



**Figure S2** Genome-wide association studies of seed mass in 2009 and 2010. (A) Manhattan plot of CMLM for 2009 seed mass. Significance threshold is denoted by the gray dashed line. The 10 sorghum chromosomes are plotted against the negative base-10 logarithm of the association P value. The areas highlighted in green indicate confidence intervals for seed size determined by QTL mapping. Heterochromatin and centromeres are indicated by the gray areas and the black dots individually. (B) Manhattan plot of CMLM for 2010 seed mass.