



Figure S6. Reordering of B73 AGPv2 reference genome contigs around GRMZM2G085873. A snippet of maize B73 reference genome around chromosome 1, positions 260,361,563 – 260,395,575, is shown on top. Sequence from this region is aligned to our complete GRMZM2G085873 sequence using Mauve 2.4.0 (Darling *et al.* 2004). Red blocks represent the alignment from exon 2 to exon 6 between our sequence and the reference genome. Green blocks represent the alignment from 5' UTR to part of intron 1 between our sequence and the reference genome. Intron 1 either has multiple sequence errors in the reference genome or a portion missing from the reference genome. Based on our sequencing results, the contig spanning chr1: 260,377,789-260,388,002 should be oriented in an opposite direction. Also, those contigs spanning chr1: 260,367,665-260,377,688 should be moved elsewhere, either upstream or downstream of GRMZM2G085873.