{#patient}

# Whole Exome Sequencing Report

## Patient Information

- \*\*Name:\*\* {d.name}

- \*\*Sex/Age:\*\* {d.sexAge}

- \*\*Date Received:\*\* {d.dateReceived}

- \*\*Indication:\*\* {d.indication}

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## Sequencing Platform

\*\*Whole Exome Sequencing on the Illumina Novaseq 6000 NGS Platform\*\*

### Clinical Indication:

{d.clinicalIndication}

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## Likely Pathogenic Variant Detected Related to the Clinical Phenotype

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## Key Findings

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene&Transcript | Location | Variant | Zygosity | Inhertance | ClinicalSignificance |
| {gene.geneAndTranscript} | {d.gene.location} | {d.Variant} | {d.gene.zygosity} | {d.omimPhneotype} | {d.clinicalSignificance |

\*Genetic test results are reported based on the recommendations of American College of Medical Genetics\*

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## Variant Interpretation & Clinical Correlation

\*\*{d.gene.geneName}\*\*: {d.gene.variant}

The submitted sample shows {d.gene.zygosity} variant in {d.gene.locationDetails} of gene {d.gene.geneName} ({d.gene.genomicPosition}). {d.gene.variantDescription}

### Variant Characteristics:

- {d.gene.variantEffect}

- {d.gene.inSilicoPredictions}

- {d.gene.populationFrequency}

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## Variant Evidence

### Gene Impact

- \*\*Gene:\*\* {d.gene.geneName}

- \*\*Effect:\*\* {d.gene.effect}

- \*\*Exon:\*\* {d.gene.exon}

- \*\*Transcript:\*\* {d.gene.transcript}

- \*\*Protein:\*\* {d.gene.proteinChange}

- \*\*Coding:\*\* {d.gene.codingChange}

Based on above evidence, this variant ({d.gene.geneName}::{d.gene.variant}) is classified as {d.gene.classification}.

### OMIM Phenotype:

{d.gene.omimDescription}

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## Recommendations

1. {d.recommendations.1}

2. {d.recommendations.2}

3. {d.recommendations.3}

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## Methodology

- {d.methodology.1}

- {d.methodology.2}

- {d.methodology.3}

- {d.methodology.4}

- {d.methodology.5}

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## Limitations/Disclaimer

- {d.limitations.1}

- {d.limitations.2}

- {d.limitations.3}

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