Defective NTHL1 truncation mutants do not bind thymine glycol (Tg)

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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. ↗

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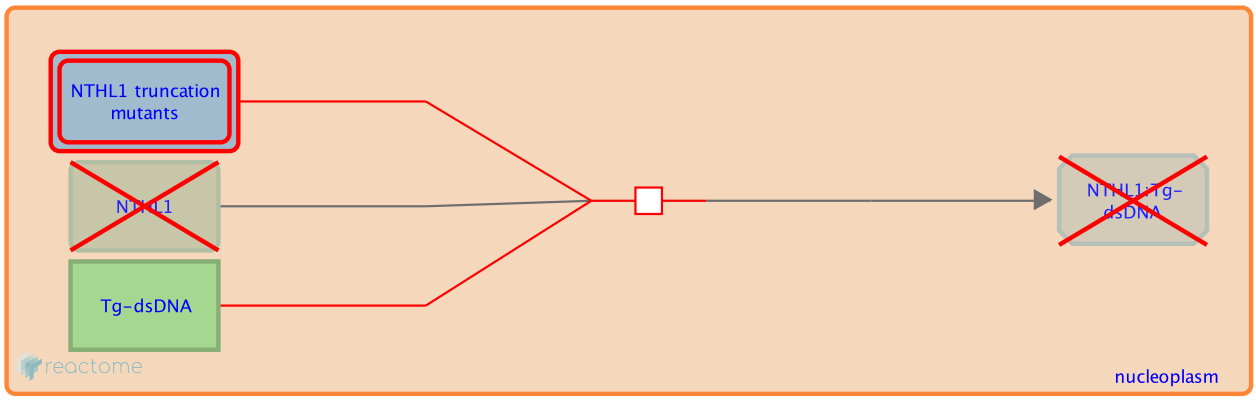
Stable identifier: R-HSA-9630043

Type: transition

Compartments: nucleoplasm

Diseases: cancer



NTHL1 Q90TER (NTHL1 Q90*) truncation mutant (Weren et al. 2015) lacks the DNA binding domain and the glycosylase domain and is thus predicted to be unable to recognize and bind damaged DNA, including damaged DNA containing thymine glycol (Tg), although this has not been experimentally tested. NTHL1 Q287TER (NTHL1 Q287*) truncation mutant (Broderick et al. 2017) lacks a portion of the DNA binding domain, including glutamine residue Q287, important for substrate recognition (Robey-Bond et al. 2017) and is predicted to be unable to recognize and bind damaged DNA, including damaged DNA containing thymine glycol (Tg), although this has not been experimentally tested.

Literature references

Broderick, P., Dobbins, SE., Chubb, D., Kinnersley, B., Dunlop, MG., Tomlinson, I. et al. (2017). Validation of Recently Proposed Colorectal Cancer Susceptibility Gene Variants in an Analysis of Families and Patients-a Systematic Review. *Gastroenterology, 152*, 75-77.e4.

Weren, RD., Ligtenberg, MJ., Kets, CM., de Voer, RM., Verwiel, ET., Spruijt, L. et al. (2015). A germline homozygous mutation in the base-excision repair gene NTHL1 causes adenomatous polyposis and colorectal cancer. *Nat. Genet., 47*, 668-71.

Editions

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