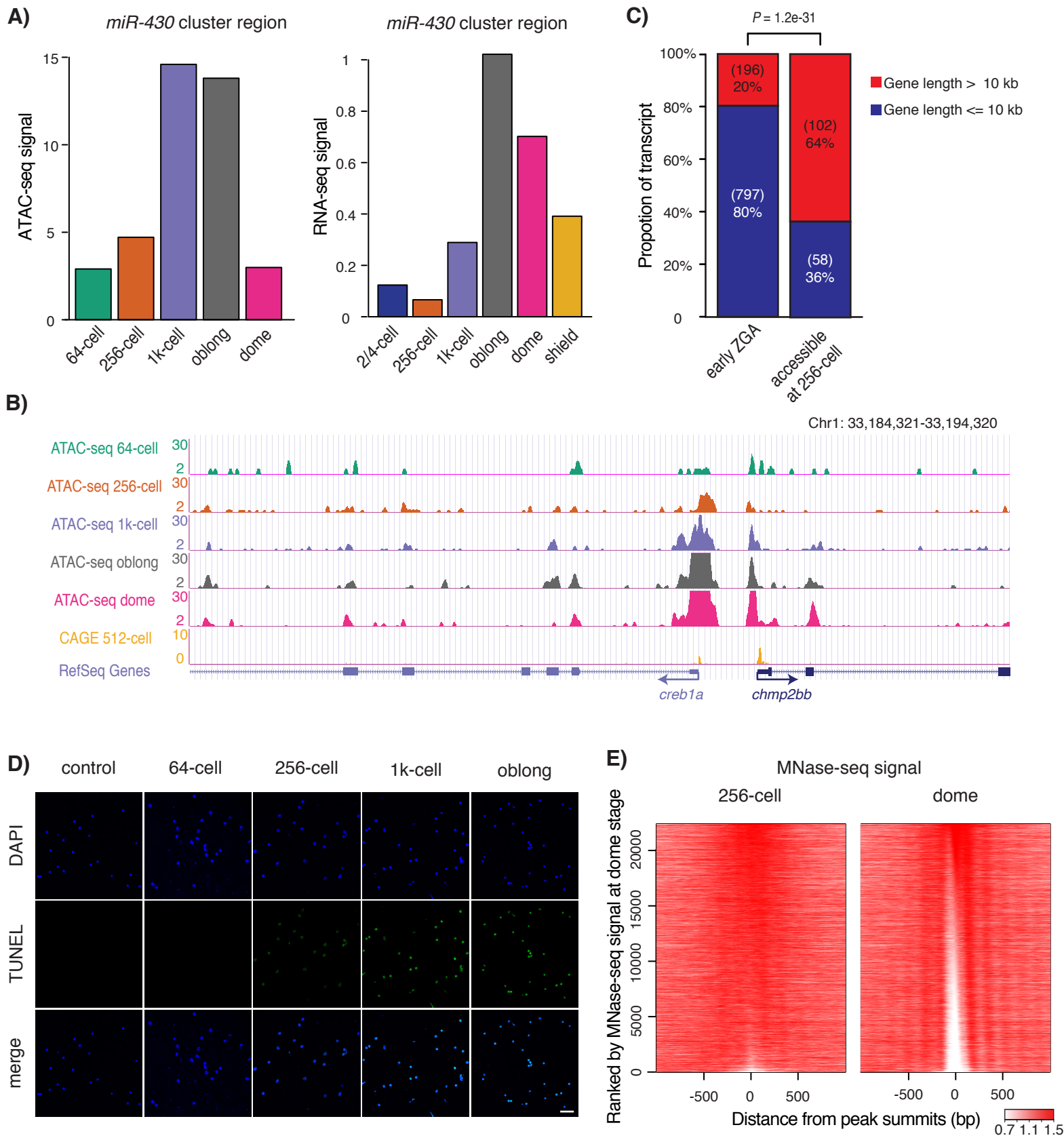


Supplemental_Fig_S2



Supplemental Figure S2. Establishment of accessible chromatin during the minor phase of ZGA. (A) The box plot shows continuously elevated trend until the dome stage on the normalized ATAC-seq and RNA-seq signals for the *miR-430* cluster, which was reported to play roles in the clearance of maternal mRNAs. The *miR-430* cluster region is indicated by the dashed box in Fig. 1B. (B) The genome browser view shows the ATAC-seq signals at the *creb1a* locus as a representative example of accessible chromatin that appears at the 256-cell stage. (C) The bar plots show the proportion of long (> 10 kb) and short (≤ 10 kb) genes for the reported early ZGA genes and genes with accessible promoters at the 256-cell stage. *p-values* were calculated by Chi-squared test. (D) Confocal images of DNase I TUNEL assay for chromatin accessibility during ZGA. Cell nuclei were stained with DAPI (blue), and chromatin accessibility were labelled with DNase I TUNEL (green). Control is embryos at oblong stage without DNase I digestion. Scale bar: 50 μ m. (E) Heatmap of nucleosome organization profiles of 256-cell stage (left panel) and dome stage (right panel) across chromatin regions detected as accessible in dome stage and inaccessible in 256-cell stage. Regions were ranked by the average MNase-seq signals of the central 50 bp window at dome stage. Regions with very low MNase-seq signals (average signal of the 2 kb window < 0.8) were not shown.