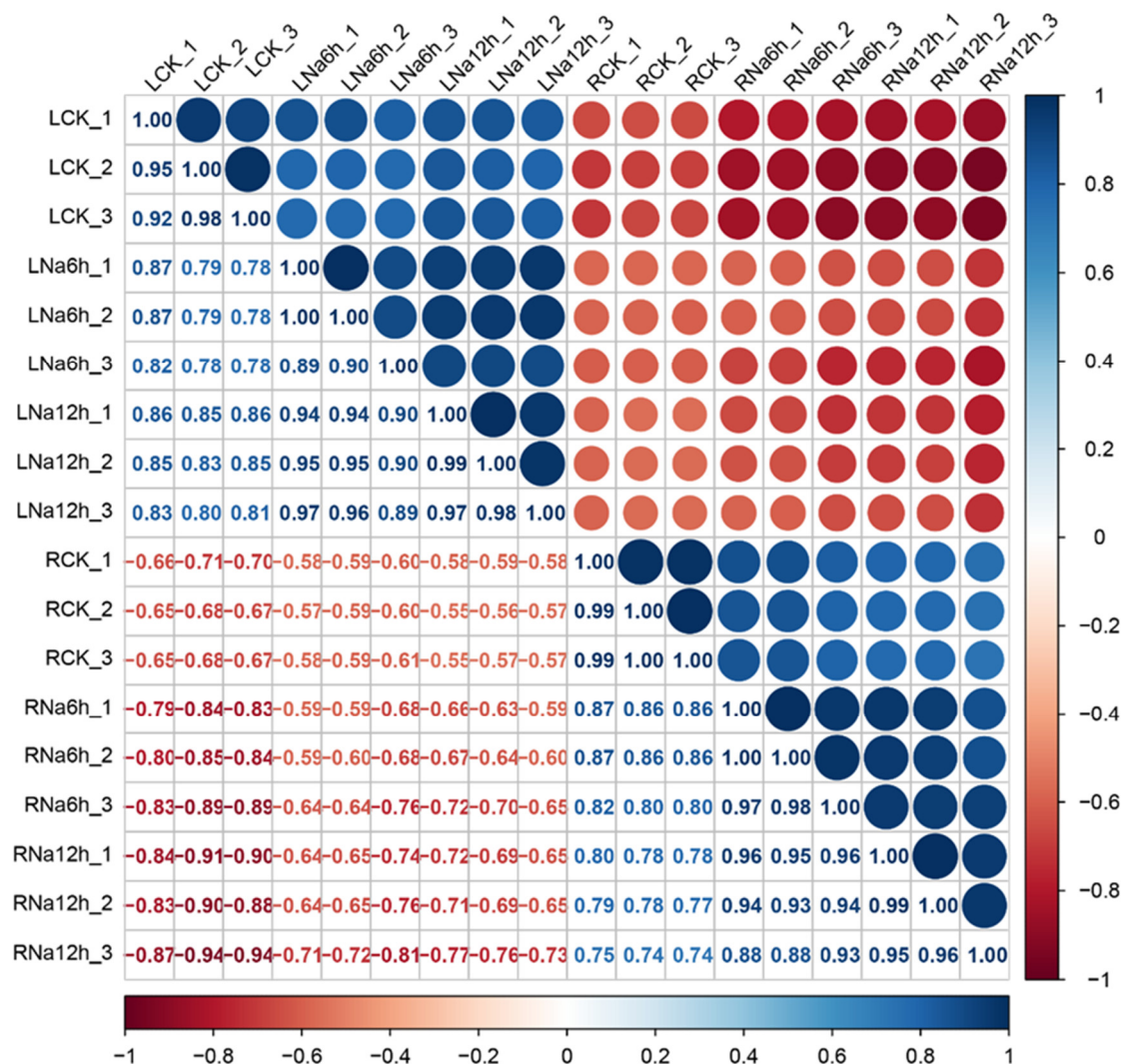


**Supplementary Figure S1.** Correlation heat maps of t Pearson correlation for 18 samples. Pearson correlation was calculated using Log2 (FPKM) of expression values. LCK: the leaves of control LNa6h: the leaves under saline-alkali stress at 6 h LNa12h: the leaves under saline-alkali stress at 12 h RCK: the roots of control RNa6h: the roots under saline-alkali stress at 6 h RNa12h: the roots under saline-alkali stress at 12 h



**Supplementary Table S1.** Sample reads quality of 18 libraries

Sample	Raw_reads	Raw_bases	Clean_reads	Clean_bases	Error_rate	Q20	Q30	GC_pct
LCK_1	47893940	7.18G	45173146	6.78G	0.03	97.45	92.85	47.75
LCK_2	47998592	7.2G	43732092	6.56G	0.03	97.72	93.31	46.4
LCK_3	52162424	7.82G	49901076	7.49G	0.03	97.35	92.48	47.84
LNa6h_1	45989142	6.9G	43514088	6.53G	0.03	97.43	92.72	47.23
LNa6h_2	46022154	6.9G	43203508	6.48G	0.03	97.23	92.22	47.6
LNa6h_3	44850488	6.73G	41650554	6.25G	0.03	96.71	91.04	46.43
LNa12h_1	44102478	6.62G	41714000	6.26G	0.03	97.38	92.59	47.18
LNa12h_2	45964412	6.89G	43417572	6.51G	0.03	97.27	92.34	47.14
LNa12h_3	45002476	6.75G	41702990	6.26G	0.03	97.63	93.18	46.7
RCK_1	45829908	6.87G	43426242	6.51G	0.03	97.45	92.66	45.6
RCK_2	50391166	7.56G	46671834	7.0G	0.03	97.44	92.65	44.9
RCK_3	46468958	6.97G	43680678	6.55G	0.03	97.1	91.94	45.71
RNa6h_1	45698972	6.85G	44501112	6.68G	0.03	97.46	92.68	46.37
RNa6h_2	43450222	6.52G	41848308	6.28G	0.03	97.48	92.76	45.71
RNa6h_3	43843240	6.58G	41814864	6.27G	0.03	97.64	93.12	45.49
RNa12h_1	43086974	6.46G	41200432	6.18G	0.03	97.59	93.11	46.06
RNa12h_2	42640688	6.4G	40659818	6.1G	0.03	97.26	92.35	46.11
RNa12h_3	45594650	6.84G	43494484	6.52G	0.03	97.47	92.81	45.58

**Supplementary Table S2.** Phenotypic data of 18 samples

Sample	SOD activity(U/g)	CAT activity(U/g)	POD activity(U/g)	PPO activity(U/g)	Na+/K+ ratio
LCK_1	59.26	13.22	530.53	15.96	0.74
LCK_2	61.04	12.66	431.66	14.87	0.84
LCK_3	61.51	11.85	506.27	15.41	0.79
LNa6h_1	104.57	8.33	664.45	21.31	0.80
LNa6h_2	105.35	7.64	615.80	22.71	0.70
LNa6h_3	109.25	8.28	723.52	19.81	0.75
LNa12h_1	90.17	26.80	1317.37	19.09	1.14
LNa12h_2	97.39	30.64	1577.45	20.86	1.42
LNa12h_3	99.51	28.41	1518.36	19.92	1.28
RCK_1	49.13	22.27	615.80	32.41	2.25
RCK2_	53.16	25.18	612.72	42.26	2.74
RCK3_	54.41	27.41	689.79	31.53	2.45
RNa6h_1	42.90	40.73	1677.45	106.12	6.19
RNa6h_2	48.20	41.35	1648.64	125.51	6.77
RNa6h_3	49.24	40.71	1647.73	87.72	5.77
RNa12h_1	39.66	105.26	2966.67	78.74	9.84
RNa12h_2	43.23	113.58	2992.22	66.76	9.42
RNa12h_3	42.07	109.34	3037.35	77.74	9.45

**Supplementary Table S3.** Primer sequences for RT-qPCR testing in this study

Name	Forward primer	Reverse primer
(q)MdPP2C29Like	GCTTGTTGGTTGTGCTAA	TCAGTTATATCCTCAGTGTTCA
(q)MdCIPK19	AAGCACATCAAGTTCTACATT	GTAATCTTTCTTCTGGTCTCAA
(q)MdbHLH80Like	ATCAGTGACCGCATAAGG	TCATCTAACATATCCGCAGTAT
(q)MdPP2C39	GGACTATGGAAGGTGATGA	CCGAAATCTTACGACTATACAG
(q)MdMYB5Like	ACAGATGGTCACTAATAGCA	CCTCTTCTTCTTATTGTTCTCAT
(q)MdWRKY31	TCATTGGCGGATCTTACT	CATTGGCATTGTTGTTGTT
(q)MdWRKY23	TTGTTGTGACTACTTATGAAGG	ACGGCTCTACTTGTTGAT
(q)MdWRKY69	GCCACTATCACTATCATATTCTC	AAGATTGTTAGTCCTCCTCAT
(q)MdPHL7Like	CACTCAAAGCGTCAGATG	TAGAGGCAGATTAGATGTAGC
(q)MdCML18	AAGTCTCCAGCCAATTCA	ATCTCCGTTACGATCCATT
(q)MdWRKY10	TGCTGATGAACCTAATGC	CTGTGACCGTCTTATGTG
(q)MdNAC1	ATATTATGACGGAGACCTCAA	ATTCATCAACTGCCACATC
(q)MdActin	TGACCGAATGAGCAAGGAAATTACT	TACTCAGCTTTGGCAATCCACATC