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.26C>A (p.Ser9Ter)

Version: 2.0

CA396451339

651982 (ClinVar)

Gene: CDH1 (HGNC:999)
Condition: CDH1-related diffuse gastric and lobular breast cancer (MONDO:0100488)
Inheritance Mode: Autosomal dominant inheritance
UUID: 137479c7-fb2b-49f0-b469-1224ccbcb1c3
Approved on: 2023/8/25
Published on: 2023/8/25

HGVS expressions

NM_004360.5:c.26C>A
NM_004360.5(CDH1):c.26C>A (p.Ser9Ter)
NC_000016.10:g.68737441C>A
CM000678.2:g.68737441C>A
NC_000016.9:g.68771344C>A
CM000678.1:g.68771344C>A
NC_000016.8:g.67328845C>A
NG_008021.1:g.5150C>A
ENST00000261769.10:c.26C>A
ENST00000261769.9:c.26C>A
ENST00000422392.6:c.26C>A
ENST00000566510.5:c.26C>A
ENST00000566612.5:c.26C>A
ENST00000611625.4:c.26C>A
ENST00000612417.4:c.26C>A
ENST00000621016.4:c.26C>A
NM_004360.3:c.26C>A
NM_001317184.1:c.26C>A
NM_001317185.1:c.-1590C>A
NM_001317186.1:c.-1794C>A
NM_004360.4:c.26C>A
NM_001317184.2:c.26C>A
NM_001317185.2:c.-1590C>A
NM_001317186.2:c.-1794C>A

Pathogenic

Met criteria codes 4

PVS1 PM2_Supporting PM5_Supporting PS4_Moderate

Not Met criteria codes 22

BS1 BS4 BS3 BS2 BP5 BP7 BP4 BP3 BP1 BP2 PS1 PS2 PS3 PM1 PM3 PM4 BA1 PM6 PP1 PP2 PP3 PP4

Expert Panel

CDH1 VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen CDH1 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines Version 3.1*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence Links 0

Evidence submitted by expert panel

CDH1 VCEP

The c.26C>A (p.Ser9Ter) variant is predicted to result in a premature stop codon in exon 1 that leads to a truncated or absent protein (PVS1, PM5_Supporting). This variant is absent in the gnomAD cohort (PM2_supporting; http://gnomad.broadinstitute.org). Two families meet HDGC phenotypic criteria (PS4_moderate; SCV000947495.1 and internal contributor). In summary, this variant meets criteria to be classified as pathogenic based on the ACMG/AMP criteria applied as specified by the CDH1 Variant Curation Expert Panel (Variant Interpretation Guidelines Version 3.1): PVS1, PM2_supporting, PS4_moderate, PM5_Supporting.

Met criteria codes

PVS1	✔	Loss of CDH1 function is a known mechanism of disease. This variant creates a premature translational stop signal at the codon 9 for Serin, exon 1 of the in the CDH1 gene. It is expected to result in an absent or disrupted protein product.
PM2_Supporting	✔	absent in gnomAD, 1000 Genomics and ESP with good coverage.
PM5_Supporting	✔	Apply PM5_Supporting to nonsense/frameshift variants that are predicted/proved to undergo NMD.
PS4_Moderate	✔	Two families meet HDGC phenotypic criteria (SCV000947495.1 and internal contributor).

Not Met criteria codes

BS1	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS4	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS3	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS2	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP5	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP7	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

BP4	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP3		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP2	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS2	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS3	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM1		✖	This variant is in the exon 1 for signal peptide.
PM3		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM4	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BA1	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM6	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP1	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP2		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP3	ℹ	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

PP4	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

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.

ClinGen Terms of Use.

¤ Powered by BCM's Genboree.