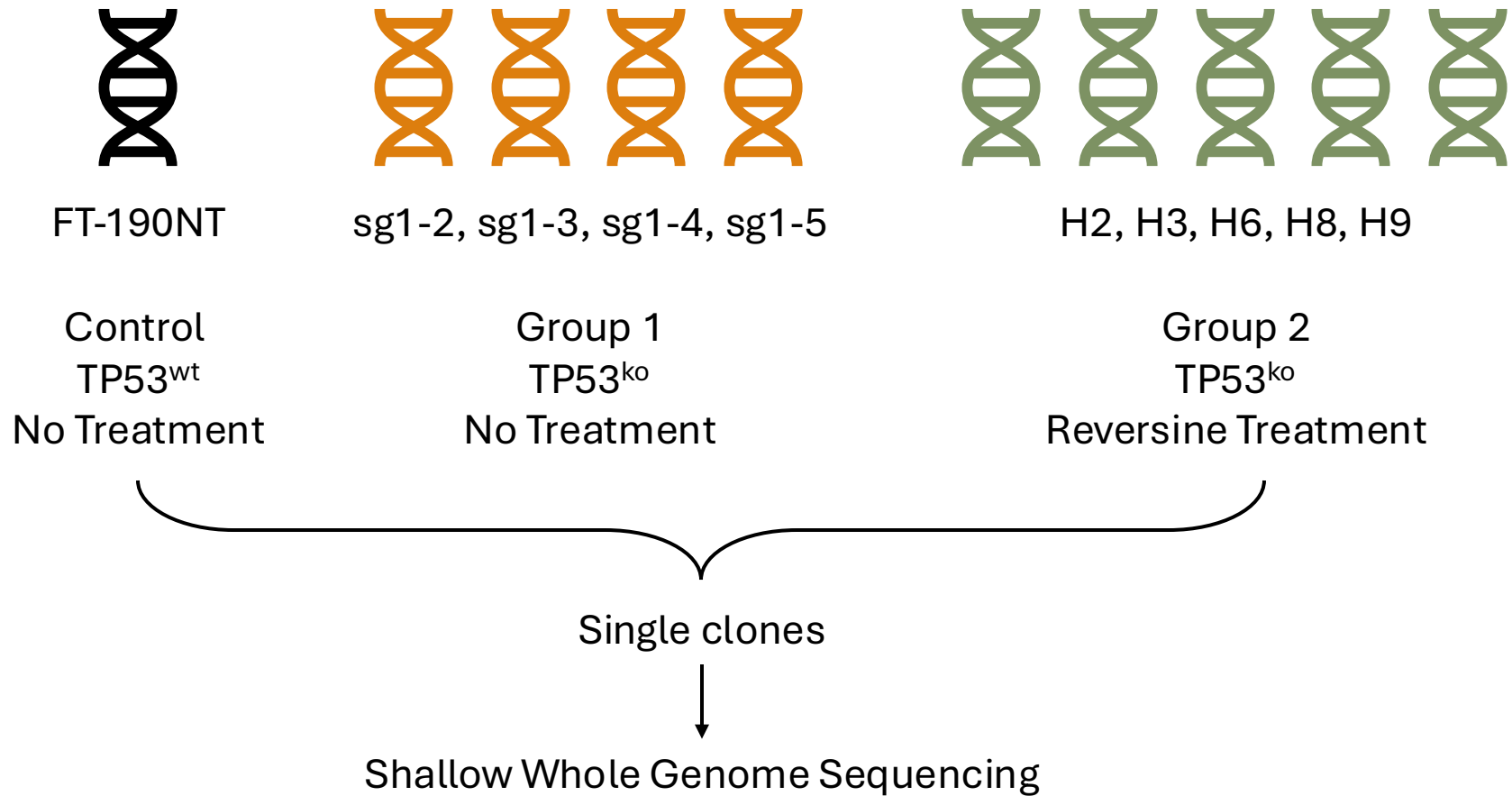


# Shallow Whole Genome Sequencing

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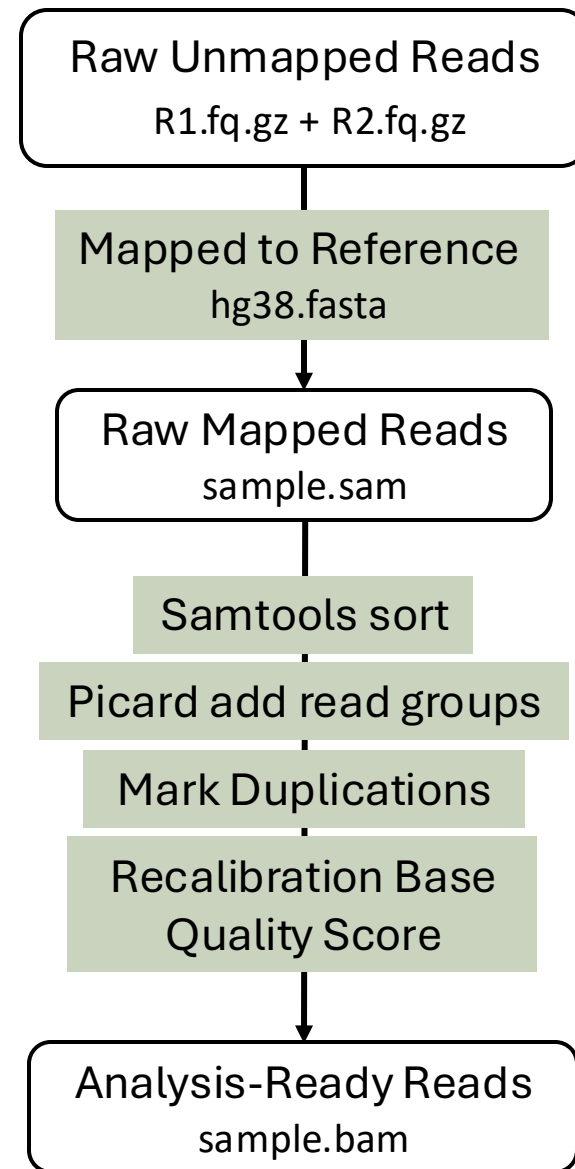
Project 3

# Background



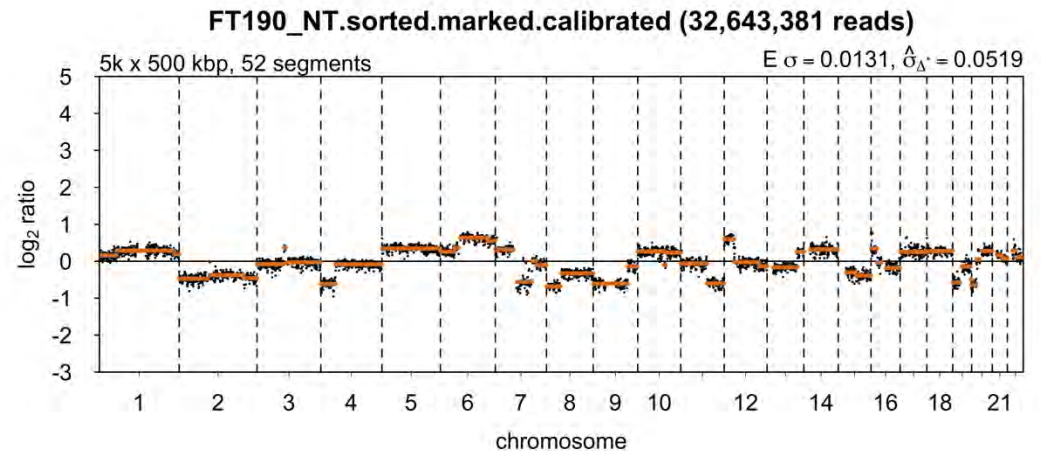
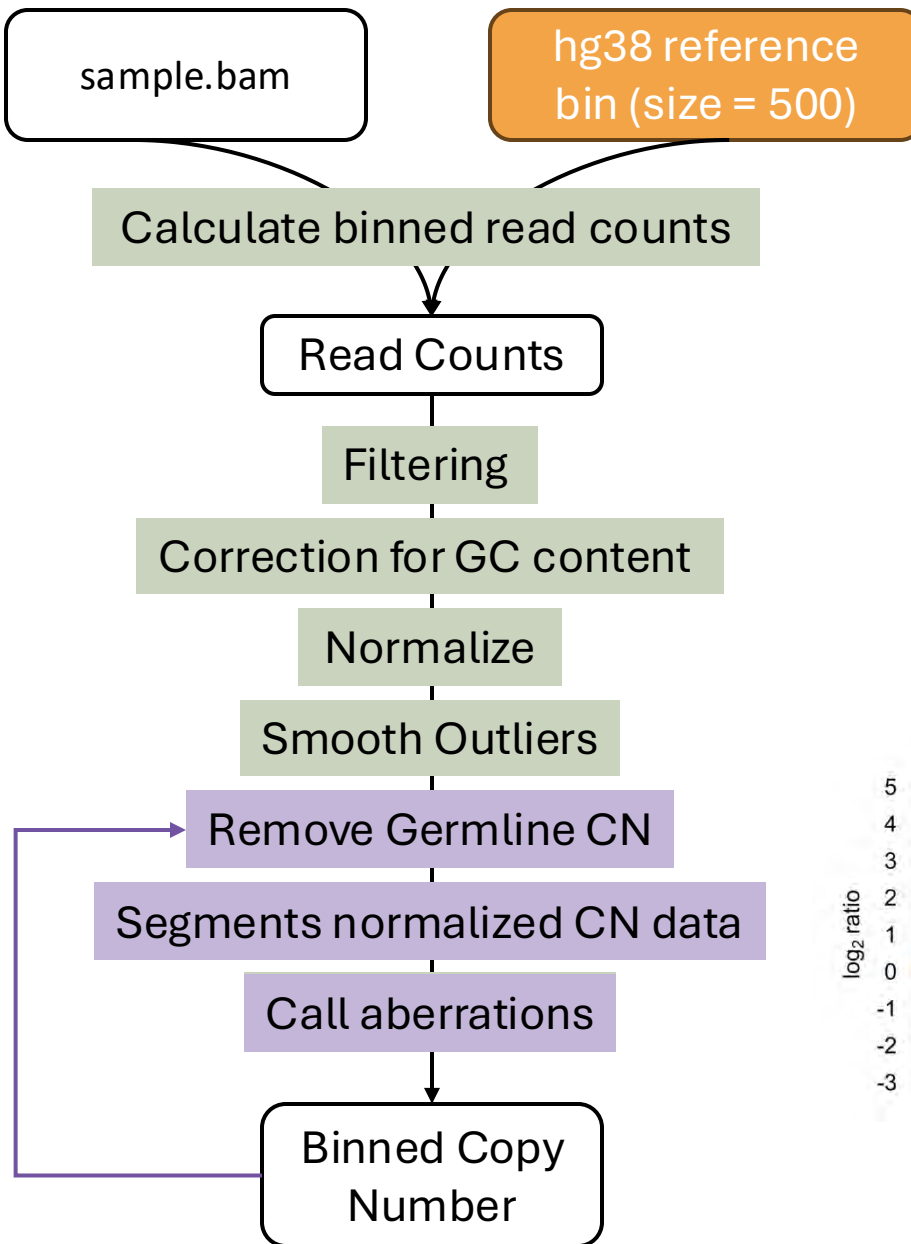
# GATK Data-Preprocessing Pipeline

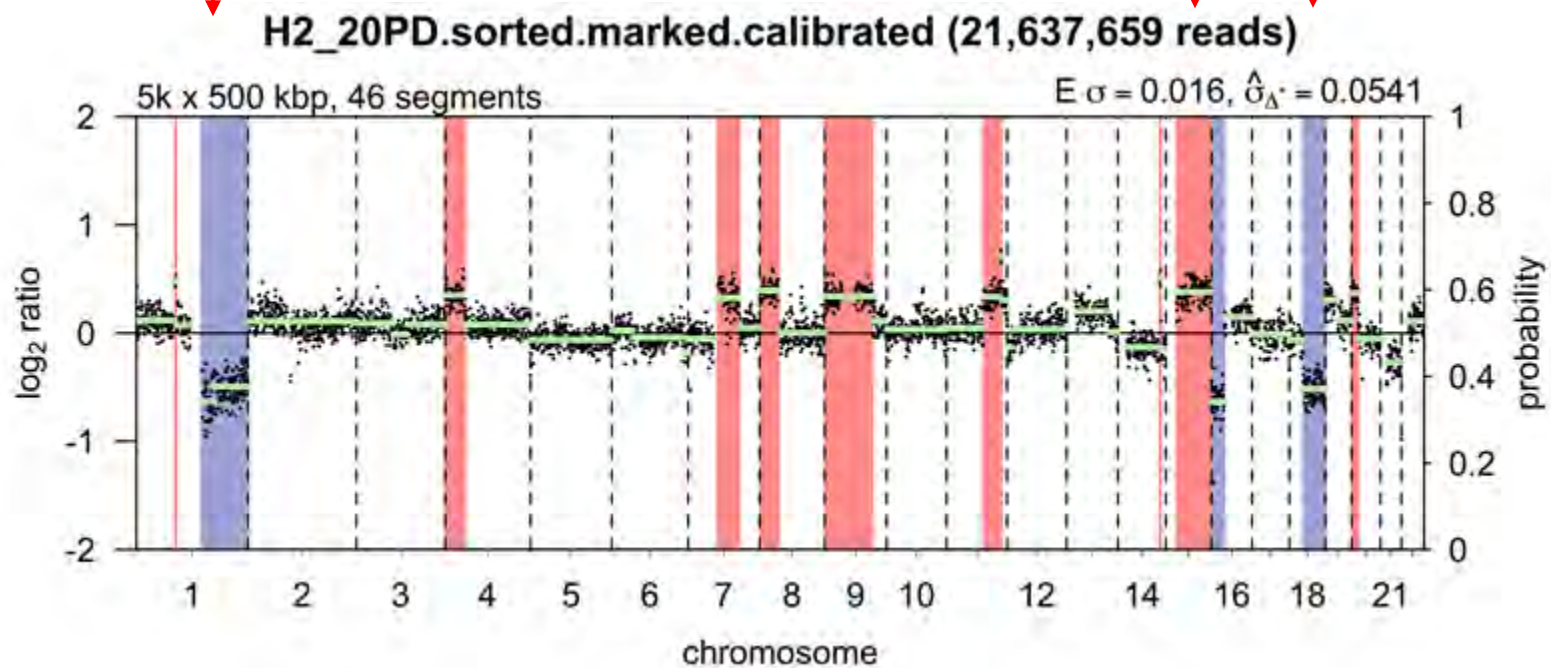
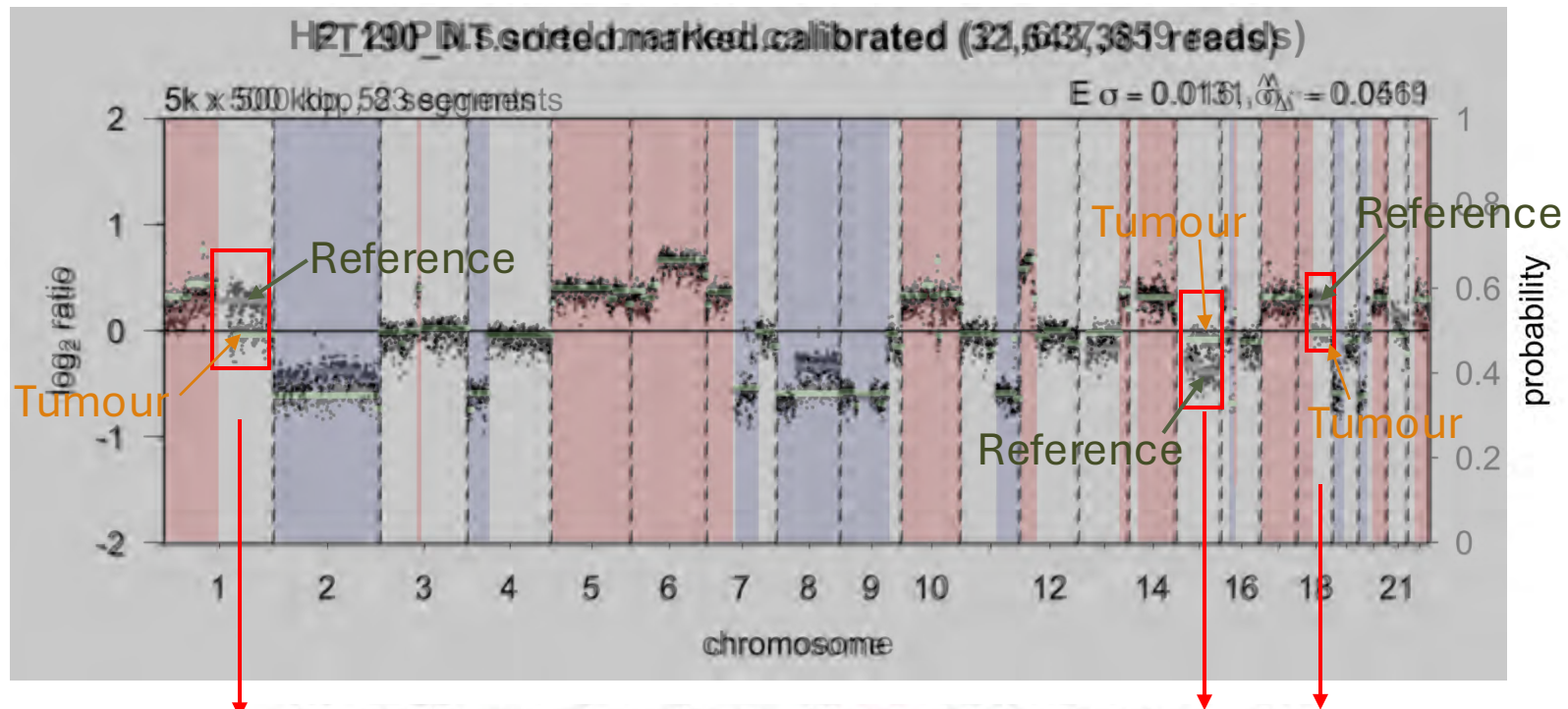
Quality of bam checked by samtools stats, average percentage of properly paired reads: 98.75%



# Analyzing Chromosomal Aberrations Using QDNA-seq

<https://bioconductor.org/packages/devel/bioc/vignettes/QDNAseq/inst/doc/QDNAseq.pdf>

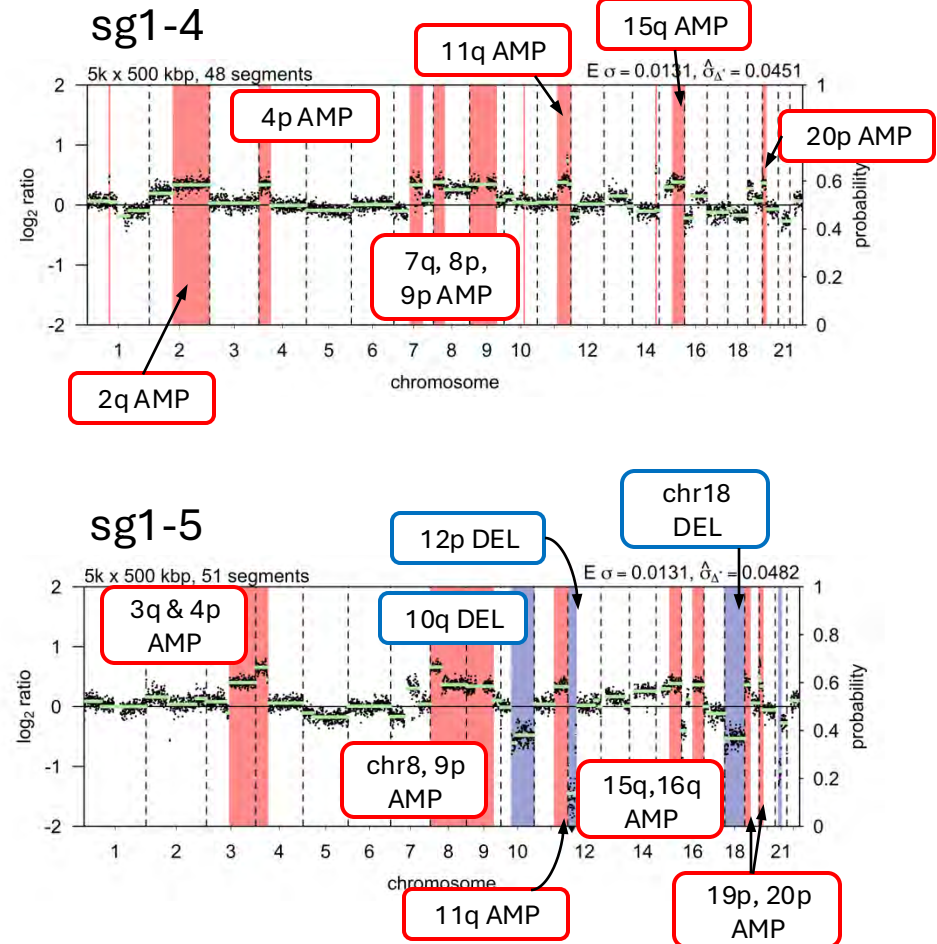
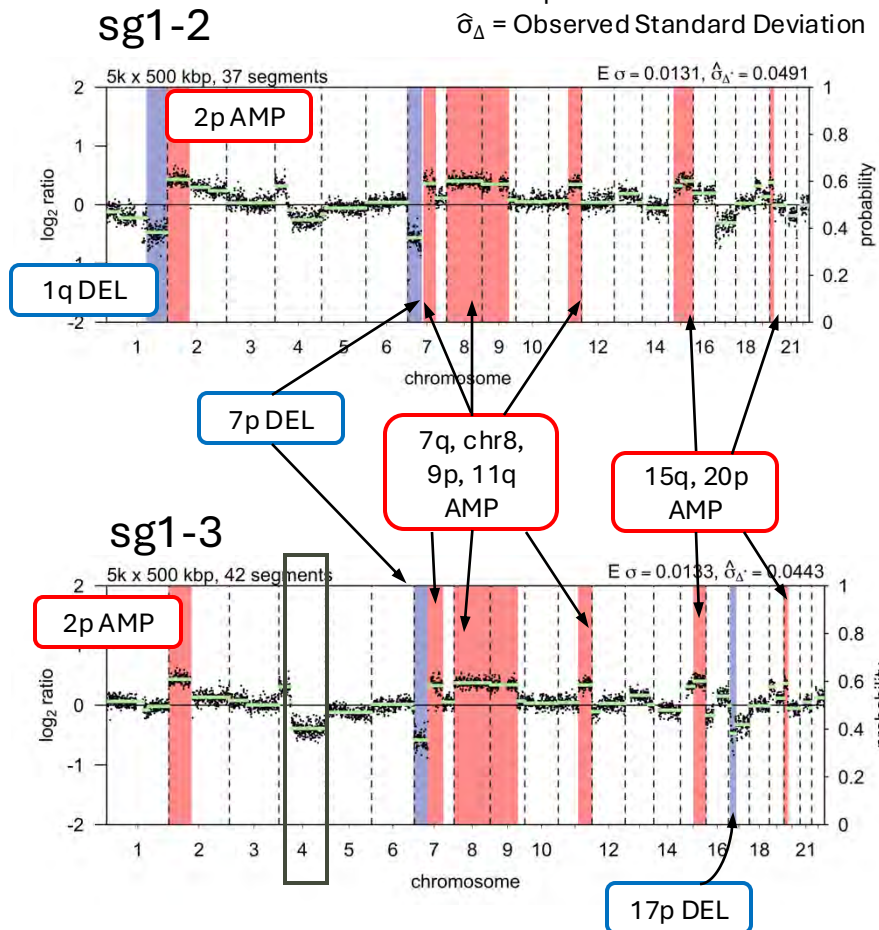




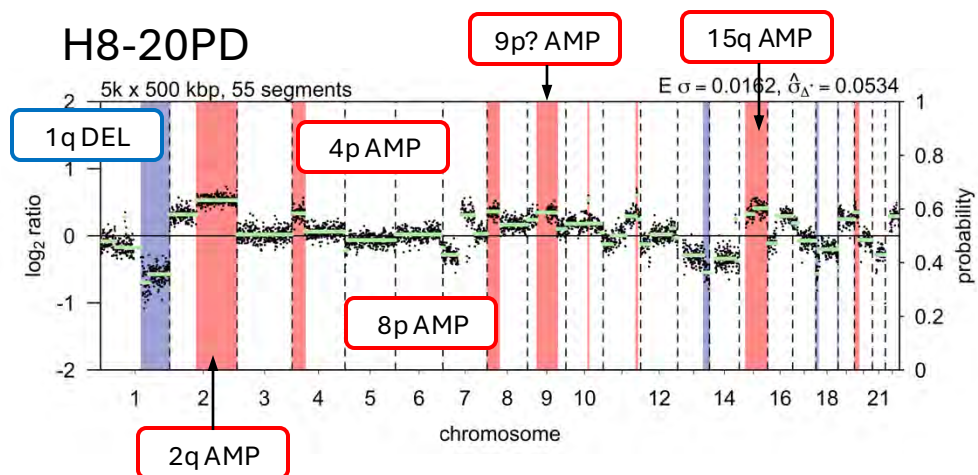
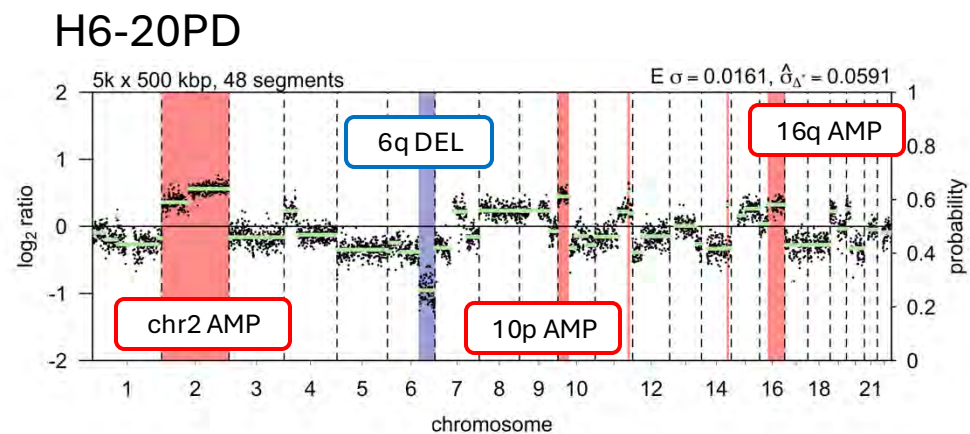
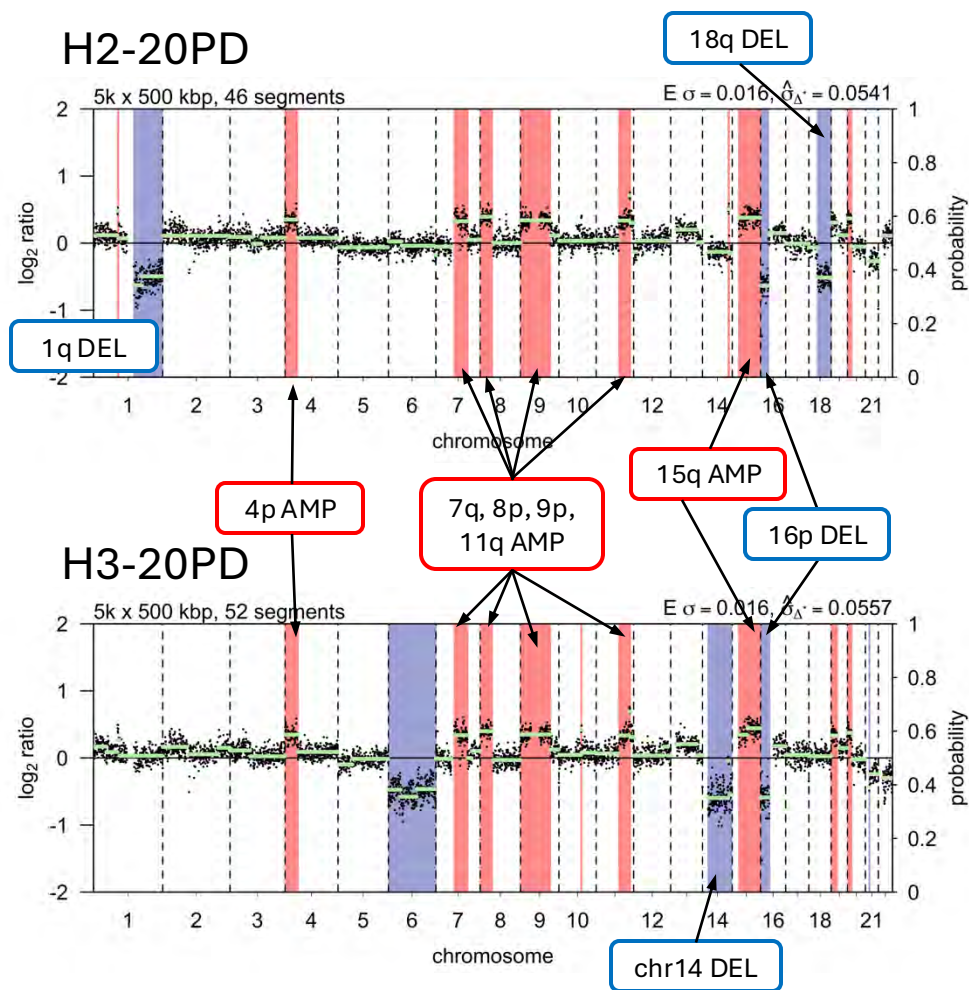


# TP53<sup>ko</sup> + no treatment

$E\sigma$  = Expected Standard Deviation  
 $\hat{\sigma}_\Delta$  = Observed Standard Deviation



# TP53<sup>ko</sup> + Reversine



# TP53<sup>ko</sup> + Reversine

