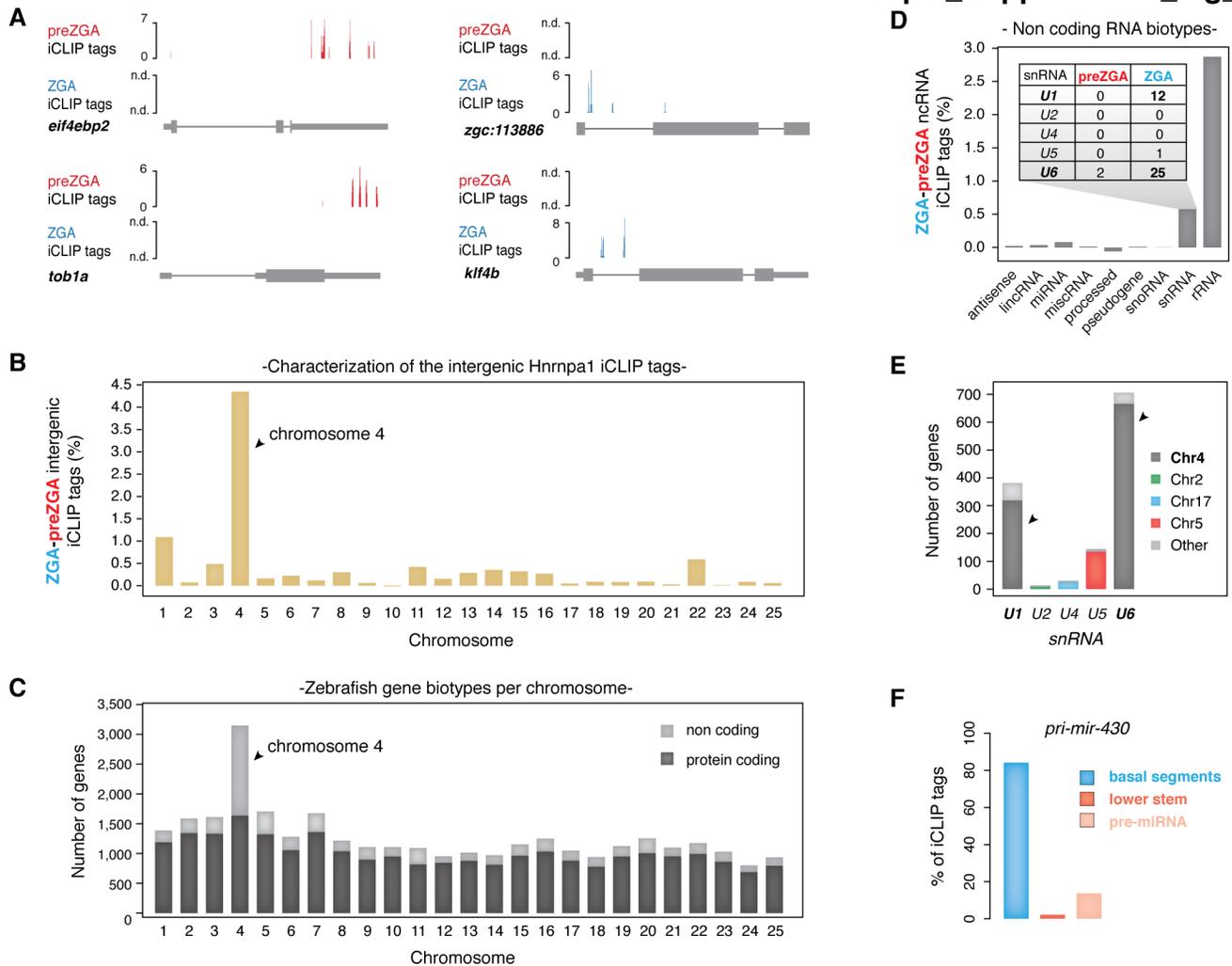


Despic_Supplemental_Fig_S5



Supplemental Figure S5 (related to Figure 4 and 5). Comparison of preZGA and ZGA Hnrnpa1 iCLIP data. (A) UCSC genome browser tracks display examples of the top preZGA- (left, red) and ZGA-specific (right, blue) Hnrnpa1 mRNA targets. Note the appearance of intronic iCLIP tags at the ZGA stage. **(B)** Barplot presenting chromosome-specific increase in intergenic Hnrnpa1 iCLIP tags at ZGA. Majority of the elevated intergenic iCLIP tags were mapped to chromosome 4. **(C)** Barplot showing the number of non-coding and protein-coding genes per chromosome. Note that chromosome 4 is particularly rich in non-coding genes in comparison to all other chromosomes. **(D)** Barplot displaying relative increase of non-coding iCLIP tags at the ZGA stage per transcript biotype. The inset shows the number of different snRNA targets per developmental stage. Note that *U1* and *U6* snRNAs are one of the most prominent Hnrnpa1 targets at ZGA. **(E)** Barplot presenting the number of annotated snRNA genes in zebrafish genome per chromosome. *U1* and *U6* snRNA genes are the most numerous and mainly localized on chromosome 4. **(F)** Barplot shows relative abundance of Hnrnpa1 iCLIP tags derived from uniquely mapped reads across different types of *pri-mir-430* regions.