

Variant: *NM_000059.4(BRCA2):c.7792GAA[1] (p.Glu2599del)*

Version: 1.0

CA025277 [↗](#)

52409 (ClinVar) [↗](#)

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

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

Inheritance Mode: Autosomal dominant inheritance

UUID: 41597833-4998-4a1f-ae06-ff349b2c6c89

Approved on: Mon, 21 Sep 2026 00:00:00 +0000

Published on: Mon, 21 Sep 2026 00:00:00 +0000

HGVS expressions

NM_000059.4(BRCA2):c.7792GAA[1] (p.Glu2599del)

NM_000059.4:c.7792GAA[1]

NM_000059.4:c.7795_7797del

NC_000013.11:g.32357919_32357921del

CM000675.2:g.32357919_32357921del

NC_000013.10:g.32932056_32932058del

CM000675.1:g.32932056_32932058del

NC_000013.9:g.31830056_31830058del

NG_012772.3:g.47440_47442del

ENST00000470094.2:c.7795_7797del

ENST00000528762.2:c.7795_7797del

ENST00000530893.7:c.7426_7428del

ENST00000665585.2:c.7795_7797del

ENST00000666593.2:c.7795_7797del

ENST00000700202.2:c.7795_7797del

ENST00000700202.1:c.262_264del

ENST00000380152.8:c.7795_7797del

ENST00000544455.6:c.7795_7797del

ENST00000614259.2:c.7795_7797del

ENST00000665585.1:c.360_362del

ENST00000680887.1:c.7795_7797del

ENST00000380152.7:c.7795_7797del

ENST00000544455.5:c.7795_7797del

ENST00000614259.1:n.7795_7797del

NM_000059.3:c.7795_7797del

Likely Pathogenic

Met criteria codes **2**

PP4_Strong PP3

Not Met criteria codes **4**

BS1 BP7 BA1 PM2

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 1.2

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

Evidence submitted by expert panel

ENIGMA BRCA1 and BRCA2 VCEP

The c.7795_7797del variant in BRCA2 is predicted to cause a change in the length of the protein due to an in-frame deletion of 1 amino acid (p.(Glu2599del)). The Total GrpMax filtering allele frequency (the lower threshold of the 95% CI) in gnomAD v4.1 is 0.00000028 in the Non-Finnish European genetic ancestry group (based on 2/1179946 alleles) which is below the ENIGMA BRCA1/2 VCEP threshold (>0.00002) for BS1_Supporting and does not meet any population code (BA1, BS1, BS1_Supporting, PM2_Supporting are not met). This BRCA2 in-frame deletion variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.64, above the recommended threshold of 0.30 for prediction of impact on BRCA2 function via protein change. A SpliceAI score of 0.03 predicts no impact on splicing (score threshold ≤ 0.1) (PP3 met). Multifactorial likelihood ratio analysis using clinically calibrated data produced a combined LR for this variant of 2883172307.4 (based on Cosegregation LR=10545472; Pathology LR=0.93; Co-occurrence LR=1.03; Family History LR=285.42), above the thresholds for very strong evidence towards pathogenicity (LR >350) (PP4_Very strong met; PMID: 34597585, 31853058, 31131967). This is an in-frame variant inside a key functional domain. Impact via the protein change has not been assessed yet. mRNA experimental analysis indicates no impact on splicing (PMIDs: 22505045, 27886673) but is not applied as strong evidence against pathogenicity since missense impact has not been excluded (BP7_Strong (RNA) not met). 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 (PP3, PP4_Very strong).

Met criteria codes

PP4_Strong			at Very strong level: Multifactorial likelihood ratio analysis using clinically calibrated data produced a combined LR for this variant of 2883172307.4 (based on Cosegregation LR=10545472; Pathology LR=0.93; Co-occurrence LR=1.03; Family History LR=285.42), above the thresholds for very strong evidence towards pathogenicity (LR >350) (PP4_Very strong met; PMID: 34597585, 31853058, 31131967).
PP3			This BRCA2 in-frame deletion variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.64, above the recommended threshold of 0.30 for prediction of impact on BRCA2 function via protein change. A SpliceAI score of 0.03 predicts no impact on splicing (score threshold ≤ 0.1) (PP3 met).

Not Met criteria codes

BS1			The Total GrpMax filtering allele frequency (the lower threshold of the 95% CI) in gnomAD v4.1 is 0.00000028 in the Non-Finnish European genetic ancestry group (based on 2/1179946 alleles) which is below the ENIGMA BRCA1/2 VCEP threshold (>0.00002) for BS1_Supporting and does not meet any population code (BA1, BS1, BS1_Supporting, PM2_Supporting are not met).
BP7			This is an in-frame variant inside a key functional domain. Impact via the protein change has not been assessed yet. mRNA experimental analysis indicates no impact on splicing (PMIDs: 22505045, 27886673) but is not applied as strong evidence against pathogenicity since missense impact has not been excluded (BP7_Strong (RNA) not met).
BA1			The Total GrpMax filtering allele frequency (the lower threshold of the 95% CI) in gnomAD v4.1 is 0.00000028 in the Non-Finnish European genetic ancestry group (based on 2/1179946 alleles) which is below the ENIGMA BRCA1/2 VCEP threshold (>0.00002) for BS1_Supporting and does not meet any population code (BA1, BS1, BS1_Supporting, PM2_Supporting are not met).

PM2	✖	The Total GrpMax filtering allele frequency (the lower threshold of the 95% CI) in gnomAD v4.1 is 0.00000028 in the Non-Finnish European genetic ancestry group (based on 2/1179946 alleles) which is below the ENIGMA BRCA1/2 VCEP threshold (>0.00002) for BS1_Supporting and does not meet any population code (BA1, BS1, BS1_Supporting, PM2_Supporting are not 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.