



Figure S8. A regional Manhattan plot of the *nas5* gene. Scatter plot of association results from a mixed model analysis of Zn (a) and Fe (b) grain concentration and linkage disequilibrium (LD) estimates (r^2) for a genomic region that contains the peak SNPs (Zn: 7-179962589, locus 33; Fe: 7-180077496) at the *nas5* gene. 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 179,962,589 bp and 180,077,496 bp (B73 RefGen_v4) on chromosome 7 for Zn and Fe, respectively. The yellow triangle indicates the peak SNP for Fe in the Zn Manhattan plot, and vice versa. The red and green horizontal dashed lines indicate the $-\log_{10} P$ -value of the least statistically significant SNP at a genome-wide false discovery rate of 5% (Zn) and 20% (Fe), respectively. The yellow vertical line indicates the genomic position of the *nicotianamine synthase5* (*nas5*) gene (Zm00001d022557). 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.