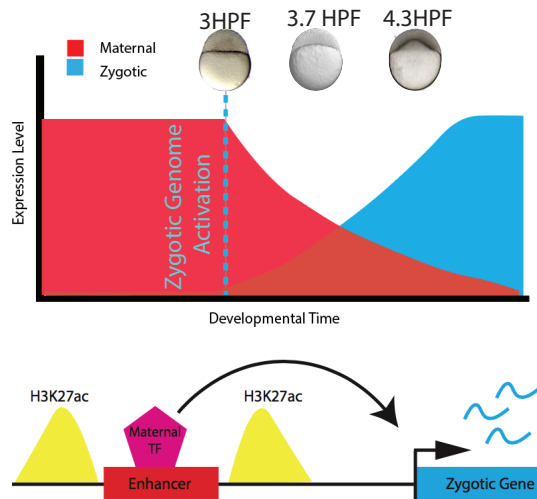


Utilizing CUT&RUN to Characterize Putative Enhancers during Zebrafish Embryogenesis

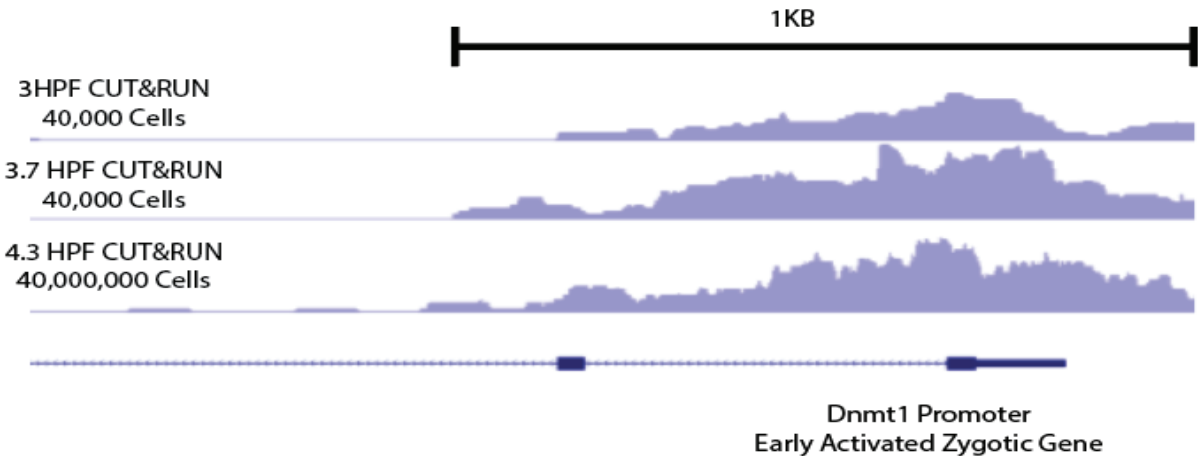
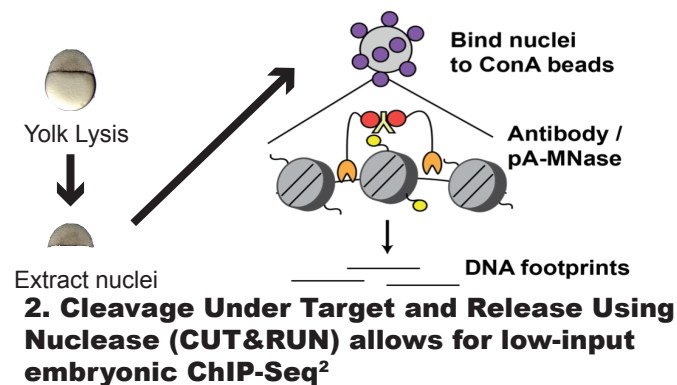
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1. Maternal factors engage cis-regulatory elements to drive transcription of the quiescent genome

Maternal transcription factors engage zygotic chromatin to drive transcriptional competence¹. H3K27ac marks active enhancers, but low cell counts limit attempts to characterize them by ChIP-Seq



3. CUT&RUN captures regulatory sequences confirmed by standard ChIP-Seq

A UCSC genome browser track shows H3K27ac signal across three experiments at the promoter of an early activated zygotic gene. 3HPF ("1000 cell") and 3.7HPF ("Oblong") CUT&RUN, alongside publicly available ChIP-Seq data at dome stage (4.3hpf)³. C&R shows both strong overlap with available ChIP as well as a pattern of signal increase over developmental time

4. A set of putative enhancers identified across developmental time

A set of core shared regions across all three experiments show strong enrichment for H3K27ac signal. Further characterization on enhancer and promoter dynamics will be done shortly to better characterize these putative enhancers and active promoters

