Transcription of POU5F1 (OCT4)

May, B., Wang, J.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

20/04/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

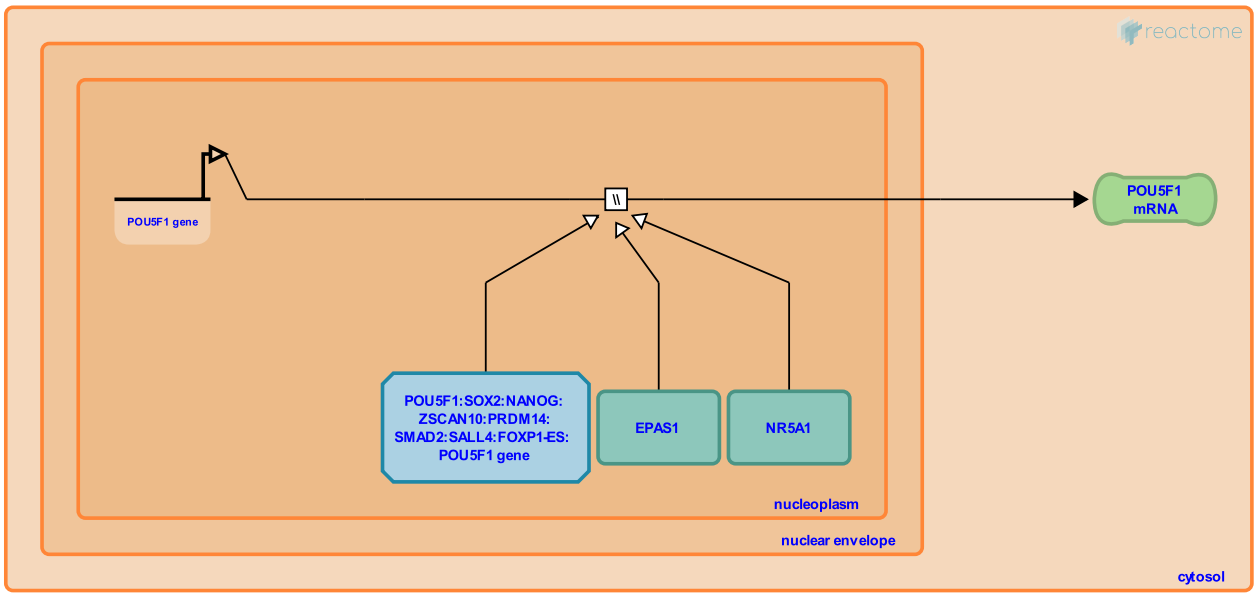
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Transcription of POU5F1 (OCT4) ↗

Stable identifier: R-HSA-452392

Type: omitted

Compartments: nucleoplasm, cytosol



The POU5F1 (OCT4) gene is transcribed to yield mRNA and the mRNA is translated to yield protein (Rao et al. 2004, Richards et al. 2004, Cauffman et al. 2005, Tai et al. 2005, Gerrard et al. 2005, Li et al. 2006, Adewumi et al. 2007,Assou etal. 2007). POU5F1 mRNA and protein are found in the cytoplasm of oocytes and cleavage-stage embryos (Cauffman et al. 2005). POU5F1 protein becomes nuclear during compaction, and protein and mRNA are present in inner cell mass and trophectoderm (Cauffman et al. 2005). Transcripts are also detectable in some differentiated tissues (Cauffman et al. 2005). POU5F1 is expressed in adult stem cells and cancers (Tai et al. 2005). POU5F1, SOX2, NANOG, SALL4, and SF-1(NR5A1) bind the promoter of the POU5F1 gene and enhance transcription (Matin et al. 2004, Chew et al. 2005, Boyer et al. 2005, Babaie et al. 2007, Greber et al. 2007, Wang et al. 2007, Yang et al. 2010, Chia et al. 2010). POU5F1 and SOX2 bind adjacent sites at the promoter and form a heterodimer on the DNA. SALL4 binds the promoter of the POU5F1 gene and activates transcription of POU5F1 (Yang et al. 2010). POU5F1 activates SALL4 expression thus forming a self-reinforcing loop. Activation-induced cytidine deaminase (AID) binds the methylated promoter of the POU5F1 gene, demethylates it, and enhances expression of POU5F1 (Bhutani et al. 2009). Hypoxia acts via HIF3A and EPAS1 (HIF2A) to enhance expression of POU5F1 (Forristal et al. 2010). LIN28 binds the POU5F1 mRNA and increases translation (Qiu et al. 2009).

Literature references

Richards, M., Bongso, A., Tan, SP., Chan, WK., Tan, JH. (2004). The transcriptome profile of human embryonic stem cells as defined by SAGE. *Stem Cells, 22*, 51-64. ↗

Gifford, DK., Jaenisch, R., Lee, TI., Young, RA., Kumar, RM., Guenther, MG. et al. (2005). Core transcriptional regulatory circuitry in human embryonic stem cells. *Cell, 122*, 947-56. ↗

Ruotti, V., Antosiewicz-Bourget, J., Thomson, JA., Vodyanik, MA., Stewart, R., Tian, S. et al. (2007). Induced pluripotent stem cell lines derived from human somatic cells. *Science, 318*, 1917-20. ↗

Andrews, PW., Matin, MM., Draper, JS., Gokhale, PJ., Moore, HD., Bahrami, AR. et al. (2004). Specific knockdown of Oct4 and beta2-microglobulin expression by RNA interference in human embryonic stem cells and embryonic carcinoma cells. *Stem Cells, 22*, 659-68. ↗

Houghton, FD., Forristal, CE., Oreffo, RO., Wright, KL., Hanley, NA. (2010). Hypoxia inducible factors regulate pluripotency and proliferation in human embryonic stem cells cultured at reduced oxygen tensions. *Reproduction, 139* , 85-97. ↗

Editions

2010-11-12	Authored, Edited	May, B.
2014-01-23	Reviewed	Wang, J.