

Supplementary Table S7. Predictive Modelling of Rice Salt Tolerance Using Lasso Regularization - details of metrics (Germination stage)

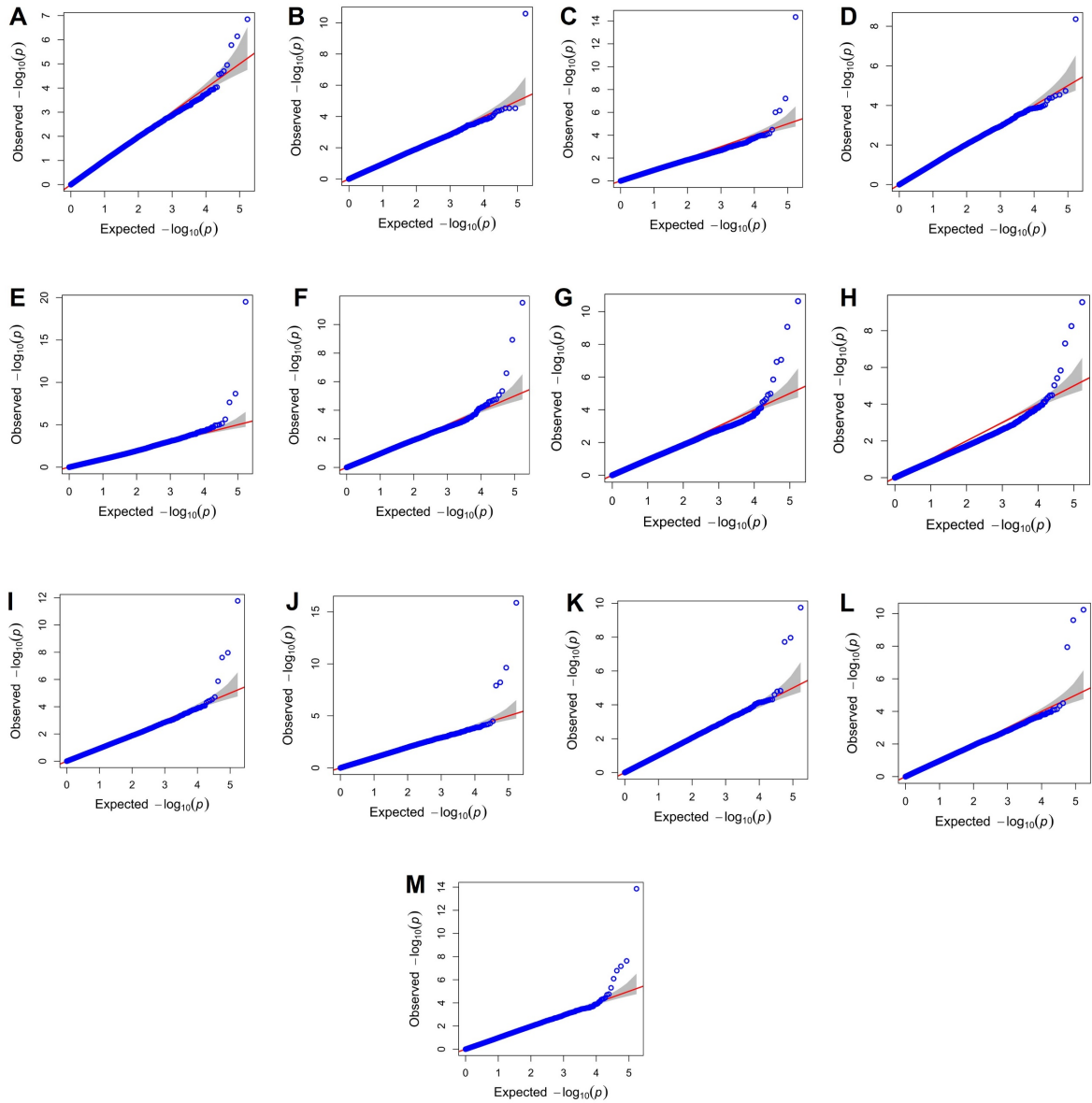
Alpha	MSE	RMSE	NMSE	R2	Adjusted_R2	λ _Min	λ _1SE
0	3.45595E-05	0.0059	0.0010	0.9990	0.9990	0.0255	0.0255
0.1	3.22461E-05	0.0057	0.0009	0.9991	0.9990	0.0153	0.0168
0.2	3.28481E-05	0.0057	0.0009	0.9991	0.9990	0.0111	0.0122
0.3	3.47971E-05	0.0059	0.0010	0.9990	0.9990	0.0089	0.0098
0.4	3.20719E-05	0.0057	0.0009	0.9991	0.9990	0.0067	0.0073
0.5	3.44053E-05	0.0059	0.0010	0.9990	0.9990	0.0059	0.0064
0.6	3.38185E-05	0.0058	0.0010	0.9990	0.9990	0.0049	0.0054
0.7	3.33707E-05	0.0058	0.0009	0.9991	0.9990	0.0042	0.0046
0.8	3.34279E-05	0.0058	0.0009	0.9991	0.9990	0.0037	0.0040
0.9	3.43032E-05	0.0059	0.0010	0.9990	0.9990	0.0033	0.0036
1*	3.19707E-05	0.0057	0.0009	0.9991	0.9991	0.0027	0.0032

*Alpha value of 1 has the lowest MSE and highest R^2 ; MSE, Mean Squared Error; RMSE, Root Mean Squared Error; NMSE, Normalized Mean Squared Error; R^2 , Coefficient of Determination; Adjusted R^2 , Adjusted Coefficient of Determination; λ _Min, regularization parameter value that gives the minimum cross-validated error; λ _1SE, regularization parameter value within one standard error of the minimum cross-validated error.

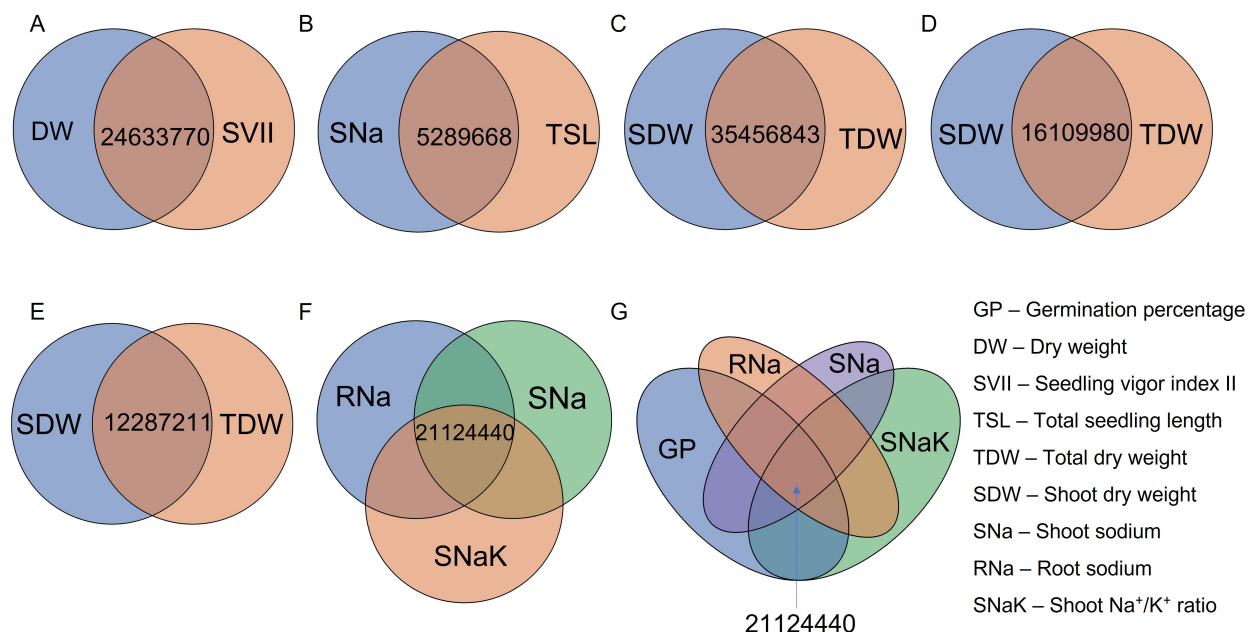
Supplementary Table S8. Predictive Modelling of Rice Salt Tolerance Using Lasso Regularization - details of metrics (Early seedling stage)

Alpha	MSE	RMSE	NMSE	R2	Adjusted_R2	λ _Min	λ _1SE
0	2.98E-05	0.00546	0.0010	0.9990	0.9989	0.0335	0.0368
0.1*	2.81E-05	0.00530	0.0009	0.9991	0.9990	0.0167	0.0183
0.2	2.91E-05	0.00539	0.0009	0.9991	0.9989	0.0110	0.0121
0.3	3.02E-05	0.00549	0.0010	0.9990	0.9989	0.0081	0.0089
0.4	2.97E-05	0.00545	0.0010	0.9990	0.9989	0.0061	0.0066
0.5	2.91E-05	0.00539	0.0009	0.9991	0.9990	0.0048	0.0053
0.6	2.91E-05	0.00539	0.0009	0.9991	0.9990	0.0040	0.0044
0.7	2.96E-05	0.00544	0.0010	0.9990	0.9989	0.0035	0.0038
0.8	3.05E-05	0.00553	0.0010	0.9990	0.9989	0.0030	0.0033
0.9	2.90E-05	0.00538	0.0009	0.9991	0.9990	0.0025	0.0030
1	3.04E-05	0.00551	0.0010	0.9990	0.9989	0.0022	0.0022

*Alpha value of 0.1 has the lowest MSE and highest R^2 ; MSE, Mean Squared Error; RMSE, Root Mean Squared Error; NMSE, Normalized Mean Squared Error; R^2 , Coefficient of Determination; Adjusted R^2 , Adjusted Coefficient of Determination; λ _Min, regularization parameter value that gives the minimum cross-validated error; λ _1SE, regularization parameter value within one standard error of the minimum cross-validated error.



Supplementary Figure S1. Quantile–quantile (Q–Q) plot showing the distribution of observed and expected $-\log_{10}(p)$ values obtained from the BLINK model: A. Germination percentage, B. Dry weight, C. Seedling vigor index II (Germination stage), D. Total Seedling Length, E. Shoot fresh weight, F. Shoot dry weight, G. Total dry weight, H. Root Na^+ , I. Root K^+ , J. Root Na^+/K^+ , K. Shoot Na^+ , shoot K^+ , and shoot Na^+/K^+ ratio (Early seedling stage)



Supplementary Figure S2. Co-association of significant marker–trait associations across chromosomes: A. Dry weight and seedling vigor index II (germination stage, Chr 1); B. Shoot sodium and Total seedling length (early seedling stage, Chr 4); C. Shoot dry weight and Total dry weight (early seedling stage, Chr 2); D. Shoot dry weight and Total dry weight (early seedling stage, Chr 3); E. Shoot dry weight and Total dry weight (early seedling stage, Chr 6); F. Root sodium, shoot sodium, and shoot Na⁺/K⁺ (early seedling stage, Chr 12); G. Germination percentage, root sodium, shoot sodium, and shoot Na⁺/K⁺ (germination and early seedling stages, Chr 12). Numbers indicate genomic positions of common SNPs; Ch denotes chromosome