

Variant: NM_001085049.3(MRAS):c.453G>A (p.Pro151=)

Version: 1.0

CA2637031 [↗](#)

496410 (ClinVar) [↗](#)

Gene: MRAS ([HGNC:22808](#))

Condition: RASopathy ([MONDO:0021060](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: c4b0ae99-0a60-41ae-9906-724b163297e7

Approved on: 2024/12/3

Published on: 2025/3/25

HGVS expressions

NM_001085049.3(MRAS):c.453G>A (p.Pro151=)

NM_001085049.3:c.453G>A

NC_000003.12:g.138400539G>A

CM000665.2:g.138400539G>A

NC_000003.11:g.138119381G>A

CM000665.1:g.138119381G>A

NC_000003.10:g.139602071G>A

ENST00000423968.7:c.453G>A

ENST00000289104.8:c.453G>A

ENST00000423968.6:c.453G>A

ENST00000464896.5:c.225G>A

ENST00000474559.1:c.453G>A

ENST00000478647.1:n.331G>A

ENST00000494949.5:c.225G>A

ENST00000614350.4:c.225G>A

ENST00000621127.4:c.225G>A

NM_001085049.2:c.453G>A

NM_001252090.1:c.453G>A

NM_001252091.1:c.225G>A

NM_001252092.1:c.225G>A

NM_001252093.1:c.225G>A

NM_012219.4:c.453G>A

NM_001252090.2:c.453G>A

NM_001252092.2:c.225G>A

NM_001252093.2:c.225G>A

Benign

Met criteria codes **1**

BA1

Evidence Links **0**

Expert Panel

[RASopathy VCEP](#) [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen RASopathy Expert Panel
Specifications to the ACMG/AMP Variant Interpretation
Guidelines for MRAS Version 1.4.0

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

Evidence submitted by expert panel

RASopathy VCEP

The **c.453G>A (p.Pro151=)** variant in **MRAS** is a synonymous variant at position 151. This variant has a filtering allele frequency of **1.748%** in the South Asian population in gnomAD v2, which is higher than the ClinGen RASopathy VCEP threshold (**>0.0005**) for BA1, and therefore meets this criterion (BA1). In summary, this variant meets the criteria to be classified as benign for autosomal dominant RASopathy based on the ACMG/AMP criteria applied, as specified by the ClinGen RASopathy VCEP: BA1 (RASopathy VCEP specifications version 1.4; 12/3/2024)

Met criteria codes

BA1



This variant has a minor allele frequency of 1.875% (1707/91024) in the South Asian population in gnomAD v4, >0.05%

Curation History [↗](#)

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