*Variant: NM_001754.4(RUNX1):c.*4188G>C*

Version: 1.0

CA10644605

339794 (ClinVar)

Gene: RUNX1 (HGNC:861)
Condition: hereditary thrombocytopenia and hematologic cancer predisposition syndrome (MONDO:0011071)
Inheritance Mode: Autosomal dominant inheritance
UUID: 912add43-9404-4257-a2a6-c545861ad7ef
Approved on: 2021-05-26
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HGVS expressions

NM_001754.4:c.*4188G>C
NM_001754.4(RUNX1):c.*4188G>C
NC_000021.9:g.34787947C>G
CM000683.2:g.34787947C>G
NC_000021.8:g.36160244C>G
CM000683.1:g.36160244C>G
NC_000021.7:g.35082114C>G
NG_011402.2:g.1201765G>C
ENST00000675419.1:c.*4188G>C
ENST00000300305.7:c.*4188G>C
ENST00000344691.8:c.*4188G>C
ENST00000437180.5:c.*4188G>C
NM_001001890.2:c.*4188G>C
NM_001001890.3:c.*4188G>C
NM_001754.5:c.*4188G>C

Likely Benign

Met criteria codes 1

BS1

Not Met criteria codes 25

PVS1 BA1 BS2 BS4 BS3 BP5 BP7 BP4 BP3 BP1 BP2 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

Evidence submitted by expert panel

Myeloid Malignancy VCEP

This 3' UTR c.*4188G>C variant is located at a non-conserved nucleotide per an evolutionary conservation prediction algorithm (PhyloP = -0.665764 in GRCh38). The variant is present in gnomAD at an allele frequency between 0.015% and 0.15% in a general continental

population (European, non-Finnish, subpopulation: 0.03528% in v3) with >5 variant alleles and a minimum of 2000 total alleles (BS1) and has not been described in the literature. 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: BS1.

Met criteria codes

BS1	✔	Variant is present in >=5 alleles in the European (non-Finnish) population (has required minimum of 2000 alleles) with an MAF of 0.03528% (v3.1.1), which is within the BS1 thresholds (0.015%-0.15%). - gnomAD v2.1.1: ALL: 0.009554% (3/31402) - NFE: 0.01297% (2/15424) - OTH: 0.09208% (1/1086) - gnomAD v3.1.1: ALL: 0.02168% (33/152196) - NFE: 0.03528% (24/38024) - AMR: 0.02616% (4/15290) - ASJ: 0.05760% (2/3472) - OTH: 0.09579% (2/2088)

Not Met criteria codes

PVS1	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BA1	✖	Variant is present in >=5 alleles in the European (non-Finnish) population (has required minimum of 2000 alleles) with an MAF of 0.03528% (v3.1.1), which is within the BS1 thresholds (0.015%-0.15%). - gnomAD v2.1.1: ALL: 0.009554% (3/31402) - NFE: 0.01297% (2/15424) - OTH: 0.09208% (1/1086) - gnomAD v3.1.1: ALL: 0.02168% (33/152196) - NFE: 0.03528% (24/38024) - AMR: 0.02616% (4/15290) - ASJ: 0.05760% (2/3472) - OTH: 0.09579% (2/2088)
BS2	✖	Not applicable
BS4	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS3	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP5	✖	Not applicable
BP7	✖	3'UTR variant that is located at a non-conserved nucleotide (PhyloP = -0.665764 in GRCh38), and the variant is the reference nucleotide in one primate and/or 3 mammals.
BP4	✖	No donor/acceptor gains or losses predicted (SpliceAI Δ score <= 0.2), but does not apply for UTR variants.
BP3	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP1	✖	Not applicable
BP2	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

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 literature found in HGMD, Google+Google Scholar searches, or COSMIC.
PP1	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP2	✖	Not applicable
PP3	✖	No donor/acceptor gains or losses predicted with SpliceAI Δ score >= 0.38.
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	✖	Variant is present in >=5 alleles in the European (non-Finnish) population (has required minimum of 2000 alleles) with an MAF of 0.03528% (v3.1.1), which is within the BS1 thresholds (0.015%-0.15%). - gnomAD v2.1.1: ALL: 0.009554% (3/31402) - NFE: 0.01297% (2/15424) - OTH: 0.09208% (1/1086) - gnomAD v3.1.1: ALL: 0.02168% (33/152196) - NFE: 0.03528% (24/38024) - AMR: 0.02616% (4/15290) - ASJ: 0.05760% (2/3472) - OTH: 0.09579% (2/2088)

Curation History

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