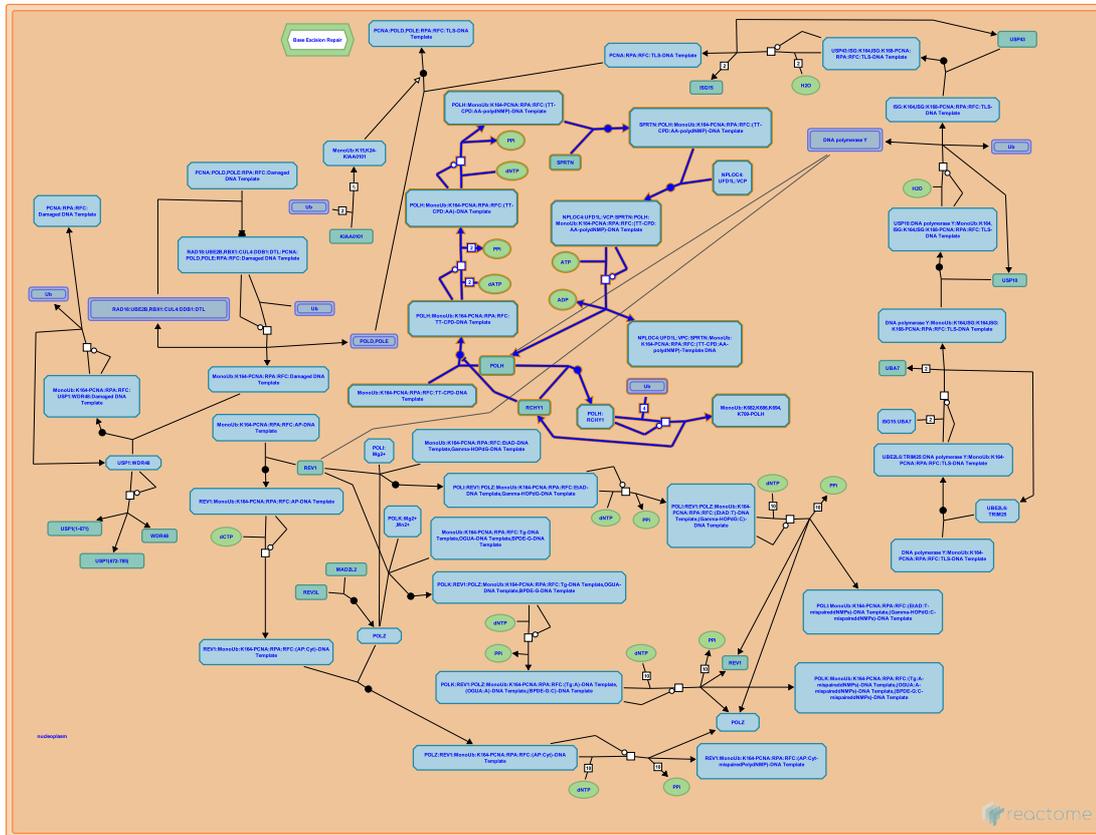


Translesion Synthesis by POLH



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

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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.

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. [↗](#)
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- 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: 70

This document contains 1 pathway and 8 reactions ([see Table of Contents](#))

POLH binds monoUb:K164-PCNA at damaged TT-CPD-DNA template ↗

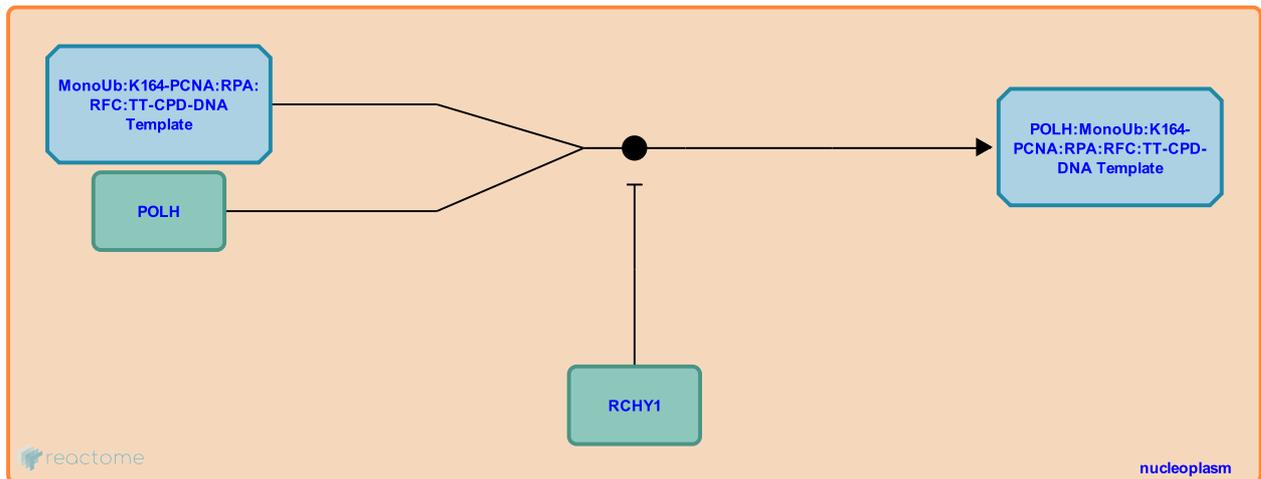
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-110316

Type: binding

Compartments: nucleoplasm

Inferred from: [POLH binds monoUb:K164-PCNA at damaged TT-CPD-DNA template \(Homo sapiens\)](#)



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: [Insertion of correct bases opposite the lesion by POLH](#)

Insertion of correct bases opposite the lesion by POLH ↗

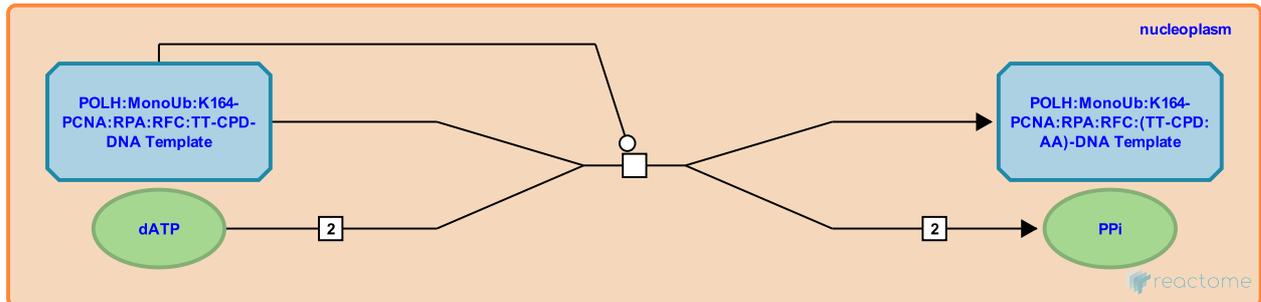
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-110317

Type: transition

Compartments: nucleoplasm

Inferred from: [Insertion of correct bases opposite the lesion by POLH \(Homo sapiens\)](#)



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.

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Preceded by: [POLH binds monoUb:K164-PCNA at damaged TT-CPD-DNA template](#)

Followed by: [Elongation by POLH](#)

Elongation by POLH ↗

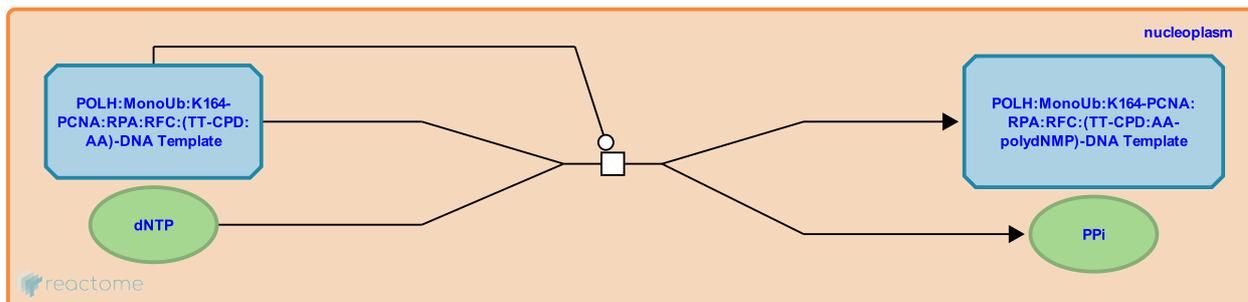
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-110319

Type: transition

Compartments: nucleoplasm

Inferred from: [Elongation by POLH \(Homo sapiens\)](#)



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: [Insertion of correct bases opposite the lesion by POLH](#)

Followed by: [SPRTN binds monoUb:K164-PCNA associated with POLH](#)

RCHY1 binds POLH [↗](#)

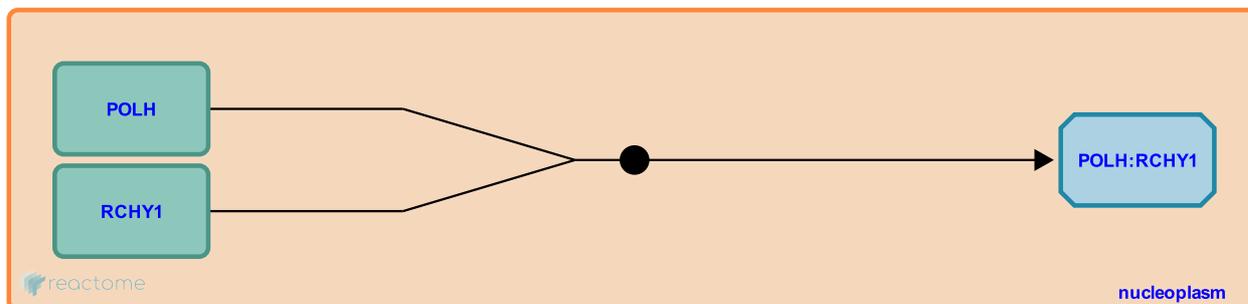
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-5655142

Type: binding

Compartments: nucleoplasm

Inferred from: [RCHY1 binds POLH \(Homo sapiens\)](#)



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: [RCHY1 monoubiquitinates POLH](#)

RCHY1 monoubiquitinates POLH ↗

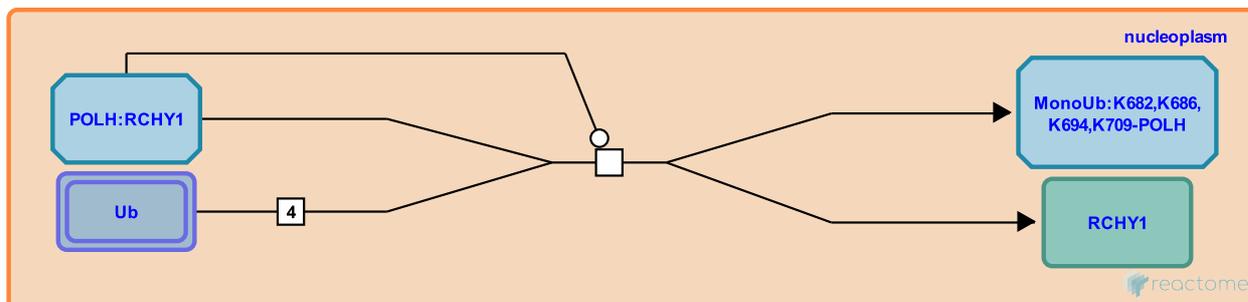
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-5655170

Type: transition

Compartments: nucleoplasm

Inferred from: [RCHY1 monoubiquitinates POLH \(Homo sapiens\)](#)



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: [RCHY1 binds POLH](#)

SPRTN binds monoUb:K164-PCNA associated with POLH ↗

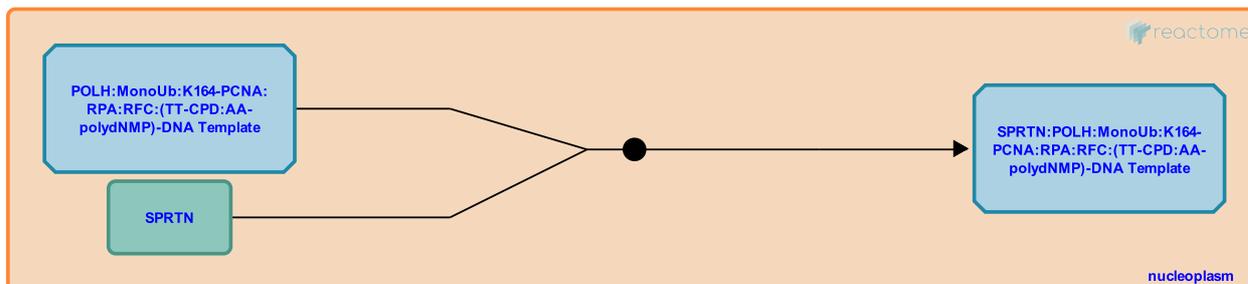
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-5654986

Type: binding

Compartments: nucleoplasm

Inferred from: [SPRTN binds monoUb:K164-PCNA associated with POLH \(Homo sapiens\)](#)



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: [Elongation by POLH](#)

Followed by: [SPRTN recruits VCP to monoUb:K164-PCNA associated with POLH](#)

SPRTN recruits VCP to monoUb:K164-PCNA associated with POLH ↗

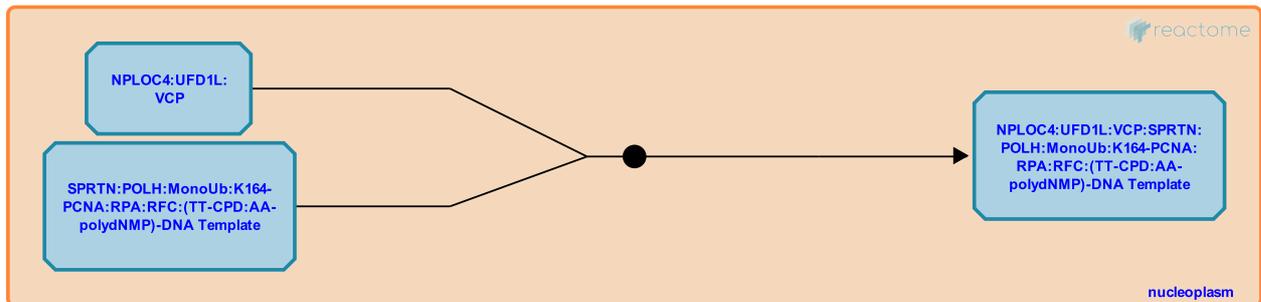
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-5654985

Type: binding

Compartments: nucleoplasm

Inferred from: [SPRTN recruits VCP to monoUb:K164-PCNA associated with POLH \(Homo sapiens\)](#)



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: [SPRTN binds monoUb:K164-PCNA associated with POLH](#)

Followed by: [SPRTN:VCP-mediated release of POLH from monoUb:K164-PCNA](#)

SPRTN:VCP-mediated release of POLH from monoUb:K164-PCNA ↗

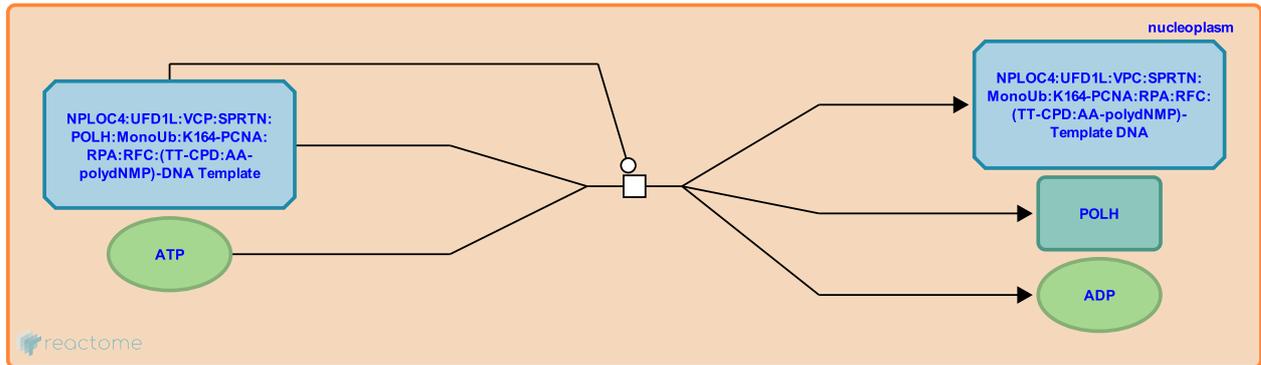
Location: [Translesion Synthesis by POLH](#)

Stable identifier: R-CFA-5654989

Type: transition

Compartments: nucleoplasm

Inferred from: [SPRTN:VCP-mediated release of POLH from monoUb:K164-PCNA \(Homo sapiens\)](#)



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: [SPRTN recruits VCP to monoUb:K164-PCNA associated with POLH](#)

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