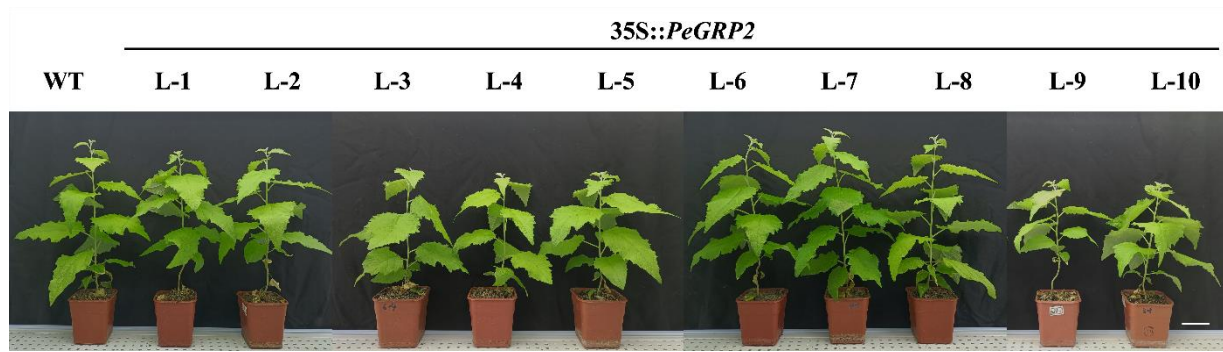


Supplementary Table S1. Primers used for qRT-PCR.

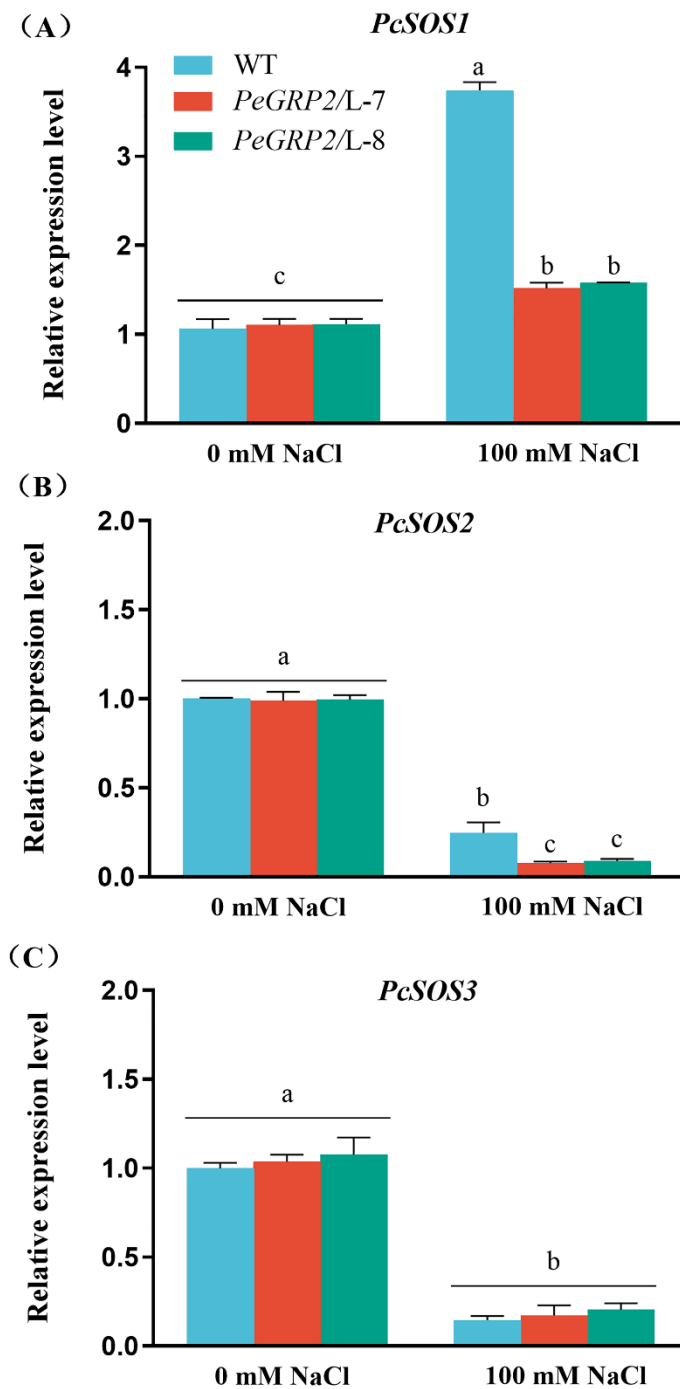
<i>Gene name</i>	<i>Primer sequences (5'-3')</i>	
<i>PeGRP2</i>	<i>F: ATTACAGTGACGAGGACCACC</i>	<i>R: GGAAGGGACAAACGGAGACT</i>
<i>PeActin7</i>	<i>F: ATTGGCCTTGGGGTTAAGAG</i>	<i>R: CACACTGGAGTGATGGTTGG</i>
<i>PcUBQ</i>	<i>F: AGACCTACACCAAGCCCAAGAAGAT</i>	<i>R: CCAGCACCGCACTCAGCATTAG</i>
<i>PcPETC</i>	<i>F: ATTTCTTTGTCCCTTCTGGAC</i>	<i>R: GTTCCATGGCACAACACAC</i>
<i>PcPSBR</i>	<i>F: AACCTGAGGAACGGGTTA</i>	<i>R: AAGGATTCCAGCTAGGGTAA</i>
<i>PcPSBY</i>	<i>F: TACCACTCATACCAGCCATA</i>	<i>R: ATAGAATAGCAGGAGCAACG</i>
<i>PcPSB28</i>	<i>F: CCTACTCCCTATTCAATGGC</i>	<i>R: AAGGTGAATATCGCCATACC</i>
<i>PcCAB5</i>	<i>F: CACTTGGATGTGTCTTTCT</i>	<i>R: CTGTACCCTTCAACGAATCC</i>
<i>PcCAB6</i>	<i>F: CCATTGAATTCGTTGCCATT</i>	<i>R: ACCAGGATAAGCTGTTTGT</i>
<i>PcRBCMT</i>	<i>F: CTCTTTTGTACTGGACACGA</i>	<i>R: GACCACTTGAAAGTCTCCAT</i>
<i>PcLIL3-1</i>	<i>F: CTGCAATGATTGGGTCTTC</i>	<i>R: TAGGGATGGAAGATGTCTCA</i>
<i>PcPSB01</i>	<i>F: TCACCATTAAACAGTTGGTTG</i>	<i>R: AGGGTGATTTTACCTGTTGA</i>
<i>PcPSB02</i>	<i>F: AACCTTTCTGTCATGGTCAC</i>	<i>R: TATTGTTTCCCATCGATCAC</i>
<i>PcLFNR</i>	<i>F: CTTGGAAGTGGAACTGGTAT</i>	<i>R: TTTGTTTGCTCTCTACTGACT</i>
<i>PcPOD42</i>	<i>F: CTATCTCCCAGACCACAATG</i>	<i>R: CCTCACATATTGGACAGCTT</i>
<i>PcPOD47</i>	<i>F: CAAAAATAGGTTGAGTGACCC</i>	<i>R: GTTCATAGCGTAGCCCTT</i>
<i>PcSOD[Cu-Zn]2</i>	<i>F: TCATCACCGGAGACTCTAAT</i>	<i>R: CGTTCATTATCACATGGAGC</i>
<i>PcSOD[Mn]</i>	<i>F: AATCTCACTCCTGTCCAAGAA</i>	<i>R: TGGTCTCAACCACAAGTTTC</i>
<i>PcCYB1-2</i>	<i>F: GGAGGTGAAGCCATTATGAG</i>	<i>R: CCAGGGTAGAAGAACAACAT</i>
<i>PcTRX</i>	<i>F: TATGGGGATAGATTGACGGT</i>	<i>R: CTCCAAGAGAGCATCAACAT</i>
<i>PcCDSP32</i>	<i>F: AAGCTGATGGGAGATGTTTT</i>	<i>R: CTATCATTCTCGTCACCGTT</i>
<i>PcTRXM</i>	<i>F: AGTGAGTACTACCACCAGAG</i>	<i>R: ATCTGTGCTACTTGAAGTG</i>
<i>PcPRXQ</i>	<i>F: CTTTGCTTCCCACTCTTAAA</i>	<i>R: ACAAAGTCTTTCCATCCTGA</i>
<i>PcNHA1</i>	<i>F: GCTATACACACTTCAGGGAG</i>	<i>R: AAGCAGATAAGCACCAAGAA</i>
<i>PcNHE2-1</i>	<i>F: GAGATTGCAAATGTTGACCA</i>	<i>R: AGATAACAACCCCAAGTACAC</i>
<i>PcCAX3</i>	<i>F: GTTTGTGGTTCCACTTTGTG</i>	<i>R: GTTTAAGAAAAAGCACGCCC</i>
<i>PcAVP1</i>	<i>F: GGATCAATACTGTGCGATGTCT</i>	<i>R: TGGCTCTACCTTCATAAGT</i>
<i>PcAHA11</i>	<i>F: TATTTGGAGTGTAACCCCTG</i>	<i>R: GAGCAATGATAAAAGCCACC</i>
<i>PcACA8</i>	<i>F: TGAGTTTGTGGGAAGTTCA</i>	<i>R: CGATCACTTGGAGAGTTACC</i>
<i>PcACA9</i>	<i>F: ATGAGTAGCAGTTGTTTCGTC</i>	<i>R: CGAAGAATCTCGATAGGAGC</i>
<i>PcAATP</i>	<i>F: TGTCTTTTCAAATGCGTTG</i>	<i>R: TGGATTGTTTCACATCCTGT</i>
<i>PcASD</i>	<i>F: ATAAAGGACAACAGCGAGTT</i>	<i>R: CTTTCTTCTTCTGCCTCCTT</i>

Supplementary Table S2. Accession numbers of GRP orthologs used in multiple sequence alignment and phylogenetic analysis.

Sequence name	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



Supplementary Figure S1. Plant growth of wild-type *P. × canescens* and *PeGRP2*-overexpressing lines (L-1, L-2, L-3, L-4, L-5, L-6, L-7, L-8, L-9, and L-10). Tissue cultures of stem segments in MS solid medium were used to propagate the plantlets. *P. × canescens* plantlets grown in tissue culture flasks for 3-4 weeks were acclimated in hydroponics for 3 weeks before planting in individual pots for soil culture. The nursery soil contained peat, silica sand, and potting soil in a ratio of 1:1:1. Then the plantlets were transferred to a climate-controlled room for 4 weeks culture. The light intensity (photosynthetically active radiation, PAR) was 200-300 $\mu\text{mol m}^{-2} \text{s}^{-1}$ with a 16-h photoperiod (7:00 AM–11:00 PM). The room temperature was maintained at 20-25 °C. The plants were watered twice a week and representative images are shown. Scale bars = 5 cm.



Supplementary Figure Figure S2. Transcript of *PcSOS1*, *PcSOS2* and *PcSOS3* in *PeGRP2*-overexpressing *P. × canescens* under long-term salt exposure. The wild-type (WT) *P. × canescens* and *PeGRP2*-overexpressing lines (L-7 and L-8) 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 S1. Data are mean \pm SE (n = 3), and different letters indicate significant difference ($P < 0.05$).