

Variant: *NM_004360.5(CDH1):c.360dup (p.His121fs)*

Version: 1.0

[CA10583408](#)

[239903 \(ClinVar\)](#)

Gene: CDH1 ([HGNC:999](#))

Condition: CDH1-related diffuse gastric and lobular breast cancer ([MONDO:0100488](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: e116f274-4c06-47a0-a9a0-fef88440fff9

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HGVS expressions

NM_004360.5:c.360dup

NM_004360.5(CDH1):c.360dup (p.His121fs)

NC_000016.10:g.68801866dup

CM000678.2:g.68801866dup

NC_000016.9:g.68835769dup

CM000678.1:g.68835769dup

NC_000016.8:g.67393270dup

NG_008021.1:g.69575dup

ENST00000261769.10:c.360dup

ENST00000261769.9:c.360dup

ENST00000422392.6:c.360dup

ENST00000561751.1:c.127dup

ENST00000562836.5:n.431dup

ENST00000564676.5:n.642dup

ENST00000564745.1:n.355dup

ENST00000566510.5:c.360dup

ENST00000566612.5:c.360dup

ENST00000611625.4:c.360dup

ENST00000612417.4:c.360dup

ENST00000621016.4:c.360dup

NM_004360.3:c.360dup

NM_001317184.1:c.360dup

NM_001317185.1:c.-1256dup

NM_001317186.1:c.-1460dup

NM_004360.4:c.360dup

NM_001317184.2:c.360dup

NM_001317185.2:c.-1256dup

NM_001317186.2:c.-1460dup

Pathogenic

Met criteria codes **4**

PM2_Supporting

PVS1

PM5_Supporting

PS4_Supporting

Not Met criteria codes **22**

Expert Panel

Criteria Specification Information

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

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

[Guidelines Version 3.1](#)
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[Criteria Specifications for this VCEP](#)

Evidence Links 0

Evidence submitted by expert panel

CDH1 VCEP

The c.360dupG (p.His121Alafs*47) variant is predicted to result in a premature stop codon that leads to a truncated or absent protein (PVS1, PM5_Supporting). The variant is absent in the gnomAD cohort (PM2_Supporting; <http://gnomad.broadinstitute.org>). This variant has been reported in at least one family meeting HDGC clinical criteria (PS4_Supporting, SCV000288479.2). 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_Supporting, PM5_Supporting.

Met criteria codes

PM2_Supporting			This variant is absent from populations in gnomAD, ExAC, 1000 Genomes and ESP.
PVS1			This variant occurs in exon 3 and is predicted to result in a premature stop codon that leads to a truncated or absent protein.
PM5_Supporting			Apply PM5_Supporting to nonsense/frameshift variants that are predicted/proved to undergo NMD.
PS4_Supporting			This variant was identified in a proband meeting the HDGC criteria (SCV000288479.2).

Not Met criteria codes

BA1			This variant is absent from populations in gnomAD, ExAC, 1000 Genomes and ESP.
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 frameshift variants.
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 frameshift variants.

PP4			PP4 does not apply to CDH1.
PM1			PM1 does not apply to CDH1.
PM3			PM3 does not apply to CDH1.
PM4			PM4 does not apply to frameshift variants.
PM6			To our knowledge, this variant has not been reported as de novo.
BS2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS1			This variant is absent from populations in gnomAD, ExAC, 1000 Genomes and ESP.
BS4			To our knowledge, segregation of this variant has not been reported.
BS3			BS3 does not apply to frameshift variants.
BP4			BP4 does not apply to frameshift variants.
BP3			BP3 does not apply to CDH1.
BP1			BP1 does not apply to CDH1.
BP2			To our knowledge, this variant has not been reported in cis or trans with a pathogenic variant.
BP5			To our knowledge, this variant has not been reported in a case with an alternate molecular basis for disease.
BP7			BP7 does not apply to frameshift variants.

Curation History [↗](#)

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