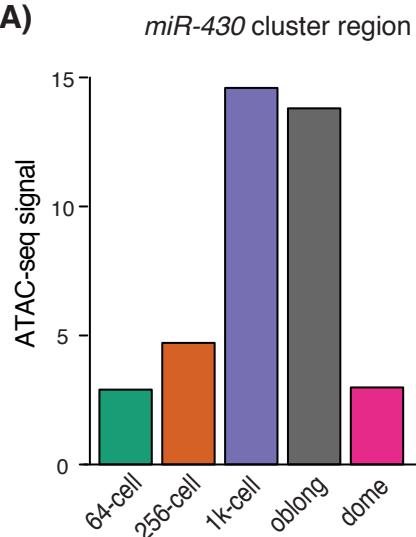
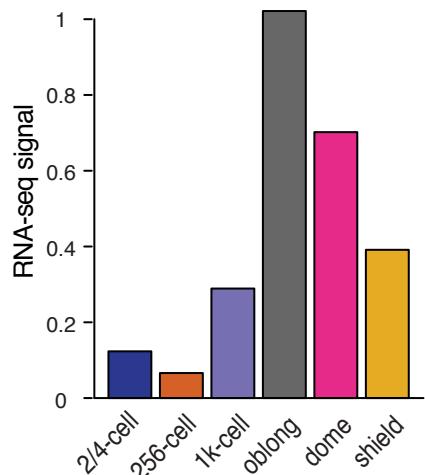


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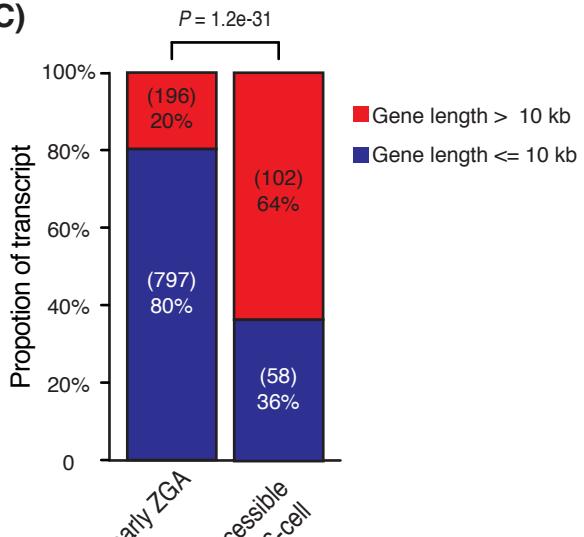
A)



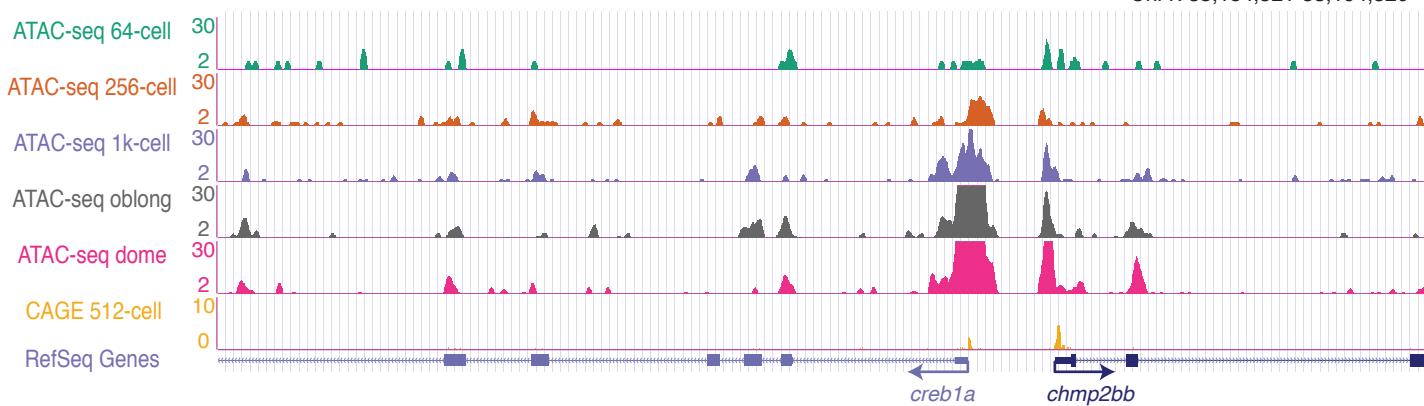
miR-430 cluster region



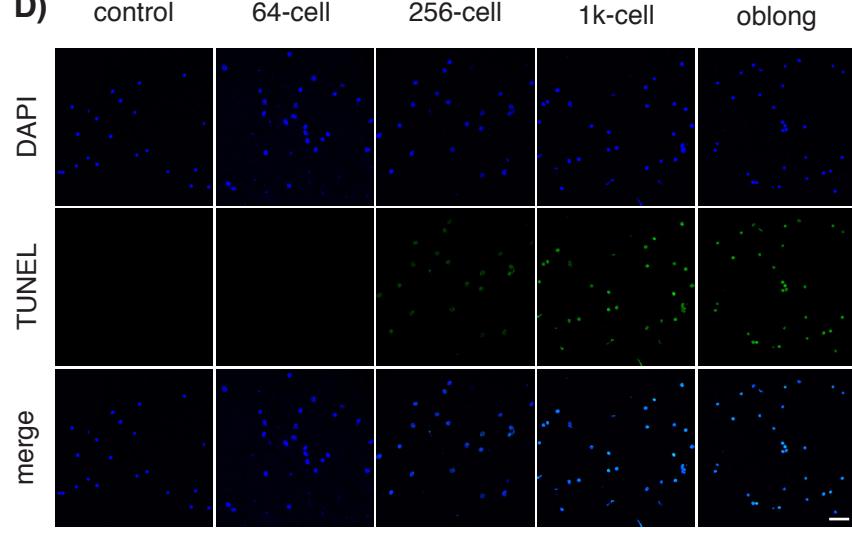
C)



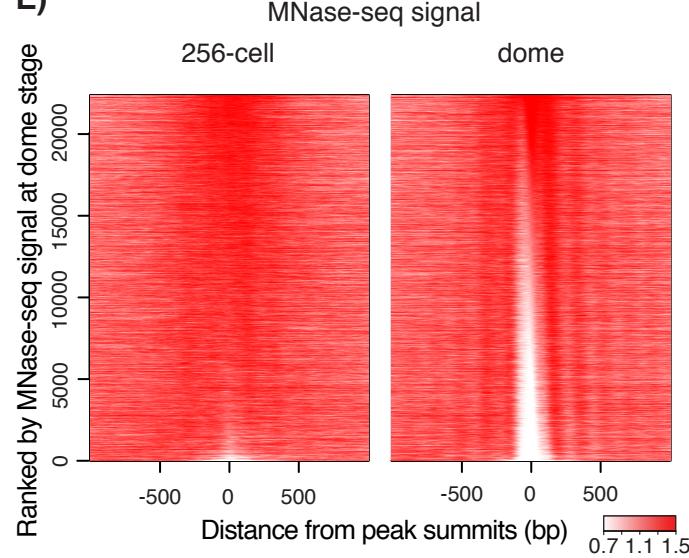
B)



D)



E)



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.