Systematic identification of gene family regulators in mouse and human embryonic stem cells.

By elsc_admin

Created 9/15/2016
By elsc_admin September 15, 2016


Abstract:

Pluripotent self-renewing embryonic stem cells (ESCs) have been the focus of a growing number of high-throughput experiments, revealing the genome-wide locations of hundreds of transcription factors and histone modifications. While most of these datasets were used in a specific context, all datasets combined offer a comprehensive view of chromatin characteristics and regulatory elements that govern cell states. Here, using hundreds of datasets in ESCs, we generated colocalization maps of chromatin proteins and modifications, and built a discovery pipeline for regulatory proteins of gene families. By comparing genome-wide binding data with over-expression and knockdown analysis of hundreds of genes, we discovered that the pluripotency-related factor NR5A2 separates mitochondrial from cytosolic ribosomal genes, regulating their expression. We further show that genes with a common chromatin profile are enriched for distinct Gene Ontology (GO) categories. Our approach can be generalized to reveal common regulators of any gene group; discover novel gene families, and identify common genomic elements based on shared chromatin features.

Journal:
Nucleic acids research

Volume:
44

Issue:
9

Pagination:
4080-9

Date Published:
2016 May 19

Custom 1:
UPCOMING EVENTS

Learn more about our exciting upcoming events!

read more

Studying at ELSC

Our Int'l Ph.D. program provides outstanding students with top-notch courses in computational neuroscience.

read more

The Building

The Jerusalem Brain Sciences Building will provide a state-of-the-art research and teaching facility for the Edmond and Lily Safra Center for Brain Sciences.

read more

ELSC Media Channel

Get into our media channel and investigate ELSC's latest videos: seminars, public lectures, courses and video articles.

read more