

Variant: *NM\_001754.5(RUNX1):c.1396A>G (p.Met466Val)*

Version: 1.1

[CA10014177](#)

[1002421 \(ClinVar\)](#)

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

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

**Inheritance Mode:** Autosomal dominant inheritance

**UUID:** 32058939-e3a4-4a3d-8d5c-78f1fe956233

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### *HGVS expressions*

**NM\_001754.5:c.1396A>G**

NM\_001754.5(RUNX1):c.1396A>G (p.Met466Val)

NC\_000021.9:g.34792182T>C

CM000683.2:g.34792182T>C

NC\_000021.8:g.36164479T>C

CM000683.1:g.36164479T>C

NC\_000021.7:g.35086349T>C

NG\_011402.2:g.1197530A>G

ENST00000675419.1:c.1396A>G

ENST00000300305.7:c.1396A>G

ENST00000344691.8:c.1315A>G

ENST00000399240.5:c.1123A>G

ENST00000437180.5:c.1396A>G

ENST00000482318.5:c.\*986A>G

NM\_001001890.2:c.1315A>G

NM\_001754.4:c.1396A>G

NM\_001001890.3:c.1315A>G

Uncertain Significance

Met criteria codes **1**

BP4

Not Met criteria codes **23**

PP1 PP2 PP4 PM1 PM3  
PM5 PM4 PM6 PM2 PVS1  
BS1 BS4 BS3 BS2 BP5 BP7  
BP3 BP1 BP2 PS1 PS2 PS3  
PS4

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 Version 2*

[PDF](#)

[Criteria Specification Approval History](#)

[Criteria Specifications for this VCEP](#)

Evidence submitted by expert panel

**Myeloid Malignancy VCEP**

**NM\_001754.5(RUNX1):c.1396A>G (p.Met466Val) is a missense variant which has a REVEL score  $\leq 0.50$  (0.203) and SpliceAI is  $\leq 0.20$  (0.00) (BP4). In summary, the clinical significance of this variant is uncertain. ACMG/AMP criteria applied, as specified by the Myeloid Malignancy Variant Curation Expert Panel for RUNX1: BP4.**

#### Met criteria codes


**BP4**   This missense variant has a REVEL score  $< 0.50$  (0.203) and a SpliceAI score  $\leq 0.20$  (0.00) (BP4).

#### Not Met criteria codes

**PP1**   No case studies found

**PP2**  This rule is not applicable for MM-VCEP

**PP4**  This rule is not applicable for MM-VCEP


**PM1**  Not located in a hotspot or a critical region

**PM3**  This rule is not applicable for MM-VCEP



**PM5**   Amino Acid location has been curated as Benign by MMVCEP

**PM4**   Not an in-frame deletion/insertion

**PM6**   No case studies found

**PM2**  gnomAD v.4.1.0: 5/1144916 alleles in European (non-Finish) sub-population, MAF: 0.0004376% This variant is present in at least one population database.

**PVS1**   Not a null/truncating variant














**BS1**   gnomAD v.4.1.0: 5/1144916 alleles in European (non-Finish) sub-population, MAF: 0.0004376% This variant does not have a MAF between 0.00015 (0.015%) and 0.0015 (0.15%) in any general continental dataset.

**BS4**   No case studies found

**BS3**   No functional studies found

**BS2**  This rule is not applicable for MM-VCEP

**BP5**  This rule is not applicable for MM-VCEP

<b>BP7</b>			Not a synonymous or intronic variant
<b>BP3</b>			This rule is not applicable for MM-VCEP
<b>BP1</b>			This rule is not applicable for MM-VCEP
<b>BP2</b>			Variant only present in gnomAD v2.1.1 and does not meet code criteria
<b>PS1</b>			Amino Acid location has been curated as Benign by MMVCEP
<b>PS2</b>			No case studies found
<b>PS3</b>			No functional studies found
<b>PS4</b>			This variant has been reported in one proband meeting at least one of the RUNX1-phenotypic criteria (PS4_Supporting; PMID: 32855275) however not confirmed as germline

Curation History [↗](#)




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