

Regulatory Network Created from Loss of Function and Gain of Function Studies of Mouse Embryonic Stem Cells

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The advent of genome-wide mRNA microarrays and RNA-seq experiments for studying the regulatory networks controlling mouse embryonic stem cells (mESCs) ushered a wealth of experimental data. The task of reusing, organizing, integrating and interpreting this data as a whole becomes critical to understanding the underlying complex regulatory mechanisms that govern stem cell self-renewal and early differentiation. Specifically, the integration and analysis of mRNA expression in loss of function (LOF) or gain of function (GOF) experiments applied to mESCs where a single gene was either knocked out or added can be used to reconstruct regulatory networks among these genes and their protein products. In addition, a library of molecular signatures, of up and down genes for different LOF or GOF can be cross referenced with information about transcription factors and their putative target genes from chip-chip and chip-seq studies. Here we describe a new database called LOGOFEA containing 27 experiments, 72 perturbations, and 127257 interactions, describing LOF and GOF experiments applied to mESCs. Such database is utilized as a web-based system that can be used to perform enrichment analysis to relate new expression data to prior studies. In addition, by combining the content of the database with chip-chip and chip-seq studies we obtained a signed and directed mESC gene regulatory network. Such data integration effort can be a useful resource for the stem cell research community.