Variant: NM_024675.4(PALB2):c.7G>T (p.Glu3Ter)

Version: 2.0

CA10583388

241571 (ClinVar)

Gene: PALB2 (HGNC:79728)
Condition: PALB2-related cancer predisposition (MONDO:0700272)
Inheritance Mode: Autosomal dominant inheritance
UUID: fe8de8d5-9fd0-4d86-9572-d14485246aff
Approved on: 2023-04-05
Published on: 2025-09-16

HGVS expressions

NM_024675.4:c.7G>T
NM_024675.4(PALB2):c.7G>T (p.Glu3Ter)
NC_000016.10:g.23641151C>A
CM000678.2:g.23641151C>A
NC_000016.9:g.23652472C>A
CM000678.1:g.23652472C>A
NC_000016.8:g.23559973C>A
NG_007406.1:g.5207G>T
ENST00000561514.3:c.-846G>T
ENST00000565038.2:c.7G>T
ENST00000566069.6:c.7G>T
ENST00000697377.2:c.-233G>T
ENST00000697379.2:c.-139G>T
ENST00000561514.2:c.-1737G>T
ENST00000697374.1:c.-1328G>T
ENST00000697376.1:c.-1049G>T
ENST00000697377.1:c.-1124G>T
ENST00000697379.1:c.-1030G>T
ENST00000697382.1:c.-1788G>T
ENST00000697383.1:c.7G>T
ENST00000697384.1:n.161G>T
ENST00000261584.9:c.7G>T
ENST00000261584.8:c.7G>T
ENST00000567003.1:n.151G>T
ENST00000568219.5:c.-862G>T
NM_024675.3:c.7G>T

Pathogenic

Met criteria codes 3

PVS1 **PM2_Supporting** **PM5_Supporting**

Not Met criteria codes 1

BP7

Evidence Links 0

Expert Panel

Hereditary Breast, Ovarian and Pancreatic Cancer VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Hereditary Breast, Ovarian and Pancreatic Cancer Expert Panel Specifications* *to the ACMG/AMP Variant Interpretation Guidelines for PALB2 Version 1.0.0*

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Hereditary Breast, Ovarian and Pancreatic Cancer VCEP

The c.7G>T (p.Glu3Ter) variant in PALB2 is a nonsense variant predicted to cause a premature stop codon in biologically-relevant-exon 1 leading to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism. This alteration results in a termination codon upstream of the most C-terminus pathogenic alteration (PALB2 p.Tyr1183*) as classified by the HBOP VCEP and is expected to be more deleterious. This variant is absent from gnomAD v2.1.1. In summary, this variant meets criteria to be classified as pathogenic for autosomal dominant hereditary breast and pancreatic cancer and autosomal recessive FANCN based on the ACMG/AMP criteria applied as specified by the HBOP VCEP. (PVS1, PM5_supporting, PM2_supporting)

Met criteria codes

PVS1	ℹ	✓	The c.7G>T (p.Glu3Ter) variant in PALB2 is a nonsense variant predicted to cause a premature stop codon in biologically-relevant-exon 1/13 leading to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism.
PM2_Supporting	ℹ	✓	This variant is absent from gnomAD v2.1.1 (PM2_Supporting).
PM5_Supporting	ℹ	✓	This alteration results in a termination codon upstream of the most C-terminus pathogenic alteration (PALB2 p.Tyr1183*) as classified by the ClinGen HBOP Variant Curation Expert Panel, and is expected to be more deleterious (PM5_Supporting).

Not Met criteria codes

BP7	ℹ	✗	No impact on splicing by SpliceAI

Curation History

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