



Figure S4. A regional Manhattan plot of locus 7. Scatter plot of association results from a mixed model analysis of Cu concentration and linkage disequilibrium (LD) estimates (r^2) for a genomic region that contains the peak SNP (8-136857539) at locus 7. Each vertical line represents the $-\log_{10} P$ -value of a SNP. Triangles are the r^2 values of each SNP relative to the peak SNP (indicated in red) at 136,857,539 bp (B73 RefGen_v4) on chromosome 8. The red horizontal dashed line indicates the $-\log_{10} P$ -value of the least statistically significant SNP at a genome-wide false discovery rate of 5%. The yellow vertical line indicates the genomic position of the *calcium pump1* (*cap1*) gene Zm00001d011013. The open triangles indicate SNPs that are within the candidate gene. The light blue rectangle demarcates the ± 100 kb candidate gene search space surrounding the peak SNP.