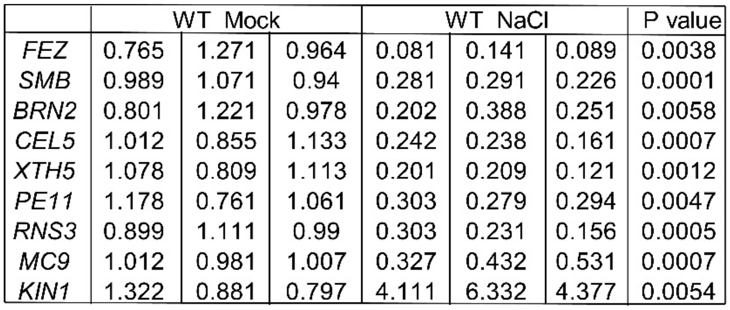

	WT Mock			WT NaCl			P value
FEZ	0.765	1.271	0.964	0.081	0.141	0.089	0.0038
SMB	0.989	1.071	0.94	0.281	0.291	0.226	0.0001
BRN2	0.801	1.221	0.978	0.202	0.388	0.251	0.0058
CEL5	1.012	0.855	1.133	0.242	0.238	0.161	0.0007
XTH5	1.078	0.809	1.113	0.201	0.209	0.121	0.0012
PE11	1.178	0.761	1.061	0.303	0.279	0.294	0.0047
RNS3	0.899	1.111	0.99	0.303	0.231	0.156	0.0005
MC9	1.012	0.981	1.007	0.327	0.432	0.531	0.0007
KIN1	1.322	0.881	0.797	4.111	6.332	4.377	0.0054

Extended Data Fig. 8 | RT-qPCR analysis of the root cap cycle genes in response to salt. The analysis was conducted on 5-day-old wild-type root tips in response to NaCl treatment (200 mM, 2 h). The gene expression levels were normalized to the expression of *UBQ10* in each sample. The gene expression level without salt treatment was valued as 1 in WT. The ratio of each marker gene expression after salt treatment was determined. The triplate sample data are presentated. The average gene expression ratio from triplicate samples was calculated and is presented in Fig. 6d. The statistical P-value was analyzed by comparing the results between Mock and salt treatment.