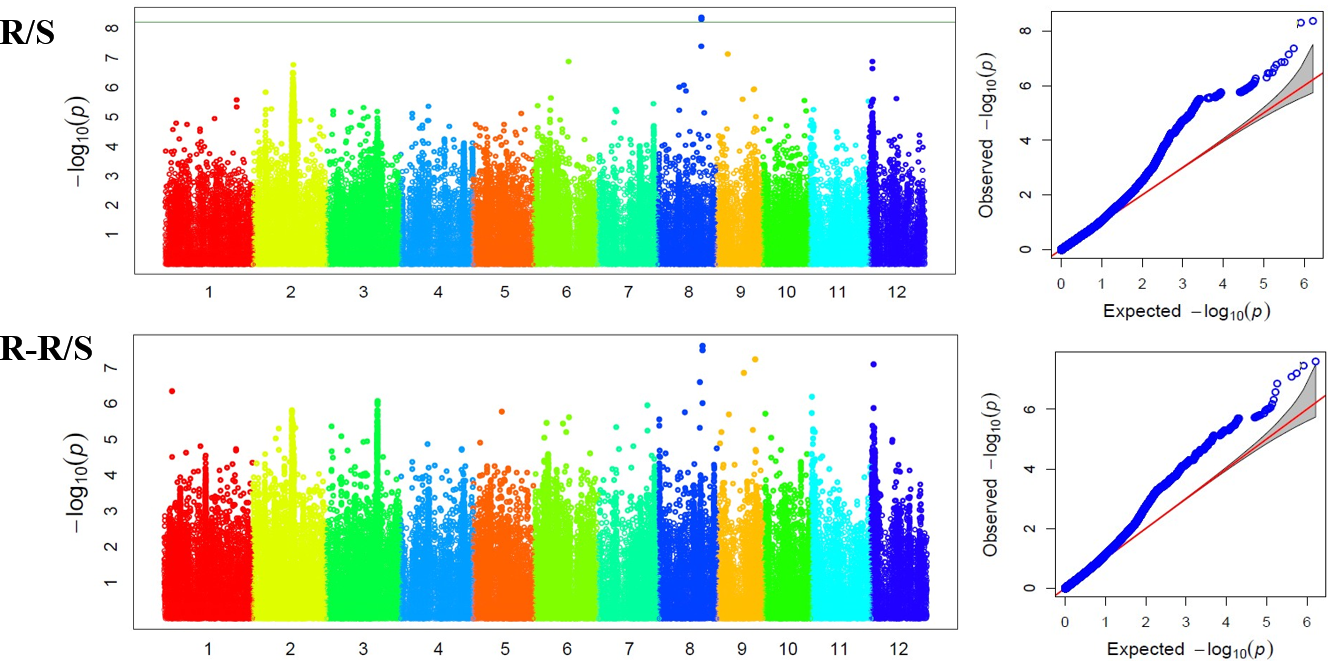
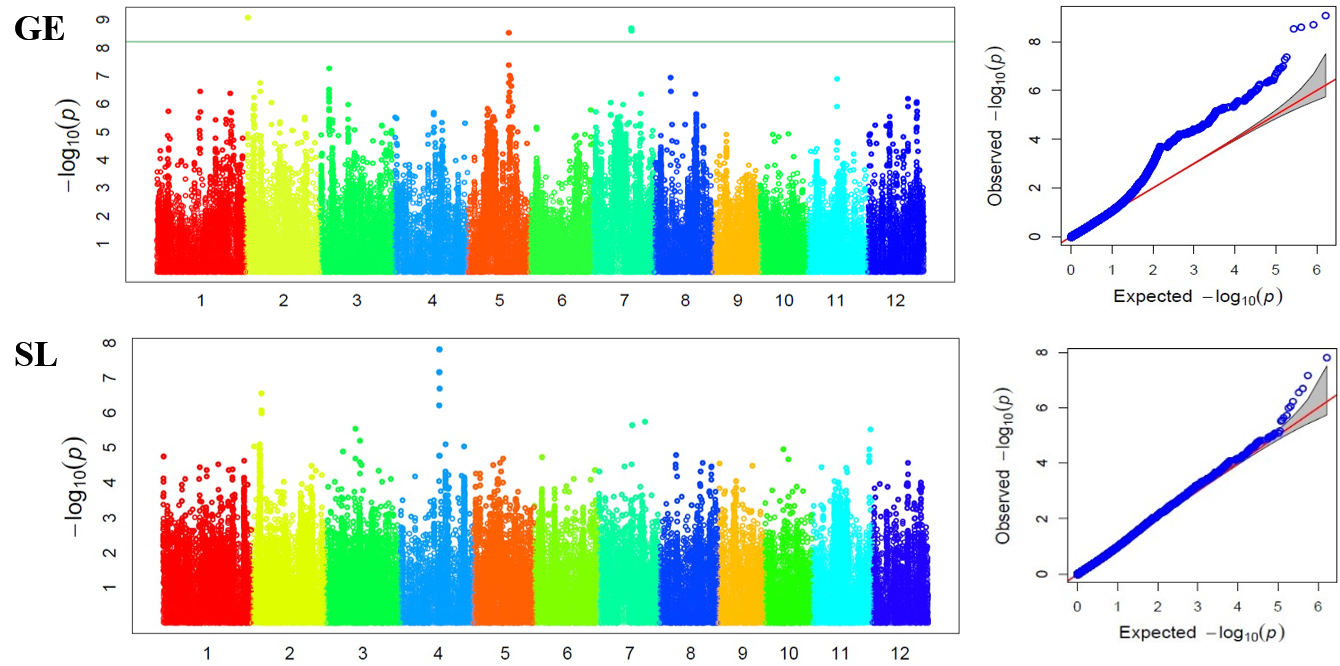


**Fig. S1** Scree plot determining the appropriate number of principal components. The most obvious eigenvalues change in slope in the scree plot occurs at component 2 in both genotype (**a**) and phenotype (**b**), suggesting that PC1 and PC2 can explain most proportion of total eigenvalues. The appropriate number of principal components is two.



**Fig. S2** Manhattan plots and QQ plots for several salt tolerance phenotypes identified by the genome-wide association study that did not show strong associations. –Log10 (*P*) values from a genome-wide scan are plotted against position on each of the 12 chromosomes. GE: Germination Energy; SL: Shoot Length; R/S: root / shoot ratio; R-R/S: relative root / shoot ratio.