



**Figure S9.** A regional Manhattan plot of locus 32. Scatter plot of association results from a mixed model analysis of Zn grain concentration and linkage disequilibrium (LD) estimates ( $r^2$ ) for a genomic region that contains the peak SNP (5-195765640) at locus 32. 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 195,765,640 bp (B73 RefGen\_v4) on chromosome 5. 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 *yellow stripe-like2* (*ysl2*) gene (Zm00001d017427). The open triangles indicate SNPs that are within the candidate gene. The light blue rectangle demarcates the  $\pm 100$  kb candidate gene search space surrounding the peak SNP.