LABORATORY REPORT

Redcliffe labs

Patient Name	:	Bill Date	:
DOB/Age/Gender	:	Sample Collected	:
Patient ID / UHID	:	Sample Received	:
Referred By	:	Report Date	:
Sample Type	:	Barcode No	:
Client	:	Report Status	:

CYTOGENETICS REPORT

Karyotyping: Blood Lympho Culture, Couple

Wife :

CLINICAL INDICATION	Blighted ovum
SUMMARY OF RESULTS	**NORMAL FEMALE KARYOTYPE**
NOMENCLATURE	**46,XX** *(As per International System for Human Cytogenomic Nomenclature, ISCN,2020)*

CLINICAL INTERPRETATION

The patient is showing a normal female karyotype along with the increase in the length of the heterochromatin on the long arm of chromosome 9 in all the metaphases analyzed.

Traditionally chromosome polymorphism (CPM) particularly in the heterochromatin region of chromosomes 1, 9, 16 and Y are considered as normal variant with no phenotypic or functional variation as they are also known to occur in the general population (*Boragoankar DS Chromosomal variation in man: a catalogs of chromosomal variants and anomalies. New York: Wiley-Liss, 1997*). Since heterochromatin also plays an essential role in spindle attachment and sister chromatid cohesion (*Karpen and Endow et al.,* 1998**).** The current clinical studies also highlight the modifications in heterochromatin region of chromosome that could be associated with primary infertility, bad obstetric history (BOH) including recurrent pregnancy loss in patients *[Minocherhomji et al., Fertility Sterility Vol.92, No.1, July 2009)* [*Madon et al., 2005; Gutierrez et al.,2009, Cheng et.al, 2017, Cao et al., 2022].*

Within the limits of standard cytogenetic methodologies, the chromosomes of the patient showed Normal G-banding patterns with no evidence of aneuploidy or without apparent structural abnormality or rearrangement. The following possibilities, although rare, cannot be ruled out: a) low level mosaicism, b) very subtle rearrangements, c) genetic disorders that cannot be detected beyond the resolution of by standard cytogenetic methods.

RECOMMENDATION	Genetic Counseling for the family is recommended.
SAMPLE DESCRIPTION	The sample was of optimal quality for conventional cytogenetics culture techniques. The 72 hours of stimulated peripheral blood sample was initiated in karyotyping medium yielded analyzable metaphases for karyotype.

Dr. Ashish Fauzdar
PhD (Genetics), AIIMS
Head of Clinical Genomics & Cytogenetics

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Patient Name	:	Bill Date	:
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Husband :

CLINICAL INDICATION	Wife has H/O Blighted ovum
SUMMARY OF RESULTS	**NORMAL MALE KARYOTYPE**
NOMENCLATURE	**46,XY** *(As per International System for Human Cytogenomic Nomenclature, ISCN,2020)*

CLINICAL INTERPRETATION

Within the limits of standard cytogenetic methodologies, the chromosomes of the patient showed Normal Male Karyotype G-banding patterns with no evidence of aneuploidy or without apparent structural abnormality or rearrangement. The following possibilities, although rare, cannot be ruled out: a) low level mosaicism, b) very subtle rearrangements, c) genetic disorders that cannot be detected beyond the resolution of by standard cytogenetic methods.

RECOMMENDATION	Genetic Counseling for the family is recommended.
SAMPLE DESCRIPTION	The sample was of optimal quality for conventional cytogenetics culture techniques. The 72 hours of stimulated peripheral blood sample was initiated in karyotyping medium yielded analyzable metaphases for karyotype.

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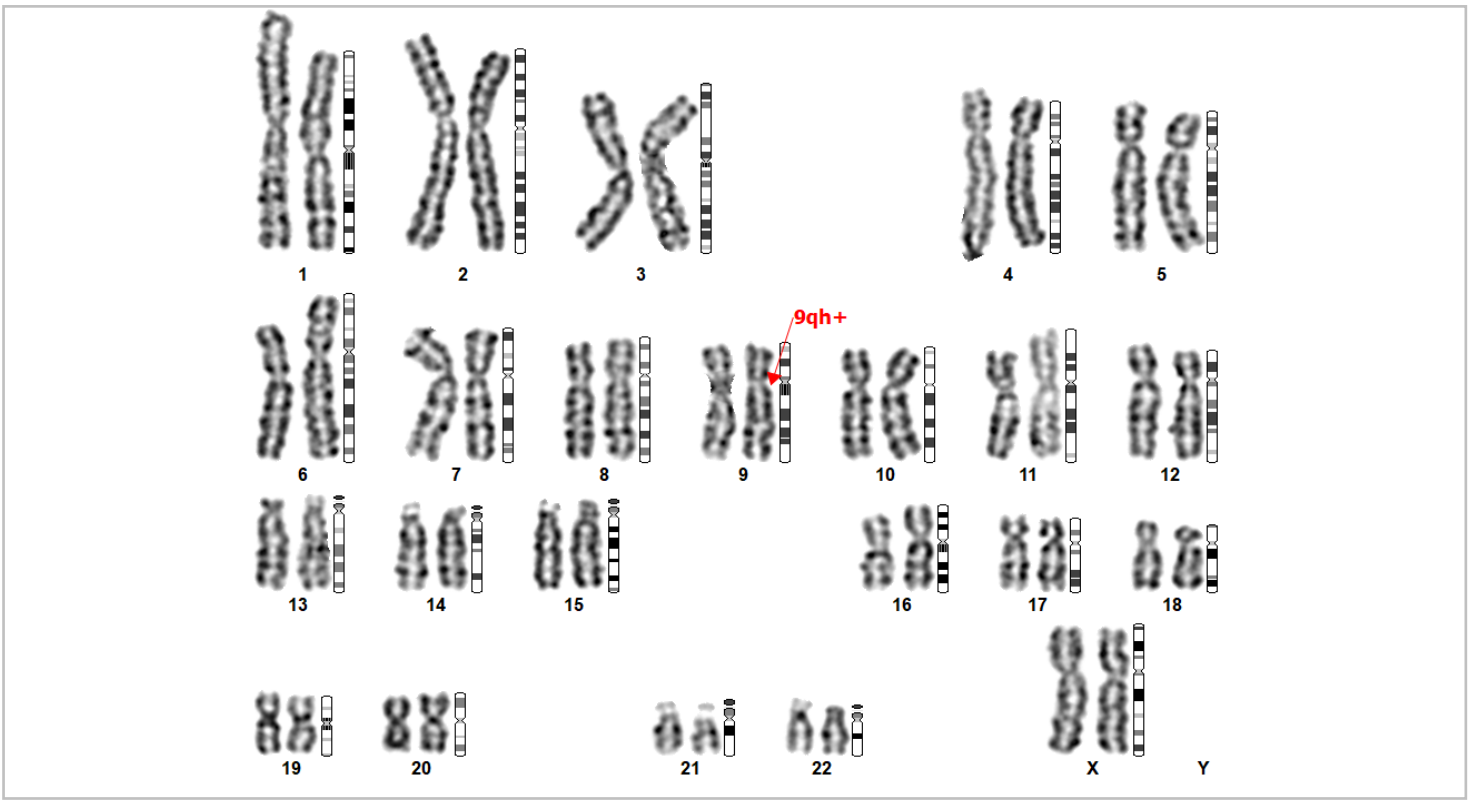
KARYOTYPE IMAGE:



KIRAN **Karyotype: 46,XX** **Barcode No: CG002944**

METHOD:	G-BANDING
Metaphase Counted:	20
Metaphase Analyzed:	10
Metaphase Karyotyped:	10
Banding Resolution:	**700**
Metaphase Quality:	**Good**

Ms. Ritu (Jr. Scientist)
Cytogenetics

Dr. Ashish Fauzdar
PhD (Genetics), AIIMS
Head of Clinical Genomics

Reviewed and Signed out on: 04-Apr-2023

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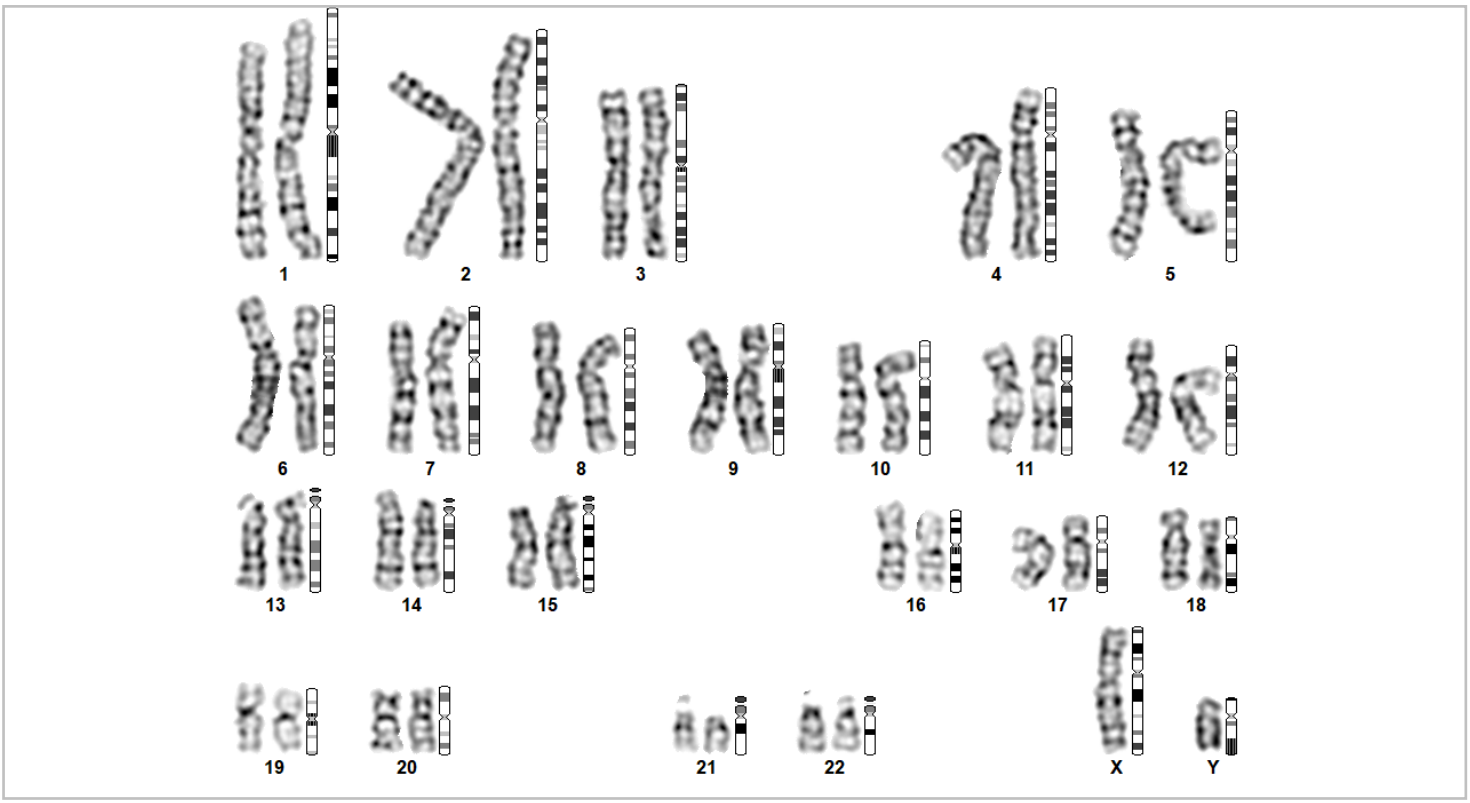
KARYOTYPE IMAGE:



DEEPAK **Karyotype: 46,XY** **Barcode No: CG002944**

METHOD:	G-BANDING
Metaphase Counted:	20
Metaphase Analyzed:	10
Metaphase Karyotyped:	10
Banding Resolution:	**650**
Metaphase Quality:	**Good**

Ms. Ritu (Jr. Scientist)
Cytogenetics

Dr. Ashish Fauzdar
PhD (Genetics), AIIMS
Head of Clinical Genomics

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