The ClinGen Evidence Repository is an **FDA-recognized human genetic variant database** containing expert-curated assertions regarding variants' pathogenicity and supporting evidence summaries. [Disclaimer]

Variant: NM_004360.5(CDH1):c.940A>T (p.Lys314Ter)

Version: 2.0

CA396459763

428632 (ClinVar)

Gene: CDH1 (HGNC:999)
Condition: CDH1-related diffuse gastric and lobular breast cancer (MONDO:0100488)
Inheritance Mode: Autosomal dominant inheritance
UUID: 8277d227-4d10-4ebb-bc74-fee3cba23a52
Approved on: 2023/8/25
Published on: 2023/8/25

HGVS expressions

NM_004360.5:c.940A>T
NM_004360.5(CDH1):c.940A>T (p.Lys314Ter)
NC_000016.10:g.68811791A>T
CM000678.2:g.68811791A>T
NC_000016.9:g.68845694A>T
CM000678.1:g.68845694A>T
NC_000016.8:g.67403195A>T
NG_008021.1:g.79500A>T
ENST00000261769.10:c.940A>T
ENST00000261769.9:c.940A>T
ENST00000422392.6:c.940A>T
ENST00000561751.1:c.562A>T
ENST00000562836.5:n.1011A>T
ENST00000566510.5:c.784A>T
ENST00000566612.5:c.940A>T
ENST00000611625.4:c.940A>T
ENST00000612417.4:c.940A>T
ENST00000621016.4:c.940A>T
NM_004360.3:c.940A>T
NM_001317184.1:c.940A>T
NM_001317185.1:c.-676A>T
NM_001317186.1:c.-880A>T
NM_004360.4:c.940A>T
NM_001317184.2:c.940A>T
NM_001317185.2:c.-676A>T
NM_001317186.2:c.-880A>T

Pathogenic

Met criteria codes 4

PVS1 PM2_Supporting PS4_Supporting PM5_Supporting

Not Met criteria codes 22

PS1 PS2 PS3 PP1 PP2 PP3 PP4 PM1 PM3 PM4 PM6

Expert Panel

CDH1 VCEP

Criteria Specification Information

Criteria Specification: *ClinGen CDH1 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines Version 3.1*

BA1 BS1 BS4 BS3 BS2 BP5
BP7 BP4 BP3 BP1 BP2

Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence Links 0

Evidence submitted by expert panel

CDH1 VCEP

The c.940A>T (p.Lys314Ter) variant is predicted to result in a premature termination codon in exon 7 (PVS1, PM5_Supporting). The variant is absent from the gnomAD population database (PM2_Supporting; https://gnomad.broadinstitute.org/). This variant has previously been reported in one individual meeting IGCLC criteria for HDGC (PS4_Supporting; PMID: 26182300). In summary, this variant meets criteria to be classified as pathogenic based on ACMP/AMP criteria as specified by the CDH1 Variant Curation Expert Panel (Variant Interpretation Guidelines Version 3.1): PVS1, PM2_Supporting, PS4_Supporting, PM5_Supporting.

Met criteria codes

PVS1	✔	This variant results in a premature termination codon in exon 7.
PM2_Supporting	✔	This variant is absent from populations in gnomAD, ExAC, 1000 Genomes and ESP.
PS4_Supporting	✔	This variant was reported in one individual meeting IGCLC criteria for HDGC based on a personal and family history of diffuse gastric cancer (PMID: 26182300).
PM5_Supporting	✔	Apply PM5_Supporting to nonsense/frameshift variants that are predicted/proved to undergo NMD.

Not Met criteria codes

PS1	✖	PS1 does not apply to this variant.
PS2	✖	To our knowledge, this variant has not been reported as de novo.
PS3	✖	PS3 does not apply to this variant.
PP1	✖	To our knowledge, segregation of this variant has not been reported.
PP2	✖	PP2 does not apply to CDH1.
PP3	✖	PP3 does not apply to this variant.
PP4	✖	PP4 does not apply to CDH1.

PM1		✖	PM1 does not apply to this variant.
PM3		✖	PM3 does not apply to CDH1.
PM4	ℹ	✖	PM4 does not apply to this variant.
PM6	ℹ	✖	To our knowledge, this variant has not been reported as de novo.
BA1	ℹ	✖	This variant is absent from populations in gnomAD, ExAC, 1000 Genomes and ESP.
BS1	ℹ	✖	This variant is absent from populations in gnomAD, ExAC, 1000 Genomes and ESP.
BS4	ℹ	✖	To our knowledge, segregation of this variant has not been reported.
BS3	ℹ	✖	BS3 does not apply to this variant.
BS2	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP5	ℹ	✖	To our knowledge, this variant has not been reported in a case with an alternate molecular basis for disease.
BP7	ℹ	✖	BP7 does not apply to this variant.
BP4	ℹ	✖	BP4 does not apply to this variant.
BP3		✖	BP3 does not apply to CDH1.
BP1		✖	BP1 does not apply to CDH1.
BP2	ℹ	✖	To our knowledge, this variant has not been observed in cis or trans with a known pathogenic variant.

Curation History

Showing 1 to 2 of 2 rows

The information on this website is not intended for direct diagnostic use or medical decision-making without review by a genetics professional. Individuals should not change their health behavior solely on the basis of information contained on this website. If you have questions about the information contained on this website, please see a health care professional.