

Fig. S4. RNA read depth of protein-coding genes and 2 kb flanking regions in the *Arabidopsis* mtDNA based on the combined data sets of the three biological samples. Only genes for which promoters have been experimentally identified (Table S2) are included. The slopes of the read depth (filled circles) were calculated every 50 bp in the 2 kb region upstream of each gene or coding units. Gray bars represent genes and dark gray bars are exons. Green and red squares represent start of transcription and 3' termini, respectively, which were identified experimentally [36,42,44]. Blue squares indicate sequences identical to reported promoters for other genes. The higher values of the slopes that fall within a 100 bp window around the transcription start sites identified experimentally are shown as green circles. The higher values of the slopes found upstream of the transcription start sites identified experimentally are shown as blue circles. Below each graph, the mtDNA coordinates of the strand in which the gene is located are shown. For each intron-containing gene, the spliced version of the gene is also shown, and the coordinates of the spliced reference sequence are depicted below each graph.





















































