**The genetic basis for panicle traits variation in switchgrass (*Panicum virgatum*)**

**Running head: Panicle genetics in switchgrass**

Li Zhang1\*, Xiaoyu Weng1, Kathrine D. Behrman1, Jason Bonnette1, John L. Reilley2, Francis M. Rouquette Jr3, Philip A. Fay4, Yanqi Wu5, Felix B. Fritschi6, Robert B. Mitchell7, David B. Lowry8, Arvid R. Boe9, Thomas E. Juenger1\*



Supplemental Fig. S1. The histograms of F2 plant survival at all 10 filed sites (All sites) and by removing data from one field site at a time using panicle length as example. This plot displays rare plant mortalities at each site, neither in TX sites (OVTN, PKLE, and TMPL) nor in South Dakota (BRKG). Further examination of the raw data showed NA values at some sites due to data lost but not due to mortalities.



Supplemental Fig. S2. The genomic prediction using the independent genotypes from the three sites (KBSM, CLMB, and PKLE) for panicle length (PL), number of primary branches (PBN), and number of secondary branches (SBN). Statistical measures of r and %bias represent the prediction accuracy and percentage of bias between observed and predicted values. This analysis was performed using the R package ‘BMTME’, which is a Bayesian multi-trait and multi-environment package for analyzing breeding data, and allows parameter estimation and evaluates the prediction performance (Montesinos-López et al. 2019).

Reference

Montesinos-López OA, Montesinos-López A, Luna-Vázquez FJ, Toledo FH, Pérez-Rodríguez P, Lillemo M, Crossa J (2019) An R Package for Bayesian Analysis of Multi-environment and Multi-trait Multi-environment Data for Genome-Based Prediction. G3: Genes|Genomes|Genetics 9:1355