (15 mM or 0.5 mM) in the nutrient medium. Scale bar represents 15 cm.

Table S1. Conserved amino acids motifs and residues and their positions in SaCLCa2 and SaCLCc2 sequences.

Conserved amino acids motifs and residues	SaCLCa2	SaCLCc2
Gating Glu	E 225	E 142
Proton Glu	E 292	E 209
(1) residues in the selectivity filter, a.a.	G PGIPE 181–186	G SGIPE 98–103
(2) GKxGPxxH, a.a.	GKEGPLVH 223–230	GKEGPMVH 140–147
(3) PxxGxLF, a.a.	PVGGVLF 282–288	PVGGVLF 199–205
CBS1, a.a.	619–677	535–587
CBS2, a.a.	733–786	646–697

Table S2. The composition of the nutrient media used in the research.

№	15 mM NO ₃ ⁻		№	0.5 mM NO ₃ ⁻	
1.	0 mM NaCl	4 mM Ca(NO ₃) ₂ 7 mM KNO ₃ 1 mM KH ₂ PO ₄ 2 mM MgSO ₄	4.	0 mM NaCl	4 mM CaCl ₂ 6.5 mM KCl 0.5 mM KNO ₃ 1 mM KH ₂ PO ₄
2.	250 mM NaCl	50 µM FeSO ₄ 50 µM Na ₂ EDTA 50 µM H ₃ BO ₃ 10 µM MnCl ₂	5.	250 mM NaCl	2 mM MgSO ₄ 50 µM FeSO ₄ 50 µM Na ₂ EDTA 50 µM H ₃ BO ₃
3.	750 mM NaCl	1 µM ZnSO ₄ 0.5 µM CuSO ₄ 0.1 µM Na ₂ MoO ₄	6.	750 mM NaCl	10 µM MnCl ₂ 1 µM ZnSO ₄ 0.5 µM CuSO ₄ 0.1 µM Na ₂ MoO ₄

Table S3. List of the primers used in the research.

Primer name	Nucleotide sequences (5'-3')	Primer designation
SaCLCa2R	GCCCTCAAATCTTGCCTT	Amplification of 3'- and 5'-ends <i>SaCLCa2</i> transcript sequences
SaCLCa2_5'RACE_R1	GATCTTAACAAGCAATGTTGGTGCT	
SaCLCa2_5'RACE_R2	GCCCCTGTCAACGTAATCAGC	
SaCLCa2_3'RACE_F1	TCTTTGGGAGCATTGGAGC	
SaCLCa2F	TCCCGGAGAATTTTCATCCAC	
pVR2_SaCLCa2_F	AAGGATCAAAACCATCATATGGAAGCAAGTGCGGAA TCACCA	Cloning of <i>SaCLCa2</i> into pVR2 vector
pVR2_SaCLCa2_R	ACTGACTCGACCCTATCATTCTGCTTTTGGATTTTGCT	
pMB1_SaCLCa2_F	ACACACATAAAACAAACCATGGAAGCAAGTGCGGAATCACCA	Cloning of <i>SaCLCa2</i> into pMB1 vector
pMB1_SaCLCa2_R	ATCGATACCGTCGACCTCGAGTCATTTCTGCTTTTGGATTTTGCTACA	
SaCLCa2_P182S_F	CCTACTGCTGCTGGGTCTGGTATCCCTG	Site-directed mutagenesis of <i>SaCLCa1(C544T)</i>
SaCLCa2_528_R	AGCAAAGAAAACAACCAGCAGCGTAG	
SaCLCc2F	TGTCCTCCTGAACTGCGAGA	Amplification of 3'- and 5'-ends <i>SaCLCc2</i> transcript sequences
SaCLCc2R	GCCTAATTCCCGAAACAACACT	
SaCLCc2_5'RACE_R1	GTTGTAAACATGAGTGAGGCAAGATC	
pVR2_SaCLCc2_F	CGAAGGATCAAAACCATCATAGAGACATTTGAATAGCTGTGAGGTGA	Cloning of <i>SaCLCc2</i> into pVR2 vector
pVR2_SaCLCc2_R	CAGTACTGACTCGACCCTAAAGGGAAACTGCTCCTCAACATTGTA	
pMB1_SaCLCc2_F	ACACACATAAAACAAACCATGGAAAATGAACTTTTAAAGAGGATTGGA	Cloning of <i>SaCLCc2</i> into pMB1 vector
pMB1_SaCLCc2_R	ATCGATACCGTCGACCTCGAGCTACTTGTGGACTTCGAGGTGC	
SaClCa1_F1	GAGACCTTGCTGAAGCCAAGC	RT-qPCR
SaClCa1_R1	TGTCCCTTCACTAGTAAGGATTG	

SaCLCa2_F1	GTCCCAGAAAGACAAGGCACG	
SaClCa2_R1	CCCATGTAAACTTCTCTCGCAC	
SaClCc1_F1	GGCAAAGTATTTCTCTGAGGAG	
SaClCc1_R1	AGATATATCCTCCAATGTGAGCC	
SaClCc2_F1	CGACCAAATTGTTAAGATGAAGG	
SaClCc2_R1	TGATCGTCCCAACTCTTTCAAC	
SaClCd_F1	GGCTTCCTGTGATAGATC	
SaClCd_R1	CACCTCTTGAATCACTAGGC	
SaClCg_F1	GGCTCCATGAGAATGACT	
SaClCg_R1	TGAAACCATCAGCCACG	
SaClCf_F1	GAAATGCTGCTGTTGCC	
SaClCf_R1	CAGAAGCAGAACAGATGTCA	
SaAct7_F1	AGATTCCGTTGCCCAG	
SaAct7_R1	ATTCCTTGCTCATACGGTCA	
SaeEF1alfa_F1	TGAGATGTGTGGCAATCC	
SaeEF1alfa_R1	GTTGCTTCTGACTCCAAGAAT	
pMB1_F	CATGGTTTGTGTTATGTGTGTTTATTC	Amplification of a linear form of pMB1 vector
pMB1_R	CTCGAGGTCGACGGTATCGATAAGC	