

S3 Table. Phenotypic correlation coefficients (Pearson coefficient) among the traits in BR CSSL population (n=74) and RIL populations. The top right half of the table represents values calculated for the CR-RIL (normal font) and BRRIL (bold font) populations. Correlation coefficients calculated for the CSSL population is given in the bottom half. *, **, *** indicates significance at P <0.001, P <0.01, and P <0.05, respectively. NA: data not available.

Trait	PH	PL	FLL	FLW	SH or BTS ^a	GermARS	GL	GW	TGW
PH		0.753*** 0.583***	0.679*** NA	-0.045 NA	-0.251** -0.102	0.037 -0.038	0.073 -0.074	0.019 -0.112	0.107 -0.028
PL	0.540***		0.723*** NA	0.149 NA	-0.176 -0.026	-0.022 -0.081	0.158 0.067	-0.055 -0.166*	-0.108 -0.025
FLL	0.592***	0.507***		0.061 NA	-0.217* NA	-0.024 NA	0.153* NA	0.019 NA	0.175* NA
FLW	0.228	0.031	0.452***		-0.012 NA	-0.249** NA	0.022 NA	0.087 NA	0.164* NA
SH or BTS	-0.033	-0.009	0.143	0.002		-0.018 0.072	-0.224** -0.154	-0.090 0.042	-0.232** -0.022
GermARS	0.144	-0.104	0.149	0.110	0.157		0.148* -0.043	-0.145 0.001	0.093 -0.012
GL	0.022	0.226	0.329**	0.101	0.183	-0.004		-0.132 0.071	0.555*** 0.457***
GW	-0.117	0.128	0.151	-0.081	-0.007	0.150	0.569***		0.401*** 0.537***
TGW	-0.149	-0.003	0.144	-0.022	0.145	-0.011	0.736***	0.679***	

PH, plant height; PL, panicle length; FLL, flag leaf length; FLW, flag leaf width; SH, seed shattering; BTS, breaking tensile strength; germARS, arcsine transformed value of germination%; GL, grain length; GW, grain width; TGW, thousand grain width.

^a Seed shattering scores were used in RIL populations but BTS values were used in CSSL population.