

Variant: *NM_004360.5(CDH1):c.2062_2063TG[1]*
(*p.Cys688_Glu689delinsTer*)

Version: 2.0

CA163542 [↗](#)

140781 (ClinVar) [↗](#)

Gene: [CDH1](#)

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

Inheritance Mode: Autosomal dominant inheritance

UUID: 3f59f180-03c4-40bf-8632-9084331cc8d5

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HGVS expressions

NM_004360.5:c.2062_2063TG[1]

NM_004360.5(CDH1):c.2062_2063TG[1] (p.Cys688_Glu689delinsTer)

NC_000016.10:g.68823526_68823527del

CM000678.2:g.68823526_68823527del

NC_000016.9:g.68857429_68857430del

CM000678.1:g.68857429_68857430del

NC_000016.8:g.67414930_67414931del

NG_008021.1:g.91235_91236del

ENST00000261769.10:c.2064_2065del

ENST00000261769.9:c.2064_2065del

ENST00000422392.6:c.1881_1882del

ENST00000562118.1:n.282_283del

ENST00000562836.5:n.2135_2136del

ENST00000566510.5:c.*730_*731del

ENST00000566612.5:c.*304_*305del

ENST00000611625.4:c.2127_2128del

ENST00000612417.4:c.1830+1407_1830+1408del

ENST00000621016.4:c.1865+1372_1865+1373del

NM_004360.3:c.2064_2065del

NM_001317184.1:c.1881_1882del

NM_001317185.1:c.516_517del

NM_001317186.1:c.99_100del

NM_004360.4:c.2064_2065del

NM_004360.5:c.2064_2065del

NM_001317184.2:c.1881_1882del

NM_001317185.2:c.516_517del

NM_001317186.2:c.99_100del

Pathogenic

Met criteria codes **4**

PS4

PM5_Supporting

PM2_Supporting

PVS1

Not Met criteria codes **22**

Expert Panel

CDH1 VCEP [↗](#)

Criteria Specification Information

BP5

BP7

BP4

BP3

BP1

BP2

PS1

PS2

PS3

PP1

PP2

PP3

PP4

PM1

PM3

PM4

PM6

BA1

BS2

BS1

BS4

BS3

Evidence Links 0

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 submitted by expert panel

CDH1 VCEP

The c.2064_2065delTG (p.Cys688Terfs) 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 five families meeting HDGC clinical criteria (PS4; PMID: 15235021, 17545690, 21424370, 26072394, 29307626). 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: PVS1, PM2_Supporting, PS4, PM5_Supporting.

Met criteria codes

PS4	<div><div></div><div></div></div>	✓	5 families that meet HDGC clinical criteria
PM5_Supporting	<div><div></div><div></div></div>	✓	Apply PM5_Supporting to nonsense/frameshift variants that are predicted/proved to undergo NMD.
PM2_Supporting	<div><div></div><div></div></div>	✓	Absent in gnomAD v2.1.1 in a region of sufficient coverage
PVS1	<div><div></div><div></div></div>	✓	PTC created in exon 13 of 16, expected to undergo NMD

Not Met criteria codes

BP5	<div><div></div><div></div></div>	✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP7	<div><div></div><div></div></div>	✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP4	<div><div></div><div></div></div>	✗	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			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			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP1			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			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
PM1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM6			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BA1			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
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

Curation History 		
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