Chromatin structure—the genome-wide organization of DNA-associated proteins—plays a key role in cellular fate decisions. Histone modifications (HMs) are set (‘written’), removed (‘erased’) and bound (‘read’) by enzyme complexes termed Chromatin Regulators (CRs). Recent studies have demonstrated that aberrations in the function of CRs are highly implicated in diseases such as developmental abbreations and cancer. In our [previous efforts](https://www.ncbi.nlm.nih.gov/pubmed/22196736) we initiated a systematic study of the genomic organization of CRs. Following up on this, we employ our [high-throughput automated ChIP-seq approach](https://www.ncbi.nlm.nih.gov/pubmed/?term=27826357) to map CRs along differentiation and use the data to computationally identify and predict key developmental CRs. We then test these predictions by perturbing the protein levels of these candidate CRs by inducible degradation and assaying the effects on differentiation.