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# *Variant: NM_004360.5(CDH1):c.1051C>T (p.Gln351Ter)*

Version: 2.0

*CA396460000*

*532473 (ClinVar)*

**Gene**: CDH1 (HGNC:999)
**Condition**: CDH1-related diffuse gastric and lobular breast cancer (MONDO:0100488)
**Inheritance Mode**: Autosomal dominant inheritance
**UUID:** 7d455de9-958f-460b-8990-85a41ab7450a
**Approved on**: 2023/8/25
**Published on**: 2023/8/25

## *HGVS expressions*

**NM_004360.5:c.1051C>T**
**NM_004360.5(CDH1):c.1051C>T (p.Gln351Ter)**
NC_000016.10:g.68812177C>T
CM000678.2:g.68812177C>T
NC_000016.9:g.68846080C>T
CM000678.1:g.68846080C>T
NC_000016.8:g.67403581C>T
NG_008021.1:g.79886C>T
ENST00000261769.10:c.1051C>T
ENST00000261769.9:c.1051C>T
ENST00000422392.6:c.1051C>T
ENST00000561751.1:c.673C>T
ENST00000562836.5:n.1122C>T
ENST00000565810.1:n.95C>T
ENST00000566510.5:c.895C>T
ENST00000566612.5:c.1051C>T
ENST00000611625.4:c.1051C>T
ENST00000612417.4:c.1051C>T
ENST00000621016.4:c.1051C>T
NM_004360.3:c.1051C>T
NM_001317184.1:c.1051C>T
NM_001317185.1:c.-565C>T
NM_001317186.1:c.-769C>T
NM_004360.4:c.1051C>T
NM_001317184.2:c.1051C>T
NM_001317185.2:c.-565C>T
NM_001317186.2:c.-769C>T

**Pathogenic**

**Met criteria codes** 4

PS4_Supporting PVS1 PM2_Supporting PM5_Supporting

**Not Met criteria codes** 22

PP1 PP2 PP3 PP4 PM1 PM3 PM4 BA1 PM6 BS1

## Expert Panel

CDH1 VCEP

## Criteria Specification Information

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

BS4 BS3 BS2 PS1 PS2 PS3
BP5 BP7 BP4 BP3 BP1 BP2

Evidence Links 0

*Guidelines Version 3.1*

**Criteria Specification Approval History**

**Criteria Specifications for this VCEP**

Evidence submitted by expert panel

***CDH1 VCEP***

**The c.1051C>T p.(Gln351Ter) 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; SCV000760845.2). Therefore, 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**

| | | |
|---|---|---|
| **PS4_Supporting** | ✔ | Not in published studies. SCV000760845.2 - DGC in 20s (meets criteria). |
| **PVS1** | ✔ | Predicted NMD. Exon 8 of 16. |
| **PM2_Supporting** | ✔ | Absent in population databases. |
| **PM5_Supporting** | ✔ | Apply PM5_Supporting to nonsense/frameshift variants that are predicted/proved to undergo NMD. |

**Not Met criteria codes**

| | | |
|---|---|---|
| **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 |
| **BA1** |  | ✖ | 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 |
| **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 |
| **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 |
| **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** |  | ✖ | 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 |

## Curation History

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