

Table S1 Trait statistics for eight Na⁺- and K⁺-related traits under normal and salt stress conditions.

Trait	Treatment	Mean	SD	Min	Max	H_B^2	Increased fold
SNaC (mg/kg)	NT	579.31	253.70	102.60	1566.37	0.67	3.40
	SS	2547.87	937.81	895.69	6869.13	0.88	
RNaC (mg/kg)	NT	245.89	84.00	69.80	653.42	0.85	5.33
	SS	1556.98	423.59	713.17	3118.37	0.72	
SKC (mg/kg)	NT	2763.18	663.33	1061.54	5280.95	0.36	-0.52
	SS	1323.23	548.01	290.04	3095.32	0.83	
RKC (mg/kg)	NT	918.57	329.71	300.48	2377.86	0.75	-0.60
	SS	364.22	325.03	62.13	2617.45	0.66	
SNaC/SKC	NT	0.24	0.12	0.04	0.61	0.39	8.92
	SS	2.38	1.85	0.65	10.51	0.56	
RNaC/RKC	NT	0.30	0.12	0.08	1.00	0.56	18.30
	SS	5.79	2.71	0.73	22.94	0.65	
KTC	NT	3.25	1.27	1.29	9.24	0.51	0.54
	SS	5.02	3.22	0.48	18.63	0.65	
NaTC	NT	2.46	1.04	0.74	5.72	0.35	-0.26
	SS	1.81	0.89	0.51	4.72	0.89	

NT and SS represent normal treatment and salt stress, respectively.

Min, Max, H_B^2 , and SD represent minimum value, maximum value, broad-sense heritability, and standard deviation, respectively.

Increased fold = (Mean (SS)- Mean (NT)) / Mean (NT).

Sig represents the significance between the NT and SS conditions for each of the eight traits collected in this study.

*** significant at $P < 0.001$.

SNaC, shoot Na⁺ content; RNaC, root Na⁺ content; SKC, shoot K⁺ content; RKC, root K⁺ content; SNaC/SKC, shoot Na⁺ content/shoot K⁺ content; RNaC/RKC, root Na⁺ content/root K⁺ content; KTC, K⁺ transport coefficient; NaTC, Na⁺ transport coefficient.

Table S2 Pearson correlations (r) of eight Na⁺- and K⁺-related traits between NT and SS conditions.

	SKC	SNaC	SNaC/SKC	RKC	RNaC	RNaC/RKC	KTC	NaTC
SKC	1	-0.04 ^{NS}	-0.46 ^{***}	0.27 ^{***}	-0.05 ^{NS}	-0.17 ^{NS}	0.15 ^{***}	0.11 ^{NS}
SNaC	-0.02 ^{NS}	1	0.88 ^{***}	0.14 ^{NS}	0.44 ^{***}	0.24 [*]	-0.15 ^{NS}	0.61 ^{***}
SNaC/SKC	-0.63 ^{***}	-0.63 ^{***}	1	0.07 ^{NS}	0.48 ^{***}	0.26 [*]	-0.34 ^{**}	0.50 ^{***}
RKC	0.07 ^{NS}	0.01 ^{NS}	-0.11 ^{NS}	1	0.40 ^{***}	-0.48 ^{***}	-0.65 ^{***}	-0.12 ^{NS}
RNaC	-0.09 ^{NS}	-0.06 ^{NS}	-0.01 ^{NS}	0.20 ^{**}	1	0.57 ^{***}	-0.26 ^{**}	-0.36 ^{***}
RNaC/RKC	0.01 ^{NS}	-0.16 ^{NS}	-0.05 ^{NS}	-0.60 ^{***}	0.28 ^{***}	1	0.43 ^{***}	-0.31 ^{**}
KTC	0.61 ^{***}	-0.11 ^{NS}	-0.42 ^{***}	-0.43 ^{***}	-0.13 ^{NS}	0.54 ^{***}	1	-0.01 ^{NS}
NaTC	0.07 ^{NS}	0.80 ^{***}	0.50 ^{***}	0.04 ^{NS}	-0.57 ^{***}	-0.27 ^{**}	-0.05 ^{NS}	1

NT and SS represent normal treatment and salt stress, respectively.

Data above the diagonal and below the diagonal represent the Pearson correlations of traits under NT and SS conditions, respectively.

*P < 0.05, ** P < 0.01, *** P < 0.001, and NS = not significant.

SNaC, shoot Na⁺ content; RNaC, root Na⁺ content; SKC, shoot K⁺ content; RKC, root K⁺ content; SNaC/SKC, shoot Na⁺ content/shoot K⁺ content; RNaC/RKC, root Na⁺ content/root K⁺ content; KTC, K⁺ transport coefficient; NaTC, Na⁺ transport coefficient.

Table S3 Details of significant SNPs detected by FarmCPU model.

Condition	Trait	SNP	Chr	Position (bp)	P-value	SNP effect
NT	RNaC	PZE-101252072	1	296,621,512	2.95×10^{-7}	-25.64
	RNaC	SYN33050	2	42,106,477	3.15×10^{-7}	-25.24
SS	SNaC/SKC	SYN38412	3	11,534,876	1.09×10^{-7}	-0.92
	SNaC/SKC	PZE-104132392	4	215,400,346	6.90×10^{-9}	-0.90
	SNaC/SKC	SYN6394	9	124,028,957	1.76×10^{-7}	-0.56
	SNaC/SKC	PZE-110042260	10	80,616,083	9.44×10^{-8}	-0.94
	RKC	SYN26336	9	137,285,825	5.28×10^{-7}	-98.44
	KTC	SYN24195	1	62,227,891	2.33×10^{-7}	0.89
	KTC	PUT-163a-21390620-1531	2	230,934,478	1.25×10^{-7}	-1.05

NT and SS represent normal treatment and salt stress, respectively.

Chr represents chromosome.

RNaC, root Na⁺ content; SNaC/SKC, shoot Na⁺ content/shoot K⁺ content; RKC, root K⁺ content; KTC, K⁺ transport coefficient.

Table S4 All candidate genes located in the LD regions of significant SNPs detected by GWAS under NT and SS conditions.

Condition	Significant SNP	Candidate gene	Annotation
NT	PZE-101252072	<i>GRMZM2G095851</i>	Elongation factor 2
		<i>GRMZM2G559098</i>	—
		<i>GRMZM2G040369</i>	—
		<i>GRMZM5G862488</i>	—
		<i>GRMZM2G048031</i>	—
		<i>GRMZM2G051675</i>	Transmembrane and coiled-coil domain-containing protein 5B
		<i>GRMZM2G167428</i>	—
		<i>GRMZM2G113158</i>	G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300
		<i>GRMZM2G338809</i>	—
		<i>GRMZM5G883969</i>	—
		<i>GRMZM2G470422</i>	Protein SENSITIVE TO PROTON RHIZOTOXICITY 1
		<i>GRMZM5G821743</i>	—
		<i>GRMZM2G170137</i>	—
		<i>GRMZM2G470382</i>	Hypothetical protein
		<i>GRMZM2G114992</i>	—
		<i>GRMZM2G114899</i>	—
		<i>GRMZM2G035017</i>	40S ribosomal protein S4-like
		<i>GRMZM2G704150</i>	—
		<i>AC217358.3_FG005</i>	—
		<i>GRMZM5G881369</i>	—
		<i>GRMZM5G891724</i>	—
		<i>AC217358.3_FG003</i>	—
		SYN33050	
<i>GRMZM2G010238</i>	Molybdopterin biosynthesis CNX3 protein		

		<i>AC197340.3_FG010</i>	—
		<i>GRMZM2G384979</i>	Probable purine permease 11
		<i>GRMZM2G083888</i>	Casparian strip membrane protein 4
		<i>GRMZM2G083930</i>	—
		<i>AC197340.3_FG003</i>	Hypothetical protein
		<i>AC197340.3_FG004</i>	—
		<i>GRMZM2G137161</i>	Amino acid/polyamine transporter II
		<i>GRMZM2G065480</i>	Arsenical pump-driving ATPase
		<i>GRMZM2G430411</i>	—
		<i>GRMZM2G130085</i>	Protease Do-like 8 chloroplastic
		<i>GRMZM2G430365</i>	—
		<i>GRMZM2G430362</i>	ATP-dependent RNA helicase SUV3
		<i>GRMZM2G009948</i>	—
		<i>GRMZM2G337197</i>	—
		<i>GRMZM2G337196</i>	—
		<i>GRMZM2G337113</i>	Glyceraldehyde-3-phosphate dehydrogenase 1
		<i>GRMZM2G489504</i>	—
		<i>GRMZM2G012404</i>	—
		<i>GRMZM2G012328</i>	Pectinesterase 5
		<i>GRMZM2G315401</i>	Galactose mutarotase-like superfamily protein
SS	PZE-104132392	<i>GRMZM2G076896</i>	—
		<i>GRMZM2G094123</i>	—
		<i>GRMZM5G837626</i>	—
		<i>GRMZM2G591412</i>	—
		<i>GRMZM2G085361</i>	—
		<i>GRMZM2G096622</i>	Ypt/Rab-GAP domain of gyp1p superfamily protein
		<i>GRMZM2G702807</i>	—
		<i>GRMZM2G104783</i>	Putative cytochrome P450 superfamily protein
		<i>GRMZM5G876644</i>	—

PZE-110042260	<i>GRMZM2G379278</i>	—
	<i>GRMZM2G077317</i>	Monocopper oxidase-like protein SKU5
	<i>GRMZM2G077486</i>	Tricin synthase 1
	<i>GRMZM5G811235</i>	—
	<i>GRMZM2G096422</i>	—
	<i>GRMZM2G096367</i>	—
	<i>GRMZM2G333183</i>	ABC transporter B family member 14
	<i>GRMZM2G502467</i>	—
	<i>GRMZM2G446895</i>	HEAT repeat-containing protein 6
	<i>AC177873.3_FG003</i>	—
	<i>GRMZM2G154328</i>	TMPIT-like protein
	<i>GRMZM2G372475</i>	—
	<i>GRMZM2G070555</i>	—
	<i>GRMZM2G372553</i>	Androgenic embryo 3
	<i>GRMZM2G026884</i>	—
	<i>GRMZM2G008271</i>	Basal layer antifungal peptide bap-1a
	<i>GRMZM2G008403</i>	Basal layer antifungal peptide 1b bap1-b
	<i>GRMZM2G058703</i>	—
	<i>GRMZM2G054359</i>	—
SYN38412	<i>GRMZM5G830695</i>	Acyl-protein thioesterase 2
	<i>GRMZM2G013978</i>	—
	<i>GRMZM2G037505</i>	—
	<i>GRMZM2G506916</i>	—
	<i>GRMZM2G037386</i>	—
	<i>GRMZM2G061830</i>	NADH-cytochrome b5 reductase-like protein
	<i>GRMZM2G061798</i>	—
	<i>GRMZM2G039828</i>	—
	<i>GRMZM2G039799</i>	—
	<i>GRMZM2G039454</i>	Cellulose synthase 3 cesa3

	<i>GRMZM2G336437</i>	—
SYN6394	<i>GRMZM2G127853</i>	Glucan endo-1,3-beta-glucosidase 4
	<i>GRMZM5G842555</i>	KH domain-containing protein
	<i>GRMZM5G881775</i>	—
	<i>GRMZM2G372952</i>	Zinc finger protein ZAT4
	<i>AC226253.1_FG002</i>	—
	<i>GRMZM2G429110</i>	—
	<i>GRMZM2G078924</i>	Membrane-anchored ubiquitin-fold protein 1
	<i>GRMZM2G162949</i>	RING zinc finger protein-like
	<i>GRMZM2G162968</i>	—
	<i>GRMZM2G075104</i>	Probable ubiquitin conjugation factor E4
	<i>GRMZM2G372632</i>	Pentatricopeptide repeat-containing protein At4g31850, chloroplastic
	<i>GRMZM2G171428</i>	Probable WRKY transcription factor 4
	<i>GRMZM2G171401</i>	PRKR interacting protein 1
	<i>GRMZM2G472064</i>	—
	<i>GRMZM2G113345</i>	—
	<i>GRMZM2G113372</i>	—
	<i>GRMZM2G412254</i>	—
	<i>GRMZM2G163774</i>	Premnaspirodiene oxygenase
SYN26336	<i>GRMZM2G057959</i>	—
	<i>GRMZM2G053639</i>	—
	<i>GRMZM2G053652</i>	—
	<i>GRMZM2G053790</i>	—
	<i>GRMZM2G053908</i>	RNA-splicing protein MRS3
	<i>GRMZM2G083186</i>	—
	<i>GRMZM2G083190</i>	—
	<i>GRMZM2G083222</i>	—
	<i>GRMZM2G083262</i>	Eukaryotic translation initiation factor 2 subunit alpha

	<i>GRMZM2G383749</i>	—
	<i>GRMZM2G575444</i>	—
	<i>AC206223.3_FG004</i>	Actin-interacting protein 1-2
	<i>GRMZM2G700011</i>	—
	<i>GRMZM2G700014</i>	—
	<i>GRMZM5G865047</i>	—
	<i>AC206223.3_FG006</i>	Protein kinase superfamily protein
	<i>AC206223.3_FG010</i>	—
	<i>AC206223.3_FG008</i>	—
	<i>AC206223.3_FG007</i>	—
	<i>GRMZM5G832912</i>	—
	<i>AC206223.3_FG001</i>	—
	<i>GRMZM5G898471</i>	—
	<i>GRMZM2G078933</i>	—
	<i>GRMZM2G378852</i>	Putative MAPKKK family protein kinase
	<i>GRMZM2G090025</i>	—
PUT-163a-	<i>GRMZM2G308463</i>	Short-chain dehydrogenase reductase ATA1
21390620-1531	<i>GRMZM5G833998</i>	—
	<i>GRMZM5G892308</i>	Putative glutaredoxin-C14
	<i>GRMZM2G066840</i>	Short-chain dehydrogenase reductase ATA1
	<i>GRMZM2G066902</i>	—
	<i>GRMZM2G066950</i>	—
	<i>GRMZM2G082302</i>	—
	<i>GRMZM2G070444</i>	—
	<i>AC190480.1_FG007</i>	Major facilitator superfamily protein, partial
	<i>GRMZM2G372180</i>	—
	<i>GRMZM2G070371</i>	—
	<i>GRMZM2G070304</i>	Glycerol-3-phosphate acyltransferase 3
	<i>GRMZM2G107501</i>	—

	<i>GRMZM2G557893</i>	—
	<i>GRMZM2G003182</i>	Sigma-like factor2B
	<i>GRMZM2G180172</i>	Protein RETICULATA chloroplastic
	<i>GRMZM2G156127</i>	Cytokinin-N-glucosyltransferase 1
	<i>AC148152.3_FG008</i>	—
SYN24195	<i>GRMZM2G081322</i>	—
	<i>GRMZM2G082346</i>	—
	<i>GRMZM2G703582</i>	S-norcochlorogenic acid synthase 1-like
	<i>GRMZM2G421970</i>	—
	<i>GRMZM5G864300</i>	—
	<i>GRMZM2G382569</i>	—
	<i>GRMZM2G382568</i>	—
	<i>GRMZM2G063055</i>	AAA ATPase containing von Willebrand factor type A
	<i>GRMZM2G156827</i>	Protein HUA2-LIKE 2
	<i>AC204659.3_FG005</i>	—
	<i>GRMZM2G057652</i>	—
	<i>GRMZM5G845960</i>	—
	<i>GRMZM2G057674</i>	Alpha/beta-Hydrolases superfamily protein
	<i>GRMZM2G703586</i>	—
	<i>GRMZM5G811034</i>	Cyclin-dependent kinase B2-1
	<i>GRMZM2G108416</i>	—
	<i>GRMZM2G414278</i>	Phospholipase A1-II 7
	<i>GRMZM2G108523</i>	Uncharacterized PPE family protein PPE2
	<i>GRMZM2G108530</i>	Protein Mo25
	<i>GRMZM2G108576</i>	—

NT and SS represent normal treatment and salt stress, respectively.

“—” represents no functional annotations.