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THE DISTILLERY

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Using chromatin immunoprecipitation followed by whole-genome sequencing (ChIP-Seq) to identify disease-associated super-enhancer regulatory elements	Cell culture studies suggest mapping super-enhancers could help identify drug targets in cancer or other diseases. ChIP-Seq of mediator complex subunit 1 (MED1) in multiple myeloma (MM) cells identified 308 highly enriched sites of MED1 binding upstream of known oncogenic drivers, including c-Myc (MYC). These enriched MED1-bound regions were dubbed super-enhancers because they were bound by multiple transcriptional regulators of cell fate and drove target gene expression to higher levels than traditional enhancers. In MM cells, a bromodomain containing 4 (BRD4) inhibitor decreased expression of super-enhancer–regulated genes compared with that of genes not associated with super-enhancers. Next steps include identifying molecules to disrupt super-enhancer function and using super-enhancer mapping to identify drug targets.	Patent application filed for findings from both studies; licensed to Syros Pharmaceuticals Inc.	Whyte, W.A. *et al. Cell*; published online April 11, 2013; doi:10.1016/j.cell.2013.03.035 Lovén, J. *et al. Cell*; published online April 11, 2013; doi:10.1016/j.cell.2013.03.036 **Contact:** Richard Young, Whitehead Institute for Biomedical Research, Cambridge, Mass. e-mail: young@wi.mit.edu

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