

# S2 Fig. Genotyping and association analysis of the breeding panel. (a) Linkage disequilibrium (*r2*) decay plot of pair-wise markers as a function of genetic distance (cM) for the breeding panel. The fitted curve (red) shows the expected LD decay between adjacent 90K iSelect SNP array markers based on a nonlinear regression model. The critical *r2* value (dashed line) is the 95% quantile of *r2* value of unlinked SNP markers. (b) Quantile-Quantile (Q-Q) plot of three different models for population structure and kinship. The expected *P*-values were plotted against observed *P*-values for each SNP, based on three different models: the naïve model (blue), GLM with three sub-populations (red), and MLM with three sub-populations and kinship (green). The diagonal reference line (dashed line) represented the null hypothesis of no association. The Q-Q plot was based on the seedling test of isolate W009, which is the most representative Q-Q plot among all phenotypic data.