

Core MLL complex methylates H3K4Me2- Nucleosome at the THBS1 gene promoter

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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

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Reactome database release: 74

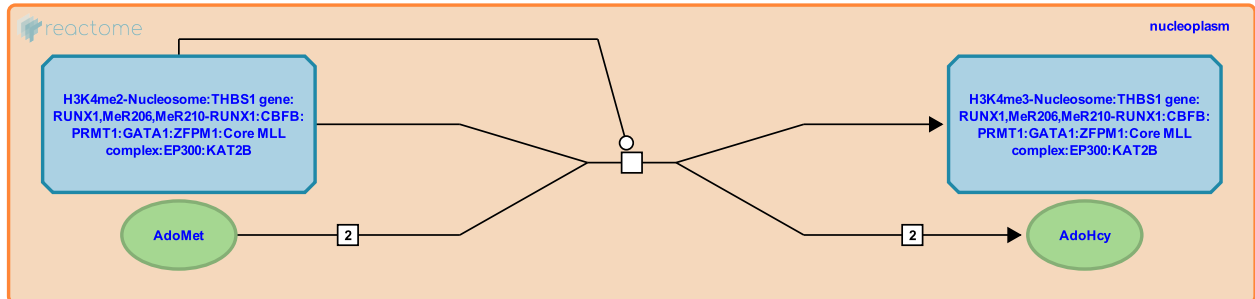
This document contains 1 reaction ([see Table of Contents](#))

Core MLL complex methylates H3K4Me2-Nucleosome at the THBS1 gene promoter ↗

Stable identifier: R-HSA-8937016

Type: transition

Compartments: nucleoplasm



The WDR5-containing histone methyltransferase MLL complex, recruited to the THBS1 (TSP-1) promoter via RUNX1 (and possibly GATA1), is assumed to methylate histone H3 on dimethylated lysine residue K4 (K5 when taking into account the initiator methionine), producing the H3K4me3 mark. The H3K4me3 mark is characteristic of nucleosome associated with transcriptionally active promoters of megakaryocyte-specific genes (Herglotz et al. 2013) and the appearance of the H3K4me3 mark at the THBS1 promoter coincides with THBS1 transactivation (Michaud-Levesque and Richard 2009).

Literature references

Michaud-Levesque, J., Richard, S. (2009). Thrombospondin-1 is a transcriptional repression target of PRMT6. *J. Biol. Chem.*, 284, 21338-46. ↗

Herglotz, J., Kuvardina, ON., Kolodziej, S., Kumar, A., Hussong, H., Grez, M. et al. (2013). Histone arginine methylation keeps RUNX1 target genes in an intermediate state. *Oncogene*, 32, 2565-75. ↗

Editions

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