a		WT Mock			WT ABA			P value	pyrpyl112458 Mock			pyrpyl	112458	ABA	P value
	FEZ	1.086	0.861	1.053	0.253	0.304	0.333	0.0007	0.736	1.174	1.089	1.020	0.601	1.007	0.5548
	SMB	0.844	1.022	1.134	0.345	0.506	0.399	0.0038	0.844	1.059	1.097	0.861	1.186	0.910	0.9164
	BRN2	1.157	1.141	0.702	0.315	0.431	0.554	0.0261	1.303	0.784	0.913	0.945	0.729	1.235	0.8942
	CEL5	0.952	0.961	1.087	0.349	0.400	0.201	0.0008	1.204	0.805	0.991	0.995	1.204	1.095	0.4932
	XTH5	0.944	0.931	1.125	0.324	0.344	0.220	0.0007	1.109	0.873	1.019	0.857	1.052	0.773	0.3786
	PE11	1.213	0.965	0.822	0.464	0.365	0.418	0.0077	1.133	0.816	1.052	0.973	0.896	1.076	0.8717
	RNS3	1.114	1.009	0.877	0.344	0.414	0.574	0.0045	0.955	1.183	0.862	0.910	1.063	0.727	0.5033
	MC9	1.104	0.849	1.047	0.741	0.581	0.714	0.0248	1.057	0.868	1.075	0.754	0.954	1.034	0.4642
	KIN1	0.872	1.299	0.829	49.112	54.965	62.523	0.0001	1.054	1.103	0.843	1.647	1.098	1.056	0.2655

b		WT(+3MBiP) Mock			WT(+3MBiP) ABA			P value	icpk(+3MBiP) Mo		Mock	icpk (-	+3MBiP)	ABA	P value
	FEZ	1.199	0.869	0.932	0.296	0.381	0.288	0.0030	0.998	1.141	0.861	0.376	0.350	0.320	0.0014
	SMB	0.878	0.891	1.231	0.317	0.298	0.385	0.0049	1.122	0.887	0.991	0.970	0.728	0.696	0.1402
	BRN2	1.249	0.901	0.850	0.429	0.438	0.565	0.0170	0.761	0.993	1.246	0.418	0.478	0.801	0.0773
	CEL5	0.865	1.094	1.041	0.305	0.192	0.203	0.0006	1.180	0.946	0.874	0.336	0.252	0.311	0.0019
	XTH5	0.905	0.792	1.303	0.198	0.243	0.209	0.0073	0.801	1.026	1.172	0.234	0.248	0.175	0.0021
	PE11	0.810	0.801	1.389	0.416	0.325	0.266	0.0290	0.774	1.048	1.178	0.828	0.728	1.198	0.6822
	RNS3	1.101	0.792	1.107	0.554	0.611	0.405	0.0169	1.010	0.862	1.128	0.666	0.933	0.789	0.1345
	MC9	0.857	1.203	0.940	0.403	0.699	0.601	0.0335	0.862	1.038	1.100	0.879	1.457	1.094	0.4775
	KIN1	0.802	0.953	1.245	50.402	40.961	51.637	0.0002	0.944	0.927	1.130	27.549	33.591	34.629	0.0002

Extended Data Fig. 7 | RT-qPCR analysis of the root cap cycle genes in response to ABA.

The analysis was conducted with 5-day-old WT and *pyrpyl112458* (a) or *icpk* (b) root tips in response to ABA (10 µM, 4 h). The gene expression levels were normalized to the expression of *UBQ10* in each sample. The gene expression level without ABA treatment was valued as 1 in WT or the mutant. The ratio of each marker gene expression was determined. The triplate sample data are presented. The average gene expression from triplicate samples was calculated and is presented in Fig. 5d and Fig. 5e. The statistical P-value was analyzed by comparing the results between Mock and ABA treatment.