

Variant: *NM_000059.4(BRCA2):c.7826G>T (p.Gly2609Val)*

Version: 1.0

CA10579757 [↗](#)

232537 (ClinVar) [↗](#)

Gene: BRCA2 ([HGNC:675](#))

Condition: BRCA2-related cancer predisposition ([MONDO:0700269](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: a90281f6-825d-4686-8119-83717a6feabf

Approved on: 2025/12/3

Published on: 2025/12/2

HGVS expressions

NM_000059.4(BRCA2):c.7826G>T (p.Gly2609Val)

NM_000059.4:c.7826G>T

NC_000013.11:g.32362543G>T

CM000675.2:g.32362543G>T

NC_000013.10:g.32936680G>T

CM000675.1:g.32936680G>T

NC_000013.9:g.31834680G>T

NG_012772.3:g.52064G>T

ENST00000470094.2:c.7826G>T

ENST00000528762.2:c.7826G>T

ENST00000530893.7:c.7457G>T

ENST00000665585.2:c.7826G>T

ENST00000666593.2:c.7826G>T

ENST00000700202.2:c.7826G>T

ENST00000700202.1:c.293G>T

ENST00000380152.8:c.7826G>T

ENST00000544455.6:c.7826G>T

ENST00000614259.2:c.7834G>T

ENST00000665585.1:c.391G>T

ENST00000680887.1:c.7826G>T

ENST00000380152.7:c.7826G>T

ENST00000544455.5:c.7826G>T

ENST00000614259.1:n.7834G>T

NM_000059.3:c.7826G>T

Likely Pathogenic

Met criteria codes **4**

PP4_Moderate

PM2_Supporting

PS3

PP3

Evidence Links **0**

Expert Panel

ENIGMA BRCA1 and BRCA2 VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen ENIGMA BRCA1 and BRCA2 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for BRCA2 Version 1.1.0

[↗](#) **Criteria Specification Approval History**

[↗](#) **Criteria Specifications for this VCEP**

ENIGMA BRCA1 and BRCA2 VCEP

The c.7826G>T variant in BRCA2 is a missense variant predicted to cause substitution of Glycine by Valine at amino acid 2609 (p.(Gly2609Val)). This variant is absent from gnomAD v2.1 (exomes only, non-cancer subset, read depth ≥25) and gnomAD v3.1 (non-cancer subset, read depth ≥25) (PM2_Supporting met). Reported by four calibrated studies to exhibit protein function similar to pathogenic control variants (PMIDs:38417439, 35190686, 39779857, 39779848) (PS3 met). This BRCA2 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.32, above the recommended threshold of 0.30 for prediction of impact on BRCA2 function via protein change. A SpliceAI score of 0.01 predicts no impact on splicing (score threshold <0.10) (PP3 met). Multifactorial likelihood ratio analysis using clinically calibrated data produced a combined LR for this variant of 6.11 (based on Co-occurrence LR=1.03; Family History LR=5.96), within the thresholds for moderate evidence towards pathogenicity (LR >4.3 & ≤18.7) (PP4_Moderate met; PMID: 31853058, Internal lab contributor). In summary, this variant meets the criteria to be classified as a Likely pathogenic variant for BRCA2-related cancer predisposition based on the ACMG/AMP criteria applied as specified by the ENIGMA BRCA1/2 VCEP (PM2_Supporting, PS3, PP3, PP4_Moderate).

Met criteria codes

PP4_Moderate			Multifactorial likelihood ratio analysis using clinically calibrated data produced a combined LR for this variant of 6.11 (based on Co-occurrence LR=1.03; Family History LR=5.96), within the thresholds for moderate evidence towards pathogenicity (LR >4.3 & ≤18.7) (PP4_Moderate met; PMID: 31853058, Internal lab contributor).
PM2_Supporting			This variant is absent from gnomAD v2.1 (exomes only, non-cancer subset, read depth ≥25) and gnomAD v3.1 (non-cancer subset, read depth ≥25) (PM2_Supporting met).
PS3			Reported by four calibrated studies to exhibit protein function similar to pathogenic control variants (PMIDs:38417439, 35190686, 39779857, 39779848) (PS3 met).
PP3			This BRCA2 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.32, above the recommended threshold of 0.30 for prediction of impact on BRCA2 function via protein change. A SpliceAI score of 0.01 predicts no impact on splicing (score threshold <0.10) (PP3 met).

Curation History



 ▾

 ▾

Showing 1 to 1 of 1 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.