ALTUM CMA REPORT

Name: AYESHA	Age/Gender: 30 Years/Female
Patient ID: 1002426112	Sample ID: 2400031174
Specimen type: POC	Sample quality: Optimum
Referring Doctor: DR. BABITA KULHARI	Referring Centre: City Hospital-Alwar
Test: Altum CMA	Collection Date: 27.05.2024
Receiving Date: 28.05.2024	Reporting Date: 10.06.2024
Indication: Non-consanguineous couple, G1 - Missed abortion at 8-10 weeks, G2 - Present pregnancy - Missed abortion at ~6 weeks.	

SUMMARY:

Gain of 90 Mb on chromosome 16 (Trisomy 16).

RESULT

Clinically relevant Copy Number Variation: **Detected**

Sr. No	Type	Chr. No	Cytoband	Size (kbp)	CN State	Gene Count	Genomic coordinates (ISCN 2016)	Interpretation
1	Gain	16	p13.3 q24.3	90,053	3	1,137	arr[GRCh38] 16p13.3q24.3 (35,881_90,088,654)x3	Pathogenic#

#Pathogenic: The CNV has been classified based on the ACMG guidelines specified by Kearney *et. al.,* 2011.

Sex of the fetus has not been disclosed in accordance with the PCPNDT Act 2003

INTERPRETATION AND CASE SUMMARY:

Chromosomal microarray analysis reveals a gain of 90 Mb on chromosome 16, spanning from 16p13.3 to 16q24.3 region. It consists of 1,137 genes (list available on request).

This finding is consistent with **complete Trisomy 16.**

Trisomy 16 results from having three copies of chromosome 16 in each cell in the body instead of the usual two copies. It is known to be associated with miscarriages in the first trimester and accounts for 30% of autosomal trisomies[3].

Trisomy 16 is incompatible with life and has never been described progressing further than the first trimester. In cases of mosaic trisomy 16, there is a high risk of abnormal outcome, cases commonly exhibiting intrauterine growth retardation (IUGR), fetal-death-in-utero, preeclampsia, preterm delivery, neonatal death, developmental delay, congenital heart defect, and other minor anomalies.

The recurrence risk of standard trisomy 16 is less as it is not inherited but occurs as a random event during the formation of egg and sperm. The recurrence risk of this condition is very low.

Clinical correlation is recommended.

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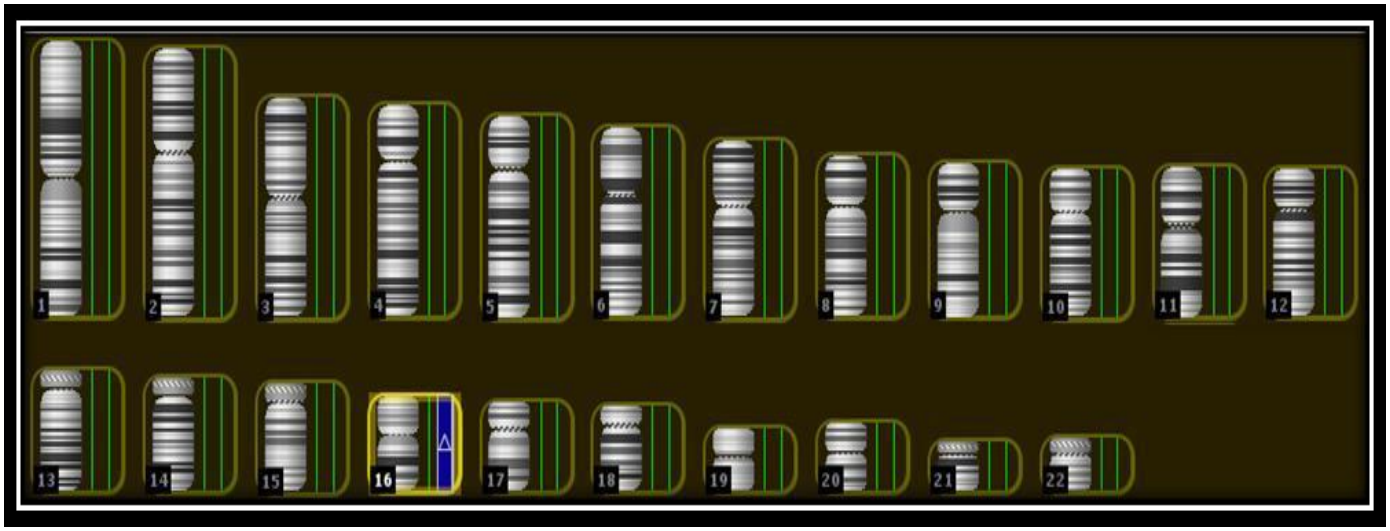

Karyoview

MATERNAL CELL CONTAMINATION RESULTS:

No significant maternal contamination detected on PCR-based VNTR analysis with a lower limit of detection of 10%.

RECOMMENDATION:

1. Genetic counselling is recommended for further genetic evaluation based on clinical correlation.

TEST METHODOLOGY:

This microarray consists of a total of 315,608 features covering control, copy number (CN) and single nucleotide polymorphism (SNP) probes. There is a total of 18K CN and 148K SNP probes uniformly spaced over the genome with enhanced interrogation of 396 regions of prenatal interest. The minimum resolution for detection is ~1MB for losses, ~2MB for gains and >5MB for LOH (loss of heterozygosity). However, LOH will be reported depending upon chromosomal location, significance and likelihood of imprinting disorder.

Genomic DNA was digested with Nsp1 and then ligated to Nsp1 adaptor followed by PCR amplification. Digested, ligated and amplified PCR products were then purified and fragmented. The fragmented products were labelled with biotin and hybridised overnight to the array. The array was stained and washed using a fluidics station and then scanned on an Affymetrix Gene Chip scanner (GCS 3000). The data file (.CEL file) generated was analysed using Chromosome Analysis Suite (ChAS). The analysis is based on the Human reference genome (GRCh38/hg38). All findings are correlated with clinical history before reporting. All VOUS (variants of unknown significance) are reported if they are found relevant to clinical history. An unrelated pathogenic or likely pathogenic finding is reported if there is sufficient empirical evidence for its involvement in a disorder.

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LIMITATIONS:

- The test can only detect gross genomic copy number imbalances (aneuploidy, deletions and duplications) and LOH in the nuclear genome.
- It cannot detect balanced chromosomal rearrangements such as balanced translocations, inversions and balanced insertions.
- Low grade mosaicism (<20%) for chromosomal abnormalities cannot be detected.
- The test cannot detect point mutations. This test detects the chromosomal abnormalities only under its limit of resolution.

DISCLAIMER:

- The above analysis is based upon the sample received in the laboratory. This is not a diagnostic test and hence should not be considered as a purpose of diagnosis of any diseases.
- Lilac Insights follows a policy of not reporting Variations of Unknown Clinical Significance (VOUS) for prenatal cases. An unrelated pathogenic or likely pathogenic finding is reported if there is sufficient empirical evidence for its involvement in a disorder.
- Clinical decisions should not be taken solely on the basis of Chromosomal Microarray Results and correlation with other clinical findings like patient history, ultrasound findings is necessary.
- The test was validated and its performance characteristics have been determined by Lilac Insights Pvt. Ltd as required by the ACMG guidelines.
- MCC is tested on the basis of the distribution of SNP markers in this assay or in selected instances it is also confirmed by performing VNTR based analysis.
- Although all precautions are taken during DNA tests the currently available data indicates that the technical error rate for all types of DNA analysis is approximately 2%. There is a slight chance of failure due to degraded DNA or contaminated sample.

REFERENCES:

1. South *et. al*., Constitutional Microarray Guidelines, Genetics in medicine, Volume 15, Number 11, November 2013.
2. CytoScan Optima Suite- Data sheet.
3. Takol Chareonsirisuthigul *et. al.,* Intrauterine Growth Retardation Fetus with Trisomy 16 Mosaicism, Case Reports in Genetics, vol. 2014, Article ID 739513, 3 pages, 2014. https://doi.org/10.1155/2014/739513.
4. Armour *et. al.,* 2018. Practice guideline: joint CCMG-SOGC recommendations for the use of chromosomal microarray analysis for prenatal diagnosis and assessment of fetal loss in Canada. Armour CM, et. al., J Med Genet 2018;55:215–221. doi:10.1136/jmedgenet-2017-105013.
5. Johnson P, Duncan K, Blunt S, Bell G, Ali Z, Cox P, Moore GE. Apparent confined placental mosaicism of trisomy 16 and multiple fetal anomalies: case report. Prenat Diagn. 2000 May;20(5):417-21. doi: 10.1002/(sici)1097-0223(200005)20:5<417::aid-pd816>3.0.co;2-m. PMID: 10820412.

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Checked by
Dr. Madhavi Pusalkar, Ph.D
General Manager: Genomics

Verified by
Dr. Yamini Jadhav
Consultant Cytogeneticist

- End of the report -

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