

Innovative use of SNPs in PGT-A allows to distinguish meiotic trisomies without parental DNA sample support

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21.PGDIS

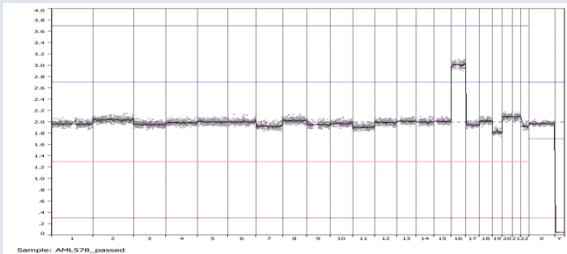
Kuala Lumpur

6.-8.5.2024

Use of SNPs in preimplantation genetic testing for aneuploidies (PGT-A)

CNV

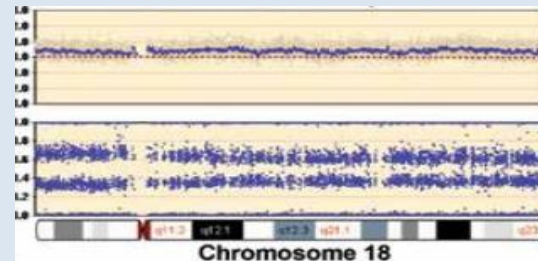
NGS



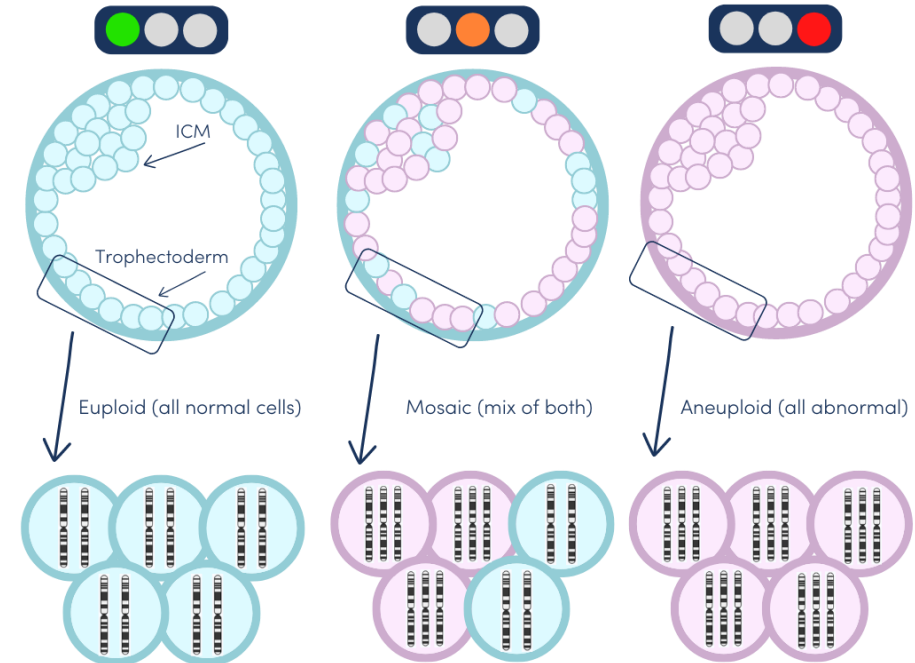
- Mosaicism detection
- High resolution
- Segmental aneuploidies

CNV + SNP analysis

NGS, SNP array



- Triploids/haploids detection
- Reduced false calls
- Fingerprinting
- Origin of aneuploidy (meiotic, mitotic, pat., mat.)



Recommended for transfer



Genetic counselling

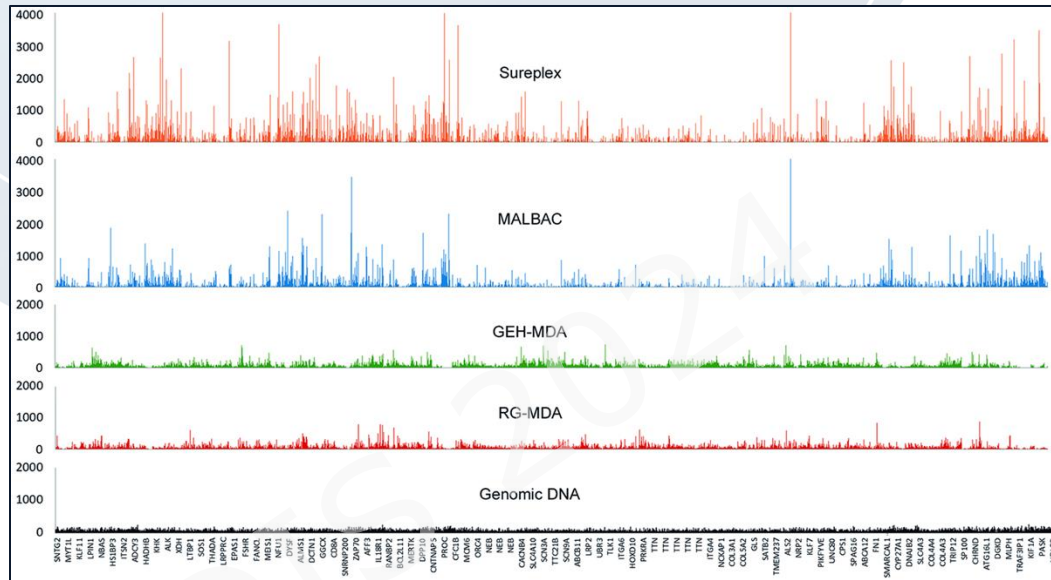
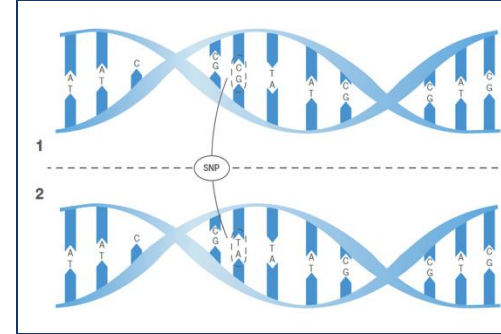


Not recommended

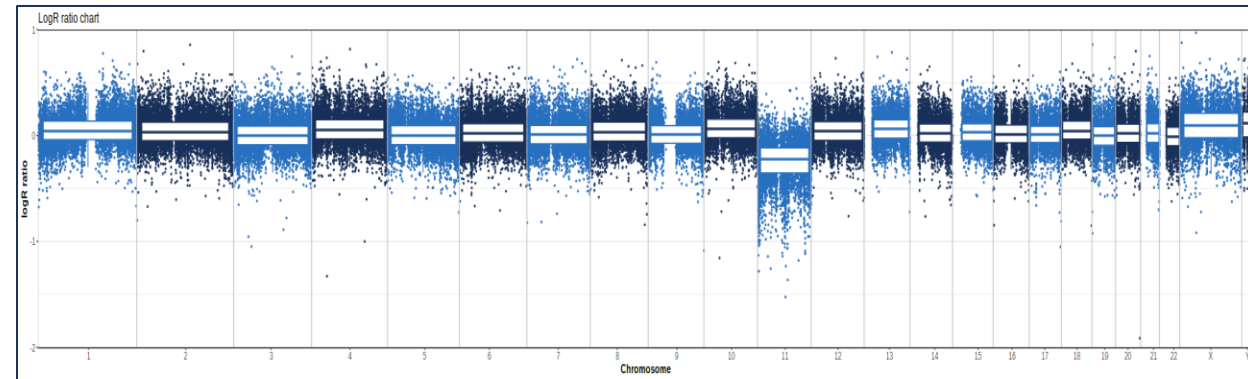
PGT-A

PGT-A + SNP analysis

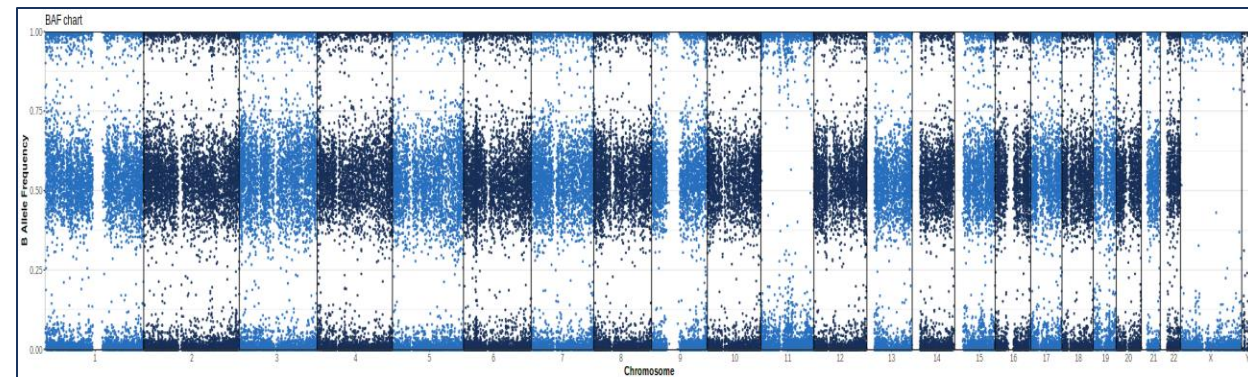
- Infinium™ Global Screening Array-24 v3.0 BeadChip
- 654,027 SNP markers
- Multiple Displacement Amplification (MDA)



Rey et al., 2018



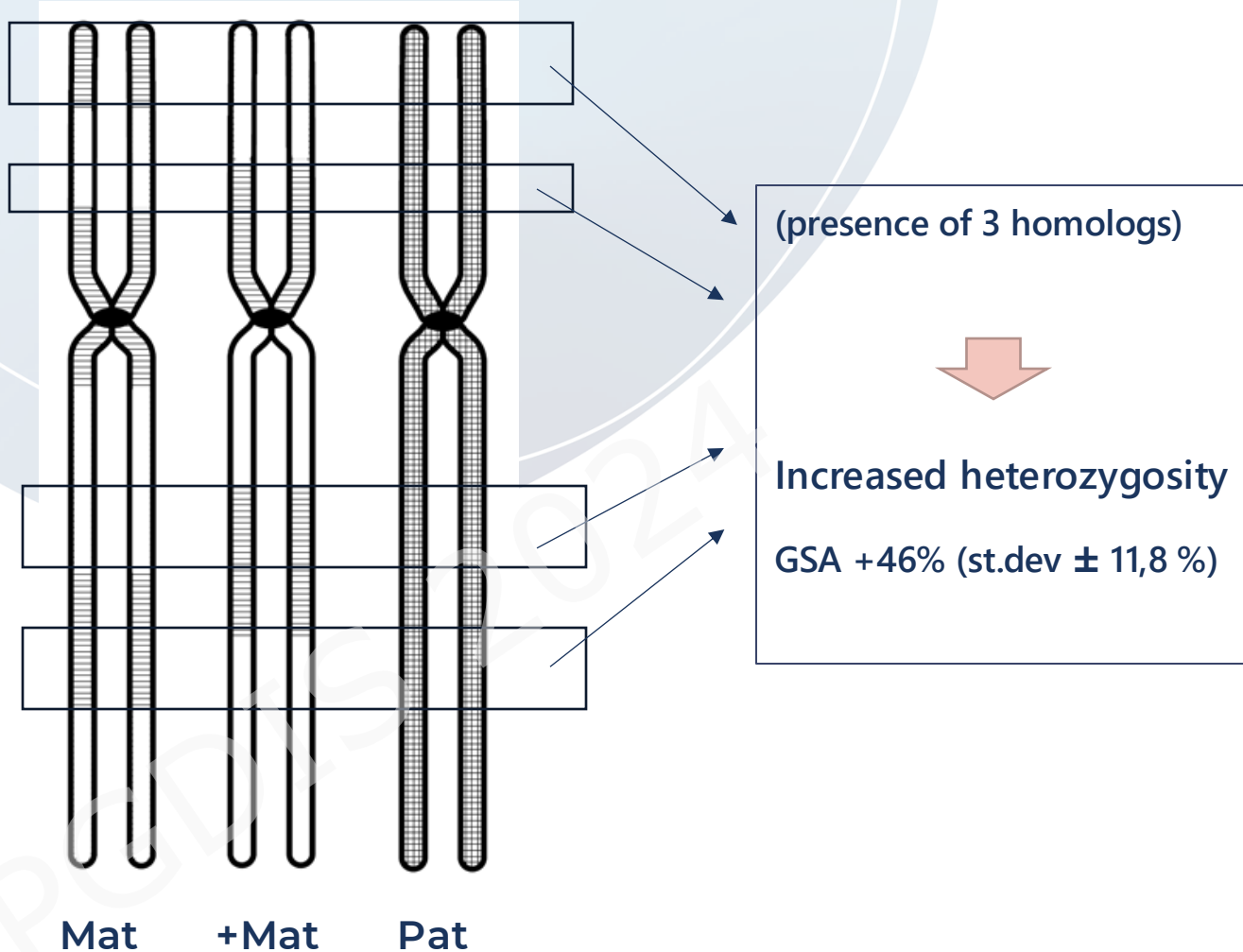
LogR (CNV)



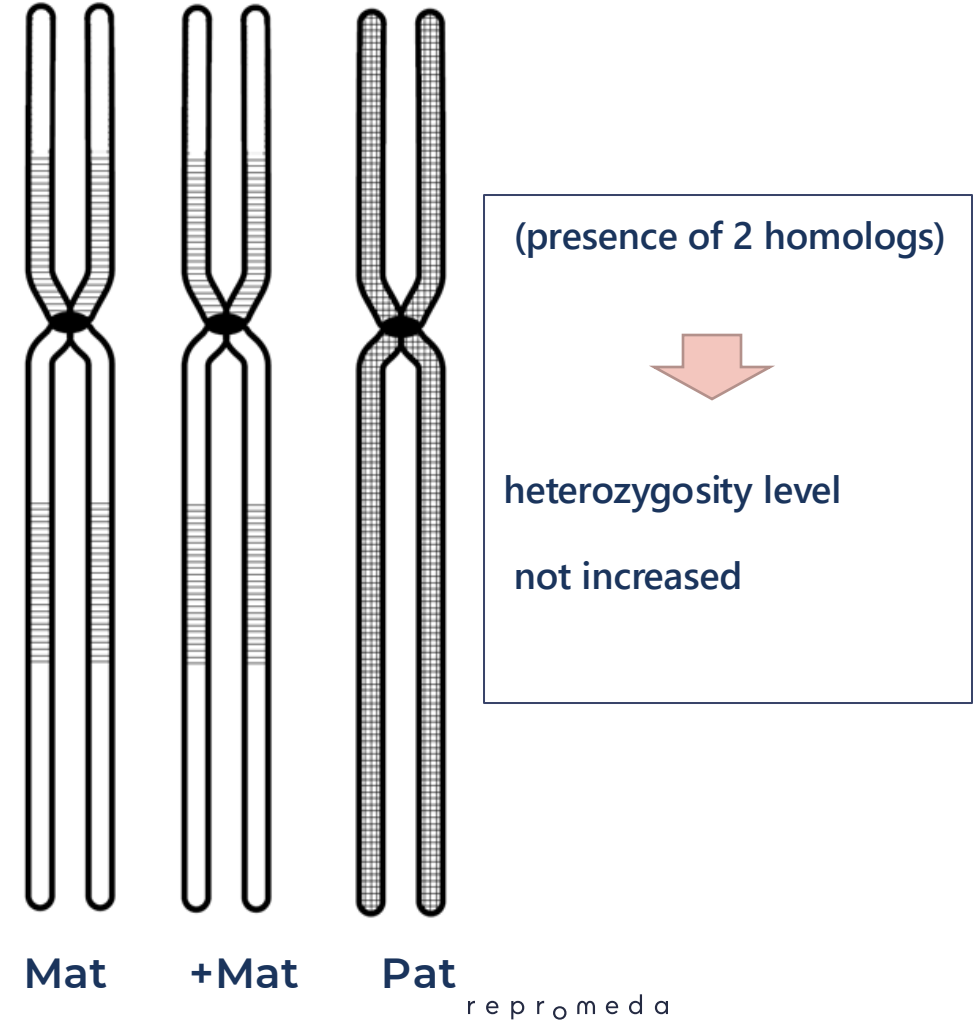
BAF

Meiotic vs. mitotic trisomies without parental DNA sample support?

Meiotic trisomy



Mitotic trisomy



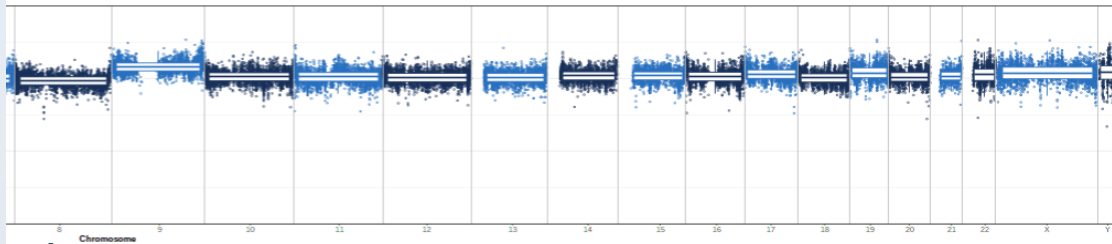
PGT-A meiotic vs. mitotic trisomies without parental DNA sample support?

Meiotic trisomy

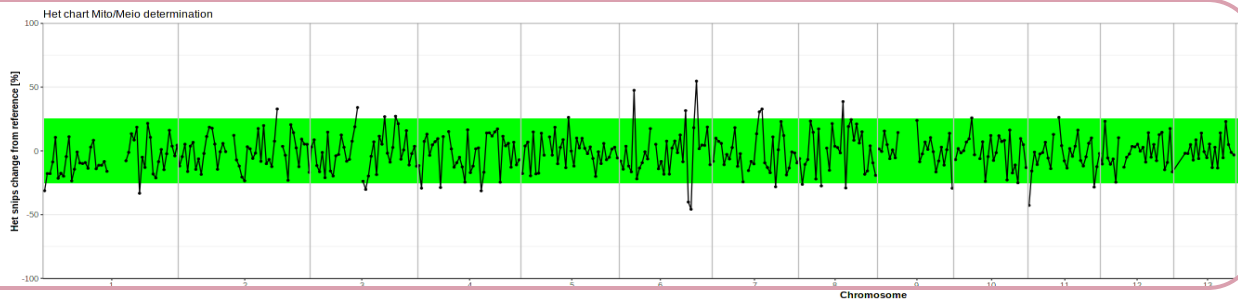
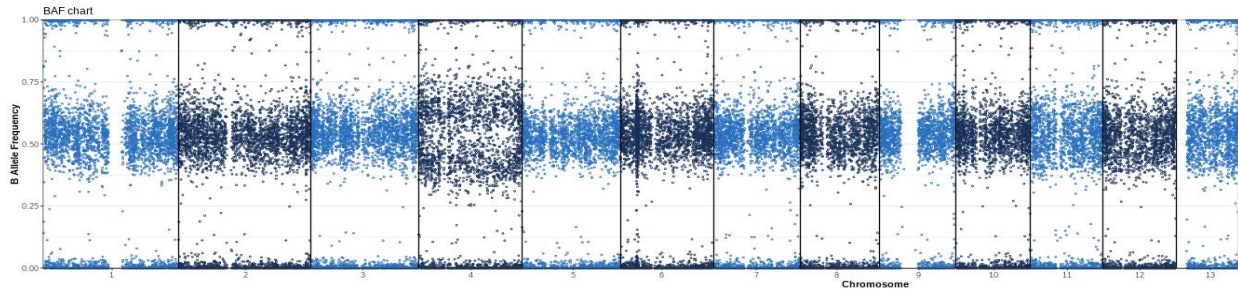
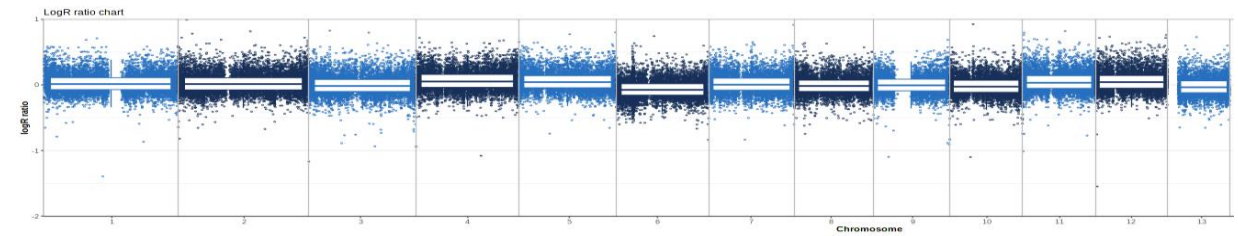
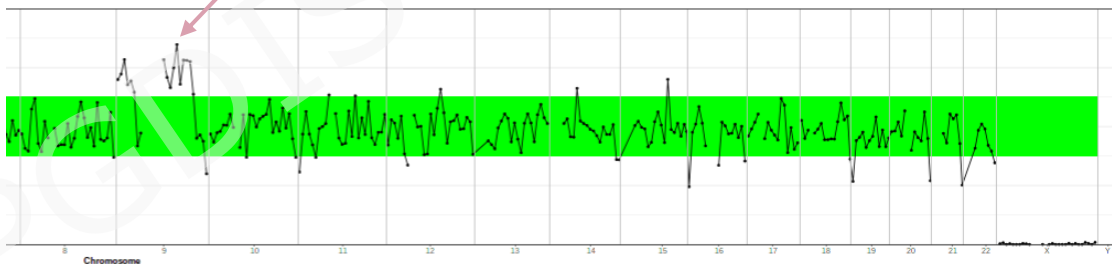
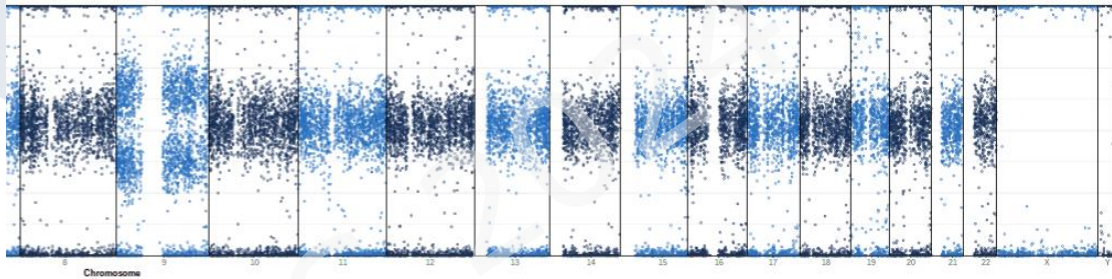
Mitotic trisomy

Normalised heterozygosity increase in TE samples enables to distinguish between meiotic and mitotic trisomy without parental DNA sample support

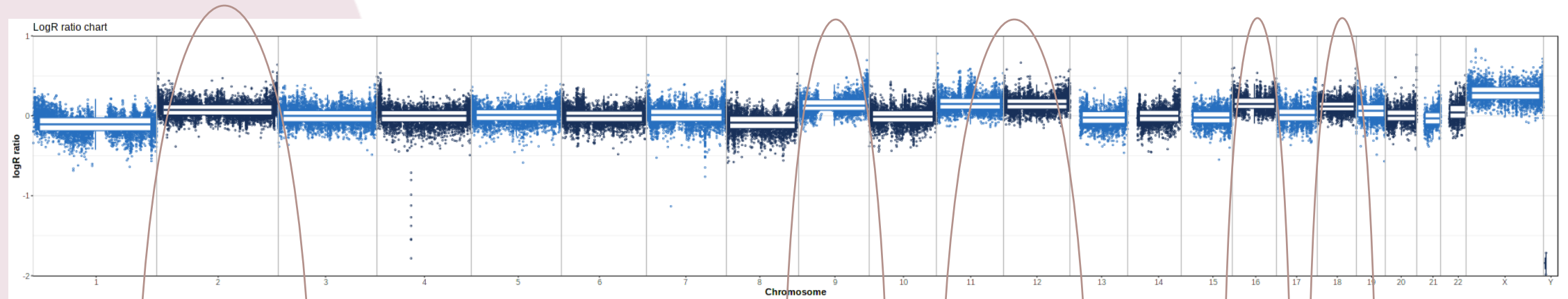
LogR (CNV)



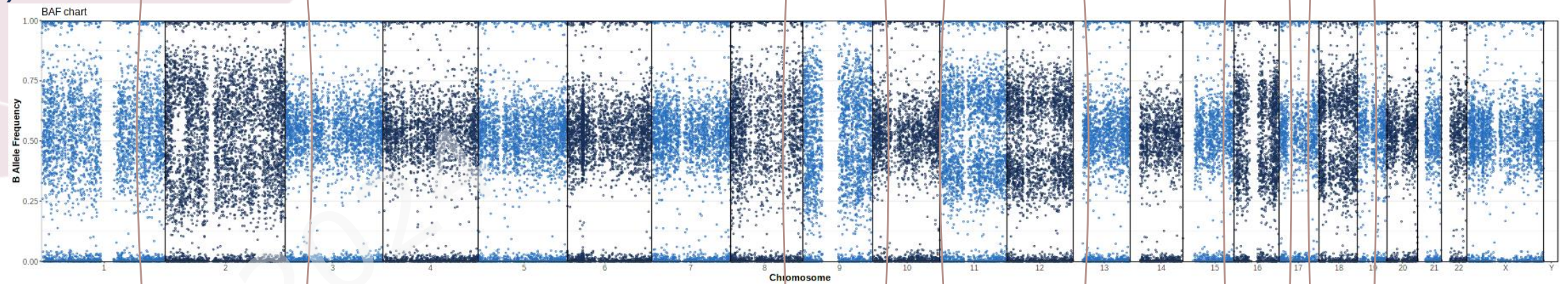
BAF



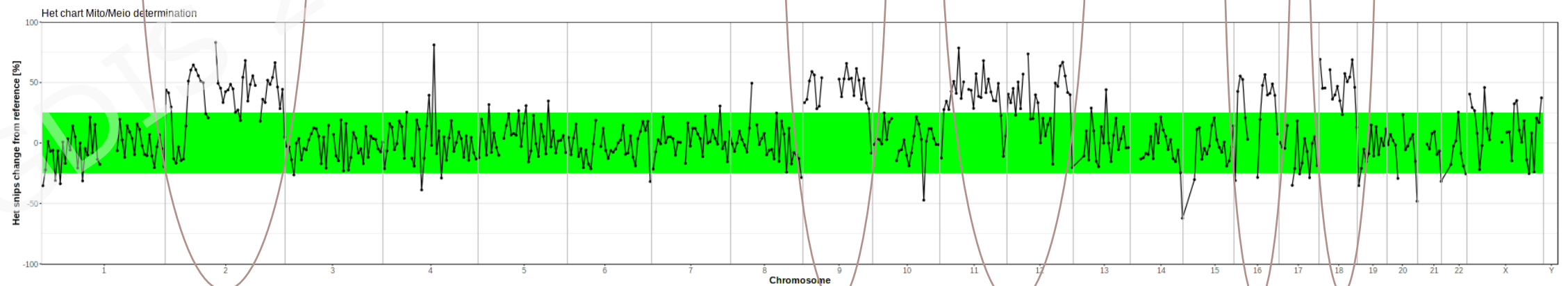
Trophectoderm sample - meiotic trisomy signature



LogR (CNV)



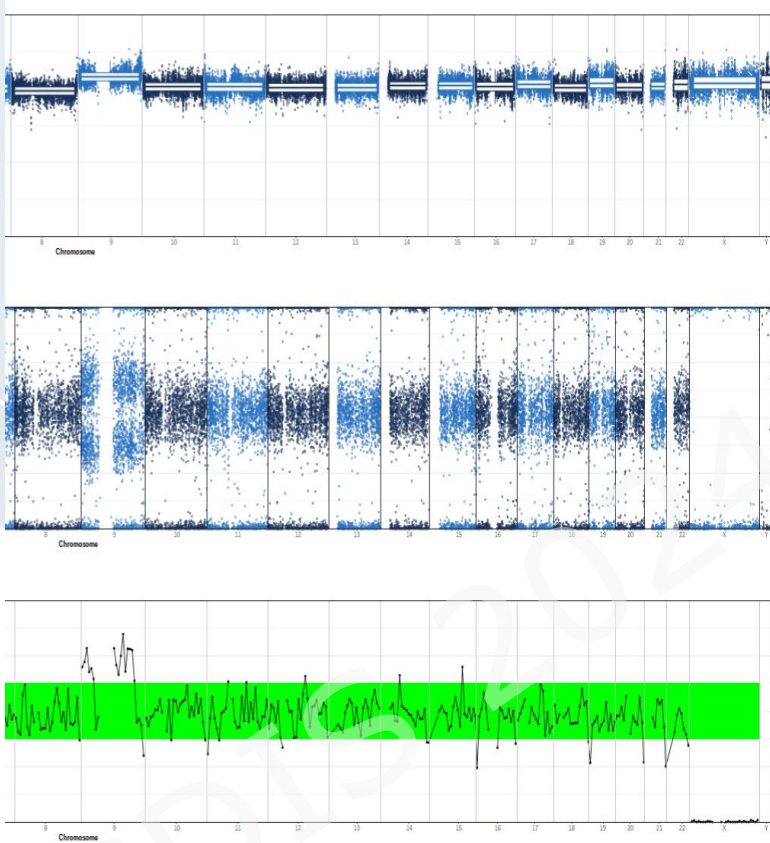
BAF



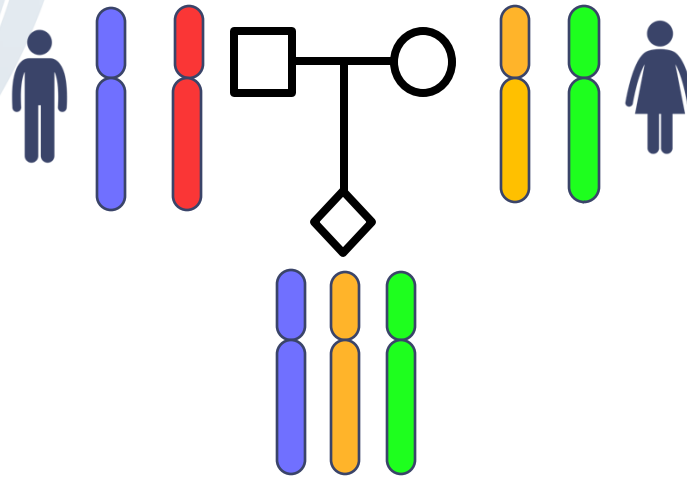
GOH

Validation of the algorithm

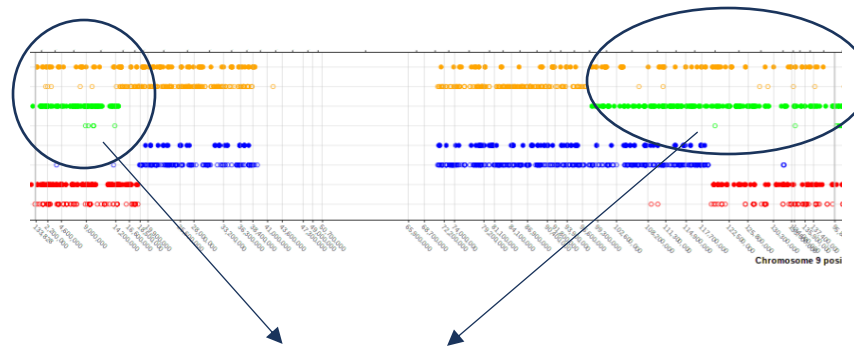
Trophectoderm sample -> meiotic pattern → Parental DNA samples analysis (biparental haplotypes)



Infinium™ Global Screening Array-24 v3.0 BeadChip



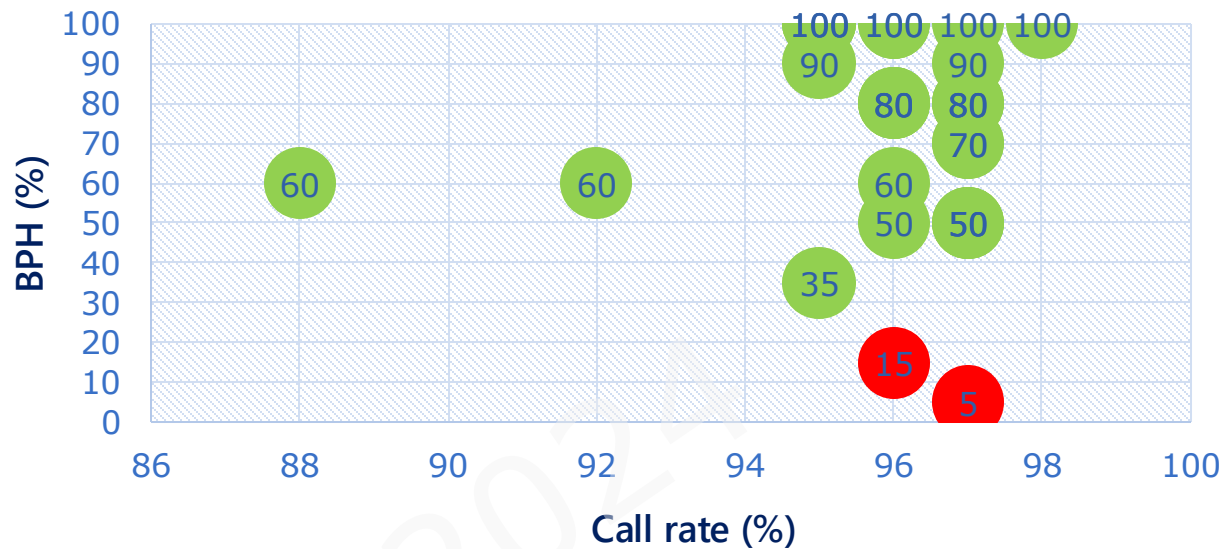
38/38 meiotic trisomies confirmed
= 100% concordance between
heterozygosity increase and
biparental haplotypes (BPH)



BPH = biparental haplotypes

Validation of the sensitivity (meiotic pattern)

Sensitivity of the meiotic pattern
detection for chr.21, 22

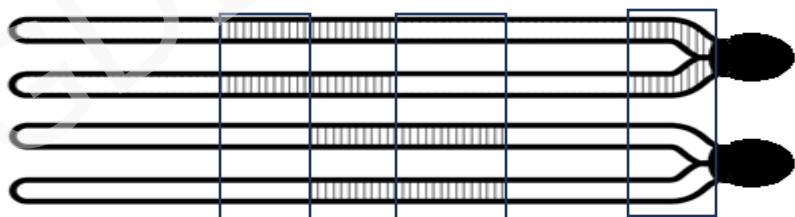


$$\text{BPH}(\%) = \text{BPH} / \text{BPH} + \text{SPH}$$

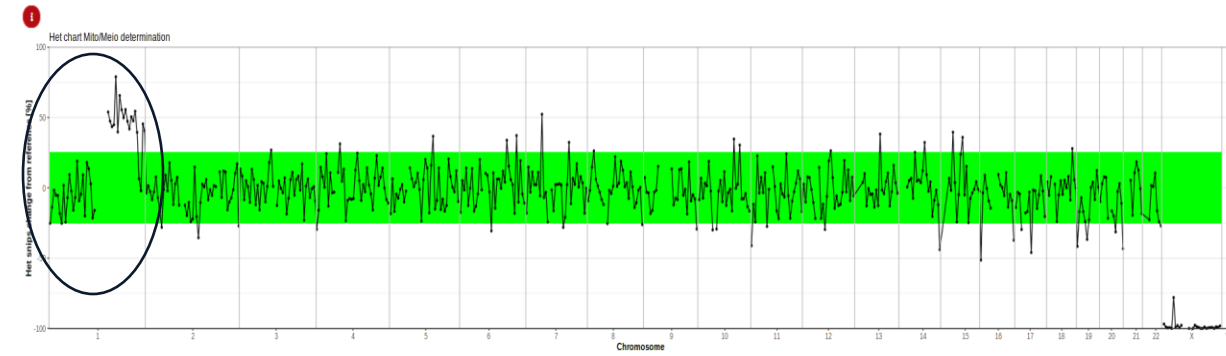
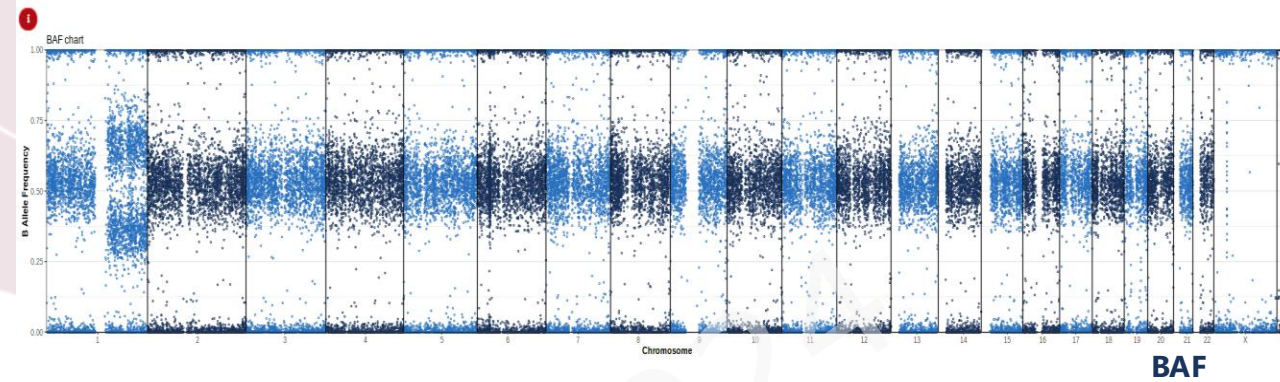
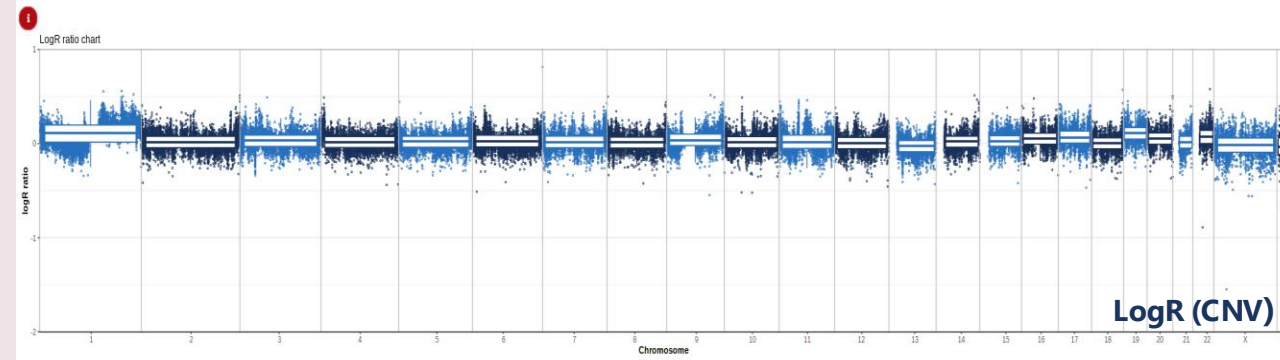
- Twenty meiotic trisomies of chr. 21, 22
(confirmed by karyomapping)

- 18/20 (90%) of meiotic trisomies
confirmed by the heterozygosity analysis

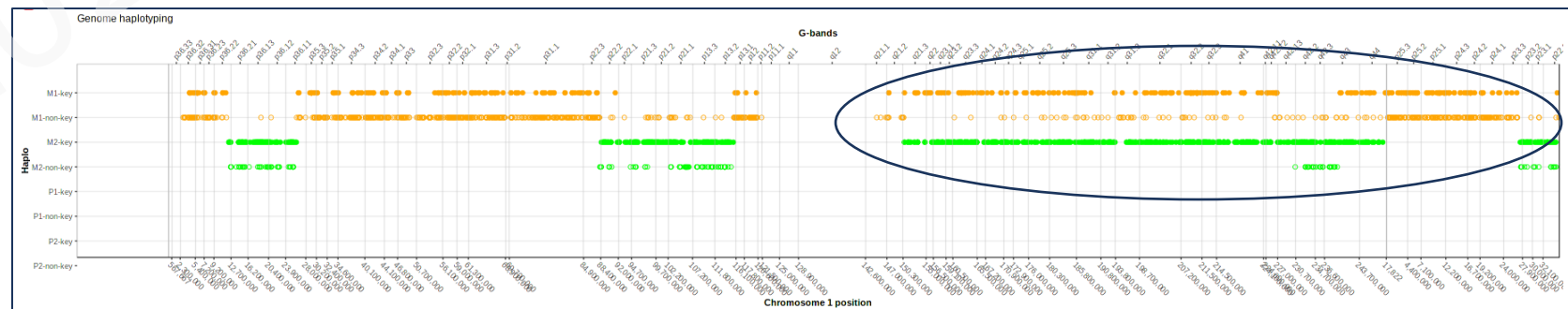
Overall sensitivity 95-98%



Segmental aneuploidy – Gain of heterozygosity algorithm



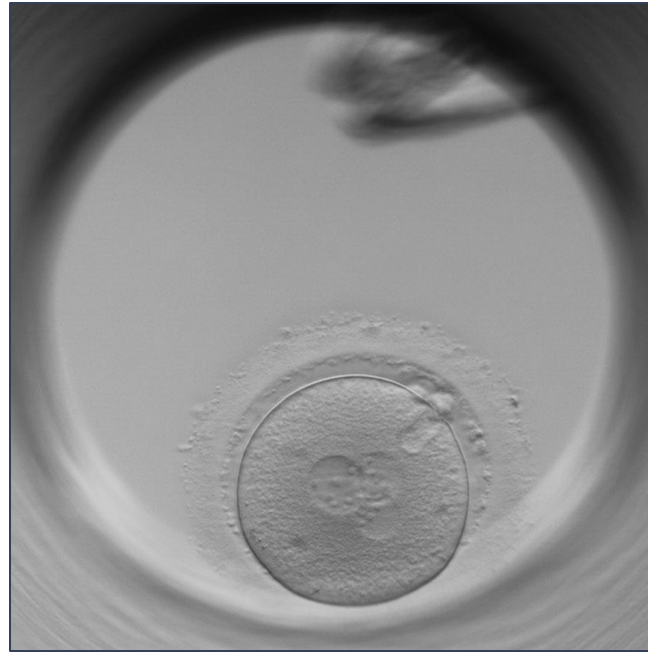
Improved diagnostics of segmentals



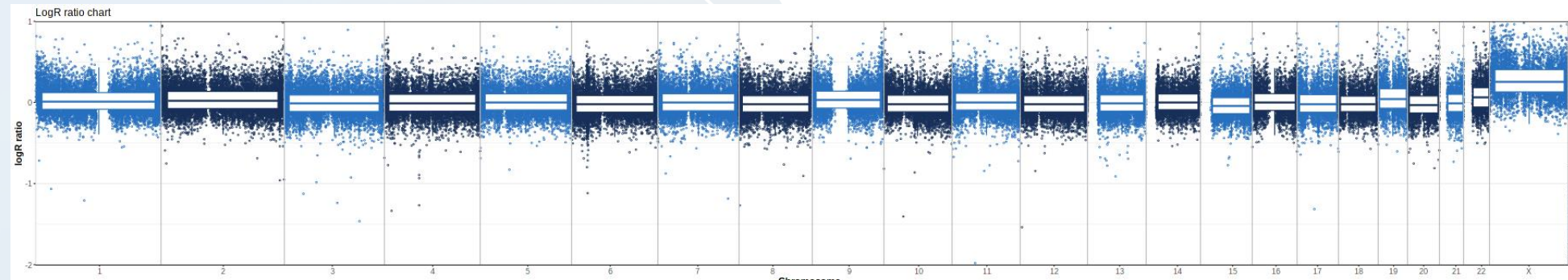
Haploblock analysis
repro media

Polyploidy detection – Gain heterozygosity algorithm

- detection of haploid embryos (1 PN check)
- detection of triploid embryos (3 PN check)



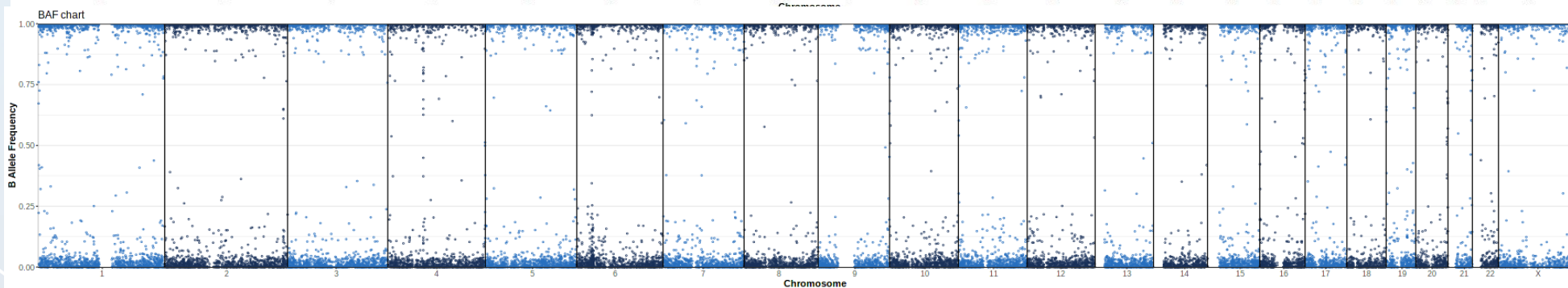
Repromeda, embryology lab



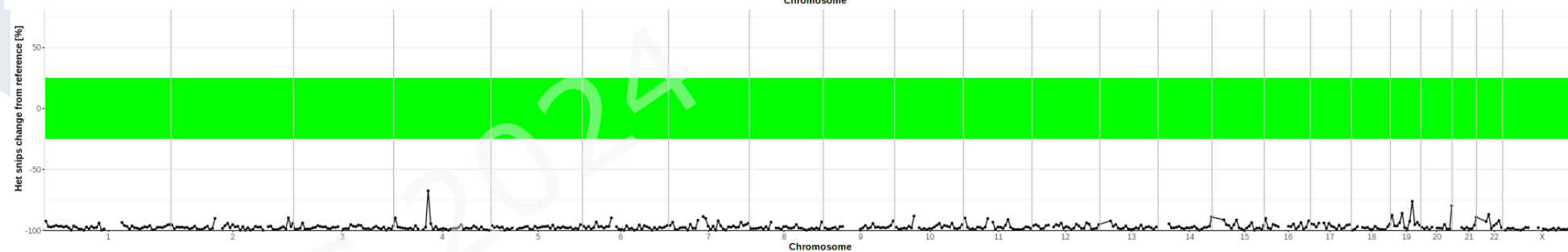
Haploid TE sample

chr. constitution =
23,X

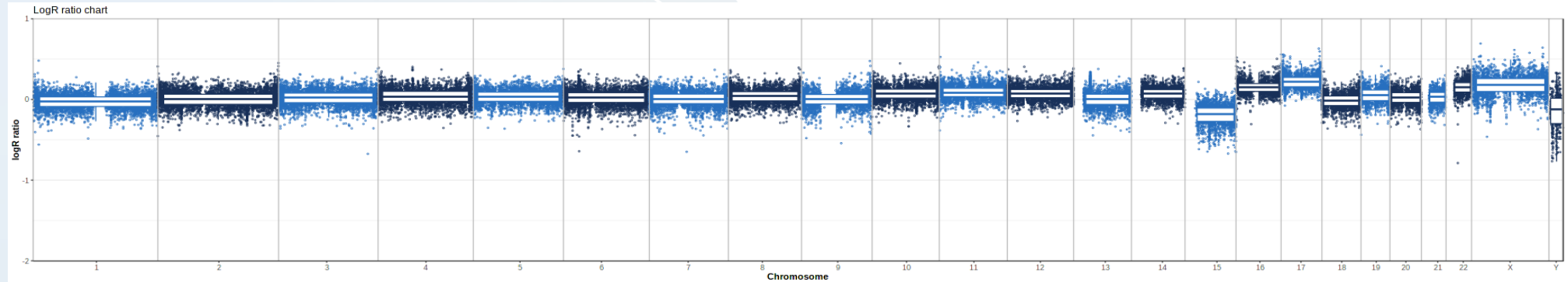
LogR (CNV)



BAF



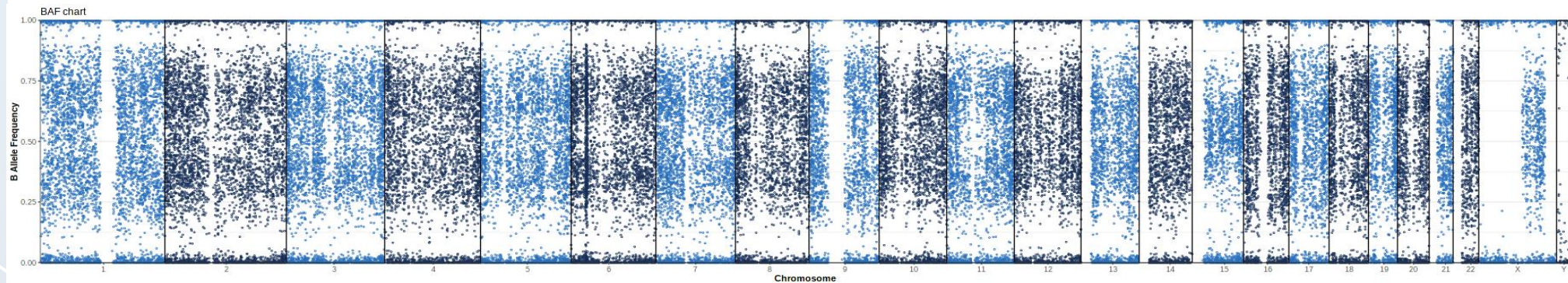
Heterozygosity
analysis



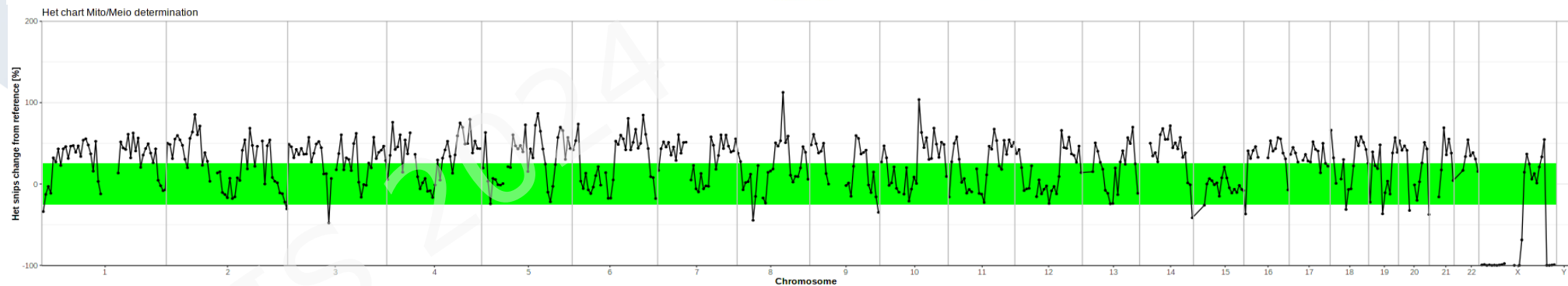
Triploid TE sample

chr. constitution =
69,XXY

LogR (CNV)



BAF

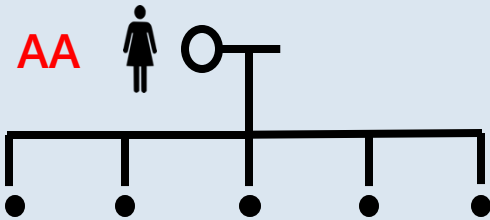


GOH

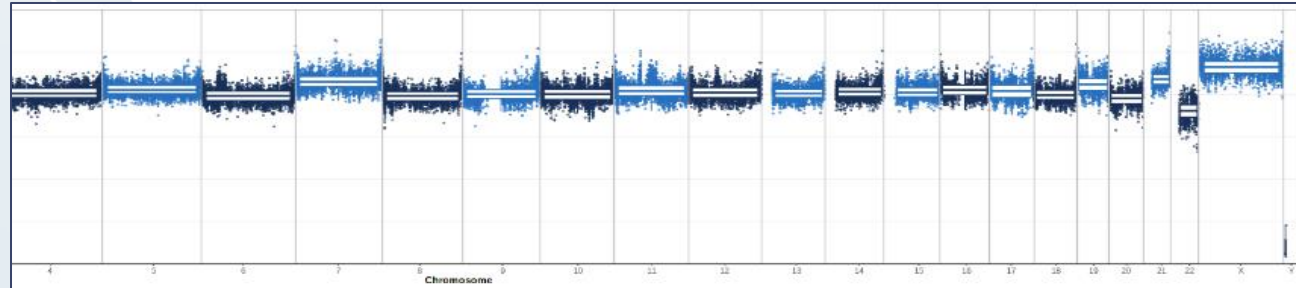
Extended SNP analysis with maternal DNA sample PGT-A+

SNP analysis

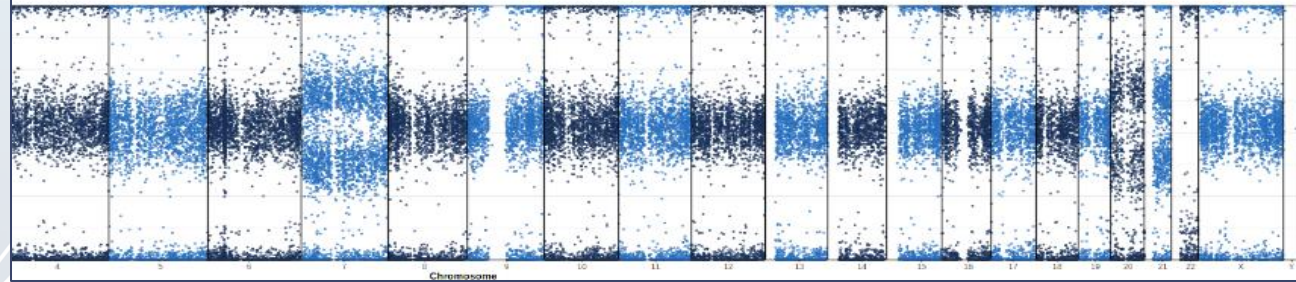
Haplotypy (SNP array)



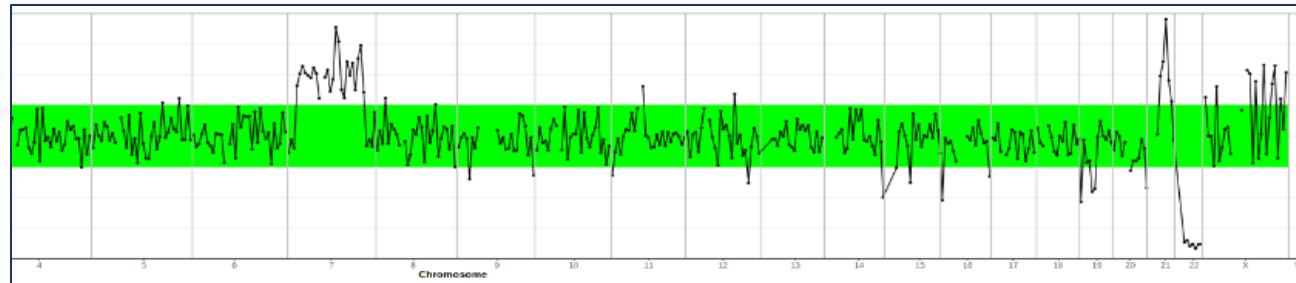
- Parental BAF chart
- Chart of increased heterozygosity
- Chromosome aneuploidy origin



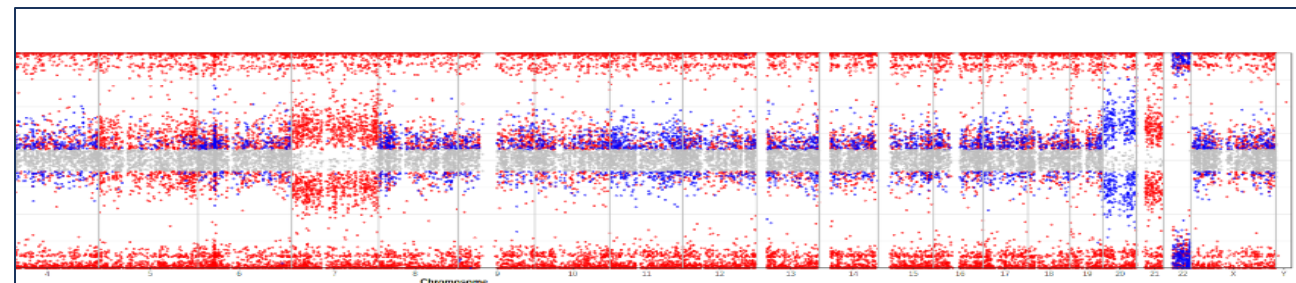
LogR (CNV)



BAF



Heterozygosity
analysis



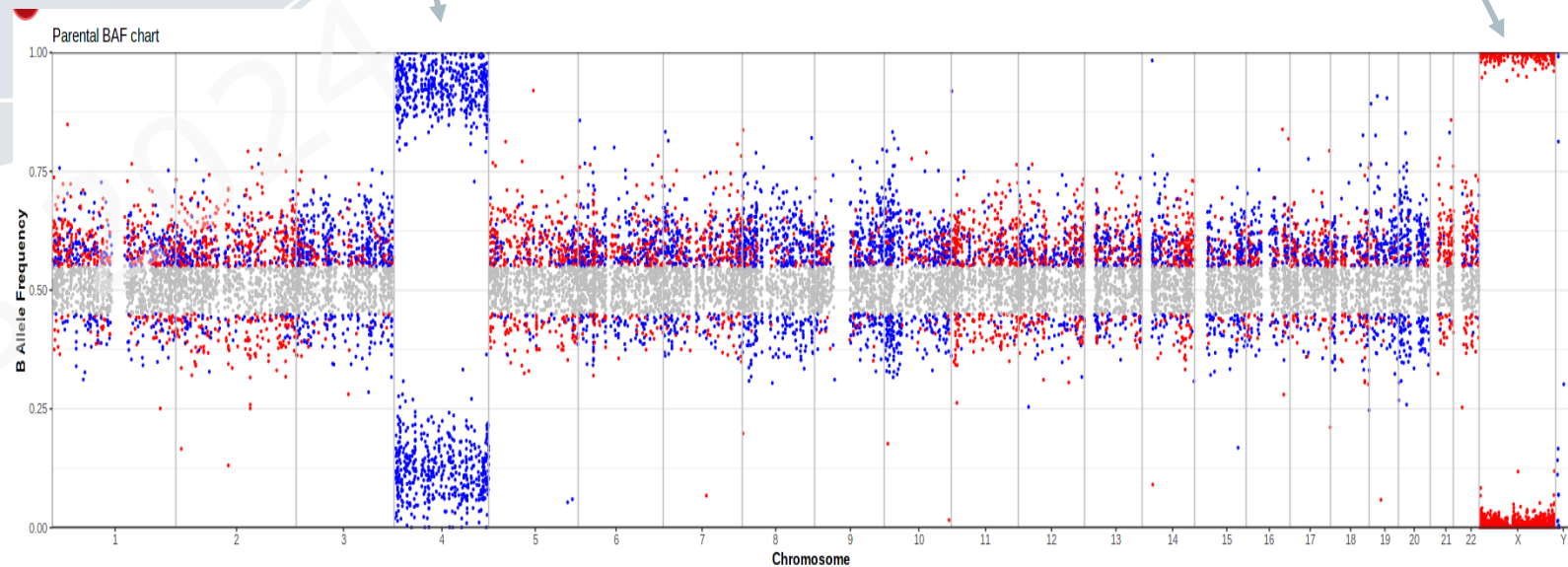
Aneuploidy origin
(mat/pat)

Extended SNP analysis with maternal DNA sample PGT-A+

- Mozaicism analysis
- Improved detection of high mosaic versus full aneuploidy – 90 % border for monosomies

90 % mosaic monosomy:
• 9:1 MDA DNA ratio
monosomy chr. 4 : disomy chr.4

100 % „monosomy“ of chr. X

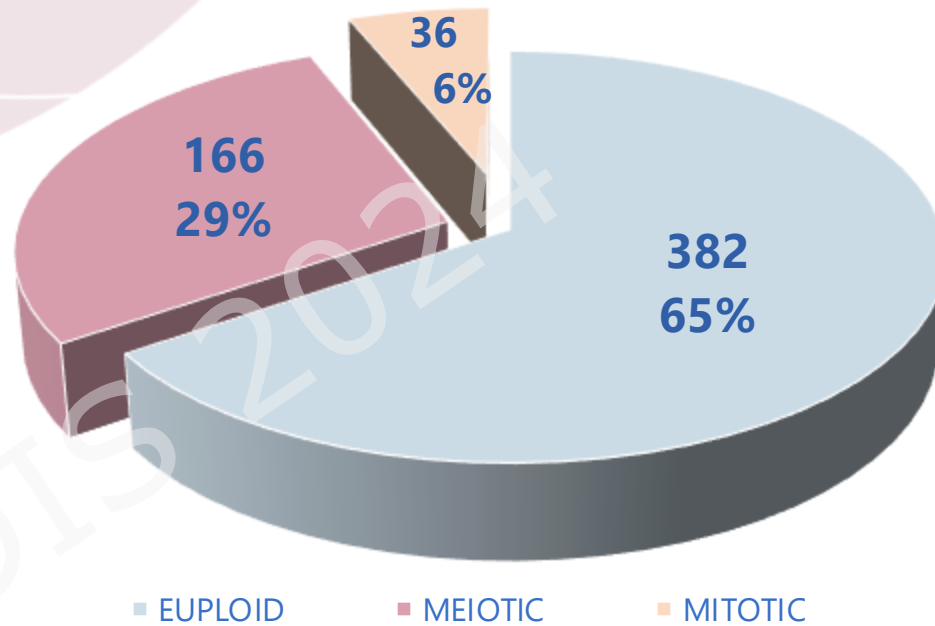


Aneuploidy statistics – whole chromosome errors

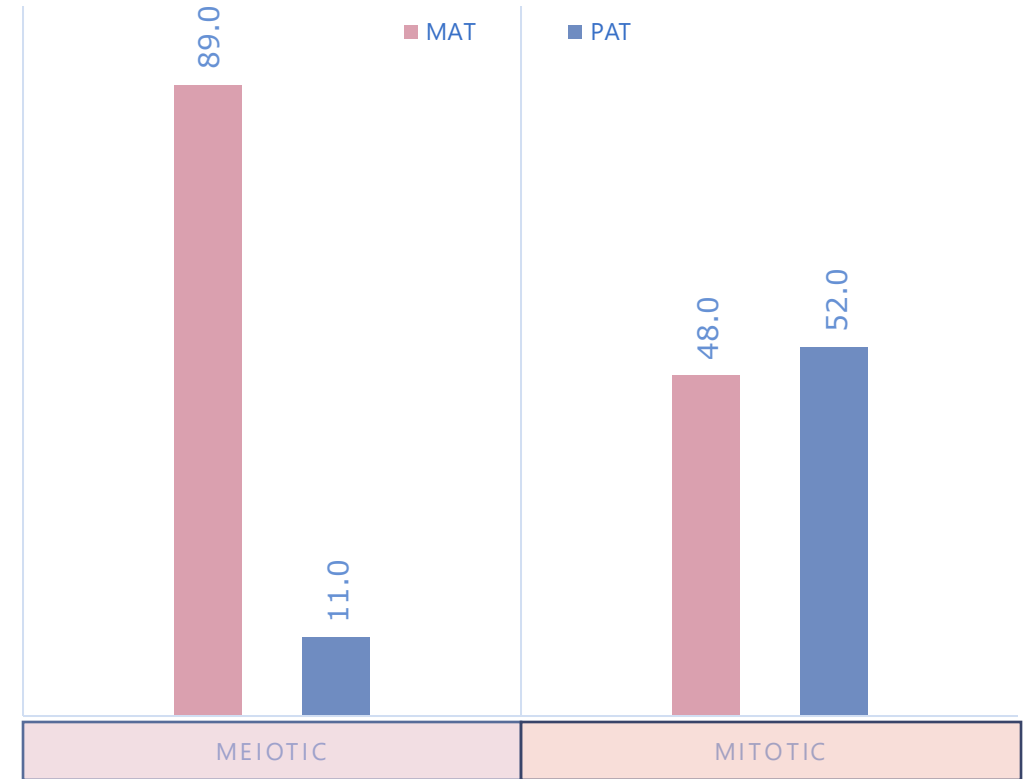
Average maternal age: 34,2 years

Embryos analysed: 625

Meiotic and mitotic aneuploidy incidence



PARENTAL ORIGIN OF ANEUPLOIDY (%)

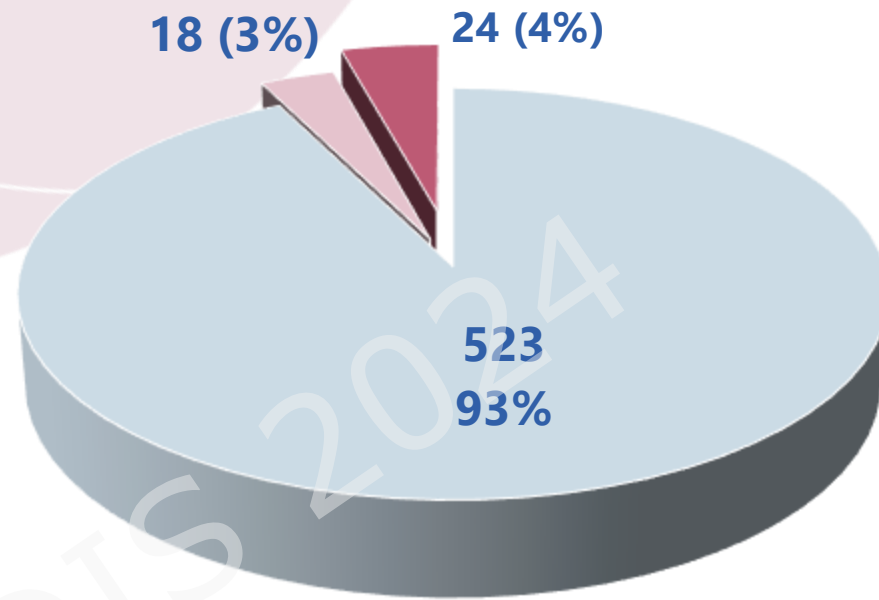


Aneuploidy statistics – segmental errors

Average maternal age: 34,2 years

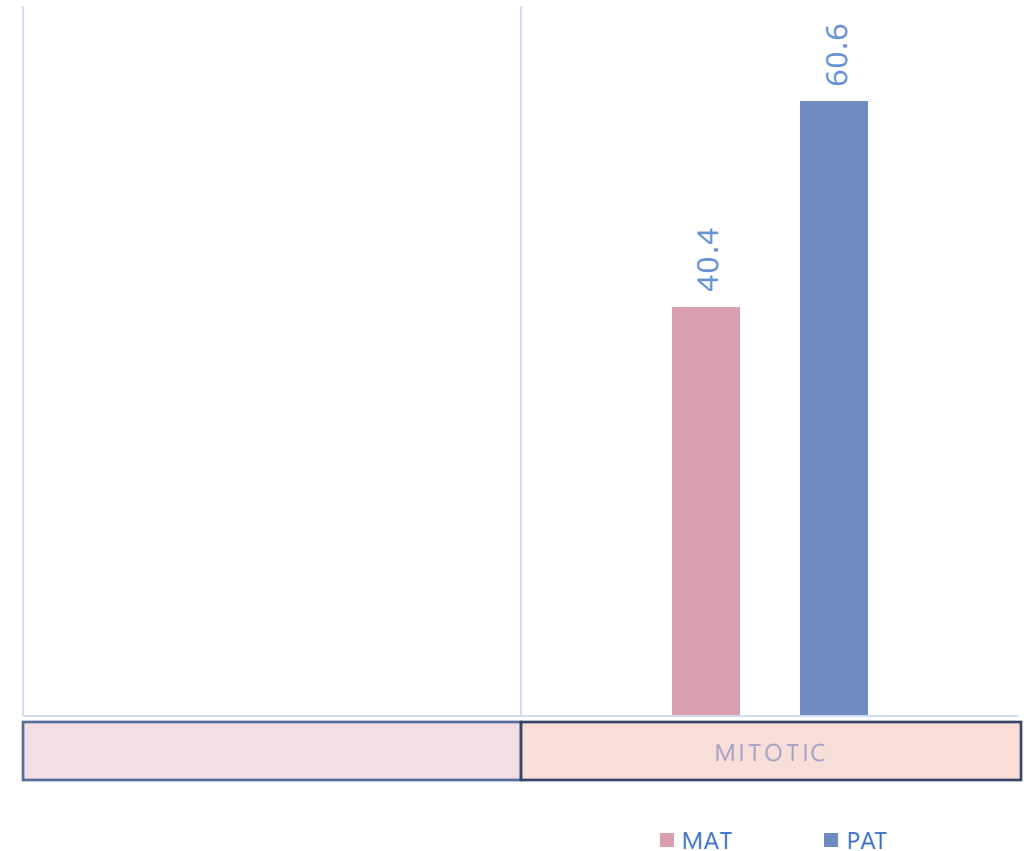
Embryos analysed: 625

Segmental aneuploidy incidence



- WITHOUT SEGMENTAL ANEUPLOIDY
- SEGMENTAL ANEUPLOIDY IN MOSAIC
- SEGMENTAL ANEUPLOIDY FULL

PARENTAL ORIGIN OF SEGMENTAL ANEUPLOIDY (%)



repromeda

Summary

- SNP analysis improve diagnostics
- Gain of heterozygosity analysis – patent pending (NGS / SNP arrays, preimplantation / prenatal samples)
 - meiotic vs. mitotic trisomy analysis
 - triploidy detection
- Analysis of aneuploidy origin – maternal DNA sample
- Recombination rate = 70% of BPH in meiotic trisomies and triploid samples
- Embryo transfer recommendation:
 - ✓ - euploid, segmentals in mosaic
 - ! - mosaic embryos, full segmentals -mitotic
 - ✗ - meiotic trisomies, triploids, haploids, segmental gains (meiotic pattern)



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Thank you for your attention

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