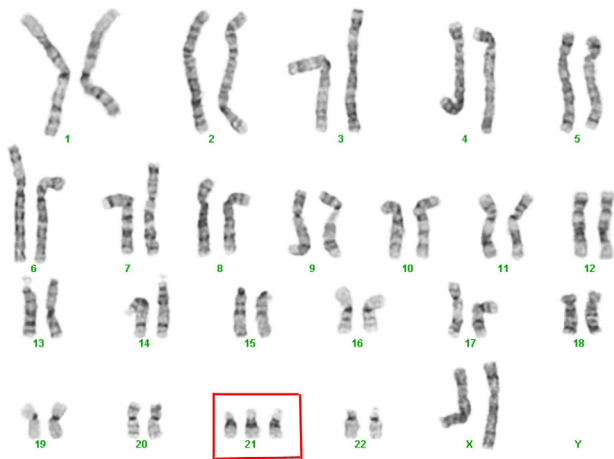


# THE PATHCARE NEWS

## CYTOGENOMIC TESTING



### CYTOGENETICS TO CYTOGENOMICS

#### What is Cytogenomics?

**CYTOGENOMICS** is used as a general term that encompasses conventional karyotyping, as well as molecular cytogenetics (fluorescence in situ hybridization-FISH), microarrays and molecular-based techniques. With advancing technologies and consequent shift towards an increasing application of molecular genetic techniques with the potential for higher resolution, as well as the application of multiple testing strategies for the **diagnosis of chromosomal disorders**, it is important that testing laboratories keep up with technology and provide guidance to this ever-changing testing scenario. These will enable Cytogenetic laboratories to operate within

acceptable standards and to offer a reliable, cost-effective service.

### Guidelines for CONSTITUTIONAL Cytogenomic Analysis

| Main clinical indications<br><b>PRENATAL DIAGNOSIS</b>   | Main clinical indications<br><b>POSTNATAL DIAGNOSIS</b>   |
|--|---|
| Abnormal foetal ultrasound   | Abnormal clinical phenotype   |
| High-risk maternal serum screening/NIPT result indicating an increased risk of a chromosomally abnormal foetus | Multiple congenital abnormalities   |
| Parental chromosome rearrangement, mosaicism or previous aneuploidy  | Clinically significant abnormal growth – short stature, excessive growth, microcephaly, macrocephaly  |
| Previous livebirth/stillbirth with a chromosome abnormality  | Primary or secondary amenorrhoea or ovarian insufficiency   |
| Possible foetal mosaicism detected by prior prenatal study   | Ambiguous genitalia   |
| Familial monogenic disorder (i.e., CF, Noonan syndrome)  | Infertility of unknown aetiology  |
|  | Sperm abnormalities – azoospermia or severe oligospermia  |
|  | A malformed foetus or stillbirth of unknown aetiology   |
|  | Third and subsequent miscarriage(s): products of conception   |
|  | Significant familial history of chromosome rearrangements   |
|  | Significant familial history of intellectual disability (ID) of possible chromosomal origin where it is not possible to study the affected individual |
|  | Carrier-ship for an X-linked recessive disorder in a female.  |
|  | <b>Microarray is the test method of choice for: Intellectual disability (ID), autism, neurodevelopmental disorders and/or congenital anomalies</b>    |

**TESTS AVAILABLE:**

**1. PRENATAL TESTING**

| TEST  | DESCRIPTION   | TAT          | SAMPLE REQUIRED   |
|---|---|--------------|---|
| <b>NIPT – Non-Invasive Prenatal Testing</b> | NIPT is a screening test with a high specificity and sensitivity. All positive results should be confirmed by chromosomal analysis / FISH.  | 7-10 days    | EDTA blood sample   |
| <b>AMNIOCENTESIS: FISH / QF-PCR</b>         | Fluorescent-in-situ-hybridization / Qualitative Fluorescent PCR – a method where chromosomal investigation of most common aneuploidies are analysed. i.e. 13,18,21, X,Y. Chromosomes 15 and 16 may be added for FISH / QFPCR performed on placental tissue. | 3-5 days     | Amniotic fluid<br>Placental tissue / POC                      |
| <b>KARYOTYPING- Chromosomal Analysis</b>    | Chromosomal analysis is performed on all 46 chromosomes.<br>Can detect abnormalities >5mb.<br>Can detect aneuploidies, translocations, and all re-arrangements  | 14 days      | Lithium Heparin blood sample                                  |
| <b>CMA – CHROMOSOMAL MICRO-ARRAY</b>        | Genome-wide microarray-based analysis (array) is used to detect chromosomal imbalances at a significantly higher resolution than routine cytogenetic analysis   | 10 – 14 days | EDTA blood sample<br>Amniotic fluid<br>Placental tissue / POC |

**2. POSTNATAL TESTING**

| TEST                                      | DESCRIPTION  | TAT          | SAMPLE REQUIRED              |
|---|--|--------------|------------------------------|
| <b>KARYOTYPING – Chromosomal Analysis</b> | Chromosomal analysis is performed on all 46 chromosomes.<br>Can detect abnormalities > 5mb<br>Can detect aneuploidies, translocations, and all re-arrangements.  | 14 days      | Lithium Heparin blood sample |
| <b>CMA – CHROMOSOMAL MICRO-ARRAY</b>      | Genome-wide microarray-based analysis (array) is used to detect chromosomal imbalances at a significantly higher resolution than routine cytogenetic analysis.   | 10 – 14 days | EDTA blood sample            |
| <b>NGS – NEXT GENERATION SEQUENCING</b>   | Although widespread application is currently prohibited both by cost and the requirement for complex algorithms and data analysis pathways, it is predicted that this will become a standard approach for genetic diagnosis in coming years. |              |                              |

- When deciding which methodology to apply, the specific referral indication and the advantages and limitations of each technique must be taken into account

## Cytogenomic Technologies: CONSTITUTIONAL Postnatal Testing

- When deciding which methodology to apply, the specific referral indication and the advantages and limitations of each technique must be taken into account

|                              | KARYOTYPING  | FISH / QF PCR  | CMA – CHROMOSOMAL MICRO-ARRAY  | NGS  |
|------------------------------|--|--|--|--|
| Whole Genome Resolution      | 5 - 10 Mb  | - 100 kb   | 20 - 200 kb  | 100 - 150 kb   |
| TAT                          | 14 days  | 5-7 days   | 21 days  | variable   |
| Targeted                     | ALL 46 chromosomes   | Single probe or multiple chromosome probes can provide reliable results in different clinical situations.  | Used to detect chromosomal imbalances at a significantly higher resolution than routine cytogenetic analysis.  | NGS is a general term for a variety of methods and it has a number of applications, including NIPT for prenatal aneuploidy screening and whole-exome sequencing (WES)  |
| Sample required              | Blood / Placental tissue   | Blood / placental tissue   | Blood placental tissue   | Blood / placental tissue   |
| Reasons of clinical referral | Abnormal clinical phenotype<br>Multiple congenital abnormalities<br>Primary or secondary amenorrhoea or ovarian insufficiency;<br>Ambiguous genitalia<br>Infertility of unknown aetiology<br>Sperm abnormalities – azoospermia or severe oligospermia<br>Repeated miscarriages<br>Significant familial history of chromosome rearrangements;<br>Routine postnatal specimen preparations<br><br>Haematological Oncology bone marrow – leukemic / lymphoma referrals | Interphase FISH<br>Numerical abnormalities; Duplications; Deletions; Sex chromosome constitution; Mosaicism; Gene amplification.<br>Metaphase FISH Marker chromosome;<br>Unknown material attached to a chromosome;<br>Identification and exclusion of small expected structural rearrangements;<br><b>QF PCR –</b> triploidy and mosaicism and genotypes the sample allowing for identification of MCC, twin pregnancies and chimeras.<br><br>Haematological Oncology bone marrow – leukemic / lymphoma referrals | ID, autism, neurodevelopmental disorders and/or congenital anomalies<br>- Carriership for an X-linked recessive disorder in a female.<br>Abnormal clinical phenotype<br>Identification and exclusion of small expected structural rearrangements;<br><br>Haematological Oncology bone marrow – leukemic / lymphoma referrals | Significant familial history of intellectual disability (ID) of possible chromosomal origin where it is not possible to study the affected individual;<br>- Carriership for an X-linked recessive disorder in a female.<br><br>Haematological Oncology bone marrow – leukemic / lymphoma referrals |
| Aneuploidy                   | YES  | YES  | YES  | YES  |
| Balanced translocation       | YES  | YES  | NO   | YES  |
| Unbalanced translocation     | YES  | YES  | YES  | YES  |
| Polyploidy                   | YES  | YES  | YES  | YES  |
| Mosaicism                    | YES  | YES  | YES  | YES  |
| UPD                          | No   | No   | YES  | YES  |
| Copy Neutral LOH             | No   | No   | YES  | YES  |
| Gene Fusions                 | YES  | No   | YES  | YES  |

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## Cytogenomic Technologies: CONSTITUTIONAL Prenatal Testing

- When deciding which methodology to apply, the specific referral indication and the advantages and limitations of each technique must be taken into account

|                          | AMNIOCENTESIS KARYOTYPING  | AMNIOCENTESIS FISH / QF PCR  | CMA – CHROMOSOMAL MICRO-ARRAY   | NGS  |
|--------------------------|--|--|---|--|
| Whole Genome Resolution  | 5 - 10 Mb  | - 100 kb   | 20 - 200 kb   | 100 - 150 kb   |
| TAT                      | 14 days  | 5-7 days   | 21 days   | variable   |
| Targeted                 | ALL 46 chromosomes   | Single probe or multiple chromosome probes can provide reliable results in different clinical situations.  | Used to detect chromosomal imbalances at a significantly higher resolution than routine cytogenetic analysis. | NGS is a general term for a variety of methods and it has a number of applications, including NIPT for prenatal aneuploidy screening and whole-exome sequencing (WES)  |
| Sample required          | Amniotic fluid / Placental tissue/cord blood   | Amniotic fluid / placental tissue / cord blood   | Amniotic fluid / placental tissue / cord blood  | Amniotic fluid / placental tissue / cord blood   |
| Reasons of referral      | Confirmation of aneuploidy;<br>Exclusion of known large structural rearrangements;<br>Identification and exclusion of small expected structural rearrangements;<br>Routine prenatal specimen preparations;<br>Prenatal specimen abnormal ultrasound referrals (in the absence of array-based analysis);<br>Routine postnatal specimen preparations | Rapid prenatal FISH<br>High risk of chromosome aneuploidy or recurrent microdeletion (e.g., abnormal ultrasound);<br>Late gestation referral.<br>Evaluation/ characterisation of interphase FISH<br>Numerical abnormalities;<br>Duplications;<br>Deletions;<br>Sex chromosome constitution;<br>Mosaicism;<br><b>QF PCR</b><br>Detects triploidy and mosaicism and genotypes the sample, allowing for identification of MCC, twin pregnancies and chimeras. | To investigate the cause of miscarriage and foetal abnormality.   | NIPT for prenatal aneuploidy screening approximately 85% of disease-causing variants have been identified in exons or at splice-junction boundaries in introns. In addition to sequence variants, structural variants or CNVs can also be detected in WES data, which increases the diagnostic yield. Although widespread application is currently prohibited both by cost and the requirement for complex algorithms and data analysis pathways, it is predicted that this will become a standard approach for genetic diagnosis in coming years. |
| Aneuploidy               | YES  | YES  | YES   | YES  |
| Balanced translocation   | YES  | YES  | NO  | YES  |
| Unbalanced translocation | YES  | YES  | YES   | YES  |
| Polyploidy               | YES  | YES  | YES   | YES  |
| Mosaicism                | YES  | YES  | YES   | YES  |
| UPD                      | No   | No   | YES   | YES  |
| Copy Neutral LOH         | No   | No   | YES   | YES  |
| Gene Fusions             | YES  | No   | YES   | YES  |

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