

Variant: NM_001313913.2:c.854_860del

Version: 1.2

CA658820951 [↗](#)

3390364 (ClinVar) [↗](#)

Gene: F9 ([HGNC:2158](#))

Condition: hemophilia B ([MONDO:0010604](#))

Inheritance Mode: X-linked inheritance

UUID: c7549989-d137-47b7-be33-3e2d6db9914d

Approved on: 2024/12/6

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HGVS expressions

NM_001313913.2:c.854_860del

NC_000023.11:g.139561654_139561660del

CM000685.2:g.139561654_139561660del

NC_000023.10:g.138643813_138643819del

CM000685.1:g.138643813_138643819del

NC_000023.9:g.138471479_138471485del

NG_007994.1:g.35919_35925del

ENST00000218099.7:c.969_975del

ENST00000643157.1:n.1636_1642del

ENST00000218099.6:c.969_975del

ENST00000394090.2:c.855_861del

NM_000133.3:c.969_975del

NM_001313913.1:c.855_861del

NM_000133.4:c.969_975del

NM_001313913.2:c.855_861del

Pathogenic

Met criteria codes **3**

PP4_Moderate

PVS1

PM2_Supporting

Not Met criteria codes **1**

PS4

Evidence Links **0**

Expert Panel

Coagulation Factor Deficiency VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen Coagulation Factor Deficiency Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for F9 Version 1.0.0

[↗](#) **Criteria Specification Approval History**

[↗](#) **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Coagulation Factor Deficiency VCEP

The NM_000133.4(F9):c.969_975del variant deletes 7bp in exon 8 of the F9 gene, causing a frameshift and premature termination of translation. NMD is not predicted to occur, but the truncation of the peptidase S1 domain is expected to be detrimental to protein function (PVS1). The variant is absent from gnomAD v2.1 (PM2_Supporting). The variant is reported in at least one individual with severe

Hemophilia B with full gene sequencing and deletion/duplication analysis in the literature (PP4_Moderate - PMID: 26612714). In summary, this variant meets criteria to be classified as pathogenic. ACMG/AMP criteria applied, as specified by the Coagulation Factor Deficiency VCEP for F9: PVS1, PP4_Moderate, PM2_Supporting.

Met criteria codes

PP4_Moderate			1 proband with severe hemophilia B. MLPA was used for deletion/duplication analysis.
PVS1			The 7-bp deletion occurs in exon 8/8 of F9 and causes a frameshift and premature termination of translation. The variant is not predicted to undergo NMD. PVS1 is applied based on the potential truncation of the peptidase S1 domain, which is determined to be critical to protein function by the CFD-VCEP.
PM2_Supporting			The variant is absent from gnomAD v2.1 and v3.1.

Not Met criteria codes

PS4			There was some concern that the proband was the same in both publications. Given this variant meets a pathogenic classification counting only one proband, we used a conservative approach to only count one proband for PP4_Moderate.
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Curation History



Showing 1 to 3 of 3 rows

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