Salinity Stress-Mediated Suppression of Expression of Salt Overly Sensitive Signaling Pathway Genes Suggests Negative Regulation by AtbZIP62 Transcription Factor in Arabidopsis thaliana

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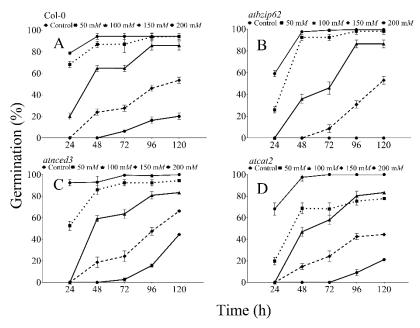


Figure S1 Arabidopsis genotypes evaluated for their germination ability on NaCl modified media **A** Germination of Col-0 wild type on different salt concentration overtime. **B** *atbzip62*, **C** *atnced3*, and **D** *atcat2* under the same conditions. Data are mean values of triplicate recorded on daily basis from 24h to 120 h after sowing.

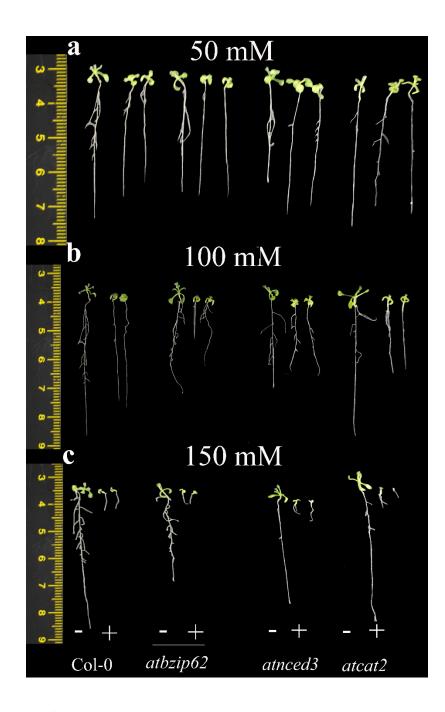


Figure S2 Phenotype of Arabidopsis Col-0 and knockout lines on gradient NaCl concentrations on MS media

The above Figure S2 shows the phenotype of Col-0 wild type, *atbzip62*, *atnced3*, and *atcat2* loss of function mutants in response to salt stress induced by gradient concentrations. **a** 50 mM, **b** 100 mM, and **c** 150 mM. Pictures were taken 10 days after sowing on MS media. Minus (-) sign represents control, and positive (+) sign indicates salt treatment.

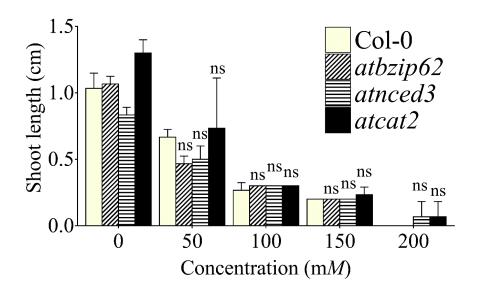


Figure S3 Salt concentration-dependent inhibition of Arabidopsis shoot growth Figure S3 shows the assessment shoot growth of *Arabidopsis* genotypes (Col-0: wild type, *atbzip62*, *atnced3* and *atcat2*) toward salinity stress on half-strength MS medium gradients concentrations (50, 100, 150 and 200 mM NaCl). Data points are the mean of triplicate while error bars indicate ±SD recorded two weeks after sowing. Data are compared with Col-0 wild type. Asterisks on top of bars are statistical significance level with 95% confidence level. *P<0.05, **P<0.01, ***P<0.001, and *ns* non-significant. Error bars are means ± SD.

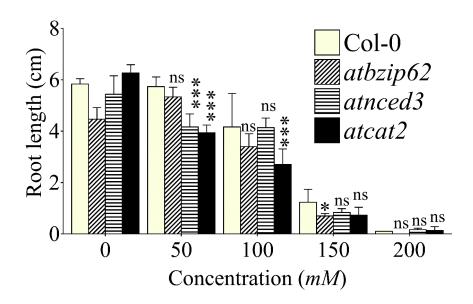


Figure S4 Inhibition of root growth by increasing NaCl-induced salt stress
Figure S4 shows the assessment root growth of *Arabidopsis* genotypes (Col-0: wild type, *atbzip62*, *atnced3* and *atcat2*) toward salinity stress on MS medium gradients concentrations (50, 100, 150 and 200 mM NaCl).
The data points are the mean values of triplicate while error bars indicate ±SD recorded two weeks after sowing. Data are compared with Col-0 wild type. Asterisks on top of bars are statistical significance level with 95% confidence level. *P<0.05, **P<0.01, ***P<0.001, and ns non-significant. Error bars are means ± SD.

Table S1 Genes for qPCR used in the study

ive genes in A	1:1 :		
Drought responsive genes in Arabidopsis			
AT1G19490	CATCGAGTTGTTGCTCGTCG	AAATCCGCCAATGCTTCTGC	Basic-leucine zipper transcription factor 62
AT2G40620	GACCTCGACACAGGCATAGC	AGCTCAGCGAGCTTATCAGG	Basic-leucine zipper transcription factor 18
AT1G06070	GCCATCAGAACCGACTTGGA	CGATTGGCTGTTGTTGGTGTC	Basic-leucine zipper transcription factor 69
AT3G17810	AGTGAGGATCGCTCGCTTTC	TCATCACACCGGTGCATACC	PYRIMIDINE 1
Salt Overly Sensitive pathway genes			
AT2G01980	TTACCAGCCCCCAAGAAACG	TCAACTGTAGGCCAGTCAGC	Arabidopsis Salt Overly Sensitive pathway gene 1
AT5G35410	TTCAAGACAAGGCTCGAGGG	CCATGAAAAGCGATGGTGCC	Arabidopsis Salt Overly Sensitive pathway gene 2
AT1G19490	GCAATGGTGTTCCTTTCGGG	GGCGGCATCAGTGTAACTCC	Arabidopsis Salt Overly Sensitive pathway gene 3
AT5G04140	CTTCTGCATGGGCGACGATA	CCTAAGGGGGTCAATGGCAG	Arabidopsis Glutamate Synthase 1
AT2G41220	GCAGCATTTAGCCAACCGTC	AGGCTCAACCTTCCCAACAG	Arabidopsis Glutamate Synthase 2
AT3G18780	AGGTTCTGTTCCAGCCATC	TTAGAAGCATTTCCTGTGAAC	Arabidopsis Actin coding gene 2
1	T2G40620 T1G06070 T3G17810 tive pathway T2G01980 T5G35410 T1G19490 T5G04140 T2G41220	T2G40620 GACCTCGACACAGGCATAGC T1G06070 GCCATCAGAACCGACTTGGA T3G17810 AGTGAGGATCGCTCGCTTTC tive pathway genes T2G01980 TTACCAGCCCCCAAGAAACG T5G35410 TTCAAGACAAGGCTCGAGGG T1G19490 GCAATGGTGTTCCTTTCGGG T5G04140 CTTCTGCATGGGCGACGATA T2G41220 GCAGCATTTAGCCAACCGTC	T2G40620 GACCTCGACACAGGCATAGC AGCTCAGCGAGCTTATCAGG T1G06070 GCCATCAGAACCGACTTGGA CGATTGGCTGTTGGTGTC T3G17810 AGTGAGGATCGCTCGCTTTC TCATCACACCGGTGCATACC tive pathway genes T2G01980 TTACCAGCCCCCAAGAAACG TCAACTGTAGGCCAGTCAGC T5G35410 TTCAAGACAAGGCTCGAGGG CCATGAAAAGCGATGGTGCC T1G19490 GCAATGGTGTTCCTTTCGGG GGCGGCATCAGTGTAACTCC T5G04140 CTTCTGCATGGGCGACGATA CCTAAGGGGGTCAATGGCAG T2G41220 GCAGCATTTAGCCAACCGTC AGGCTCAACCTTCCCAACAG