Limitations of Prenatal Cytogenetic Tests

Rapid prenatal tests

Rapid aneuploidy screening is carried out using QF-PCR for amniotic fluid samples and by chromosome analysis from direct preparations from chorionic villus samples.
The QF-PCR test measures the copy number of chromosomes 13, 18 and 21 only.
Chromosome analysis of direct preparations from chorionic villus samples will detect numerical changes for any chromosome and may detect large structural chromosome abnormalities at a low G-band resolution.

Aneuploidy screening by FISH

FISH tests will only assess the copy number of the region of the chromosomes targeted by the probes used.

Long term culture chromosome analysis

Chromosome analysis cannot guarantee to exclude the presence of mosaicism, or small structural chromosome abnormalities. If mosaicism is suspected the number of cells examined will be increased to improve the chances of detecting it.
When detected in a prenatal sample mosaicism may be difficult to interpret. Confined placental mosaicism is observed in approximately 1-2% of chorionic villus samples and further invasive testing may be required to interpret these cases.
We aim to analyse samples to meet the minimum banding resolution recommended by National Professional standards, where this has not been achieved this will be stated in our reports.
There is a small risk of overgrowth of maternal cells in amniotic fluid or chorionic villus long term cultures.
Blood samples from parents may occasionally be required in order to clarify interpretation of the cytogenetic result. If required, these will be requested in discussions with the referring department.

Prenatal array tests

- Maternal cell contamination - may be detected by an array test. This may result in the array test being non reportable
- Possible consanguinity - may be detected by an array test
- Low level mosaicism - may not be detected by an array test
- Late gestation amniotic fluid samples (30+ weeks) – may give array test results with poor quality control parameters. This may result in the array test being non reportable
- Reporting resolution – the following will be reported
    1. losses of >1 Megabases and gains of >2 Megabases where there are known protein coding genes (but which are not necessarily Online Mendelian Inheritance In Man (OMIM) or Developmental Disorders Genotype to Phenotype (DDG2P) genes), unless the region is known to be a region of polymorphism in a normal population (as defined in either the Database of Genomic Variance (DGV) or by internal data)
    2. losses of > 10 Kilobases and gains of >100 Kilobases where there are OMIM or DDG2P genes present
    3. Known pathogenic syndromes (please contact the laboratory for a full list)
    4. Regions of known susceptibility as defined in 'Recommendations for the use of Chromosome Microarray in Pregnancy' published by The Royal College of Pathologists and Royal College of Obstetricians and Gynaecologists in June 2015.