Expression of Sox9 in testis differentiation

Imaimatsu, K., Kanai, Y., May, B.

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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

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. ↗
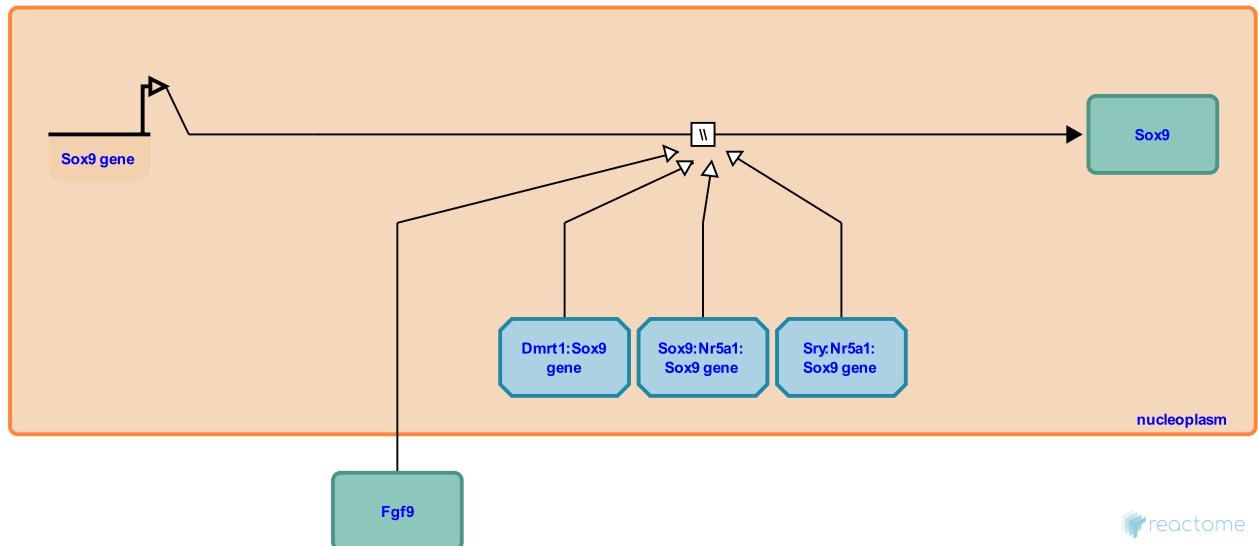
Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

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Sry and Nr5a1 bound at the TES enhancer upstream of the Sox9 gene (Sekido and Lovell-Badge 2008) and other enhancers (Gonen et al. 2017) activate transcription of Sox9 (Kidokoro et al. 2005, Sekido and Lovell-Badge 2008, Matoba et al. 2008, Gonen et al. 2017). Later in development, expression of Sry ceases and Sox9 activates expression of its own gene (Sekido and Lovell-Badge 2008). Dmrt1, itself directly activated by Sox9, also directly activates Sox9 (Matson et al. 2011, Lindeman et al. 2015). Fgf9 acting through Fgfr2 and Prostaglandin D2 activate Sox9 through less well characterized mechanisms (Kim et al. 2006).

Literature references

Harikae, K., Hiramatsu, R., Kawakami, H., Kanai, Y., Matoba, S., Tsunekawa, N. et al. (2008). Establishment of testis-specific SOX9 activation requires high-glucose metabolism in mouse sex differentiation. *Dev. Biol., 324*, 76-87. ↗

Sekido, R., Lovell-Badge, R. (2008). Sex determination involves synergistic action of SRY and SF1 on a specific Sox9 enhancer. *Nature, 453*, 930-4. ↗

Hiramatsu, R., Kawakami, H., Fujisawa, M., Kidokoro, T., Yonekawa, H., Kanai, Y. et al. (2005). Influence on spatiotemporal patterns of a male-specific Sox9 activation by ectopic Sry expression during early phases of testis differentiation in mice. *Dev. Biol., 278*, 511-25. ↗

Koopman, P., O'Neill, HC., Gonen, N., Quinn, A., Lovell-Badge, R. (2017). Normal Levels of Sox9 Expression in the Developing Mouse Testis Depend on the TES/TESCO Enhancer, but This Does Not Act Alone. *PLoS Genet., 13*, e1006520. ↗

Editions

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