Report ID [TBO/RPT/YYYY/NNNN]
Version [v1 · final]
Issued [DD Month YYYY]
info@tribro-omics.com · +91 86603 08678 · tribro-omics.com

VARIANT TRIBRO

Variant Interpretation Report

Evidence-based classification of a single variant using ACMG/AMP criteria

1 Patient and sample

Patient name	[Surname, First name]
Patient ID / MRN	[ID]
Date of birth	[DD Month YYYY]
Sex	[Female / Male / Unknown]
Sample ID	[TBO-S-YYYY-NNNN]
Sample type	[EDTA blood / extracted DNA / saliva]
Collected	[DD Month YYYY]
Received	[DD Month YYYY]
Referring clinician	[Name, institution]
Clinical indication	[Phenotype summary; HPO terms, e.g. HP:0001250]

2 Test information

Product	VARIANT Tribro — variant interpretation
Genome build	GRCh38
Requested by	[Clinician / laboratory, reference]
Reason for request	[New interpretation / reclassification / second opinion]
Source of the variant	[Report or VCF supplied, date]

3 Variant

Gene	[GENE] ([HGNC ID])
Transcript	[NM_] (MANE Select)

cDNA / protein	[c.] / [p.]
Genomic (GRCh38)	[chrN:g.]
Consequence	[Missense / nonsense / frameshift / splice / ...]
Zygosity	[Het / Hom / Hemi]
Gene–disease association	[Disease (MIM), inheritance, ClinGen validity: Definitive / Strong / ...]

CLASSIFICATION

[Pathogenic / Likely pathogenic / Uncertain significance / Likely benign / Benign]

4 Evidence (ACMG/AMP)

Code	Strength	Applied	Evidence summary
PVS1	[Very strong]	[Yes / No]	[Loss-of-function in a gene where LoF is a known mechanism]
PS / PM	[Strength]	[Yes / No]	[Functional, de novo, hotspot or absent-from-controls evidence]
PP / BP	[Supporting]	[Yes / No]	[Computational, segregation or phenotype evidence]
BA1 / BS	[Stand-alone / strong]	[Yes / No]	[Population frequency or other benign evidence]

5 Supporting data

Source	Finding
gnomAD (v4)	[Allele count / frequency; homozygotes]
ClinVar	[Classification, review status, submitters]
In silico	[REVEL, CADD, SpliceAI scores]
Literature	[Key references, functional studies]
Segregation / de novo	[Family data]

6 Interpretation

[Explain how the combined evidence reaches the classification and what additional evidence could change it.]

7 Limitations

- The classification is based on information available on the date of issue and the data supplied; the variant call itself was not re-verified unless stated.

- Variants of uncertain significance should not be used for clinical decision-making on their own.

8 Recommendations

- Re-evaluate the classification when new evidence becomes available.
- Segregation or functional studies where they would change the classification.

9 Sign-off

Role	Name and qualification	Date
Analysed by (bioinformatics)	[Name, qualification]	[DD Month YYYY]
Reviewed by (clinical scientist)	[Name, qualification]	[DD Month YYYY]
Authorised by (laboratory director)	[Name, qualification]	[DD Month YYYY]

10 Important information

This report is intended for the referring clinician and must be interpreted together with the clinical findings, family history and other test results. Variant classification follows the ACMG/AMP 2015 standards (Richards et al., Genet Med 2015) and ClinGen Sequence Variant Interpretation recommendations. Classifications reflect the evidence available on the date of issue and may change. Genetic counselling is recommended when results are discussed with the patient. Report status: [Clinical / Research use only].