

Supplementary data for Esmaeili et al, "Chromatin accessibility and histone acetylation in the regulation of competence in early development"

1. Supplementary Data 1: ATAC-seq analysis for *Xenopus* stage 10 and stage 12
 - a. ATAC-seq analysis stage 10 and 12 with p300 overlap.
 - b. Genome-wide distribution of ATAC-seq peaks.
 - c. List of promoters for which accessibility changes ≥ 2 -fold.
 - d. Putative cis-regulatory modules (pCRMs).
 - e. Δ pCRMs: pCRMs with reduced accessibility from stage 10 to stage 12.
2. Supplementary Data 2: ATAC-seq vs expression *Xenopus* stage 10
 - a. Comparison of accessibility at promoters annotated in *xenlae2* with expression at stage 10 by microarray (Livigni et al 2013).
 - b. List of genes based on high vs low promoter accessibility and high vs low expression at stage 10.
 - c. DAVID functional gene annotation.
3. Supplementary Data 3: Reduced accessibility at putative cis-regulatory modules in *Xenopus* gastrula stage ectoderm
 - a. DAVID functional gene annotation for Δ pCRMs.
 - b. List of gene names for nearest TSS within 100kb of Δ pCRM.
4. Supplementary Data 4: Motif analysis for putative cis-regulatory modules in *Xenopus* gastrula
 - a. pCRMs compared to genome background.
 - b. Δ pCRMs compared to genome background.
 - c. Δ pCRMs compared to pCRM background.
5. Supplementary Figure 1: Comparison of ATAC-Seq gastrula stage (*laevis*) and Dnase-Seq MBT (*tropicalis*)
 - a. Tracks for selected genes from *X. laevis* ATAC-Seq at stage 10 gastrula (Esmaeili et al) to *X. tropicalis* Dnase-Seq at stage 8.5 (MBT) from Gentsch et al 2019.