

Genome-wide association study dissects the genetic bases of salt tolerance in maize seedlings

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SUPPORTING INFORMATION

	Ear leaf width	100 grain weight	Ear diameter	Cob diameter	Salt tolerance	Kernel width	Ear leaf length	Tassel main axis length	Plant height	Ear height	Ear length	Kerner number perrow	cob weight	Tassel branch number	Leaf number above ear	Silking time	Pollenshed	Heading date
Ear leaf width																		
100 grain weight	0.26																	
Ear diameter	0.32	0.45																
Cob diameter	0.28	0.32	0.83															
Salt toleranca	0.14	0.01	-0.01	0.03														
Kernel width	-0.02	0.05	0.11	0.06	0.05													
Ear leaf length	0.09	0.11	0.05	0.13	0.08	0.09												
Tassel main axis length	0.09	0.13	-0.07	-0.1	-0.01	0.07	0.42											
Plant height	0.26	0.16	0.19	0.13	0.11	0.1	0.48	0.41										
Ear height	0.32	0.04	0.18	0.14	0.12	0.02	0.4	0.17	0.78									
Ear length	0.32	0.3	0.08	0.03	0.03	0.03	0.28	0.42	0.42	0.23								
Kerner number perrow	0.22	0.01	0.16	-0.05	-0.04	0.02	0.13	0.23	0.35	0.25	0.61							
cob weight	0.02	-0.03	0.02	0.08	0.01	0	0.05	0.03	0.04	0.03	-0.02	-0.03						
Tassel branch number	0.11	-0.07	-0.13	-0.05	0.04	0.04	0.24	0.09	0.22	0.42	0.02	-0.07	0.07					
Leaf number above ear	0.12	0.11	0.04	0.08	0.15	0.05	0.37	0.14	0.44	0.24	0.13	-0.01	0.01	0.24				
Silking time	0.33	-0.06	-0.07	0.04	0.23	0	0.4	0.11	0.33	0.5	0.09	-0.07	0.09	0.35	0.45			
Pollenshed	0.34	-0.06	-0.07	0.04	0.23	-0.04	0.45	0.08	0.33	0.53	0.07	-0.09	0.08	0.36	0.47	0.94		
Heading date	0.37	-0.02	-0.04	0.07	0.25	-0.02	0.45	0.05	0.35	0.54	0.1	-0.05	0.07	0.33	0.45	0.92	0.96	

Figure S1. Correlation coefficients between salt tolerance and other agronomic traits in the association population
Seventeen other agronomic traits were collected from the previously published results (Yang et al. 2014).

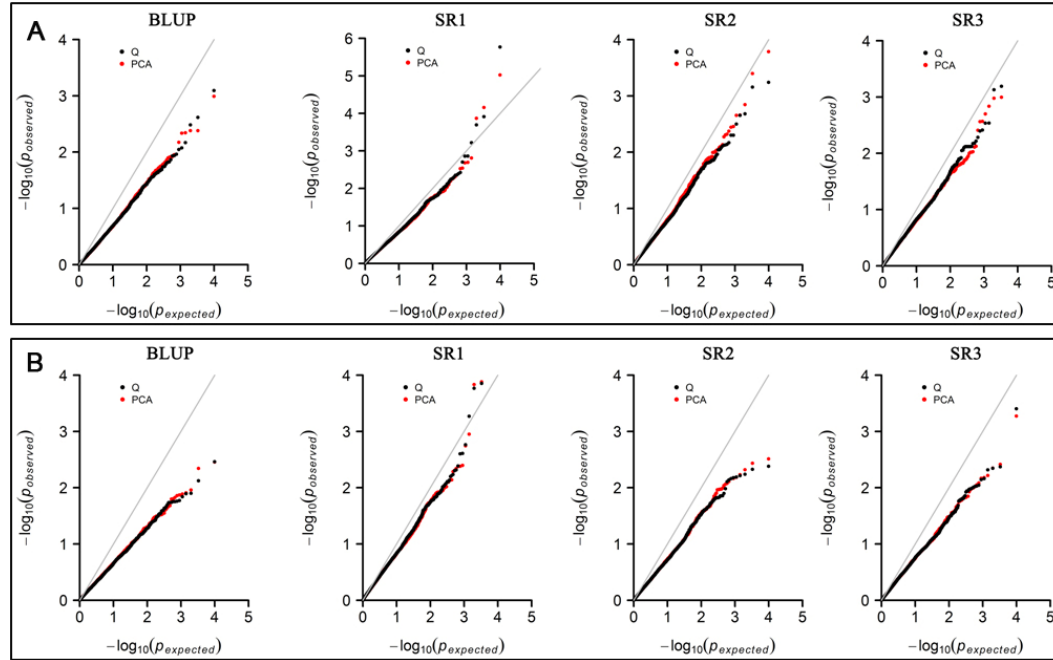


Figure S2. Comparison of false-positive controls between PCA and Q matrices

(A) Q-Q blots of BLUP, SR1, SR2 and SR3 phenotypes. Generalized linear model (GLM) was used in the analysis.

(B) Q-Q blots of BLUP, SR1, SR2 and SR3 phenotypes. Mixed linear model (MLM) was used in the analysis.

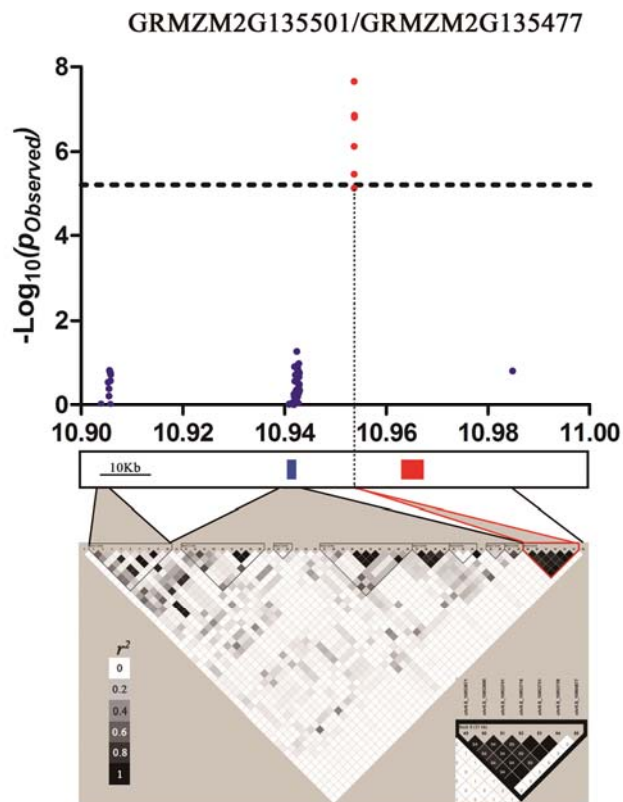


Figure S3. Candidate gene association analysis in the Chr9 10.9 Mbp-11 Mbp region

Red dots represent the significant SNPs; Various LDs of the significant SNPs are shown in different colors from gray to black according to the bar (r^2); GRMZM2G135501 and GRMZM2G135477 are indicated with blue and red boxes, respectively.

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ZmSAT32 : MGR-----SVSYDDGPVPVRSAPASLPISRSRSDDGVVPASATKPPLGGRS : 46
AtSAT32 : MGRKSQRKNATMFDSDDDTSSVSSSSSTMPSERLINPGMDEVTVLKDAILLDQS : 52

ZmSAT32 : PGSSEATQVHARQRDGSNTQDDSGERLTSAVVGSFAHHLVLAIFYSAHSPGEL : 98
AtSAT32 : LDALYEKRSSSTREQALATIVDAFNSDLQYEFVEKKFATLLHQCLHCTKKGST : 104

ZmSAT32 : DPVVTEGYQITLTGFMFLITS AFLGFMKKTLKMHDES NKQRQ---KVDDD VQ : 146
AtSAT32 : KETSLATHVIGLLALT VGLGDHAQEVLEESVTPLSQALKSGREILKITSILE : 156

ZmSAT32 : EGALPPYLLDCDQTORAKLLIYACIYMN----- : 173
AtSAT32 : CLAVITFVGGNDPEQTEKSMQIIWQMIHPKLGSNVVATKPSPAVISAVVSSW : 208

ZmSAT32 : -FLLTTIGSWRINKNSWKEPTAFLSTLLEADDRAVRMAAGEALALCFEINLL : 224
AtSAT32 : A-FLLTTVDRWTLGPKIFQETVTVTLSTLLEKDDRSVRIAAGEALAVIYEI GTL : 260

ZmSAT32 : DVSSREDDGVNTGGTT--GSKNKLFLDMQALKTKISGLATNLSTEAG----- : 269
AtSAT32 : EKFAAEVKGSANGSVKEGGVSQEALMHMHGLKAKVTKQVRELSVEAGGKGSA : 312

ZmSAT32 : -----VQGVPEPE-----KIIMLKYYVSRQ : 287
AtSAT32 : KKDLNTQRNLFKDLVEFLEDGYAPETSTKVGGDYLOTSTWYQMIQLNLYLKH : 364

ZmSAT32 : VD-----TKGRLG LG----- : 297
AtSAT32 : LGGGFIKHMQENEFLHDVFSFTPKKIGGGKLSNDEKRLFKSPNSALNKARTQ : 416

ZmSAT32 : -----GHVIA SCFTA- : 307
AtSAT32 : FLAKQRMLAKNMNVGHYAATAMEEE : 441

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Figure S4. Comparison of ZmSAT32 and AtSAT32 protein sequences

Conserved amino acids are marked in black and the conserved IFRD domains are marked with open red boxes.

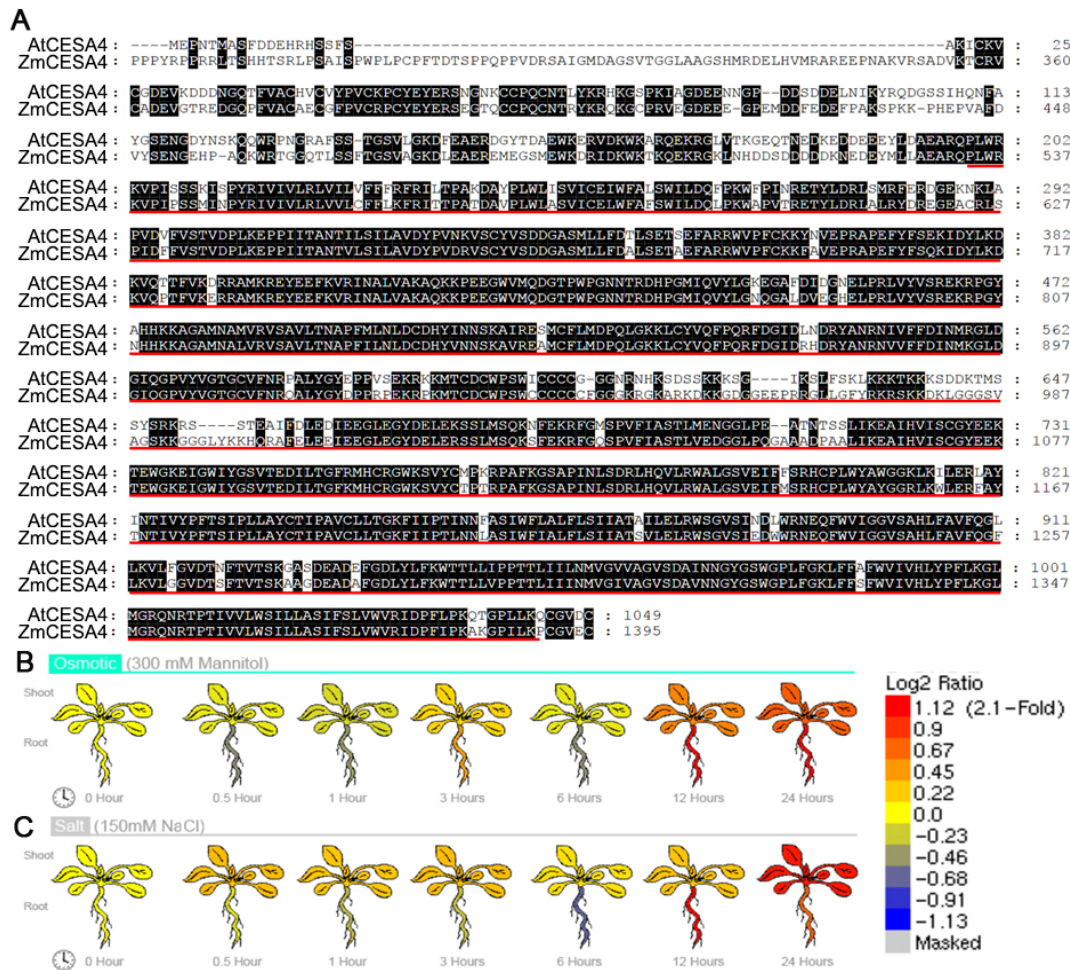


Figure S5. Sequence alignment of ZmCESA4 and AtCESA4 protein sequences

(A) Sequence comparison between ZmCESA4 and AtCESA4. Conserved amino acids are marked in black and the conserved domains are marked with pink lines.

(B) and **(C)** Expression patterns of AtCESA4 after osmotic stress (B) and salt stress (D). Different colors showing the expression levels. Data are from the *Arabidopsis* ePlant database (<http://bar.utoronto.ca/eplant/>).

Table S1. Survival rates of 445 maize inbreds

Table S2. SNPs and candidate genes significantly associated with salt tolerance

Table S3. Functional annotation of 49 candidate genes

Table S4. Primers used in this study