Transcriptional regulation of pluripotent stem cells

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references


Reactome database release: 79

This document contains 3 pathways and 12 reactions (see Table of Contents)
Transcriptional regulation of pluripotent stem cells

Stable identifier: R-HSA-452723

Compartments: cytosol, nucleoplasm


Pluripotency is maintained by a self-reinforcing loop of transcription factors (Boyer et al. 2005, Rao et al. 2006, Matoba et al. 2006, Player et al. 2006, Babaie et al. 2007, Sun et al. 2008, Assou et al. 2009, reviewed in Kashyap et al. 2009, reviewed in Dejosez and Zwaka 2012). In vivo, initiation of pluripotency may depend on maternal factors transmitted through the oocyte (Assou et al. 2009) and on DNA demethylation in the zygote (recently reviewed in Seisenberger et al. 2013) and hypoxia experienced by the blastocyst in the reproductive tract before implantation (Forristal et al. 2010, reviewed in Mohyeldin et al. 2010). In vitro, induced pluripotency may initiate with demethylation and activation of the promoters of POU5F1 (OCT4) and NANOG (Bhutani et al. 2010). Hypoxia also significantly enhances conversion to pluripotent stem cells (Yoshida et al. 2009). POU5F1 and NANOG, together with SOX2, encode central factors in pluripotency and activate their own transcription (Boyer et al. 2005, Babaie et al. 2007, Yu et al. 2007, Takahashi et al. 2007). The autoactivation loop maintains expression of POU5F1, NANOG, and SOX2 at high levels in stem cells and, in turn, complexes containing various combinations of these factors (Remenyi et al. 2003, Lam et al. 2012) activate the expression of a group of genes whose products are associated with rapid cell proliferation and repress the expression of a group of genes whose products are associated

Comparisons between human and mouse embryonic stem cells must be made with caution and for this reason inferences from mouse have been used sparingly in this module. Human ESCs more closely resemble mouse epiblast stem cells in having inactivated X chromosomes, flattened morphology, and intolerance to passaging as single cells (Hanna et al. 2010). Molecularly, human ESCs differ from mouse ESCs in being maintained by FGF and Activin/Nodal/TGFbeta signaling rather than by LIF and canonical Wnt signaling (Greber et al. 2010, reviewed in Katoh 2011). In human ESCs POU5F1 binds and directly activates the FGF2 gene, however Pou5f1 does not activate Fgf2 in mouse ESCs (reviewed in De Los Angeles et al. 2012). Differences in expression patterns of KLF2, KLF4, KLF5, ESRRB, FOXD3, SOCS3, LIN28, NODAL were observed between human and mouse ESCs (Cai et al. 2010) as were differences in expression of EOMES, ARNT and several other genes (Ginis et al.2004).

Literature references


Editions

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Expression of EPAS1 (HIF2A)

Location: Transcriptional regulation of pluripotent stem cells

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