The ClinGen Evidence Repository is an **FDA-recognized human genetic variant database** containing expert-curated assertions regarding variants' pathogenicity and supporting evidence summaries. [Disclaimer]

Variant: NM_030662.3(MAP2K2):c.919+4C>T

Version: 1.2

CA9090795

40834 (ClinVar)

Gene: MAP2K2 (HGNC:5605)
Condition: RASopathy (MONDO:0021060)
Inheritance Mode: Autosomal dominant inheritance
UUID: 246061da-c54d-4473-bf35-633ebf160104
Approved on: 2019/7/25
Published on: 2019/12/3

HGVS expressions

NM_030662.3:c.919+4C>T
NM_030662.3(MAP2K2):c.919+4C>T
NC_000019.10:g.4099197G>A
CM000681.2:g.4099197G>A
NC_000019.9:g.4099195G>A
CM000681.1:g.4099195G>A
NC_000019.8:g.4050195G>A
NG_007996.1:g.29932C>T
ENST00000394867.9:n.1358+4C>T
ENST00000687128.1:n.1362C>T
ENST00000688002.1:n.1217C>T
ENST00000689792.1:n.823+4C>T
ENST00000262948.10:c.919+4C>T
ENST00000262948.9:c.919+4C>T
ENST00000394867.8:c.628+4C>T
ENST00000593364.5:n.870C>T
ENST00000595715.1:n.734+4C>T
ENST00000597263.5:n.169+1822C>T
ENST00000599021.1:c.29+1822C>T
ENST00000600584.5:n.1479+4C>T
ENST00000601786.5:n.1220+4C>T
NM_030662.4:c.919+4C>T

Likely Benign

Met criteria codes 2
BP7 BP4

Not Met criteria codes 2
BS2 BS1

Evidence Links 0

Expert Panel
RASopathy VCEP

Criteria Specification Information
Criteria Specifications for this VCEP

Evidence submitted by expert panel

RASopathy VCEP

The variant c.919+4C>T is an intronic variant at a nucleotide that is not highly conserved and is not predicted to impact splicing (BP7). Also, computational prediction tools and conservation analysis suggests that the variant does not impact the protein (BP4). In summary, the clinical significance of the c.919+4C>T variant is likely benign. RASopathy-specific ACMG/AMP criteria applied (PMID:29493581): BP4, BP7.

Met criteria codes

BP7	✔	Intronic variant not predicted to impact splicing and not evolutionarily conserved.
BP4	✔	No predicted splice impact, not conserved and present in 7 other species including several reptiles.

Not Met criteria codes

BS2	✖	Variant identified in a prenatal chorionic villus specimen obtained from a male fetus undergoing testing for Noonan Syndrome and Related Conditions on an NGS panel of 9 genes. The clinical indication was ‘Abnormal fetal ultrasound findings’ and no other pathogenic or VUS findings were reported. The final result interpretation was 'Negative' and not supporting an increased risk of Noonan syndrome or related conditions. Additionally, no numerical abnormalities for chromosomes 13, 18, 21, X and Y were identified. Mutated in colorectal cancer (MCC) analysis was performed and no contamination was detected. Chromosomal microarray results were positive for a heterozygous 79 KB interstitial deletion of 15q24.2->24.3 that was reported to span one gene (ETFA) associated with autosomal recessive glutaric academia IIA (Integrated Genetics internal data). Cannot be counted due to age requirement.
BS1	✖	Present in 8/111196 (.0035% MAF 95% CI) non-Finnish European alleles in gnomAD

Curation History

Showing 1 to 3 of 3 rows

See Report	Preferred Variant Title	Classification	Condition	Published Date	Version	Criteria Specification	Gene
View	NM_030662.3(MAP2K2):c.919+4C>T	Likely Benign	RASopathy	2019-12-03	1.2	-	MAP2K2
View	NM_030662.3(MAP2K2):c.919+4C>T	Likely Benign	RASopathy	2019-07-26	1.1	-	MAP2K2
View	NM_030662.3(MAP2K2):c.919+4C>T	Likely Benign	RASopathy	2019-07-25	1.0	-	MAP2K2

Showing 1 to 3 of 3 rows

The information on this website is not intended for direct diagnostic use or medical decision-making without review by a genetics professional. Individuals should not change their health behavior solely on the basis of information contained on this website. If you have questions about the information contained on this website, please see a health care professional.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.