Table S1. Primers used in this study.

Primer name	Forward primer (5’ to 3’)	Reverse primer (5’ to 3’)
AtActin	GGTAACATTGTGCTCAGTGGTGG	AACGACCTTAATCTTCATGCTGC
GFP	CATCTTCTTCAAGGACGA	GTGGCTGTTGTAGTTGTA
pAC402-PSA3	tacaaatctatctctctcgagATGTCCGTG ACCTCAACTAGCAC	GgatccccgggtaccgagctcAGTTTCATT ATTCTCTTGGAGAAATTGG
pAC013-PAO2	ggactctagaggatccccgggATGGAATCC GGAGCCAAGAGTAATTCCGA	gcccttgctcaccatggtacc CATTCGAGA AATTAACAAAGGTGCCGATA
BD-PAO2	atggccatggaggccgaattcATGGAATCC GGAGCCAAGA	GcaggtcgacggatccccgggCATTCGAGA AATTAACAAAGGTGC
AD-PSA3	gccatggaggccagtgaattcATGTCCGTG ACCTCAACTAGCAC	cagctcgagctcgatggatccTTAAGTTTC ATTATTCTCTTGGAGAAATT
ZYN-PAO2	atttacgaacgatagttaattaaATGGAATCC GGAGCCAAGA	actgccacctcctccactagtCATTCGAGA AATTAACAAAGGTGC
ZYC-PSA3	atttacgaacgatagttaattaaATGTCCGTG ACCTCAACTAGCAC	actgccacctcctccactagtAGTTTCATT ATTCTCTTGGAGAAATTGG
nLUC-PAO2	acgggggacgagctcggtaccATGGAATCC GGAGCCAAGA	cagtcgacgcgttgtggatccCATTCGAGA AATTAACAAAGGTGC
cLUC-PSA3	tacgcgtcccggggcggtaccATGTCCGTG ACCTCAACTAGCAC	cagtcgacgcgttgtggatccTTAAGTTTC ATTATTCTCTTGGAGAAATT
pET32a-PAO2	catggctgatatcggatccgaattcATGGAATCC GGAGCCAAGAGTAATTCCGA	agtgcggccgcaagctttgtcgacTTACATTCG AGAAATTAACAAAGGTGCCG
pGEX4T1-PSA3	aatctggttccgcgtggatccATGTCCGTG ACCTCAACTAGCAC	CtcgagtcgacccgggaattcTTAAGTTTC ATTATTCTCTTGGAGAAATT
pAC330-PSA3	catatggggctgcaggaattcATGTCCGTG ACCTCAACTAGCAC	gggactagaactagtggatccTTAAGTTTC ATTATTCTCTTGGAGAAATT
pV190-PAO2	aggactttacttaatggatccTATCGTTCG TGGTGGGGTGT	cctagacctataactggatccCAAACTTAG GTAATAGTTTTAGATCCATAAAA
pV190-PSA3	aggactttacttaatggatccGAGTCTAAA GCTTTCTATGAATTTCAAGA	cctagacctataactggatccAGCCTCATT CATCATAGCAAGGA

Figure S1. White streaks characteristic of silencing PDS in cucumber.

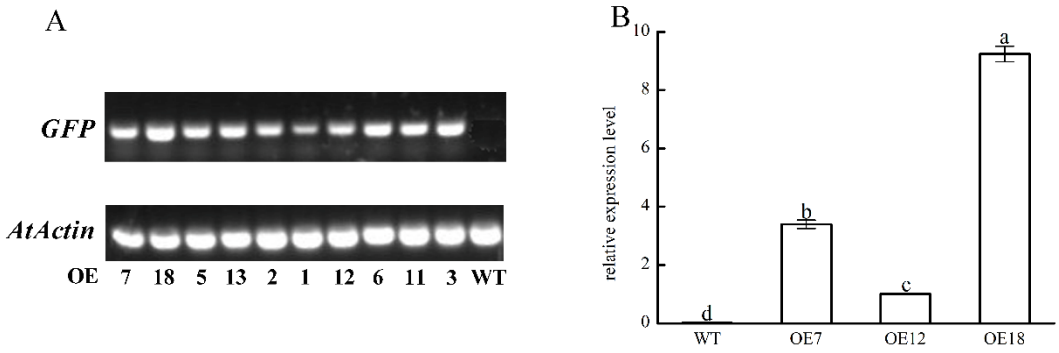

Figure S2. Semi-quantitative PCR analysis of *CsPAO2* expression and relative expression level of *CsPAO2* in OE7, OE12 and OE18. A, semi-quantitative PCR analysis; B, relative expression level of *CsPAO2* in OE7, OE12 and OE18. Relative expression level of *CsPAO2* in OE12 was taken as 1.

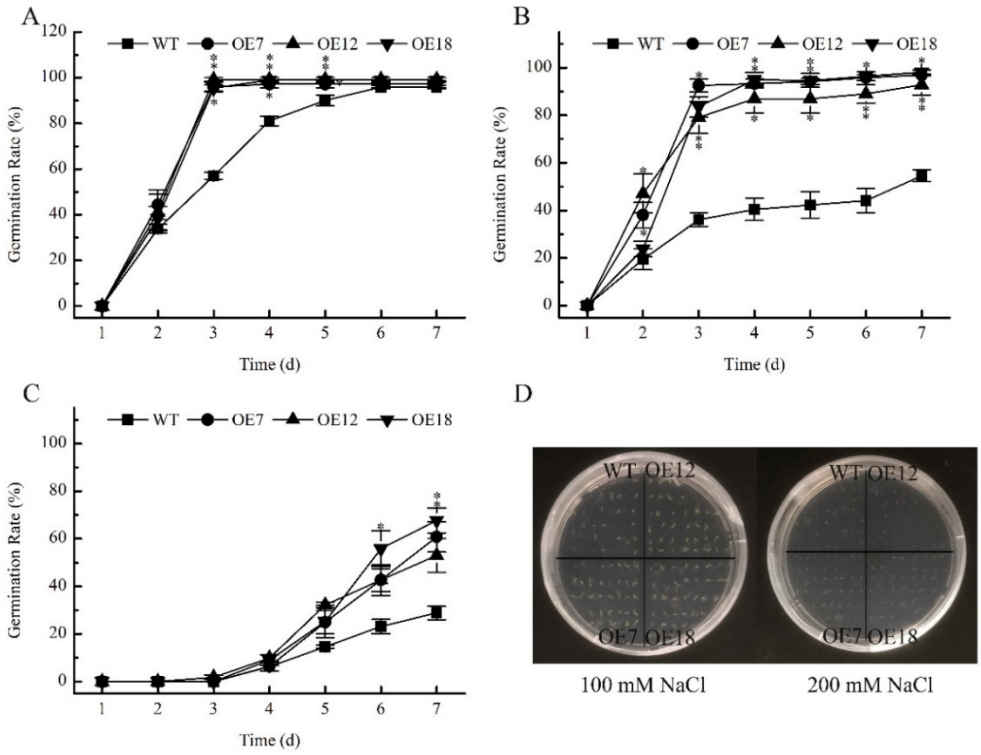

Figure S3. Seed germination rate of wild type (WT) and transgenic Arabidopsis lines (OE7, OE12 and OE18). A-C, time-course change of germination rate under 0 (A), 100 (B) and 200 (C) mM NaCl treatment. D, pictures of seeds grown on plates containing 100 and 200 mM NaCl for 7 days. Error bars represent standard error of three plates. Asterisks above lines indicate significant differences between WT and transgenic lines on the same day at $P < 0.05$ (*) according to Tukey test.

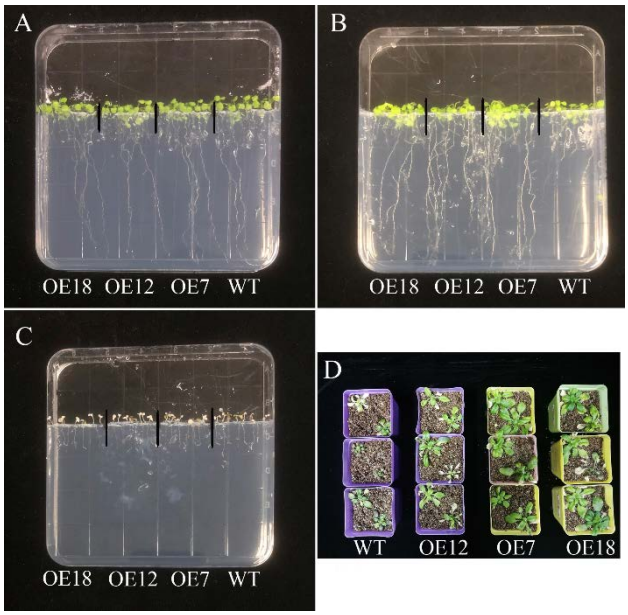

Figure S4. Root growth of wild type (WT) and transgenic plants (OE7, OE12 and OE18) under salt

stress. A-C, after 7 days of sowing on 1/2 MS medium without NaCl , seedlings were transferred onto 1/2 MS medium containing 0 (A), 100 (B) and 200 (C) mM NaCl, respectively, and pictures were taken on the seventh day. D, phenotype of Arabidopsis seedlings treated with 300 mM NaCl.

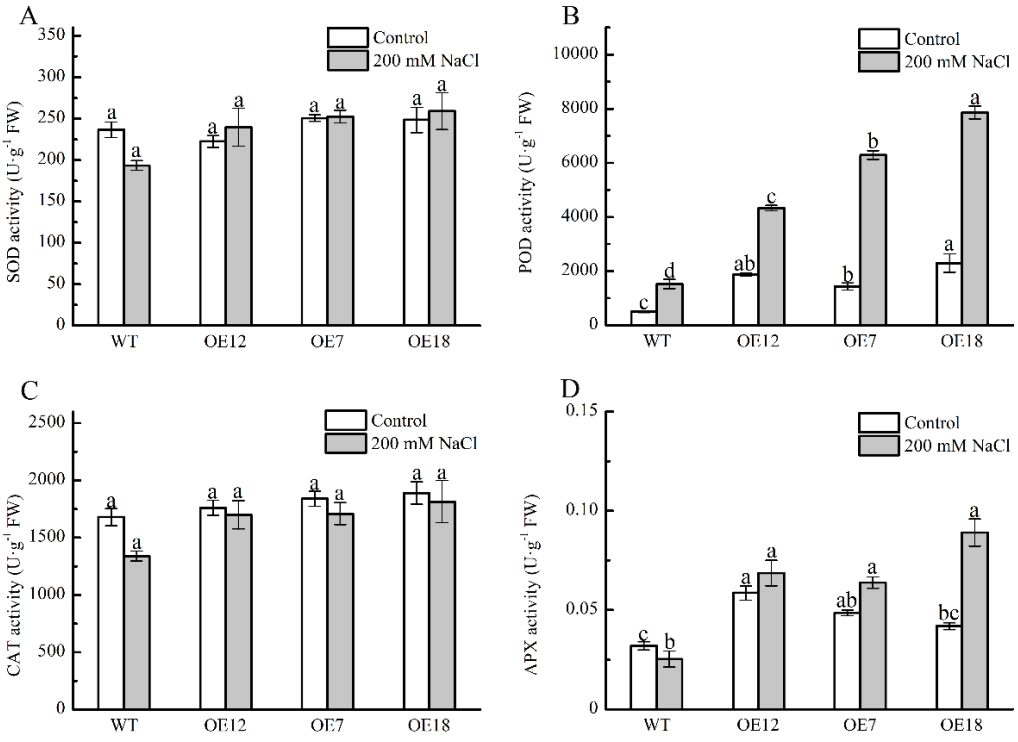

Figure S5. Antioxidant enzyme activities of wild type (WT) and transgenic Arabidopsis lines (OE12, OE7 and OE18). A, SOD; B, POD; C, CAT; D, APX. Arabidopsis seedlings cultivated in vermiculite were irrigated with 200 mM NaCl solution or water for 14 days. Error bars represent standard error of three replicates. The different letters indicate significant differences at $P < 0.05$ between different genotypes under the same treatment according to Tukey test.