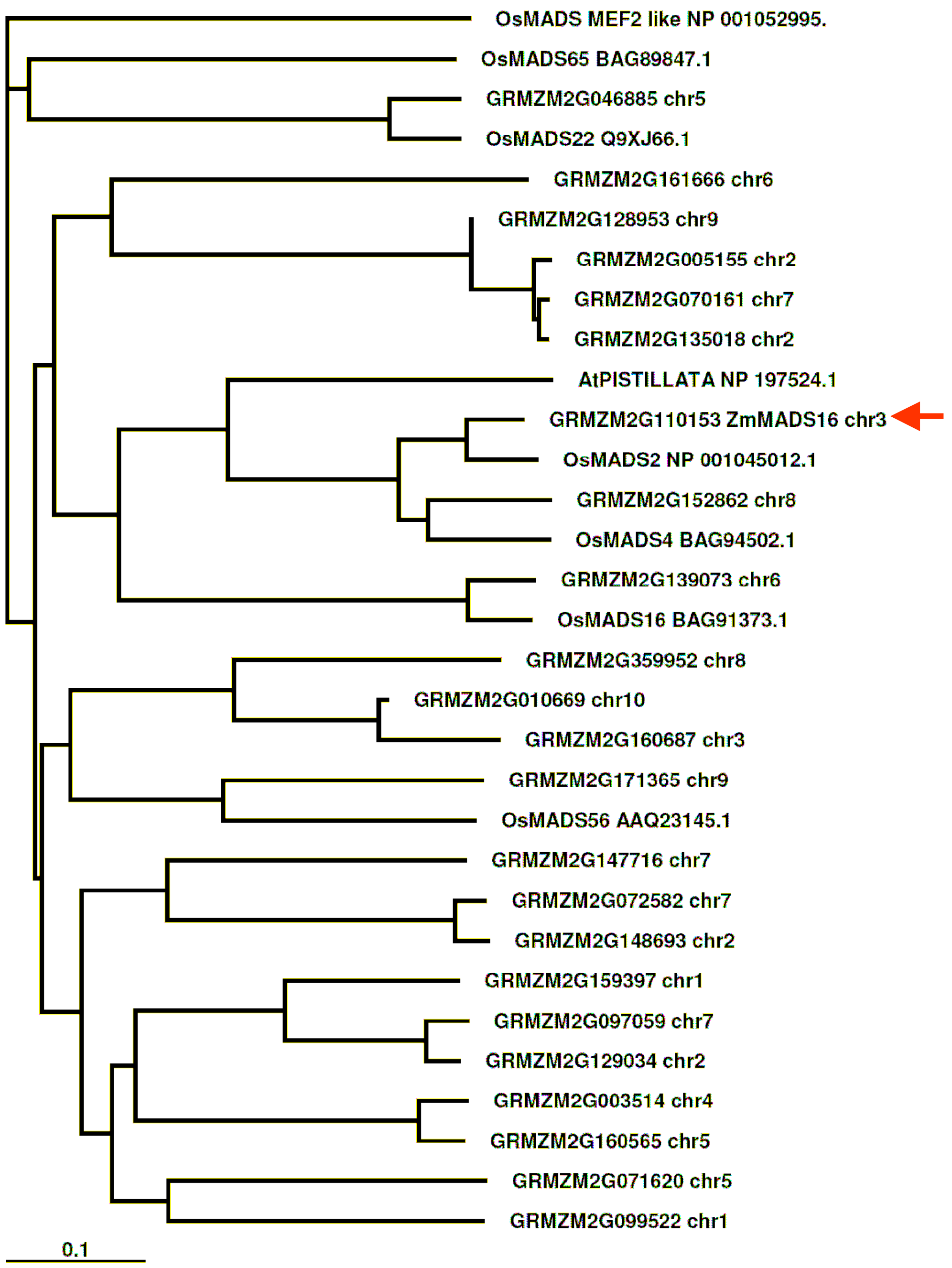
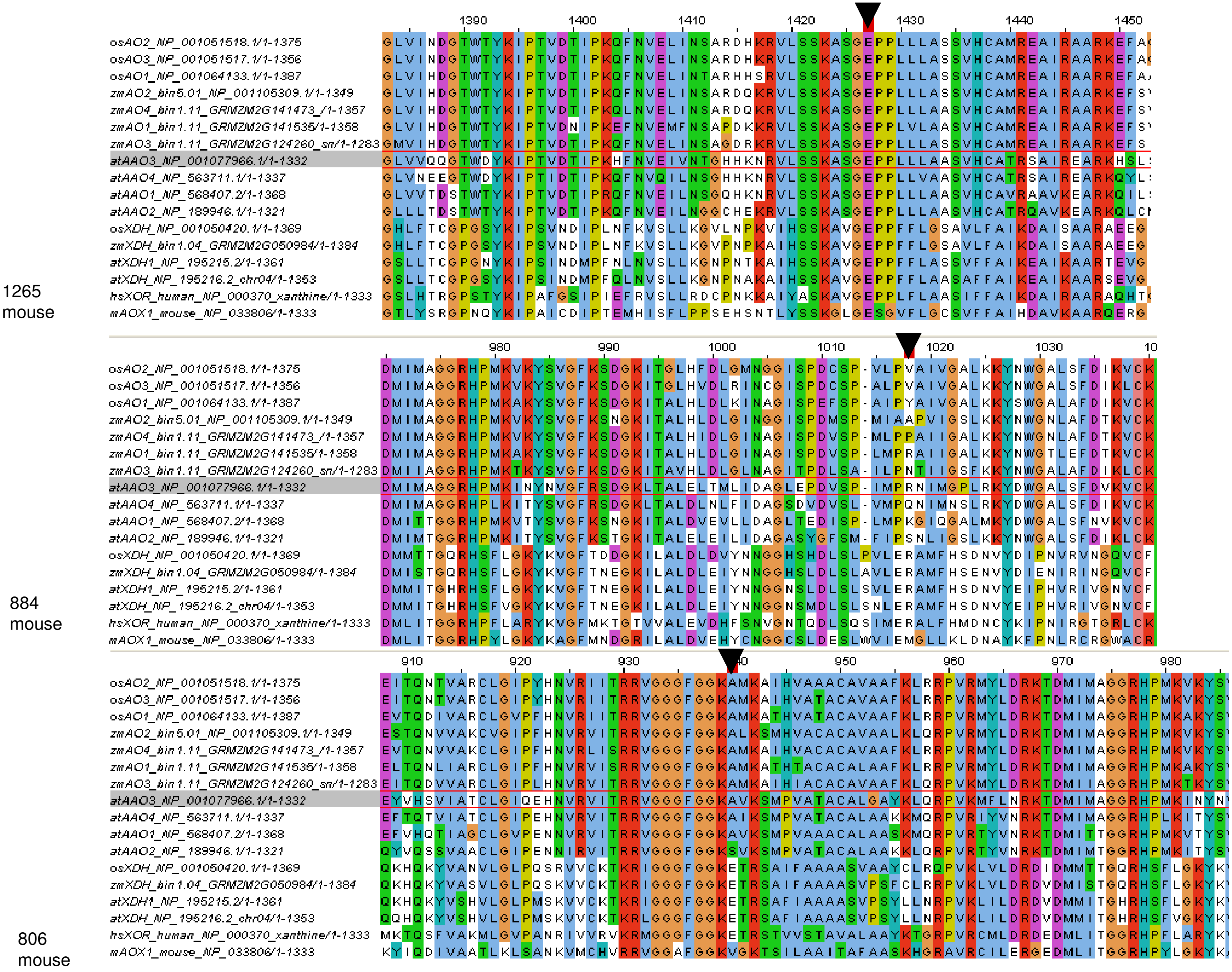
Supplement Figure S1
Setter et al. 2010



Supplement Figure 2. Alignment of amino acid sequences for aldehyde oxidases and xanthine dehydrogenases in maize (Zm), rice (Os) and Arabidopsis (At). Also shown are reference sequences from human and mouse. Maize sequences from www.maizesequence.org 4a.53. Three regions of the sequences are shown, around amino acids corresponding to mouse-1265, mouse-886, and mouse-806 (marked by arrows). See text for explanation.



Supplementary Figure S3. Plot of squared correlations of allele frequencies (r^2) against distance between polymorphic sites (SNPs) in the aldehyde oxidase ZmAO3 candidate gene. The curve shows a nonlinear regression (logarithmic) of r^2 on distance. Similar results were obtained with a Loess curve. The predicted value of r^2 rapidly declines to 0.2 by 800 bp and reaches background levels (0.1) by 3000 bp in ZmAO3. The SNPs used to generate this plot are from a 3500 bp region surrounding SNP position 285,274,032 bp on chromosome 1 in 27 diverse maize inbred lines. The investigated SNPs are an integration of HapMap SNPs (Gore et al., 2009) and loci genotyped in this study. The 27 maize inbred lines are parents of the Maize Nested Association (NAM) population and the Intermated B73 X Mo17 (IBM) population. Eight (CML103, CML228, CML247, CML277, CML322, CML333, CML52, and CML69) of the 27 lines are derived from the CIMMYT breeding program and were included in this association study.