



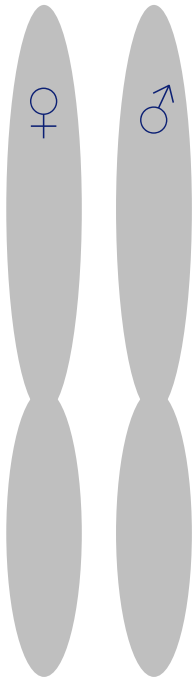
CNV detectie mbv NGS

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afdeling Pathologie
Erasmus MC, Rotterdam

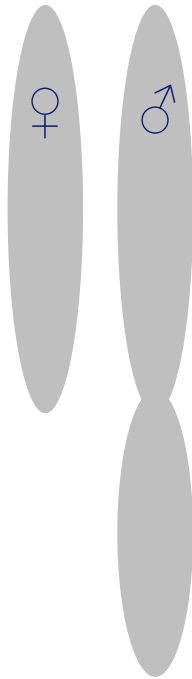
Deelnemersbijeenkomst SKML sectie Pathologie
26-05-2016

Typen grote chromosomale afwijkingen

normaal



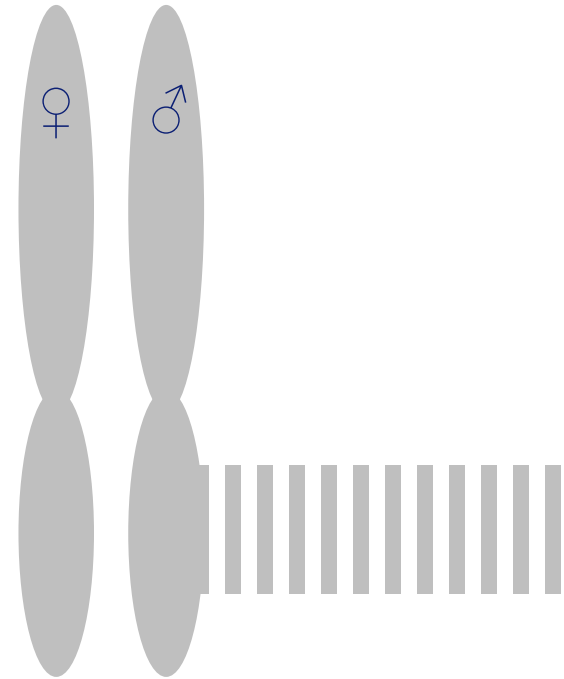
verlies



homozygote deletie



amplificatie



Methodes van diagnostische detectie van CNV

- FISH – fluorescentie in situ hybridisatie
- MLPA – multiplex ligation-dependent probe amplification
- Microsatelliet analyse



- Nieuw (binnen diagnostiek setting): SNP analyse

Single nucleotide polymorphisms (SNPs)

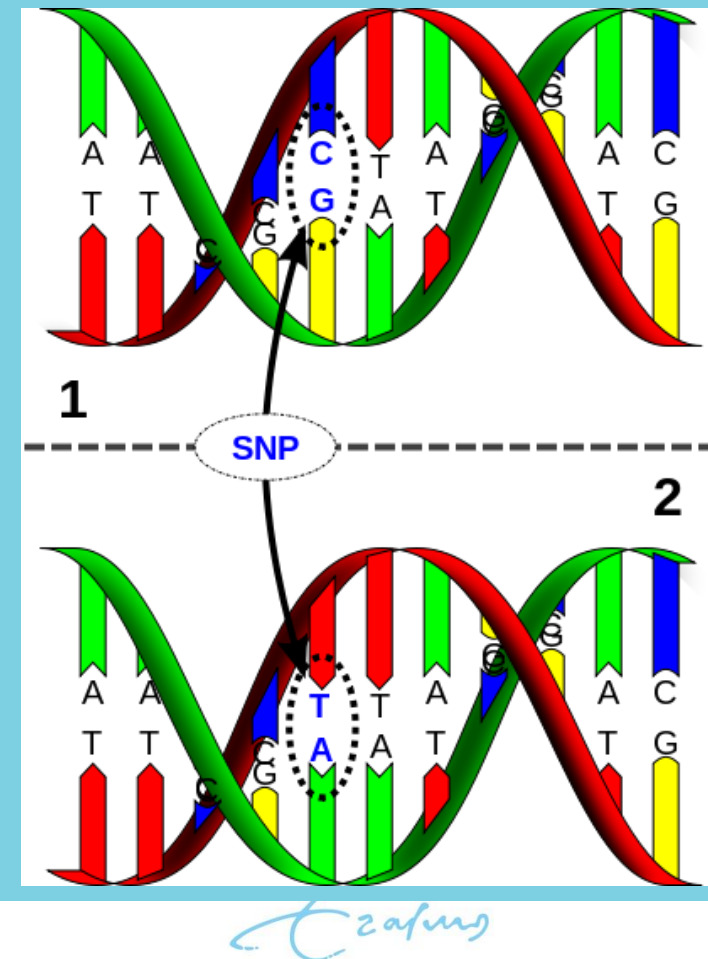
Natuurlijk voorkomende variaties die betrekking hebben op één basenpaar

Allel 1

AAGC**C**TAGCAC
TTCG**G**ATCGTG

Allel 2

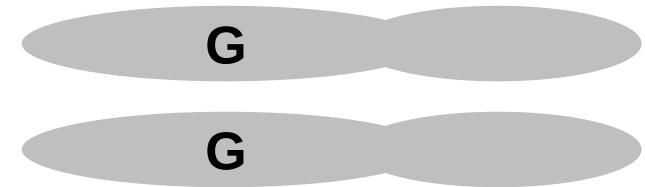
AAGC**T**TAGCAC
TTCG**A**ATCGTG



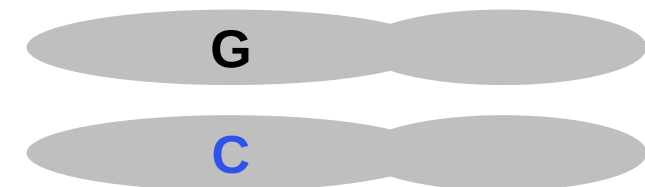
CNV analyse mbv SNPs

- Selectie hoog polymorfe SNPs in regio van interesse (bv chromosoom 1p en 19q)
- Sequencen SNPs mbv NGS analyse
- Berekenen van percentage variante allel (B-allel of minor allel frequentie)

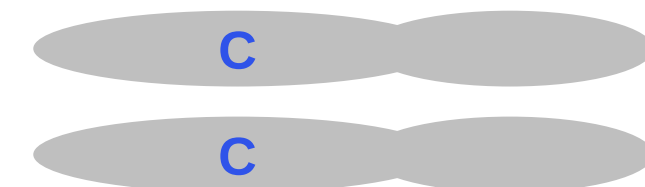
niet informatief



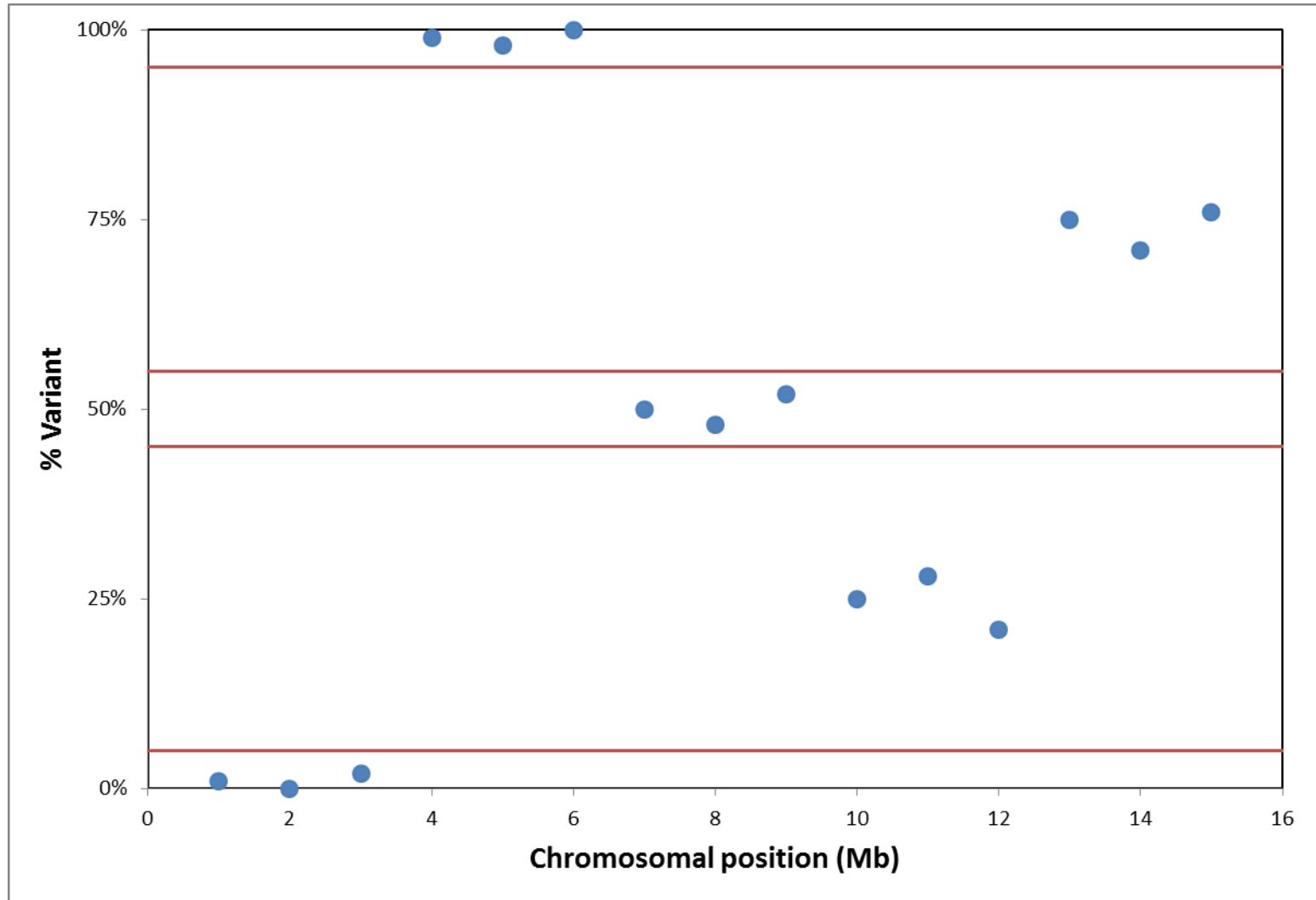
informatief



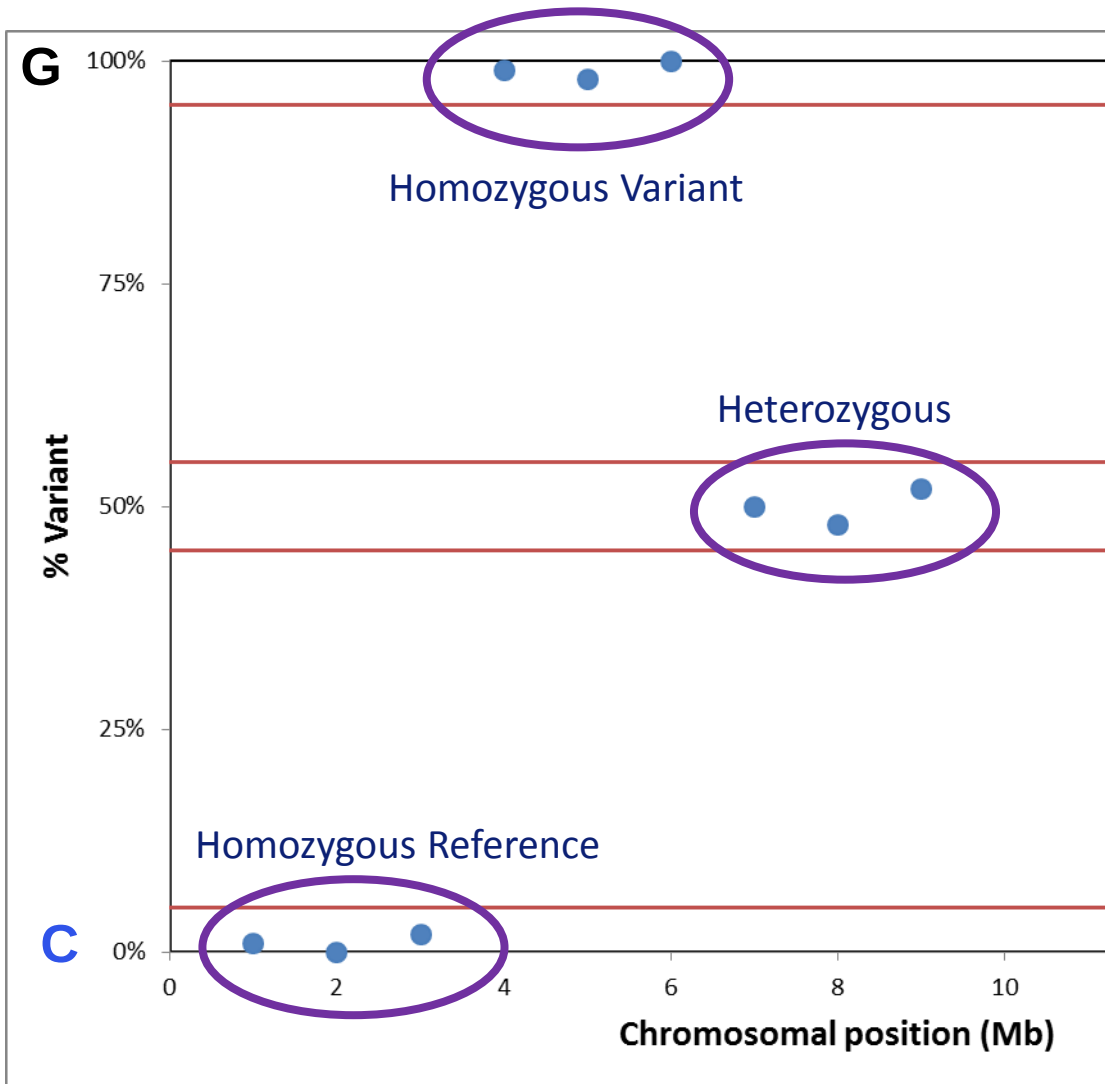
niet informatief



CNV analyse mbv SNPs



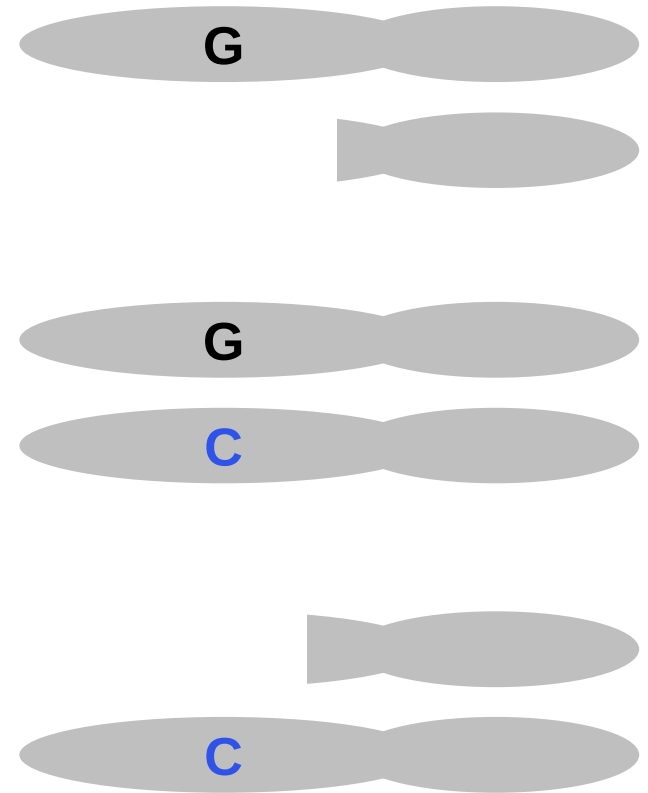
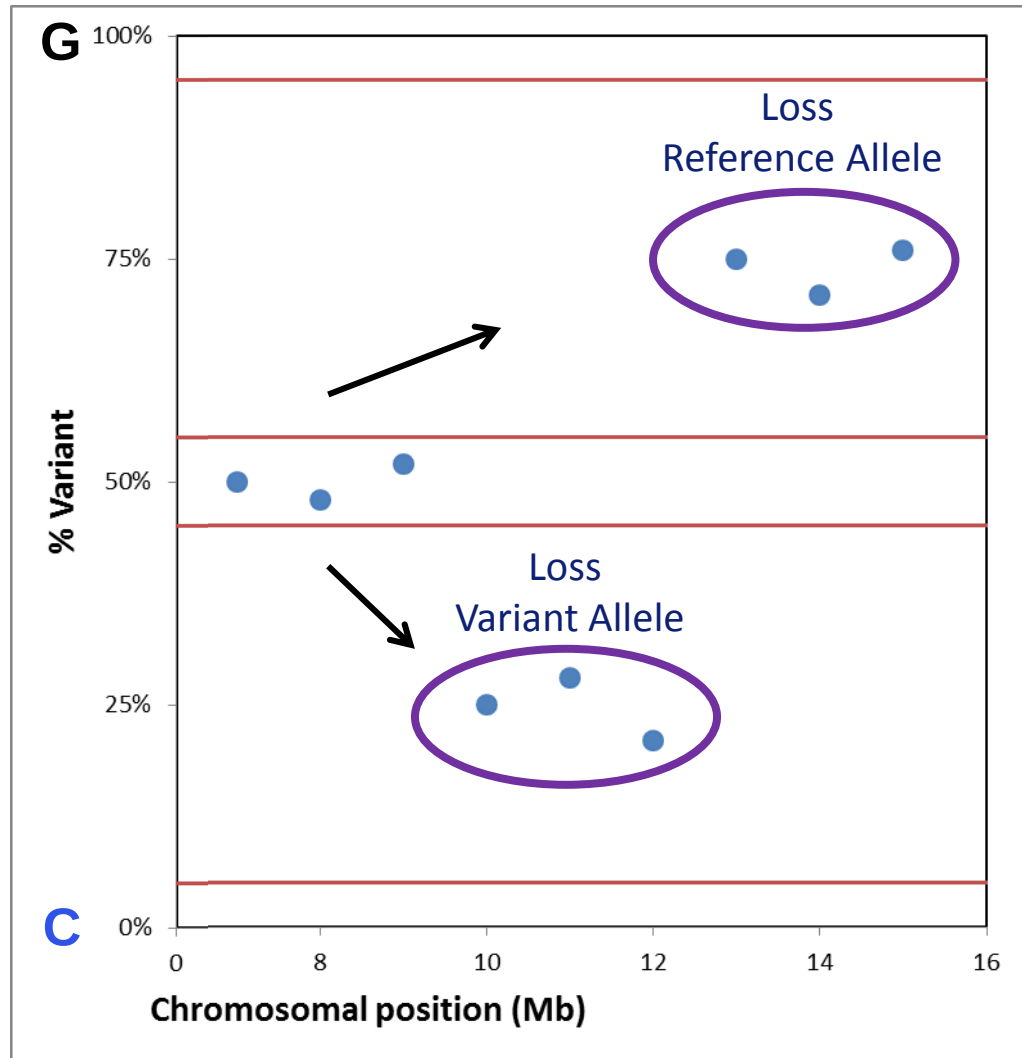
CNV analyse mbv SNPs



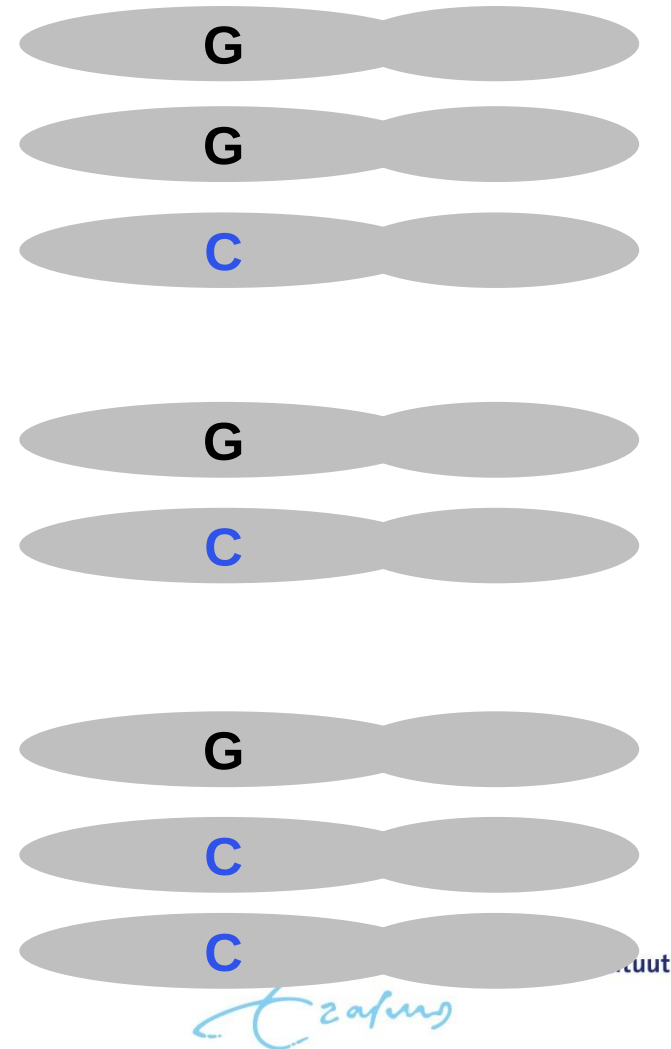
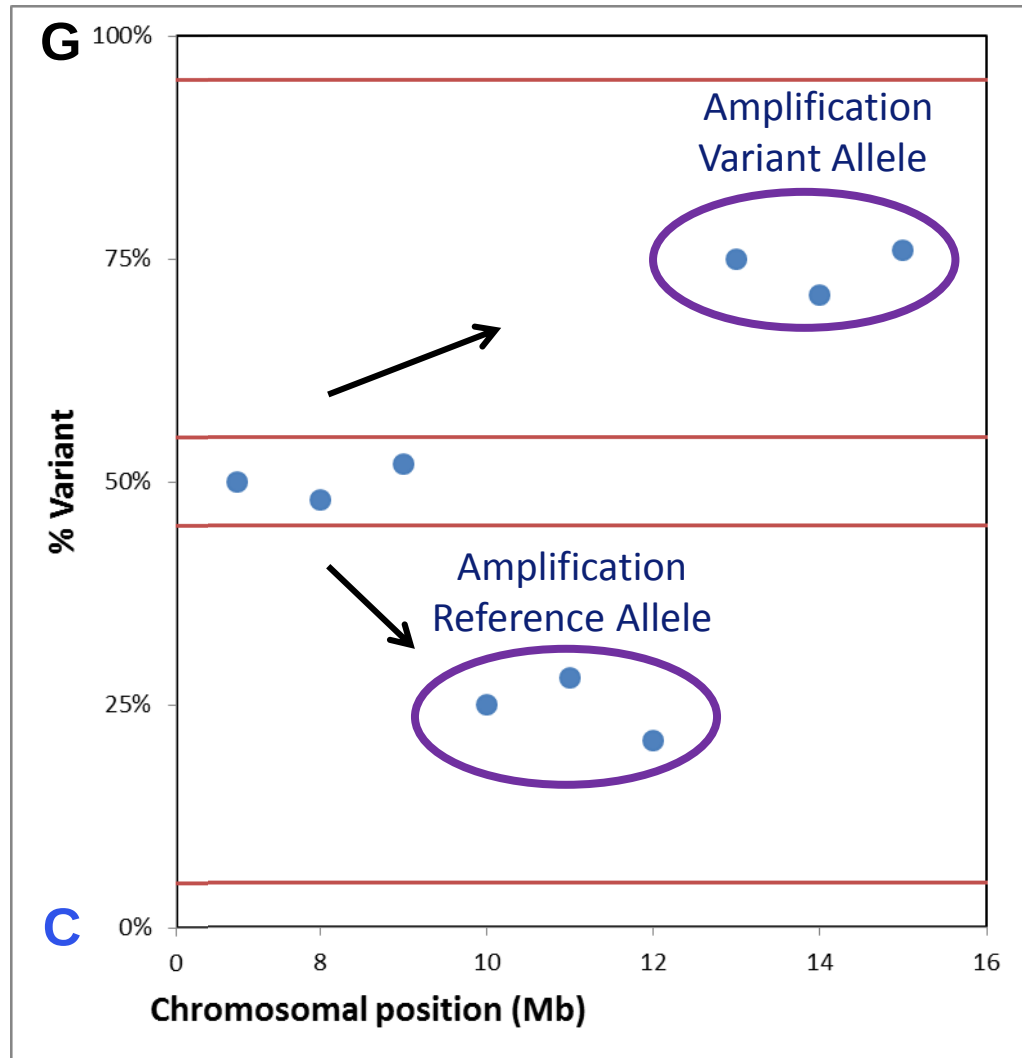
Erasmus MC

Kanker Instituut

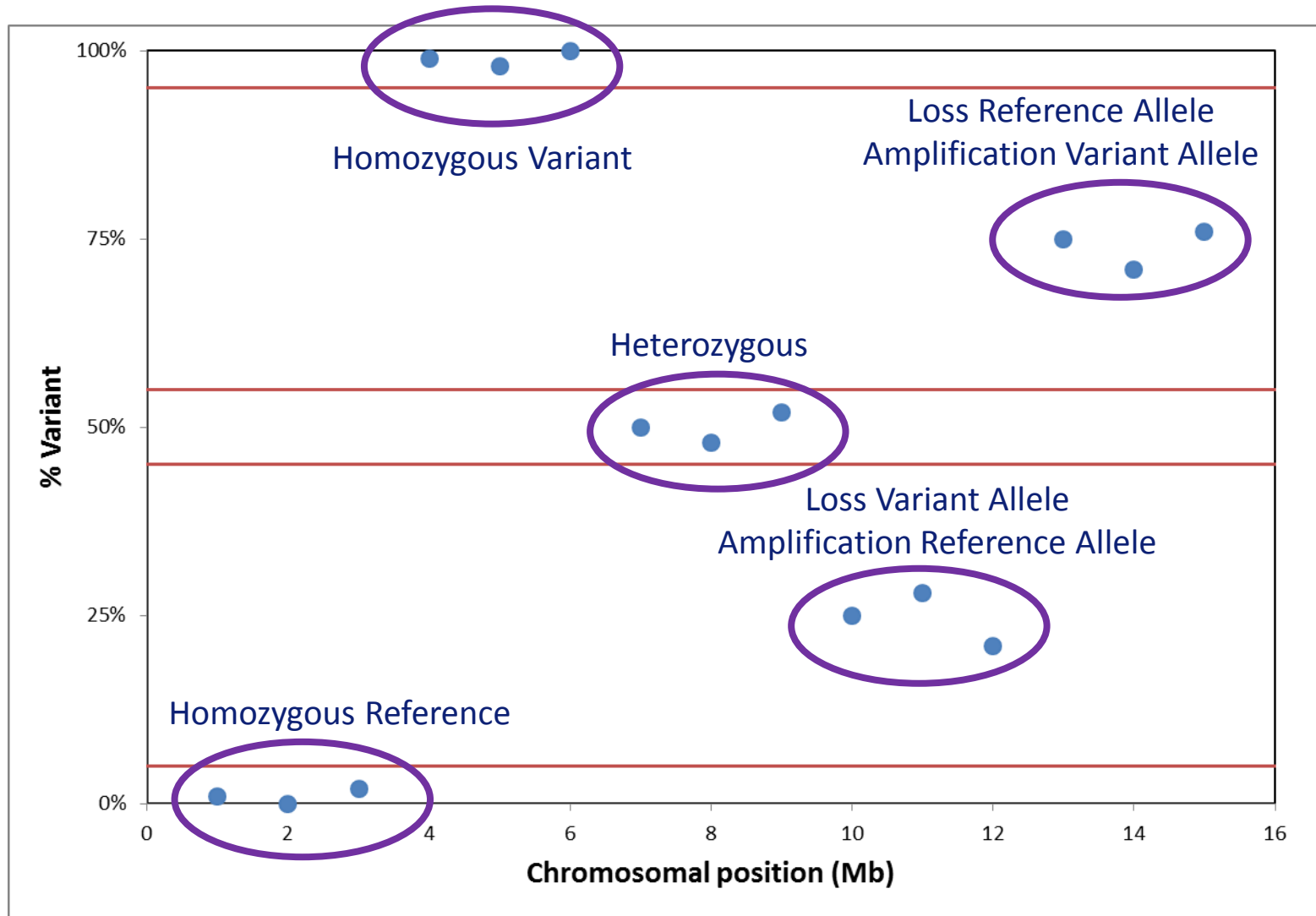
CNV analyse mbv SNPs



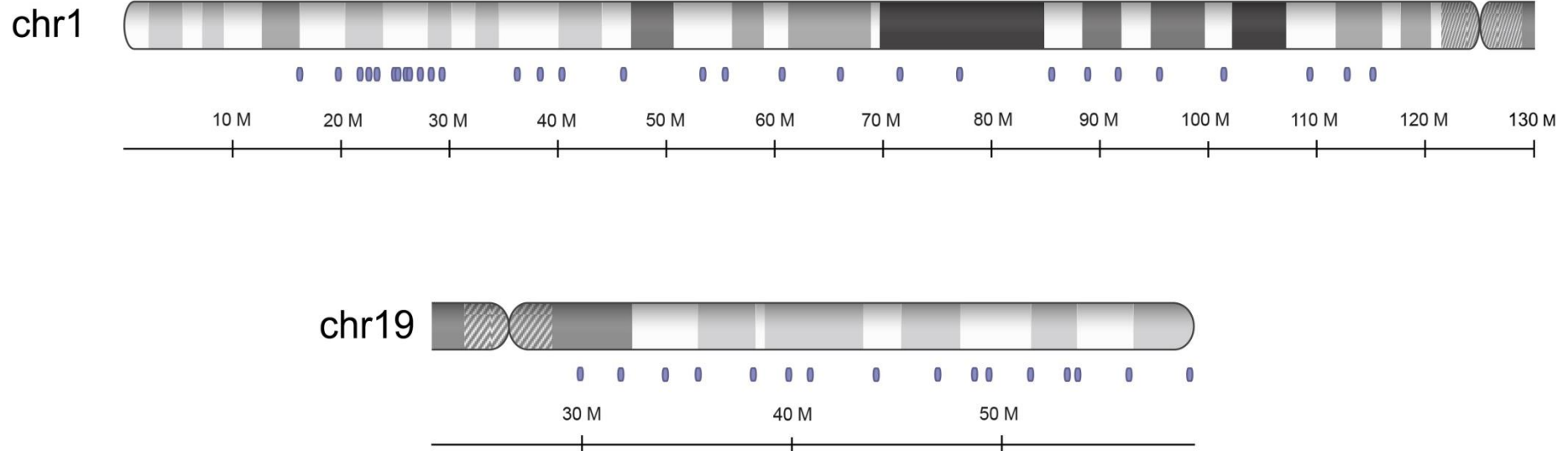
CNV analyse mbv SNPs



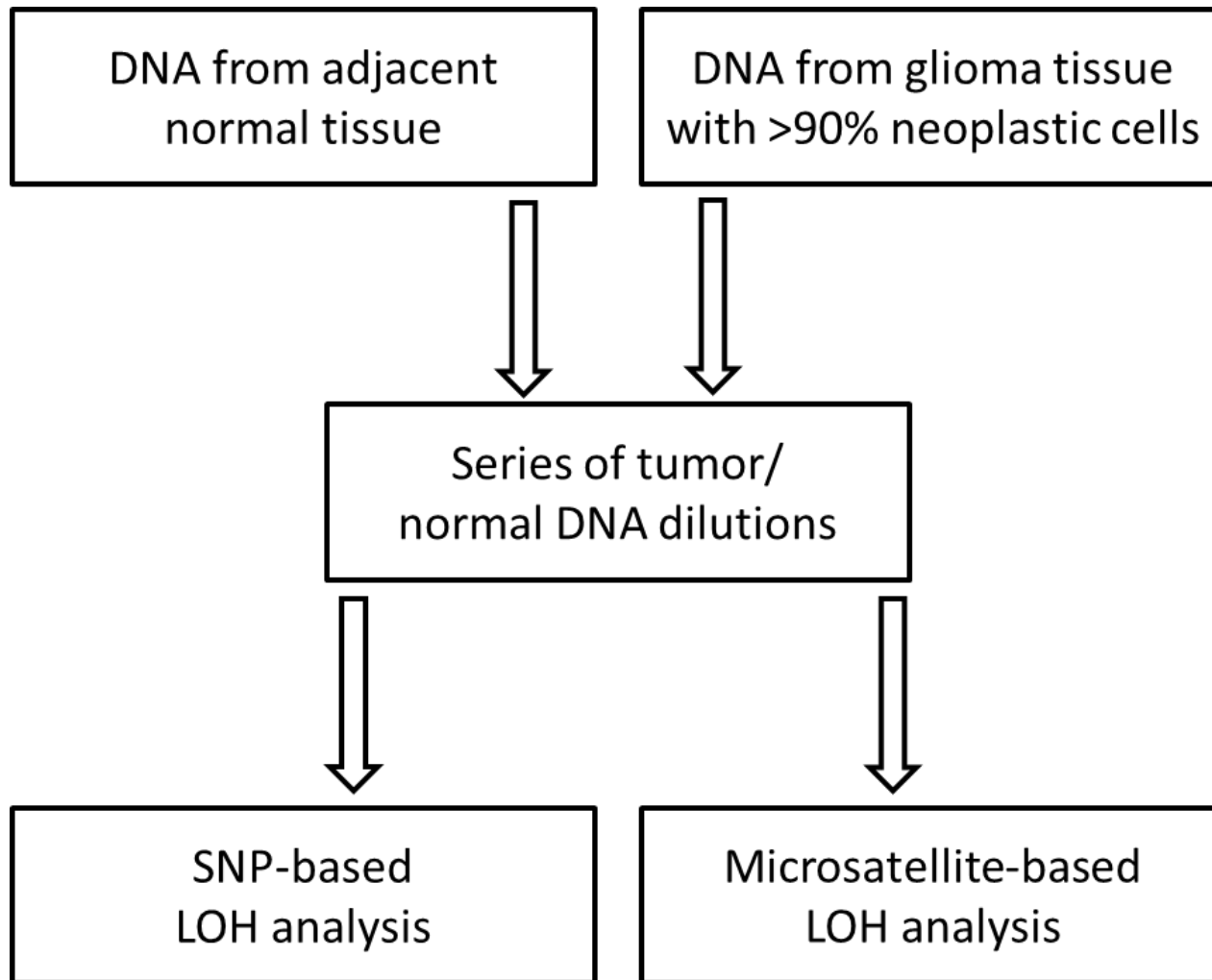
CNV analyse mbv SNPs



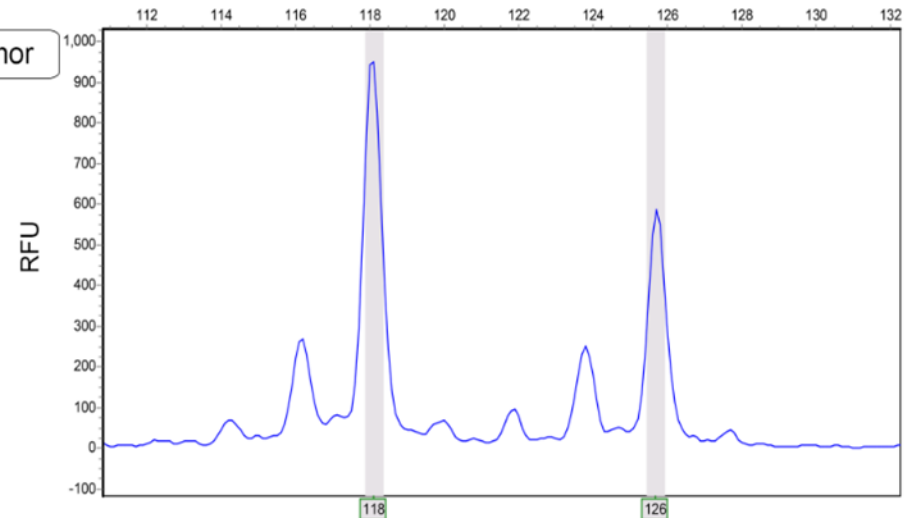
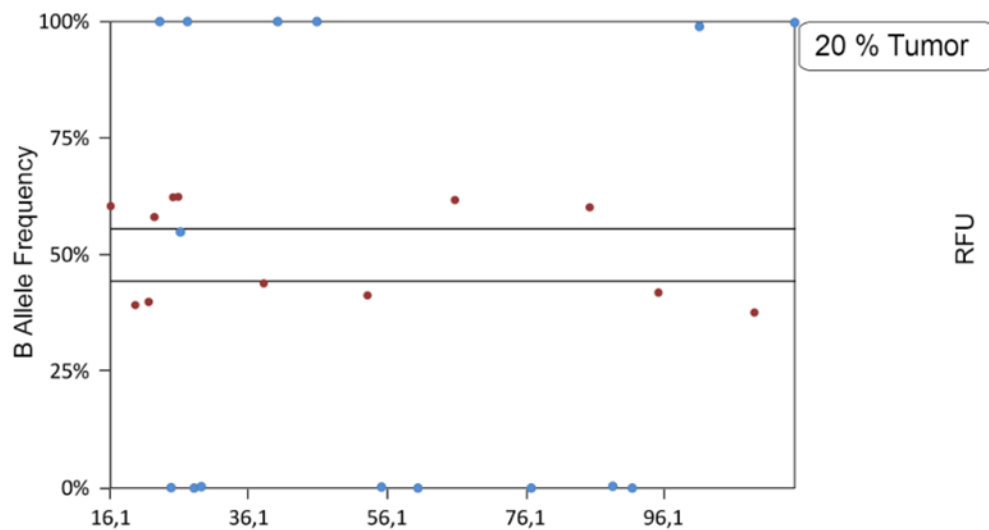
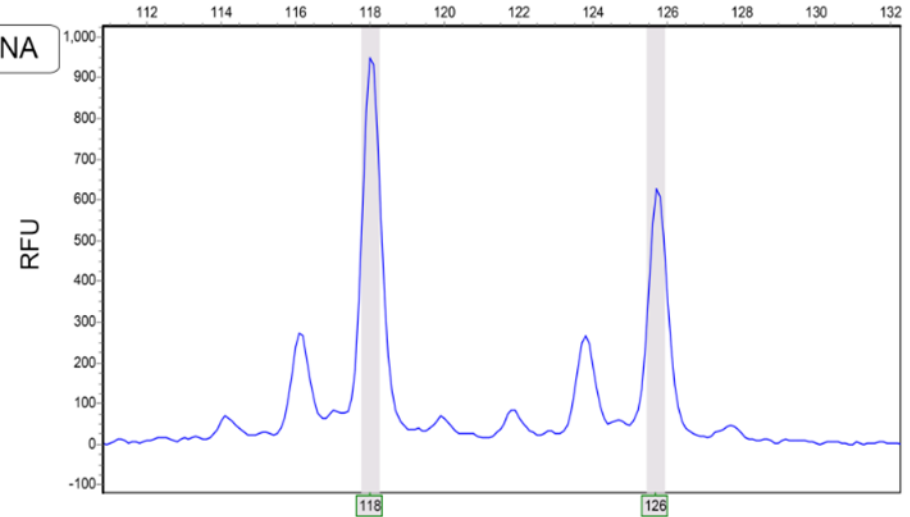
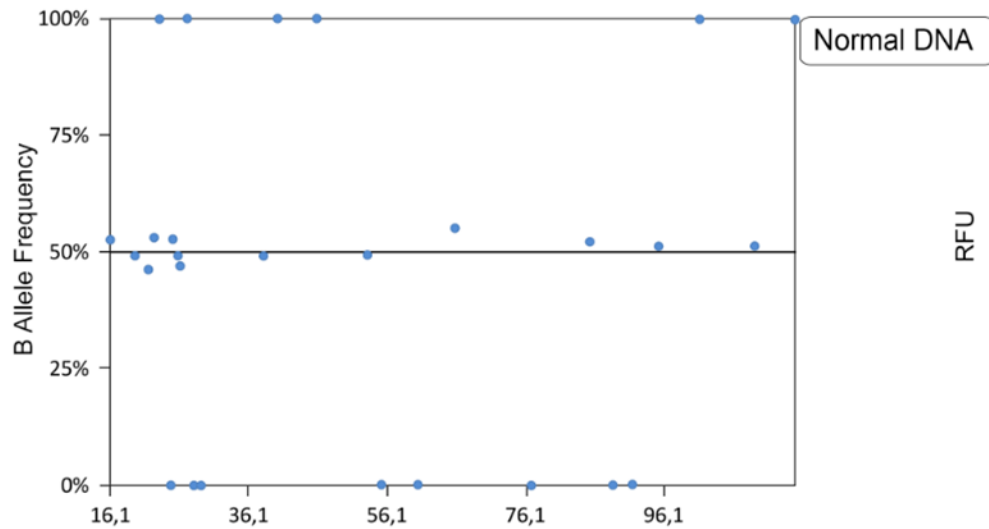
Verdeling SNPs over chromosoom 1p en 19q



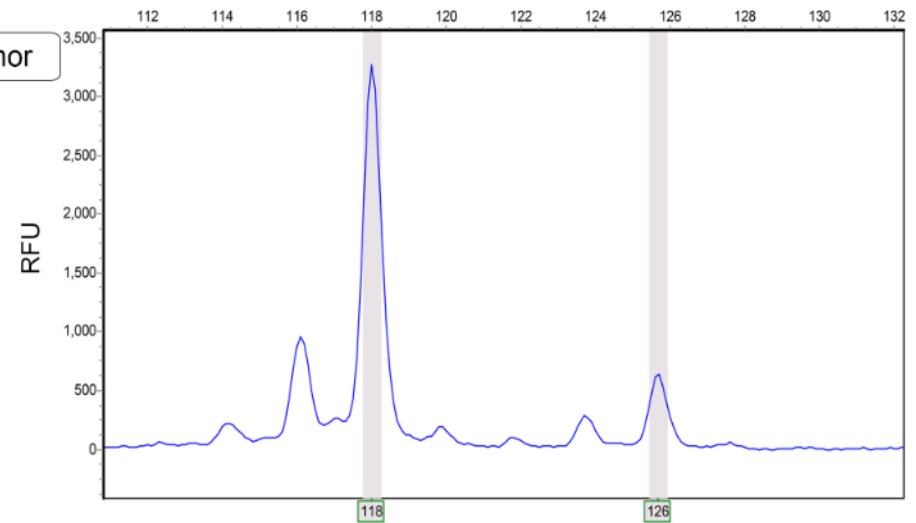
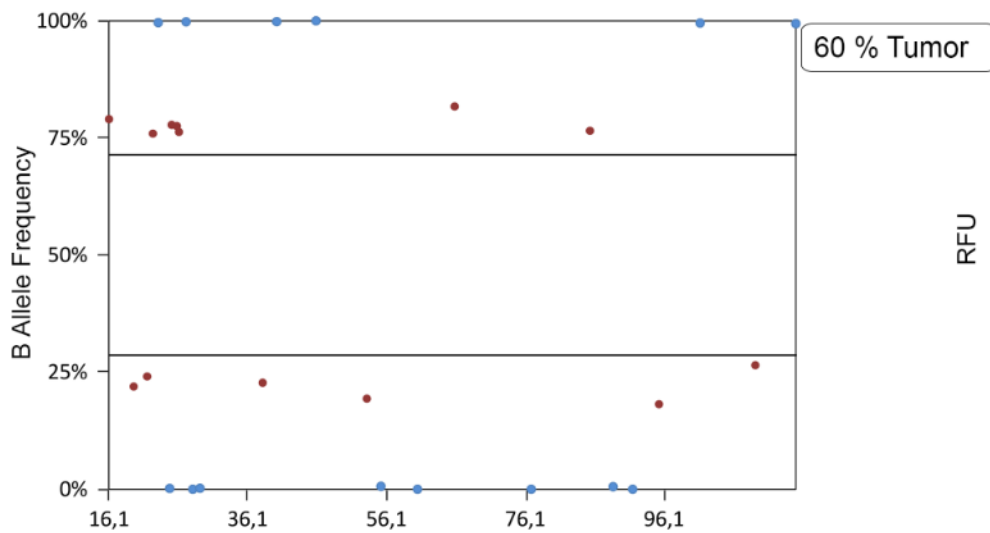
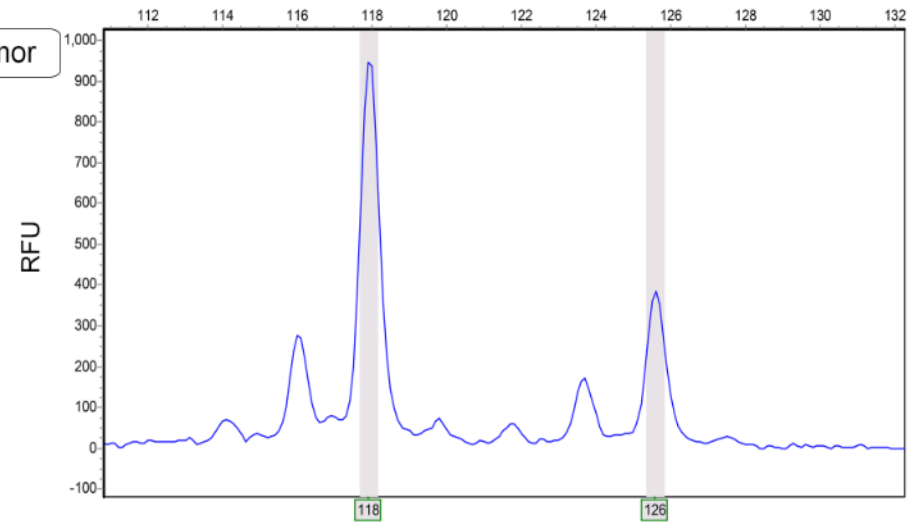
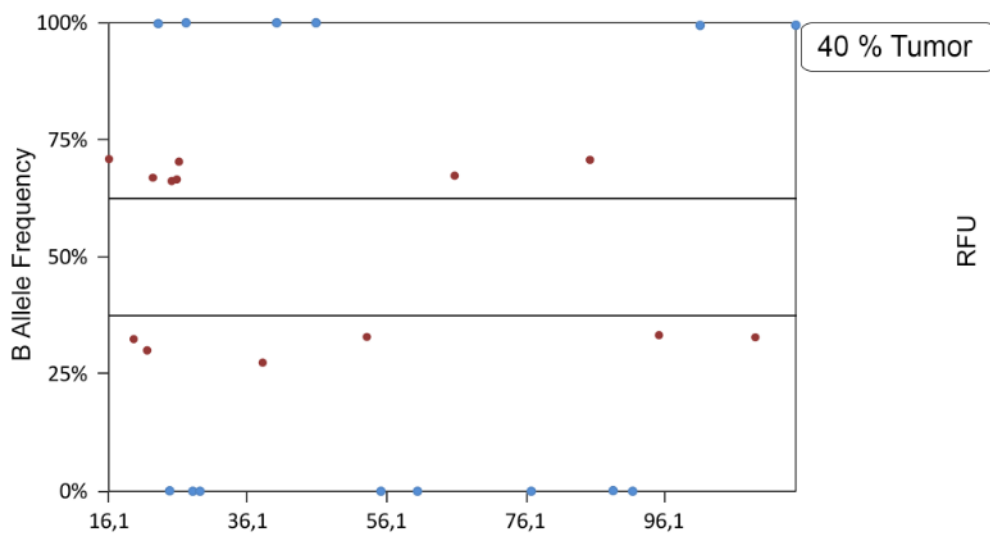
Gevoeligheid SNP vs microsatelliet LOH analyse



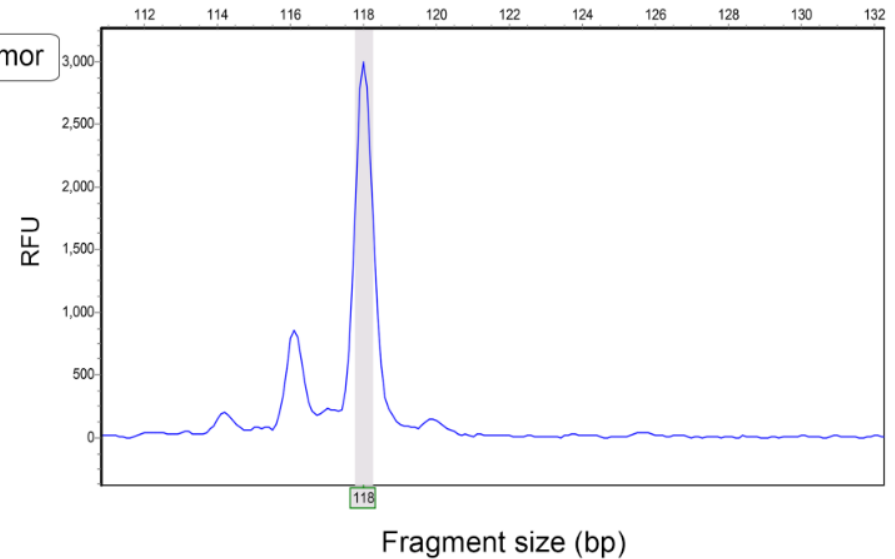
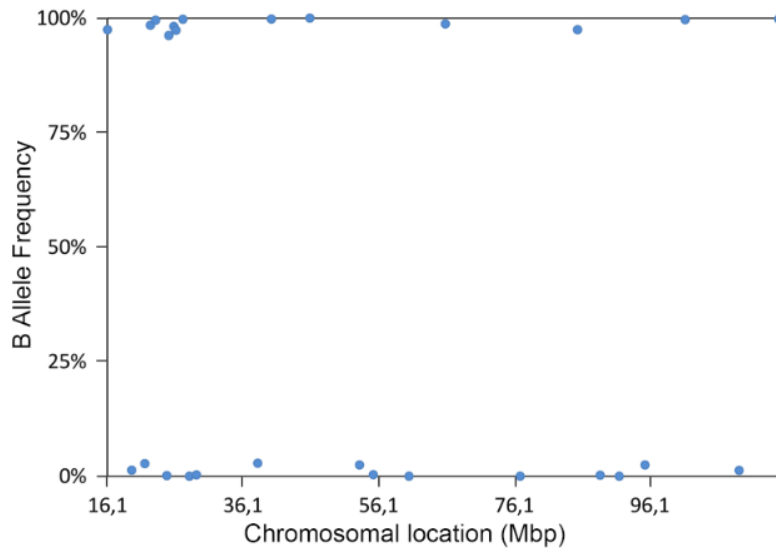
Gevoeligheid SNP vs microsatelliet LOH analyse



Gevoeligheid SNP vs microsatelliet LOH analyse



Gevoeligheid SNP vs microsatelliet LOH analyse

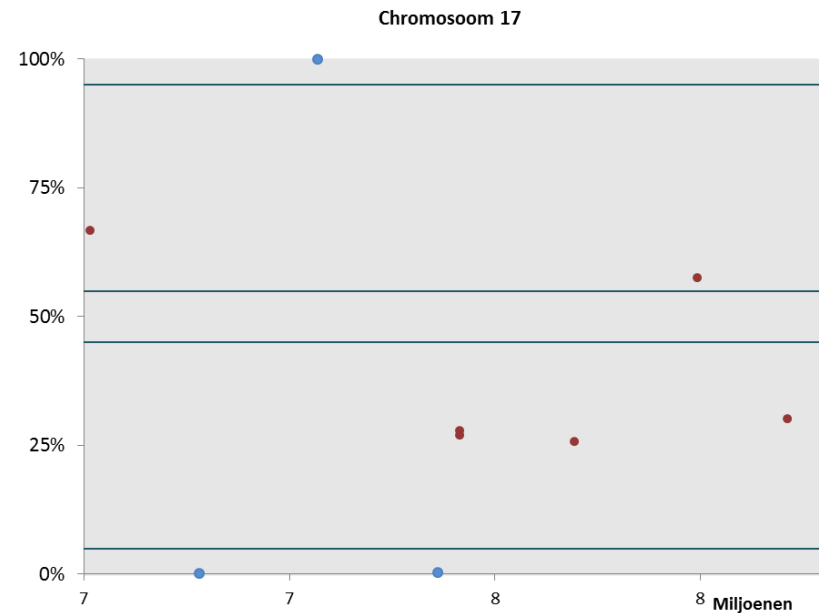
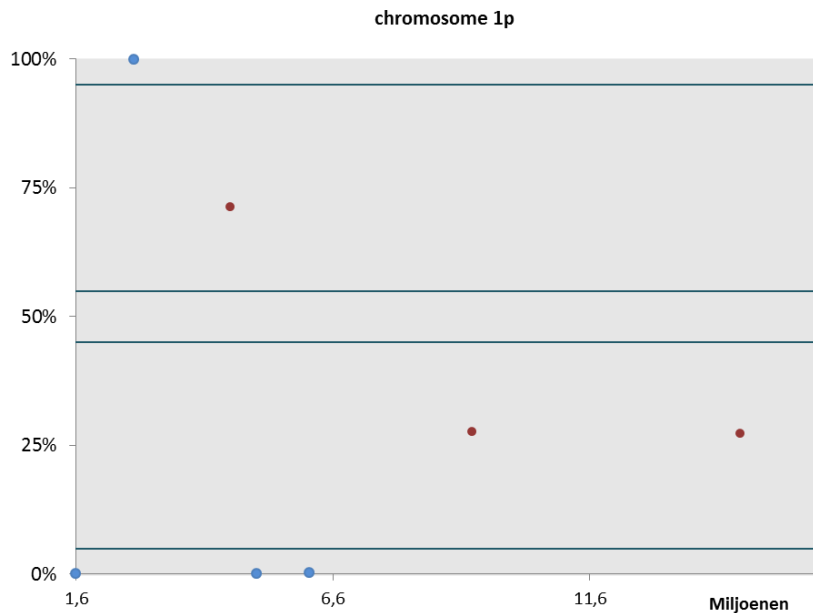
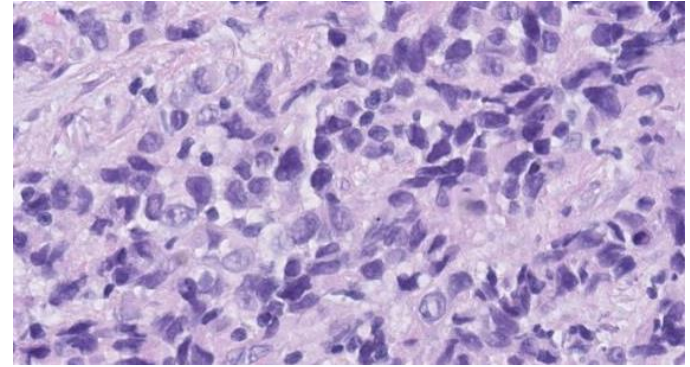


Mutatie analyse longpanel ivm therapiekeuze

Adenocarcinoom long

Percentage neoplastische cellen: 40%

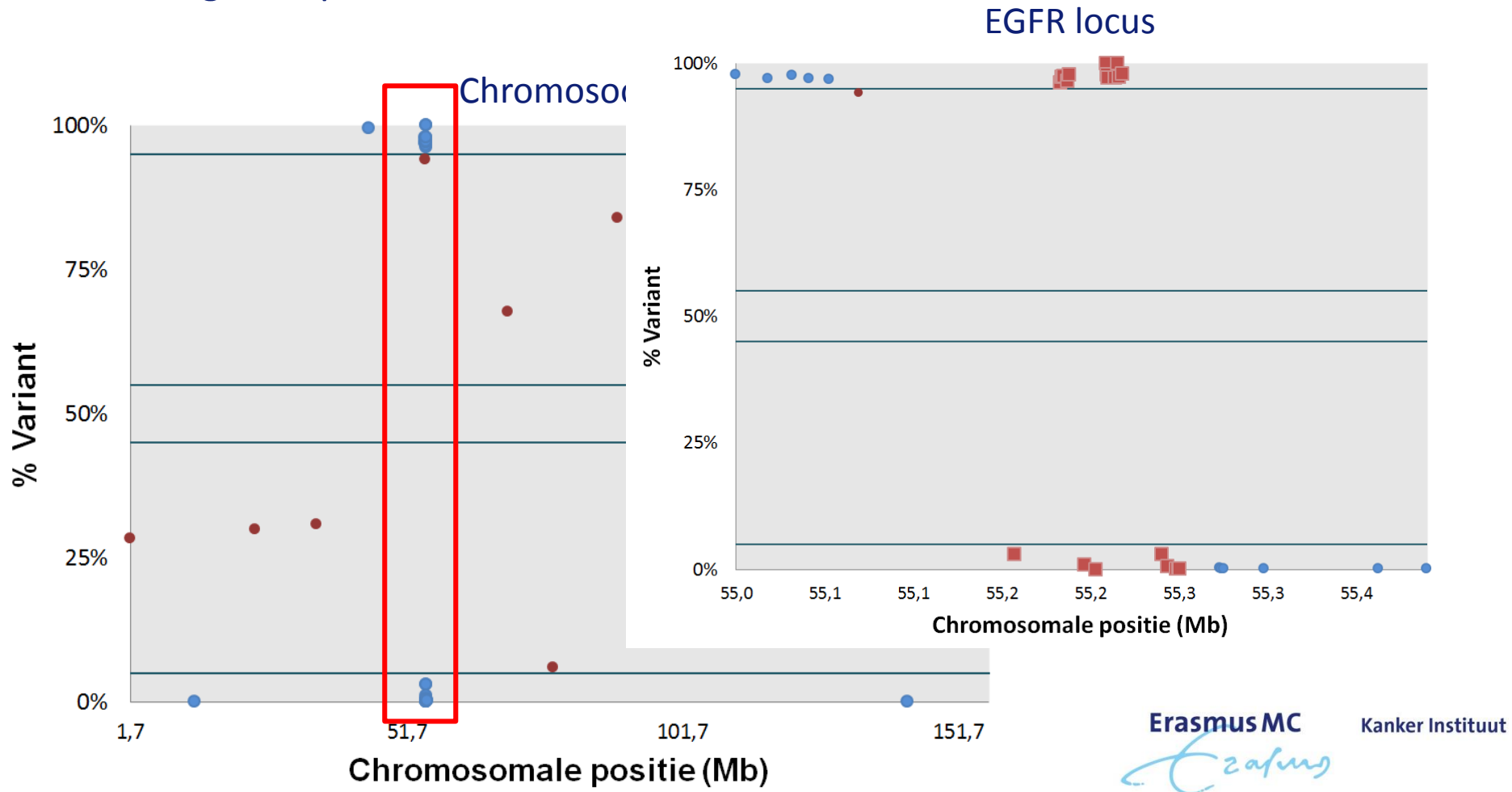
Geen mutaties gevonden met NGS



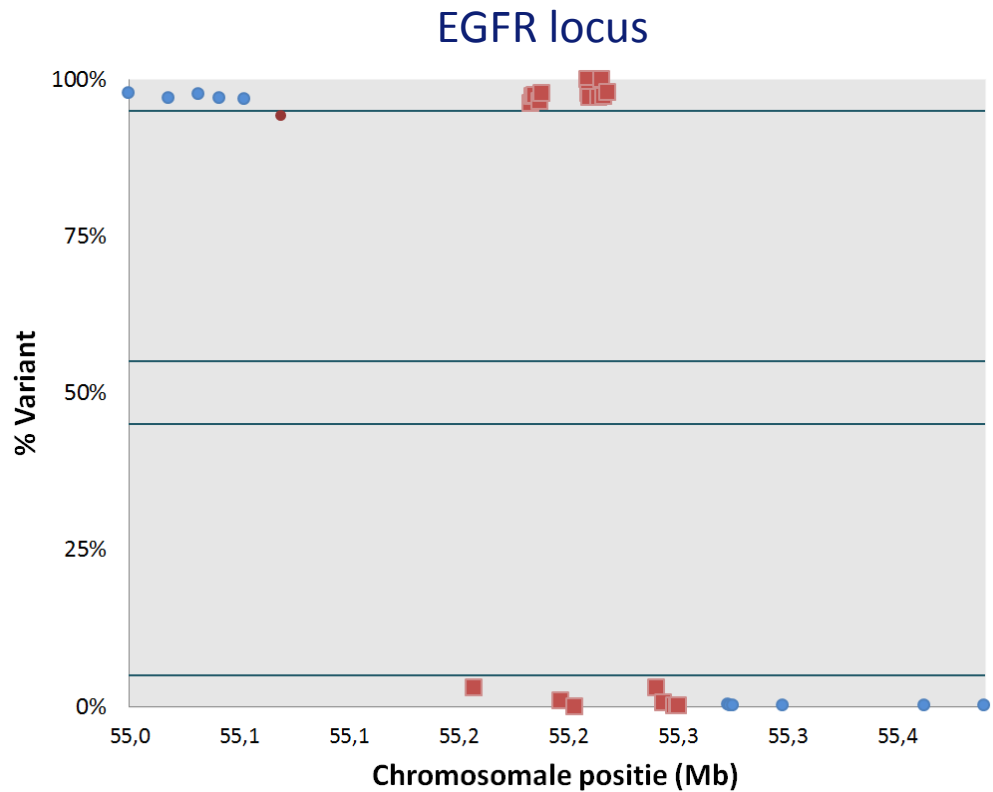
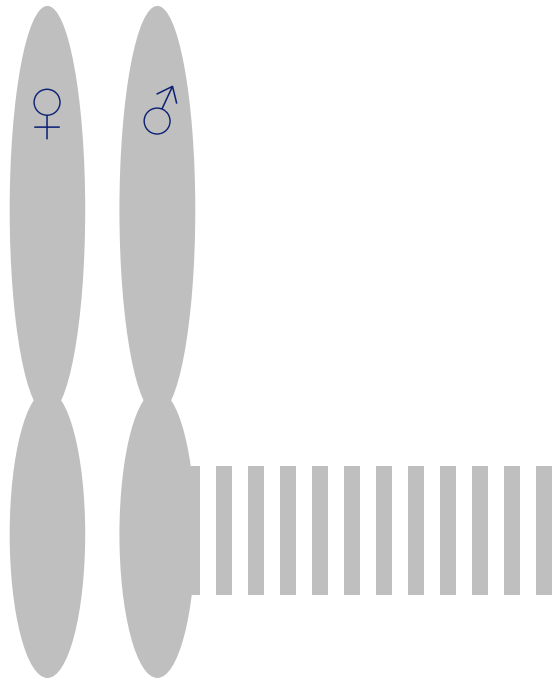
-> Afwijking past bij ongeveer 60% neoplastische cellen

Glioblastoom

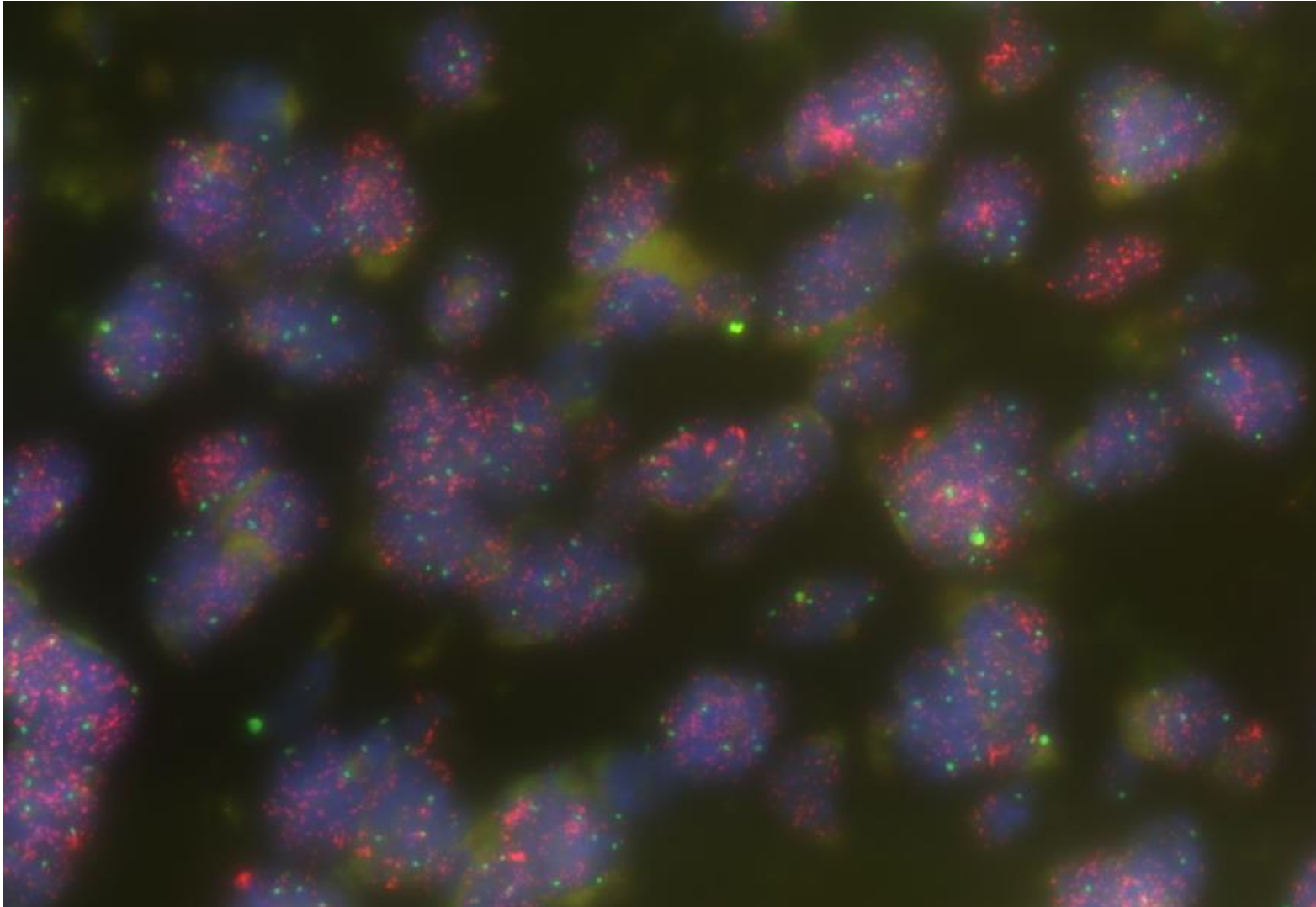
Moleculaire analyse ivm therapiekeuze/differentiaal diagnostiek
Percentage neoplastische cellen: 80%



Glioblastoom



Glioblastoom



Conclusies

- SNP analyse is een gevoelige methode voor detectie van grote chromosomale afwijkingen in routine FFPE weefsels
- Normaal referentieweefsel is niet nodig
- De analyse kan worden uitgevoerd op kleine hoeveelheden DNA (3-10 ng)
- Goed te combineren met mutatie analyse

Dankwoord

Moleculaire diagnostiek Erasmus MC Rotterdam

