

Variant: *NM_001754.4(RUNX1):c.729A>C (p.Pro243=)*

Version: 2.0

CA320603666 [↗](#)

436613 (ClinVar) [↗](#)

Gene: RUNX1 ([HGNC:861](#))

Condition: hereditary thrombocytopenia and hematologic cancer predisposition syndrome ([MONDO:0011071](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: 9f45b964-b1a9-4ec5-b6e4-e9be27b7aa84

Approved on: 2021/6/25

Published on: 2023/11/13

HGVS expressions

NM_001754.4:c.729A>C

NM_001754.4(RUNX1):c.729A>C (p.Pro243=)

NC_000021.9:g.34834486T>G

CM000683.2:g.34834486T>G

NC_000021.8:g.36206783T>G

CM000683.1:g.36206783T>G

NC_000021.7:g.35128653T>G

NG_011402.2:g.1155226A>C

ENST00000675419.1:c.729A>C

ENST00000300305.7:c.729A>C

ENST00000344691.8:c.648A>C

ENST00000358356.9:c.648A>C

ENST00000399237.6:c.693A>C

ENST00000399240.5:c.532+24988A>C

ENST00000437180.5:c.729A>C

ENST00000469087.1:n.265A>C

ENST00000482318.5:c.*319A>C

NM_001001890.2:c.648A>C

NM_001122607.1:c.648A>C

NM_001001890.3:c.648A>C

NM_001122607.2:c.648A>C

NM_001754.5:c.729A>C

Likely Benign

Met criteria codes **2**

BP4 BP7

Not Met criteria codes **23**

BA1 BS2 BS1 BS3 BP3 BP1
BP2 PVS1 BP5 PS1 PS2
PS3 PS4 PP1 PP2 PP3 PP4
PM1 PM3 PM5 PM4 PM6
PM2

Evidence Links **0**

Expert Panel

Myeloid Malignancy VCEP [↗](#)

Criteria Specification Information **!**

[↗](#) Criteria Specifications for this VCEP

Myeloid Malignancy VCEP

This synonymous variant is predicted by SSF, MES, and SpliceAI to lead to either no change/an increase/a decrease by no more than 10% in the canonical splice site score and no putative cryptic splice sites are created; in addition, evolutionary conservation prediction algorithms predict the site as not being highly conserved (PhyloP score = 0.975787 in GRCh37/1.06724 in GRCh38 or the variant is the reference nucleotide in one primate and/or three mammal species) (BP4+BP7). In summary, this variant meets criteria to be classified as likely benign. ACMG/AMP criteria applied, as specified by the ClinGen Myeloid Malignancy Variant Curation Expert Panel for RUNX1: BP4 and BP7.

Met criteria codes

BP4			This synonymous variant is predicted by SSF, MES, and SpliceAI to lead to either no change/an increase/a decrease by no more than 10% in the canonical splice site score, and no putative cryptic splice sites are created.
BP7			This synonymous variant is predicted by SSF, MES, and SpliceAI to lead to either no change/an increase/a decrease by no more than 10% in the canonical splice site score and no putative cryptic splice sites are created. However, evolutionary conservation prediction algorithms predict the site as being weakly conserved (PhyloP score = 0.975787 in GRCh37/1.06724 in GRCh38), and the variant is not the reference nucleotide in one primate and/or three mammal species (only in the lesser Egyptian jerboa and hedgehog).

Not Met criteria codes

BA1			gnomAD v2: Absent (>20x coverage) gnomAD v3: ALL:0.001410% (2/141824 alleles) - AFR:0.004832% (2/41392 alleles, no homozygotes)
BS2			Not applicable
BS1			gnomAD v2: Absent (>20x coverage) gnomAD v3: ALL:0.001410% (2/141824 alleles) - AFR:0.004832% (2/41392 alleles, no homozygotes)
BS3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP3			Not applicable
BP1			Not applicable
BP2			No homozygotes reported in gnomAD. No case reports.
PVS1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP5			Not applicable

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
PS4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP2			Not applicable
PP3			This synonymous variant is predicted by SSF, MES, and SpliceAI to lead to either no change/an increase/a decrease by no more than 10% in the canonical splice site score, and no putative cryptic splice sites are created.
PP4			Not applicable
PM1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM3			Not applicable
PM5			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
PM6			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM2			gnomAD v2: Absent (>20x coverage) gnomAD v3: ALL:0.001410% (2/141824 alleles) - AFR:0.004832% (2/41392 alleles, no homozygotes)

Showing 1 to 2 of 2 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.