



Figure S3. A regional Manhattan plot of locus 6. Scatter plot of association results from a mixed model analysis of Cu grain concentration and linkage disequilibrium (LD) estimates (r^2) for a genomic region that contains the peak SNP (8-137939692) at locus 6. 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 137,939,692 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 gene Zm00001d011063 that encodes a protein sharing amino acid sequence similarity with metallothioneins (MTs) in rice and Arabidopsis (Table S5). 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.