



Figure S5. A regional Manhattan plot of locus 10. Scatter plot of association results from a mixed model analysis of Mn grain concentration and linkage disequilibrium (LD) estimates (r^2) for a genomic region that contains the peak SNP (1-162962818) at locus 10. 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 162,962,818 bp (B73 RefGen_v4) on chromosome 1. 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 Zm00001d030846 that encodes a protein sharing amino acid sequence similarity with NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEINS (NRAMPs) 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.