



Figure S1. Genome-wide association study (GWAS) of a binary kernel color trait: white vs. non-white. The non-white class included maize inbred lines ranging from yellow to dark orange in kernel color. Scatter plot of association results from a unified mixed model analysis of the kernel color trait. Negative \log_{10} -transformed P -values (y-axis) from GWAS are plotted against physical position (B73 RefGen_v2) on each of 10 chromosomes (x-axis). Chromosomes are alternately colored. The horizontal green line indicates the $-\log_{10} P$ -value of the least statistically significant SNP at 5% false discovery rate.