Hoxb2 chromatin is activated

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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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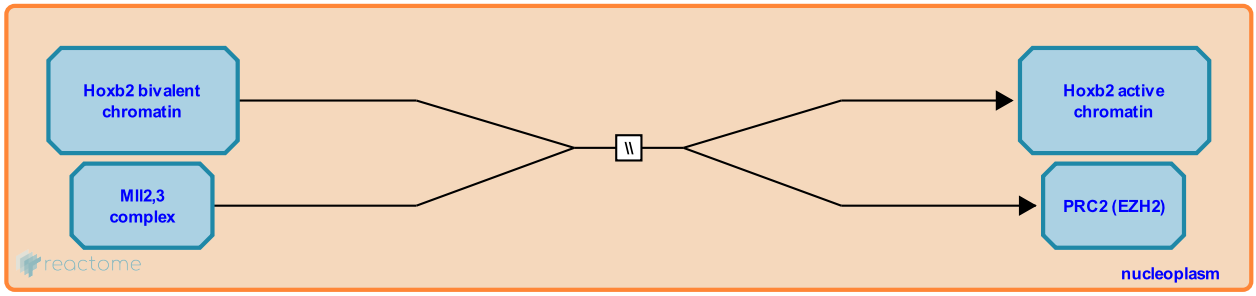
Stable identifier: R-MMU-6810170

Type: omitted

Compartments: nucleoplasm



As inferred from mouse embryonic stem cells activated by retinoic acid (Kashyap et al. 2011, Mazzoni et al. 2013) and human cell lines, methylation at lysine-27 of histone H3 (H3K27me3) is lost (Kashyap et al. 2011, Mazzoni et al. 2013), Polycomb repressive complex 2 (PRC2) is lost (Mazzoni et al. 2013), and methylation at lysine-4 (H3K4me3) is gained (Kashyap et al. 2011). The Mll2 complex methylates H3K4 at Hoxb2 in fibroblasts (Wang et al. 2009). In human cells, the histone demethylase KDM6A (UTX) binds HOXB2 chromatin and demethylates H3K27me3. Other factors may also participate in demethylation.

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Editions

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