



Supplementary Figure 4. Validation of promoter proximal antisense (a-b) and sense (c-d)

cleavage sites using 3'-RACE. Each panel displays a genome browser view of the promoter proximal region at four coding genes: Mapk4 (a), Zcchc2 (b), Ccm2 (c), Pgm2 (d) with the gene TSS denoted with a black arrow pointing towards the right. Promoter proximal 3'-end cleavage reads for uaRNA (blue) and mRNA (red) are displayed above each gene schematic shown in black. The assayed cleavage site is denoted with an asterisk and the number of reads supporting each site is displayed above each site. We validated the most prominent cleavage site (supported by the most number of reads) for each uaRNA loci. Agarose gels of 3'-RACE PCR products are displayed to the right and each assayed cleavage site (asterisk) was cloned and sequenced using Sanger sequencing methods. Scale bars are represented in black above genes. The encoded genome sequence is displayed including the sequence of the PAS (bold) and the distance between the cleavage site (blue and red arrow for uaRNA and mRNA, respectively) and the 5'-end nucleotide of the PAS is noted above.