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Variant: NM_001754.5(RUNX1):c.509G>A (p.Gly170Glu)

Version: 2.0

CA410208159

2633656 (ClinVar)

Gene: RUNX1 (HGNC:861)
Condition: hereditary thrombocytopenia and hematologic cancer predisposition syndrome (MONDO:0011071)
Inheritance Mode: Autosomal dominant inheritance
UUID: ceaec1b6-521d-4b4a-b2f8-2ccff8f9811f
Approved on: 2026/4/29
Published on: 2026/4/29

HGVS expressions

NM_001754.5(RUNX1):c.509G>A (p.Gly170Glu)
NM_001754.5:c.509G>A
NC_000021.9:g.34859578C>T
CM000683.2:g.34859578C>T
NC_000021.8:g.36231875C>T
CM000683.1:g.36231875C>T
NC_000021.7:g.35153745C>T
NG_011402.2:g.1130134G>A
ENST00000675419.1:c.509G>A
ENST00000300305.7:c.509G>A
ENST00000344691.8:c.428G>A
ENST00000358356.9:c.428G>A
ENST00000399237.6:c.473G>A
ENST00000399240.5:c.428G>A
ENST00000437180.5:c.509G>A
ENST00000467577.1:n.1G>A
ENST00000482318.5:c.*99G>A
NM_001001890.2:c.428G>A
NM_001122607.1:c.428G>A
NM_001754.4:c.509G>A
NM_001001890.3:c.428G>A
NM_001122607.2:c.428G>A

Likely Pathogenic

Met criteria codes 3

PP3 PM1_Strong PM2_Supporting

Not Met criteria codes 23

PS1 PS2 PS3 PS4 PP1 PP2 PP4 PM6 PM3 PM5 PM4 BA1 BS2 PVS1 BS1 BS4 BS3 BP5 BP7 BP4 BP3 BP1 BP2

Evidence Links 0

Expert Panel

Myeloid Malignancy VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen Myeloid Malignancy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for RUNX1 Version 3.1.0*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Myeloid Malignancy VCEP

NM_001754.5(RUNX1):c.509G>A (p.Gly170Glu) is a missense variant which affects one of the hotspot residues (G170) in the RHD (PM1_strong). This variant has a REVEL score ≥0.88 (0.95) (PP3) and a MAF ≤ 0.00005 in gnomAD v4 across all subpopulations with at least 20x coverage for RUNX1 (PM2_supporting). In summary, this variant meets criteria to be classified as likely pathogenic. ACMG/AMP criteria applied, as specified by the Myeloid Malignancy Variant Curation Expert Panel for RUNX1: PM1_strong, PP3, PM2_supporting.

Met criteria codes

PP3	✔	This missense variant has a REVEL score ≥ 0.88 (0.95) (PP3).
PM1_Strong	✔	This variant affects at least one of the following hotspot residues within the RHD: R107, K110, A134, R162, R166, S167, R169, G170, K194, T196, D198, R201, R204 (PM1_strong).
PM2_Supporting	✔	This variant has a MAF ≤ 0.00005 in gnomAD v4.0 in all subpopulations with at least 20X coverage for RUNX1 (PM2_supporting).

Not Met criteria codes

PS1	✖	There has not yet been a missense change determined to be pathogenic at this amino acid residue.
PS2	✖	De novo data for this variant has not been reported in literature.
PS3	✖	In vitro or in vivo functional data has not been reported for this variant in the literature.
PS4	✖	Proband data for this variant has not been reported in literature.
PP1	✖	Segregation data for this variant has not been reported in literature
PP2	✖	This rule is not applicable for MM-VCEP.
PP4	✖	This rule is not applicable for MM-VCEP.
PM6	✖	De novo data for this variant has not been reported in literature.
PM3	✖	This rule is not applicable for MM-VCEP.
PM5	✖	There has not yet been a different missense change determined to be pathogenic at this amino acid residue.
PM4	✖	This variant is not an in-frame deletion/insertion.

BA1	ℹ	✖	This variant does not have a MAF ≥ 0.0015 (0.15%) in any general continental population dataset.
BS2		✖	This rule is not applicable for MM-VCEP.
PVS1	ℹ	✖	This variant is not a null variant.
BS1	ℹ	✖	This variant does not have a MAF between 0.00015 (0.015%) and 0.0015 (0.15%) in any general continental dataset.
BS4	ℹ	✖	Segregation data for this variant has not been reported in literature
BS3	ℹ	✖	In vitro or in vivo functional data has not been reported for this variant in the literature.
BP5		✖	This rule is not applicable for MM-VCEP.
BP7	ℹ	✖	This variant is not a synonymous or intronic variant.
BP4	ℹ	✖	This missense variant does not have a REVEL score < 0.50.
BP3		✖	This rule is not applicable for MM-VCEP.
BP1		✖	This rule is not applicable for MM-VCEP.
BP2	ℹ	✖	This variant has not been observed in trans with a pathogenic variant for a fully penetrant dominant gene/disorder or observed in cis with a pathogenic variant in any inheritance pattern.

Curation History

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