

Variant: NM_000038.6(APC):c.933G>C (p.Lys311Asn)

Version: 1.0

CA16023349 [↗](#)

1025291 (ClinVar) [↗](#)

Gene: APC ([HGNC:324](#))
Condition: familial adenomatous polyposis 1 ([MONDO:0021056](#))
Inheritance Mode: Autosomal dominant inheritance
UUID: 25c5fc2f-b417-4d43-a9cb-4a31806c7e0c
Approved on: 2025/5/16
Published on: 2025/5/16

HGVS expressions

NM_000038.6(APC):c.933G>C (p.Lys311Asn)
NM_000038.6:c.933G>C
NC_000005.10:g.112815593G>C
CM000667.2:g.112815593G>C
NC_000005.9:g.112151290G>C
CM000667.1:g.112151290G>C
NC_000005.8:g.112179189G>C
NG_008481.4:g.128073G>C
ENST00000502371.3:c.933G>C
ENST00000504915.3:c.933G>C
ENST00000505084.2:n.989G>C
ENST00000505350.2:c.*939G>C
ENST00000507379.6:c.879G>C
ENST00000509732.6:c.933G>C
ENST00000512211.7:c.933G>C
ENST00000257430.9:c.933G>C
ENST00000257430.8:c.933G>C
ENST00000507379.5:c.879G>C
ENST00000508376.6:c.933G>C
ENST00000508624.5:c.*255G>C
ENST00000512211.6:c.933G>C
NM_000038.5:c.933G>C
NM_001127510.2:c.933G>C
NM_001127511.2:c.879G>C
NM_001354895.1:c.933G>C
NM_001354896.1:c.933G>C
NM_001354897.1:c.963G>C
NM_001354898.1:c.858G>C
NM_001354899.1:c.849G>C
NM_001354900.1:c.756G>C
NM_001354901.1:c.756G>C
NM_001354902.1:c.963G>C
NM_001354903.1:c.933G>C
NM_001354904.1:c.858G>C
NM_001354905.1:c.756G>C
NM_001354906.1:c.84G>C
NM_001127510.3:c.933G>C

NM_001127511.3:c.879G>C
NM_001354895.2:c.933G>C
NM_001354896.2:c.933G>C
NM_001354897.2:c.963G>C
NM_001354898.2:c.858G>C
NM_001354899.2:c.849G>C
NM_001354900.2:c.756G>C
NM_001354901.2:c.756G>C
NM_001354902.2:c.963G>C
NM_001354903.2:c.933G>C
NM_001354904.2:c.858G>C
NM_001354905.2:c.756G>C
NM_001354906.2:c.84G>C

Likely Pathogenic

Met criteria codes 3

PVS1_Strong PS4_Supporting
PM2_Supporting

Evidence Links 0

Expert Panel

InSiGHT Hereditary Colorectal Cancer/Polypsis VCEP

Criteria Specification Information

Criteria Specification: ClinGen InSiGHT Hereditary Colorectal Cancer/Polypsis Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for APC Version 2.1.0

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

InSiGHT Hereditary Colorectal Cancer/Polypsis VCEP

The NM_000038.6(APC):c.933G>C variant in APC is a G to non-G change at the last nucleotide of exon 9. RNA analysis demonstrated that the variant impacts splicing by an insertion of the first 66 nucleotides of intron 9, resulting in a premature stop codon (r.933_934ins933+1_933+66 p.K311_V312insVTEDYKPWSLMP*) (internal data Ambry Genetics; in Fig. 1B of the ACMG/AMP criteria specification by the ClinGen InSiGHT Hereditary Colorectal Cancer/Polypsis VCEP [HCCP VCEP] the variant was evaluated as PVS1_Supporting, but based on the additional RNA data the HCCP VCEP considers PVS1_Strong as applicable for this variant). This variant has been reported in 2 probands meeting phenotypic criteria, resulting in a total phenotype score of 1.5 (PS4_Supporting, PMID: 20685668, internal data Labcorp Genetics [formerly Invitae]). This variant is absent in gnomAD v2.1.1 (PM2_Supporting). In summary, this variant meets the criteria to be classified as Likely Pathogenic for autosomal-dominant inherited FAP based on the ACMG/AMP criteria applied, as specified by the HCCP VCEP: PVS1_Strong, PS4_Supporting, PM2_Supporting applied (VCEP specifications version v2.0.3; date of approval 7/24/2023).

Met criteria codes

PVS1_Strong



RNA analysis demonstrated that the variant impacts splicing by an insertion of the first 66 nucleotides of intron 9, resulting in a premature stop codon (r.933_934ins933+1_933+66 p.K311_V312insVTEDYKPWSLMP*) (internal data Ambry Genetics; in Fig. 1B of the ACMG/AMP criteria specification by the ClinGen InSiGHT Hereditary Colorectal Cancer/Polypsis VCEP [HCCP VCEP] the variant was evaluated as PVS1_Supporting, but based on the additional RNA data the HCCP VCEP considers PVS1_Strong as applicable for this variant).

PS4_Supporting  

This variant has been reported in 2 probands meeting phenotypic criteria, resulting in a total phenotype score of 1.5 (PS4_Supporting, PMID: 20685668, internal data Labcorp Genetics [formerly Invitae]).

PM2_Supporting  

This variant is absent in gnomAD v2.1.1 (PM2_Supporting).

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.