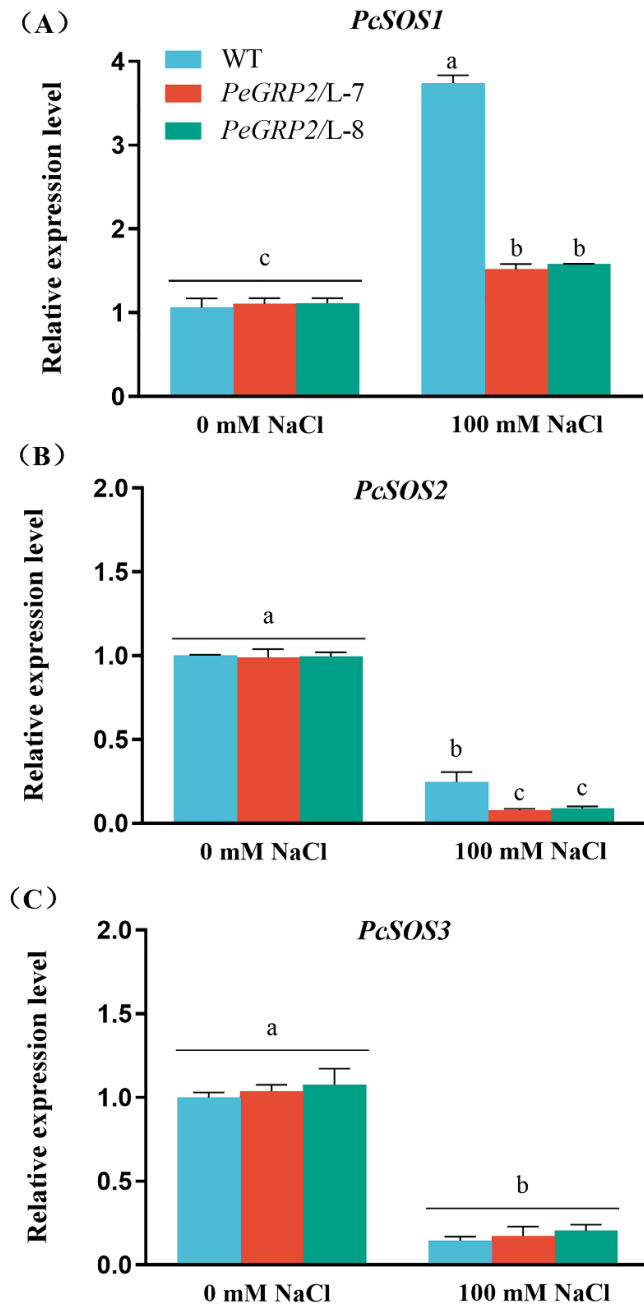


Supplemental Table S1 Accession numbers of GRP orthologs used for multiple sequence alignment and phylogenetic analysis.

GRPs	Accession number
<i>PeGRP2</i>	XP_011046516.1
<i>PtGRP2</i>	XP_024463774.1
<i>GmGRP2</i>	XP_003540832.1
<i>MdGRP2</i>	XP_008338784.2
<i>OsGRP2</i>	XP_015649739.1
<i>ZmGRP2</i>	ACN27139.1
<i>NtGRP2</i>	XP_016516220.1
<i>CsGRP2</i>	XP_010428999.1
<i>AtGRP2</i>	NP_179702.1
<i>SbGR-RNP</i>	AAG23220.1
<i>OsGRP3</i>	BAS81800.1
<i>AtGRP7</i>	NP_179760.1
<i>MhGR-RBP1</i>	HM042682.1
<i>ZjGRP</i>	AIN39847.1
<i>AtGR-RBP4</i>	NP_189025.1
<i>LbGRP1</i>	ACV33079.1

Supplemental Table S2 Primers used for qRT-PCR.

<i>Gene name</i>	<i>Primer sequences (5'-3')</i>	
<i>PcGRP2</i>	F: ATTACAGTGACGAGGACCACC	R: GGAAGGGACAAACGGAGACT
<i>PcActin7</i>	F: ATTGGCCTTGGGGTTAAGAG	R: CACACTGGAGTGATGGTTGG
<i>PcUBQ</i>	F: AGACCTACACCAAGCCCAAGAAGAT	R: CCAGCACCCGACTCAGCATTAG
<i>PcPETC</i>	F: ATTTCTTTGTCCCTTCTGGAC	R: GTTCCATGGCACAACACAC
<i>PcPSBR</i>	F: AACCTGAGGAACGGGTTA	R: AAGGATTCCAGCTAGGGTAA
<i>PcPSBY</i>	F: TACCACTCATAACCAGCCATA	R: ATAGAATAGCAGGAGCAACG
<i>PcPSB28</i>	F: CCTACTCCCTATTCAATGGC	R: AAGGTGAATATCGCCATAACC
<i>PcCAB5</i>	F: CACTTGGATGTGTCTTTCT	R: CTGTACCCTTCAACGAATCC
<i>PcCAB6</i>	F: CCATTGAATTCGTTGCCATT	R: ACCAGGATAAGCTGTTTGT
<i>PcRBCMT</i>	F: CTCTTTTGTACTGGACACGA	R: GACCACTTGAAAGTCTCCAT
<i>PcLIL3-1</i>	F: CTGCAATGATTGGGTTCTTC	R: TAGGGATGGAAGATGTCTCA
<i>PcPSBO1</i>	F: TCACCATTAAACAGTTGGTTG	R: AGGGTGATTTTACCTGTTGA
<i>PcPSBO2</i>	F: AACCTTTCTGTCATGGTCAC	R: TATTGTTTCCCATCGATCAC
<i>PcLFNR</i>	F: CTTGGAAGTGGAACTGGTAT	R: TTTGTTTGTCTCTACTGACT
<i>PcPOD42</i>	F: CTATCTCCCAGACCACAATG	R: CCTCACATATTGGACAGCTT
<i>PcPOD47</i>	F: CAAAAATAGGTTGAGTGACCC	R: GTTCATAGCGTAGCCCTT
<i>PcSOD[Cu-Zn]2</i>	F: TCATCACCCGAGACTCTAAT	R: CGTTCATTATCACATGGAGC
<i>PcSOD[Mn]</i>	F: AATCTCACTCCTGTCCAAGAA	R: TGGTCTCAACCACAAGTTTC
<i>PcCYB1-2</i>	F: GGAGGTGAAGCCATTATGAG	R: CCAGGGTAGAAGAACACAAT
<i>PcTRX</i>	F: TATGGGGATAGATTGACGGT	R: CTCCAAGAGAGCATCAACAT
<i>PcCDSP32</i>	F: AAGCTGATGGGAGATGTTTT	R: CTATCATTCTCGTCACCGTT
<i>PcTRXM</i>	F: AGTGAGTACTACCACCAGAG	R: ATCTGTGCTACTTGAACGTG
<i>PcPRXQ</i>	F: CTTTGCTTCCCACTCTTAAA	R: ACAAAGTCTTTCCATCTGA
<i>PcNHA1</i>	F: GCTATACACACTTCAGGGAG	R: AAGCAGATAAGCACCAAGAA
<i>PcNHE2-1</i>	F: GAGATTGCAAATGTTGACCA	R: AGATAACAACCCCAAGTACAC
<i>PcCAX3</i>	F: GTTTGTGGTTCCACTTTGTG	R: GTTTAAGAAAAAGCACGCCC
<i>PcAVP1</i>	F: GGATCAATACTGTCGATGTCT	R: TGGCTCTACCTTCCATAAGT
<i>PcAHA11</i>	F: TATTTGGAGTGTC AACCTG	R: GAGCAATGATAAAAAGCCACC
<i>PcACA8</i>	F: TGAGTTTGTGGGAAGTTCA	R: CGATCACTTGGAGAGTTACC
<i>PcACA9</i>	F: ATGAGTAGCAGTTGTTGCTC	R: CGAAGAATCTCGATAGGAGC
<i>PcAATP</i>	F: TGTCCTTTTCAAATGCGTTG	R: TGGATTGTTTACATCCTGT
<i>PcASD</i>	F: ATAAAGGACAACAGCGAGTT	R: CTTTCTTCTTCTGCCTCCTT
<i>PcSOS1</i>	F: GGTGGTCTTATGAGTTGGCCTGAA	R: GCAGTTGGGGAGCAGGAGTTTTTC
<i>PcSOS2</i>	F: ACGACATGTGGAACCCCGAATT	R: ACGAGTTTTAGGATTGGGATTGAGT
<i>PcSOS3</i>	F: GTTCGATCTTTGGGTGTCCTTCAT	R: GGGTCTTCGACACAAAATTCCT



Supplemental Figure S1. Transcript of *PcSOS1*, *PcSOS2* and *PcSOS3* in wildtype *P. × canescens* and *PeGRP2*-overexpressed lines under long-term salt stress. The *PeGRP2*-overexpressed lines (L-7 and L-8) wildtype (WT) and *P. × canescens* were treated with NaCl saline (0 or 100 mM) for 15 days. Leaves were collected from no-salt control and salinized plants for RT-qPCR analysis. Transcripts of salt-overly-sensitive (SOS) pathway genes *PcSOS1*, *PcSOS2* and *PcSOS3*, were examined in WT and *PeGRP2*-overexpressed poplars. The primer sequences for SOS and reference genes, *PcUBQ*, are shown in

Supplementary Table S2. Data are mean \pm SE (n = 3), and different letters indicate significant difference ($P < 0.05$).