

Patient Name:	Dummy	Case ID:	XXX
Age:	31 Years	Sample Type:	Blood
Sex:	Male	Sample collection date:	24.11.2022
Referring Clinician:	Dr. XXX	Sample collection time:	05:30PM
Test Requested:	Clinical Exome Sequencing (CES)	Reporting date:	24.01.2023

### CLINICAL INFORMATION/HISTORY

Mr. XXX, a 31 years old male who is married to Geeta Yadav, couple has bad obstetric history of three spontaneous abortions and one child expired after 6 days of life, who had congenital anomaly (cleft palate) and retrognathia. Their third pregnancy had indications of oligohydramnios. TORCH IgM result for his wife was negative. Whole exome sequencing for his wife detected a variant of uncertain significance in the *ZIC2* gene (c.1442G>T) and an additional variant of likely pathogenic significance in the *MMAB* gene (c.557G>A). Sanger Sequencing analysis done for *MMAB* gene in Mr. Manish Yadav was reported to be negative. Their karyotype reports were normal. Mr. Manish Yadav has been evaluated for carrier status of pathogenic variations.

### RESULT SUMMARY

**No pathogenic, likely pathogenic variants or variants of uncertain significance causative of the reported phenotype were identified.**

### VARIANTS RELEVANT TO INDICATION FOR TESTING

No variants were found in the sequence data which may be associated with the clinical history of the patient.

Gene & Transcript	Variant	Zygoty	Location	Disorder	Inheritance	ACMG Classification
<b><i>No significant variant related to phenotype detected</i></b>						

### FINDINGS UNRELATED TO PHENOTYPE

This section provides information on variants identified which are unrelated to the provided phenotype.

### ACMG SECONDARY FINDINGS

No clinically relevant variants associated with the ACMG recommended secondary list of genes were found in the sequence data.

### INCIDENTAL FINDINGS

No variants were detected as incidental findings in the sequenced data which may not be associated with the diagnostic indication for which the sequencing test was performed.

### CARRIER STATUS IN THE GENES RELATED TO DISEASE

The following Pathogenic or Likely Pathogenic variants were detected.

Gene & Transcript	Variant	Zygoty	Location	Disorder	Inheritance	ACMG Classification
<i>IQCE</i> NM_152558.5	c.395-1G>A p.?	Heterozygous	Intron 5	Polydactyly, postaxial, type A7 [OMIM ID: <a href="#">617642</a> ]	Autosomal Recessive	Pathogenic PM2, PVS1 & PP5

#### DETAILED VARIANT INFORMATION (VARIANTS RELEVANT TO INDICATION FOR TESTING)

##### ***IQCE* Chr. 7:2573417 – Pathogenic:**

The splice acceptor variant NM\_152558.5(*IQCE*):c.395-1G>A has been reported to ClinVar as Pathogenic with a status of (0 stars) no assertion criteria provided (Variation ID 437834 as of 2023-01-05). The c.395-1G>A variant is novel (not in any individuals) in 1kG All and in 3/241,054 (0.0012%) alleles from individuals of gnomAD All background. This variant mutates a splice-acceptor sequence and is predicted to disrupt the reading frame, resulting in nonsense mediated decay. This variant results in the loss of an acceptor splice site for the clinically relevant transcript. This variant disrupts the acceptor splice site for an exon upstream from the last coding exon resulting in a frameshift mutation that is predicted to cause nonsense mediated decay. The c.395-1G>A variant is a loss of function variant in the gene *IQCE*, which is intolerant of Loss of Function variants, as indicated by the presence of existing pathogenic loss of function variants NP\_689771.3:p.V301Sfs\*8 and NP\_689771.3:p.E451Rfs\*15. The identified variant has been previously identified in a patient affected with post-axial polydactyly phenotype in homozygous state [PMID: [28488682](#)]. For these reasons, this variant has been classified as **Pathogenic**.

##### **Polydactyly, postaxial, type A7:**

Polydactyly refers to the occurrence of supernumerary digits and is the most frequent of congenital hand and foot deformities. Based on the location of the extra digits, polydactyly can be classified into preaxial, involving the thumb or great toe; postaxial, affecting the fifth digit; and central, involving the 3 central digits. Postaxial polydactyly (PAP) is further subclassified into 2 types: in type A, a well-formed extra digit articulates with the fifth or a sixth metacarpal, whereas in type B, a rudimentary, poorly developed extra digit is present [OMIM ID [617642](#)].

#### RECOMMENDATIONS

Based on the clinical features and the observed genetic findings the following have been recommended:

1. Genetic counselling is recommended.

#### REPORTED VARIANTS STATISTICS:

Gene/Transcript	Variant	Depth	Allelic Depth	Alternate Allele Fraction	dbSNP rsID
<i>IQCE</i> NM_152558.5	c.395-1G>A	100X	45X	0.45	rs755938967

#### DATA STATISTICS

Total data generated (Gb)	7.7GB
Reads that passed alignment (%)	99.46%

<b>Data &gt; Q30 (%)</b>	<b>91.81%</b>
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## METHODOLOGY

Sequencing of the protein coding regions of approximately 30Mb of the human exome (targeting approximately 99% of regions in CCDS and RefSeq) was performed using Illumina NovaSeq platform at a mean depth of 80-100X and % of bases covered at 20X depth >90% in the target region. The individual's DNA was extracted and fragmented, with fragments from the coding regions of the selected gene panel targeted for amplification and sequencing. Reads from the sequence output were aligned to the human reference genome (GRCh37) using the Burrows-Wheeler Aligner (BWA). Duplicate reads identification and removal, base quality recalibration and re-alignment of reads based on indels were done using inbuilt DRAGEN bio-IT pipeline. Variants to the reference were called using the Genomic Analysis Tool Kit (GATK). The variants were annotated and filtered using the **Golden Helix VarSeq** and **Varsome** analysis workflow implementing the ACMG guidelines for interpretation of sequence variants. This includes comparison against the gnomAD population catalogue of variants in 123,136 exomes, the 1000 Genomes Project Consortium's publication of 2,500 genomes, the NCBI ClinVar database of clinical assertions on variant's pathogenicity and multiple lines of computational evidence on conservation and functional impact. All variants with minor allele frequency (MAF) of less than 1% in gnomAD database, and disease-causing variants reported in **HGMD**, in ClinVar are considered. The investigation for relevant variants is focused on coding exons and flanking +/-10 intronic nucleotides of genes with clear gene-phenotype evidence (based on OMIM information). All potential modes of inheritance patterns are considered. In addition, provided family history and clinical information are used to evaluate identified variants with respect to their pathogenicity and causality. This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary.

## VARIANT ASSESSMENT PROCESS

The following databases and in-silico algorithms are used to annotate and evaluate the impact of the variant in the context of human disease: 1000 genomes, gnomAD, ClinVar, OMIM, dbSNP, NCIB RefSeq Genes, ExAC Gene Constraints, VS-SIFT, VS-PolyPhen2, PhyloP, GERP++, GeneSplicer, MaxEntScan, NNSplice, PWM Splice Predictor. Analysis was reported using the to HGVS nomenclature ([www.hgvs.org/mutnomen](http://www.hgvs.org/mutnomen)) as implemented by the VarSeq transcript annotation algorithm. The reported transcript matches that used most frequently by the clinical labs submitting to ClinVar.

## LIMITATIONS

It should be noted that this test is limited to a limited number of genes and does not include all intronic and non-coding regions. This report only includes variants that meets a level of evidence threshold for cause or contribute to disease. Certain classes of genomic variants are also not covered using the NGS testing technology, including triplet repeat expansions, copy number alterations, translocations and gene fusions or other complex structural rearrangements. More evidence for disease association of genes and causal pathogenic variants are discovered every year, and it is recommended that genetic variants are re-interpreted with updated software and annotations periodically.

## VARIANT CLASSIFICATION BASED ON ACMG RECOMMENDATIONS

Genetic test results are reported based on the recommendations of American College of Medical Genetics (ACMG) as described below [1]

<b>Variant</b>	A change in a gene. This could be disease causing (pathogenic) or not disease causing (benign).
<b>Pathogenic</b>	A disease-causing variation in a gene which can explain the patients' symptoms.

<b>Likely pathogenic</b>	A variant which is very likely to contribute to the development of disease. However, the scientific evidence is currently insufficient to prove this conclusively. Additional evidence is expected to confirm this assertion of pathogenicity
<b>Variant of uncertain significance</b>	A variant which is difficult to classify either as pathogenic (disease causing) or benign (non-disease causing) based on current available scientific evidence.

**ACMG Criteria for classifying Variants**

Very Strong (PVS1)	
<b>PVS1</b>	Null variant (nonsense, frameshift, canonical $\pm 1$ or 2 splice sites, initiation codon, single or multi-exon deletion) in a gene where LOF is a known mechanism of disease.
Strong (PS)	
<b>PS1</b>	Same amino acid change as a previously established pathogenic variant regardless of nucleotide change
<b>PS2</b>	De novo variant (both maternity and paternity confirmed) in a patient with the disease and no family history.
<b>PS3</b>	Well-established in vitro or in vivo functional studies supportive of a damaging effect on the gene or gene product.
<b>PS4</b>	The prevalence of the variant in affected individuals is significantly increased compared with the prevalence in controls.
Moderate (PM)	
<b>PM1</b>	Located in a mutational hot spot and/or critical and well-established functional domain (e.g., active site of an enzyme) without benign variation
<b>PM2</b>	Absent from controls (or at extremely low frequency if recessive) in reputed databases.
<b>PM3</b>	Variant (one of the compound heterozygous), is segregating with a pathogenic variant with known phase after testing of parents.
<b>PM4</b>	An in-frame deletion/insertions in non-repeat region or stop-loss can alter the protein length.
<b>PM5</b>	A novel missense change at the same amino acid residue where a pathogenic missense variant has already been determined.
<b>PM6</b>	De novo, without testing in the family.
Supporting (PP)	
<b>PP1</b>	A variant in known gene for a disease which is co-segregating in multiple affected family members
<b>PP2</b>	Missense variants are a common mechanism of disease in a gene which has low benign missense variants.
<b>PP3</b>	A deleterious effect of the variant is predicted by multiple lines of computational evidence (conservation, evolutionary, splicing impact, etc.)
<b>PP4</b>	Patient's phenotype or family history is highly specific for a disease with a single genetic etiology.
<b>PP5</b>	Reputable source recently reports variant as pathogenic, but the evidence is not available to the laboratory to perform an independent evaluation.

**DISCLAIMER**

In accordance to the Pre-Conception and Pre-Natal Diagnostic Testing (PCPNDT) Act, 2003- Govt. of India; Lab does not disclose the gender of the fetus.

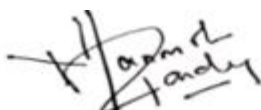
- Interpretation of variants in this report is performed to the best knowledge of the laboratory based on the information available at the time of reporting. The classification of variants can change over time and laboratory cannot be held responsible for this. Re-analysis of variants in previously issued reports in light of new evidence is not routinely performed, but may be available upon request.
- Negative results do not completely exclude the risk/carrier status for these disorders tested (residual risk)
- The sensitivity of this assay to detect large deletions/duplications of more than 10bp or copy number variations (CNV) is 70-75%. The CNVs detected have to be confirmed by alternate method.
- Due to inherent technology limitations of the assay, not all bases of the exome can be covered by this test. Accordingly, variants in regions of insufficient coverage may not be identified and/or interpreted. Therefore, it is possible that pathogenic variants are present in one or more of the genes analyzed, but have not been detected. The variants not detected by the assay that was performed may impact the phenotype.
- It is also possible that a pathogenic variant is present in a gene that was not selected for analysis and/or interpretation in cases where insufficient phenotypic information is available.
- Genes with pseudogenes, paralog genes and genes with low complexity may have decreased sensitivity and specificity of variant detection and interpretation due to inability of the data and analysis tools to unambiguously determine the origin of the sequence data in such regions.
- The mutations have not been validated/confirmed by Sanger sequencing.
- Incidental or secondary findings (if any) that meet the ACMG guidelines [2] can be given upon request.
- The report shall be generated within turnaround time (TAT), however, such TAT may vary depending upon the complexity of test(s) requested. Laboratory under no circumstances will be liable for any delay beyond aforementioned TAT.
- It is hereby clarified that the report(s) generated from the test(s) do not provide any diagnosis or opinion or recommends any cure in any manner. Laboratory hereby recommends the patient and/or the guardians of the patients, as the case may be, to take assistance of the clinician or a certified physician or doctor, to interpret the report(s) thus generated. Laboratory hereby disclaims all liability arising in connection with the report(s).
- In a very few cases genetic test may not show the correct results, e.g. because of the quality of the material provided to laboratory. In case where any test provided by laboratory fails for unforeseeable or unknown reasons that cannot be influenced by laboratory in advance, laboratory shall not be responsible for the incomplete, potentially misleading or even wrong result of any testing if such could not be recognized by laboratory in advance.
- This is a laboratory developed test and the development and the performance characteristics of this test was determined by laboratory.

**REFERENCES**

1. Hamosh, A., Scott, A. F., Amberger, J. S., Bocchini, C. A., & McKusick, V. A. (2005). Online Mendelian Inheritance in Man (OMIM), a knowledgebase of human genes and genetic disorders. Nucleic Acids Research, 33(Database Issue), D514–D517. <http://doi.org/10.1093/nar/gki033>, <https://www.omim.org/>
2. Landrum, M. J., Lee, J. M., Riley, G. R., Jang, W., Rubinstein, W. S., Church, D. M., & Maglott, D. R. (2014). ClinVar: public archive of relationships among sequence variation and human phenotype. Nucleic Acids Research, 42(Database issue), D980–D985. <http://doi.org/10.1093/nar/gkt1113> <https://www.ncbi.nlm.nih.gov/clinvar/>
3. Richards, S., Aziz, N., Bale, S., Bick, D., Das, S., Gastier-Foster, J., et al On behalf of the ACMG Laboratory Quality Assurance Committee, H. L. (2015). Standards and Guidelines for the Interpretation of Sequence Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genetics in Medicine: Official Journal of the American College of Medical Genetics, 17(5), 405–424. <http://doi.org/10.1038/gim.2015.30>.
4. Sherry ST, Ward MH, Kholodov M, Baker J, Phan L, Smigielski EM, Sirotkin K. dbSNP: the NCBI database of genetic variation. Nucleic Acids Res. 2001 Jan 1;29(1):308-11.
5. GnomAD database - <https://gnomad.broadinstitute.org/>



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**Conditions for Reporting**

1. It is presumed that specimen belongs to patient named or identified, such verification being carried out at the point of generation of said specimen.
2. A test might not be performed due to following reasons:
  - a. Specimen Quantity not sufficient (Inadequate collection/spillage during transit).
  - b. Specimen Quality not acceptable (Hemolysis/clotted/lipemic).
  - c. Incorrect sample type.
  - d. Test cancelled either on request of patient or doctor
3. In any of the above case a fresh specimen will be required for testing and reporting.
4. The results of the tests may vary from lab to lab; time to time for the same patient.
5. The reported results are dependent on individual assay methods, equipment, method sensitivity, specificity and quality of the specimen received.
6. Partial representation of report is not allowed.
7. The reported tests are for the notification of the referring doctor, only to assist him/her in the diagnosis and management of the patient.
8. Report with status "Preliminary" means one or more test are yet to be reported.
9. This report is not valid for Medico Legal Purpose.
10. Applicable Jurisdiction will be of "Delhi" for any dispute/claim concerning the test(s) & results of the test(s).

**Disclaimer: Method given in report are only indicative and can be changed depending upon type of machine and kit available at time of testing. Not all tests at all locations are under NABL scope. Availability of tests under NABL scope varies from lab to lab.**

# Terms and Conditions of Reporting

1. The presented findings in the Reports are intended solely for informational and interpretational purposes by the referring physician or other qualified medical professionals possessing a comprehensive understanding of reporting units, reference ranges, and technological limitations. The laboratory shall not be held liable for any interpretation or misinterpretation of the results, nor for any consequential or incidental damages arising from such interpretation.
2. It is to be presumed that the tests performed pertain to the specimen/sample attributed to the Customer's name or identification. It is presumed that the verification particulars have been cleared out by the customer or his/her representation at the point of generation of said specimen / sample. It is hereby clarified that the reports furnished are restricted solely to the given specimen only.
3. It is to be noted that variations in results may occur between different laboratories and over time, even for the same parameter for the same Customer. The assays are performed and conducted in accordance with standard procedures, and the reported outcomes are contingent on the specific individual assay methods and equipment(s) used, as well as the quality of the received specimen.
4. This report shall not be deemed valid or admissible for any medico-legal purposes.
5. The Customers assume full responsibility for apprising the Company of any factors that may impact the test finding. These factors, among others, includes dietary intake, alcohol, or medication / drug(s) consumption, or fasting. This list of factors is only representative and not exhaustive.

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## DISCLAIMER

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