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Issued [DD Month YYYY]
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PANEL TRIBRO

Targeted Gene Panel Report

Analysis restricted to a defined gene panel

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	PANEL Tribro — targeted gene-panel analysis
Genome build	GRCh38
Panel	[Panel name, version, number of genes]
Source of panel	[e.g. PanelApp panel name and version / custom]
Technology	[Targeted capture / amplicon / virtual panel from exome or genome]
Pipeline version	[TBO-PANEL vX.Y]

RESULT

[Positive: pathogenic / likely pathogenic variant identified that explains the phenotype] / [Negative: no reportable variant identified] / [Inconclusive: variant of uncertain significance]

3 Results

Gene	Transcript	Variant (HGVS)	Zygosity	Inheritance	Classification
[GENE]	[NM_ / MANE]	[c.] [p.]	[Het / Hom / Hemi]	[AD / AR / XL / de novo]	[Pathogenic / Likely path. / VUS]

4 Coverage of panel genes

Gene	Transcript	Mean depth	Bases ≥ 20×	Comment
[GENE]	[NM_]	[ ]×	[ ] %	[Fully covered / gaps listed]

5 Genes with incomplete coverage

[None / list genes and exons below 20×. Variants in these regions cannot be excluded.]

6 Interpretation

[Relate findings to the clinical question and the panel scope.]

7 Quality metrics

Metric	Result	Acceptance criterion
Mean depth across panel	[ ]×	≥ 200× (capture)
Panel bases at ≥ 20×	[ ] %	≥ 99 %
Contamination estimate	[ ] %	< 2 %

8 Gene list

[Complete list of genes analysed, or reference to the panel version.]

9 Methods

Target regions of [N] genes were enriched with [method] and sequenced on [platform], or extracted in silico from exome/genome data. Alignment to GRCh38 with [aligner]; variant calling with [caller]; annotation and ACMG/AMP classification as described in the Tribro-Omics standard operating procedure.

10 Limitations

- Only the genes listed are analysed; variants elsewhere in the genome are not reported.
- Large deletions and duplications are detected only where CNV analysis is stated as part of the panel.
- Regions with incomplete coverage are listed above; variants there cannot be excluded.

11 Recommendations

- Genetic counselling.
- Consider exome or genome analysis if the panel result is negative and the phenotype is suggestive of a genetic cause.

12 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]

13 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].