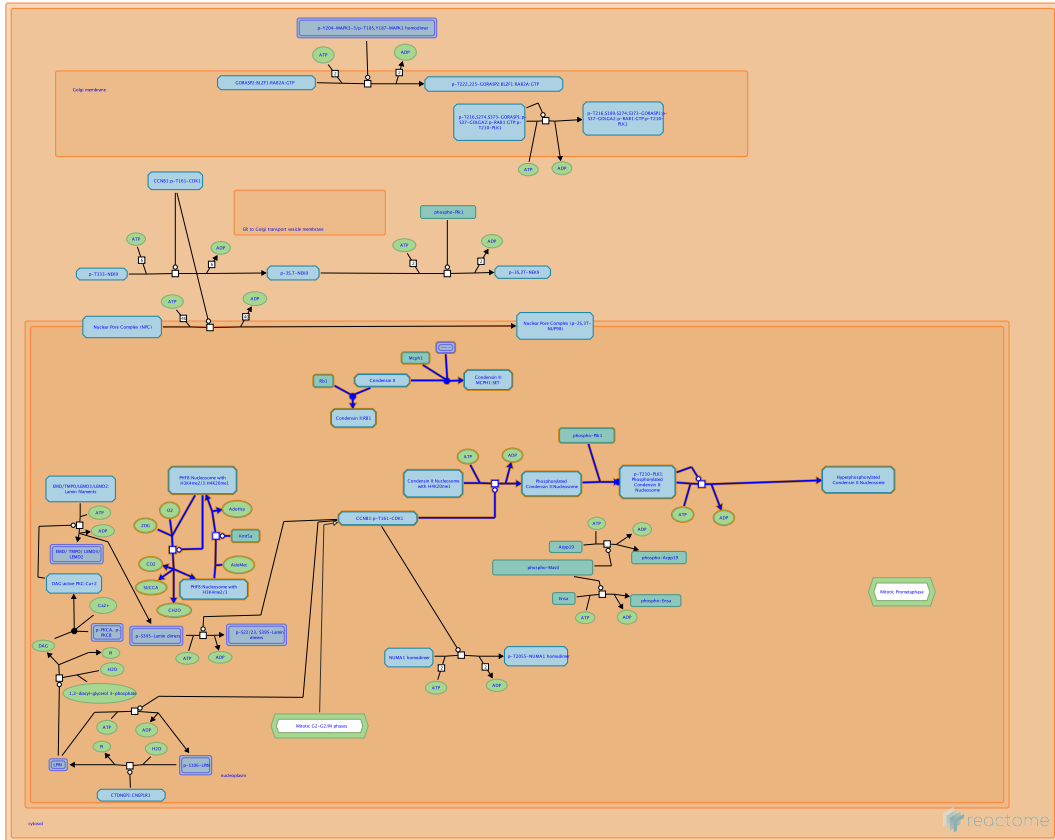


# Condensation of Prophase Chromosomes



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

## 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. [↗](#)

Reactome database release: 77

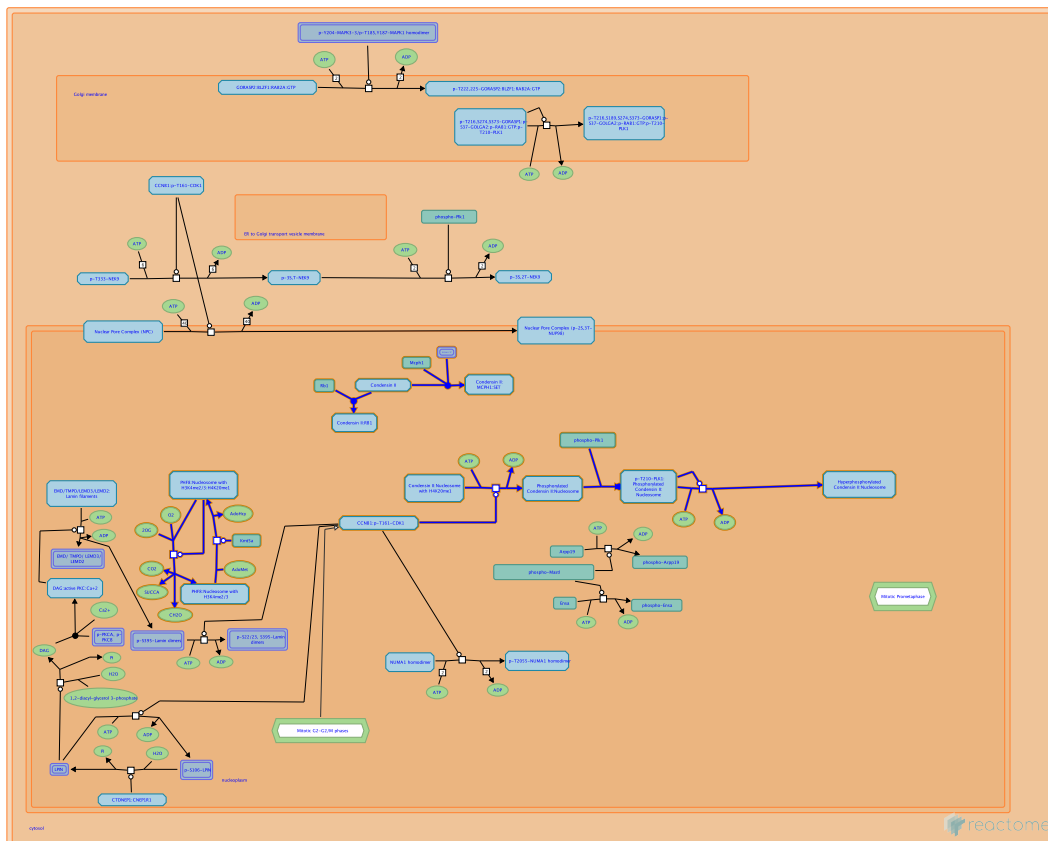
This document contains 1 pathway and 7 reactions ([see Table of Contents](#))

## Condensation of Prophase Chromosomes ↗

**Stable identifier:** R-RNO-2299718

**Compartments:** nucleoplasm

**Inferred from:** Condensation of Prophase Chromosomes (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## SETD8 monomethylates histone H4 ↗

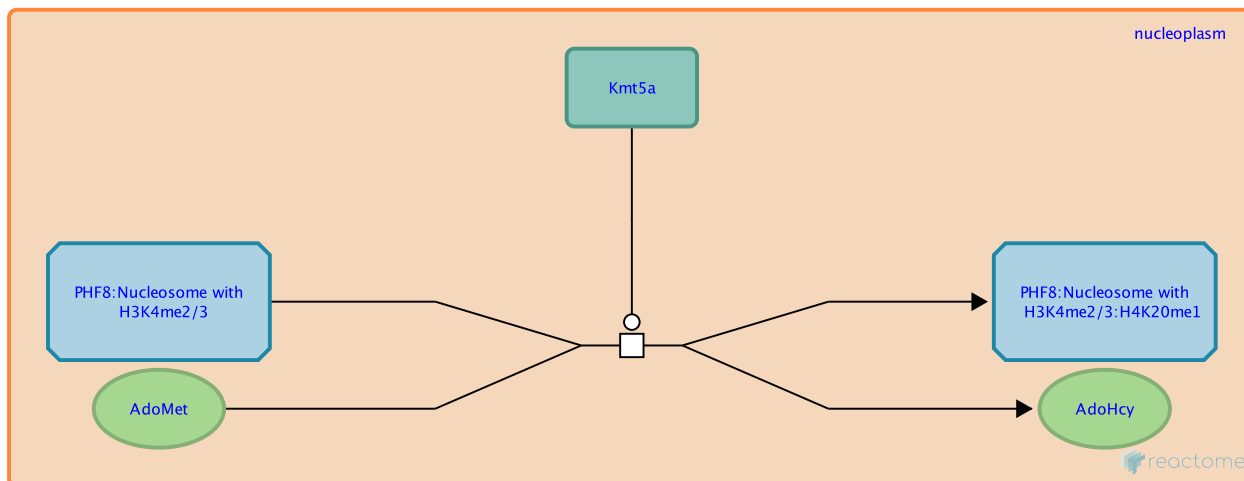
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2301205

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [SETD8 monomethylates histone H4 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [PHF8 demethylates histone H4K20me1](#)

## PHF8 demethylates histone H4K20me1 [↗](#)

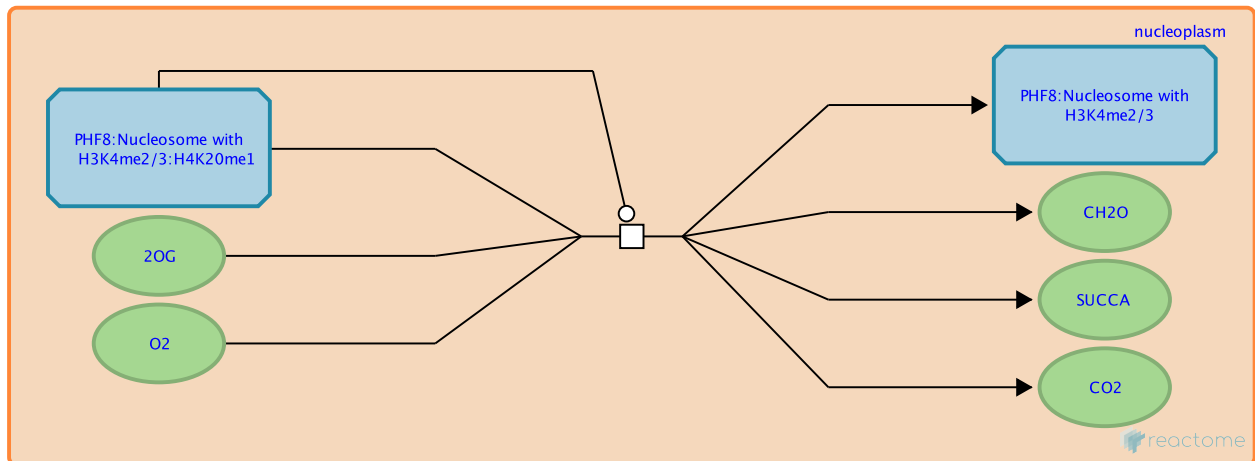
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2172678

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [PHF8 demethylates histone H4K20me1 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [SETD8 monomethylates histone H4](#)

## RB1 binds condensin II ↗

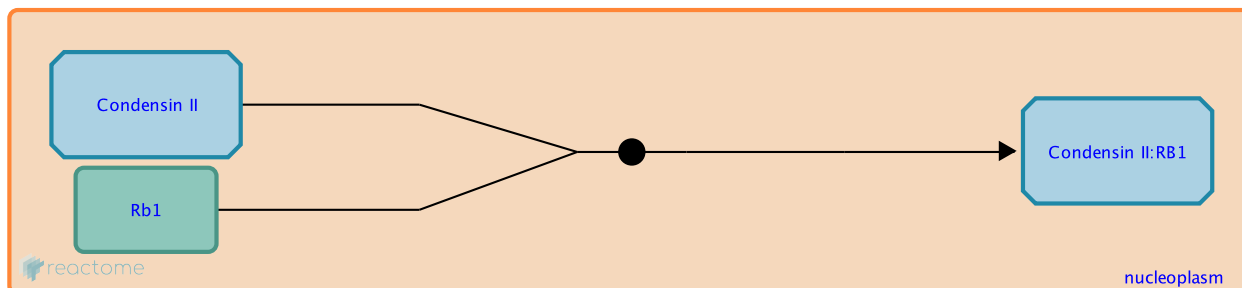
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2172666

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [RB1 binds condensin II \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## CDK1 phosphorylates condensin II subunit NCAPD3 ↗

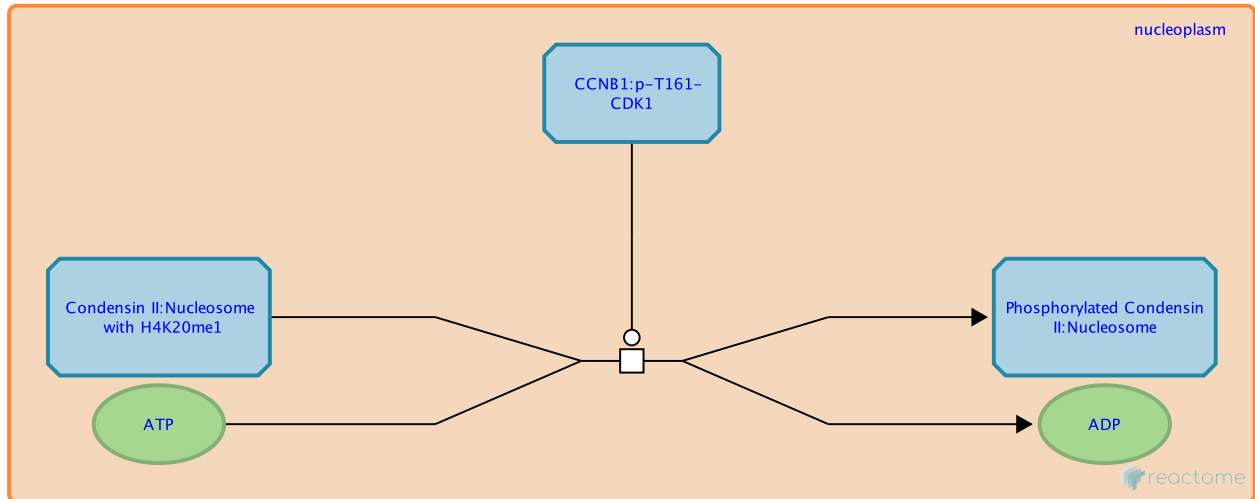
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2294600

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [CDK1 phosphorylates condensin II subunit NCAPD3 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [PLK1 binds phosphorylated condensin II complex](#)

## PLK1 binds phosphorylated condensin II complex ↗

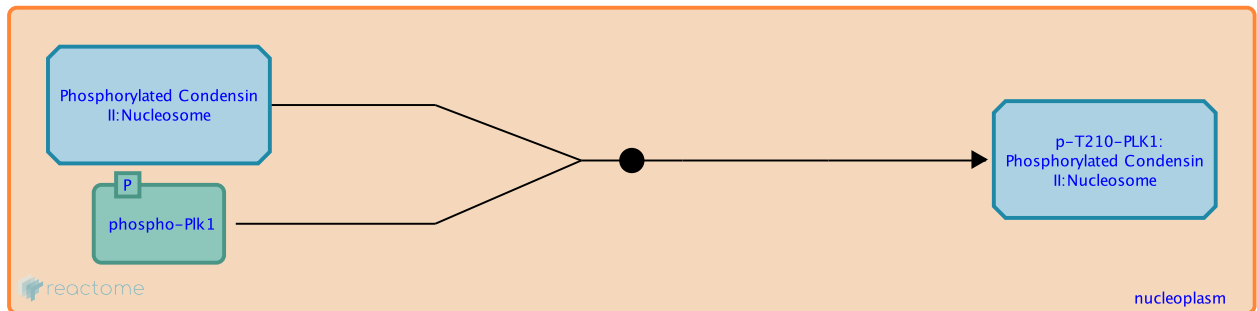
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2294590

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [PLK1 binds phosphorylated condensin II complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [CDK1 phosphorylates condensin II subunit NCAPD3](#)

**Followed by:** [PLK1 hyperphosphorylates Condensin II complex](#)



## PLK1 hyperphosphorylates Condensin II complex ↗

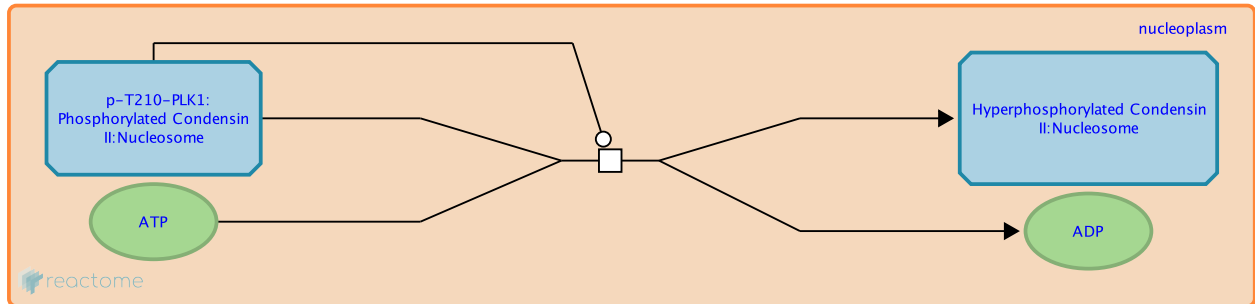
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2294580

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [PLK1 hyperphosphorylates Condensin II complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [PLK1 binds phosphorylated condensin II complex](#)

## MCPH1 sequesters condensin II ↗

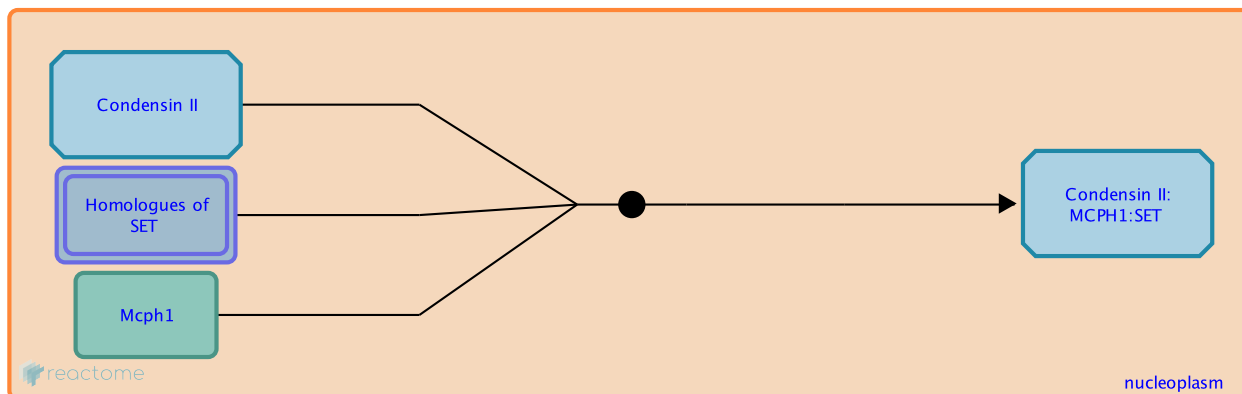
**Location:** [Condensation of Prophase Chromosomes](#)

**Stable identifier:** R-RNO-2429719

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [MCPH1 sequesters condensin II \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

# Table of Contents

Introduction	1
☞ Condensation of Prophase Chromosomes	2
☞ SETD8 monomethylates histone H4	3
☞ PHF8 demethylates histone H4K20me1	4
☞ RB1 binds condensin II	5
☞ CDK1 phosphorylates condensin II subunit NCAPD3	6
☞ PLK1 binds phosphorylated condensin II complex	7
☞ PLK1 hyperphosphorylates Condensin II complex	8
☞ MCPH1 sequesters condensin II	9
Table of Contents	10