

# Report CORIANDR: ChrOmosomal abeRration Identifier AND Reporter in R

*09 Dezember, 2020*

Sample\_ID 'r patient\_name'

unique_reads	1952144
average_length	149.896
unique_mapped_reads	3831028
SAMPLE_ID	29701.muenchen
gender	M

## Calculated numerical karyotype:

NA

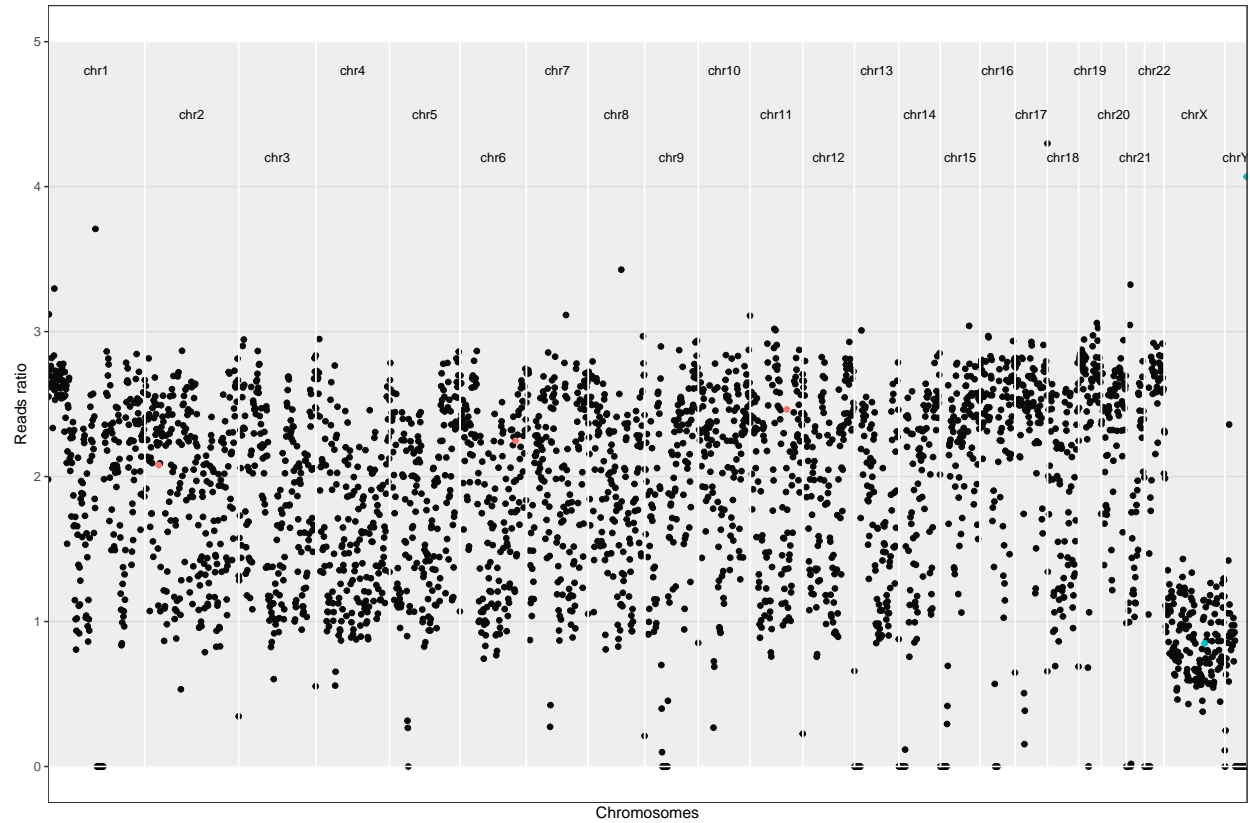
## Genes affected by CNVs\*:

id	symbol	chr	start	end	aberration
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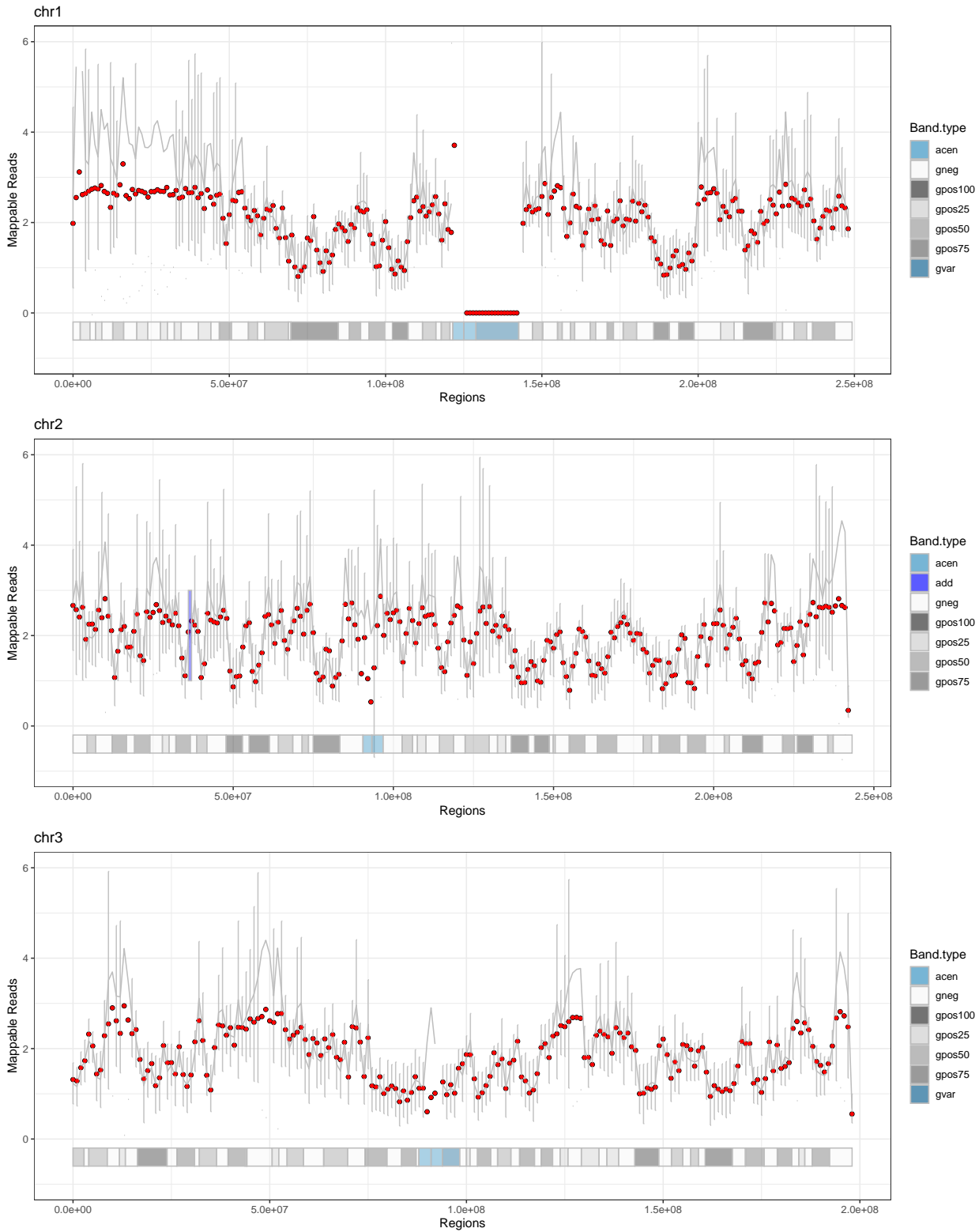
Bailey et al. (2018): Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell 173 (2), 371-385.e18. DOI: 10.1016/j.cell.2018.02.060.;

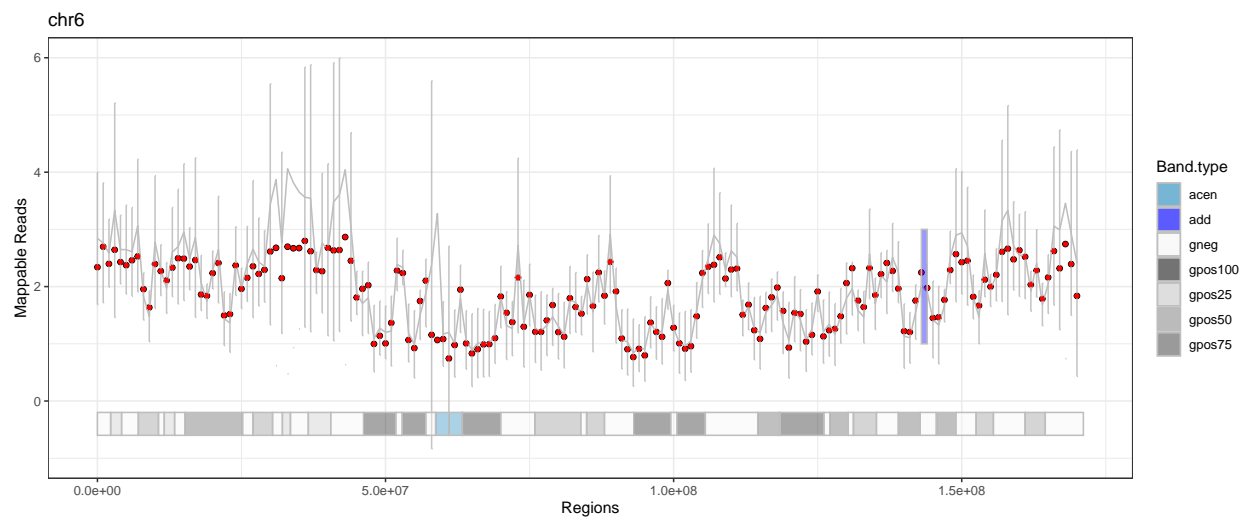
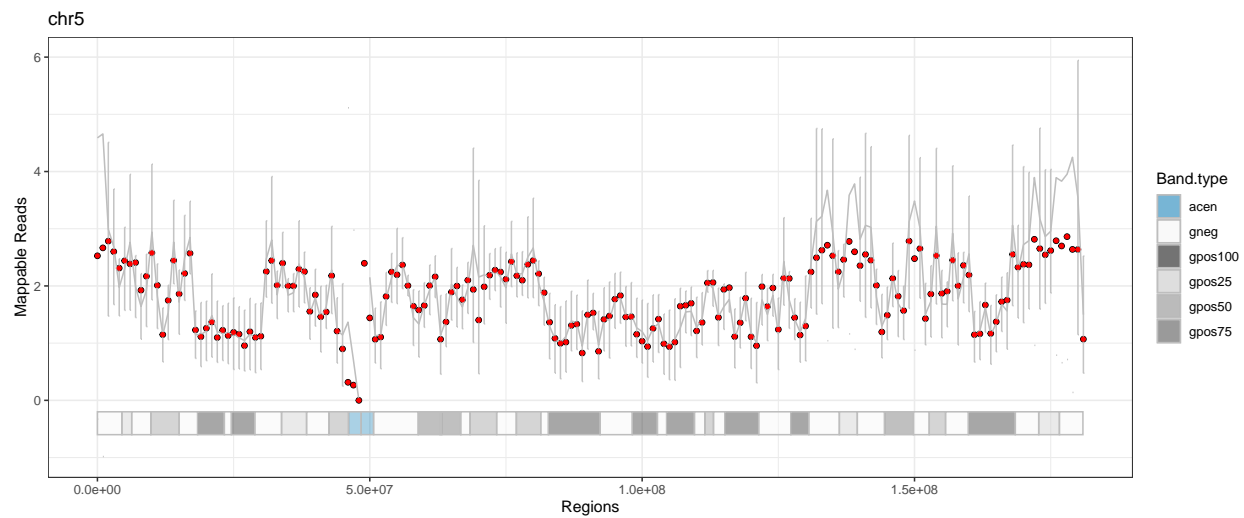
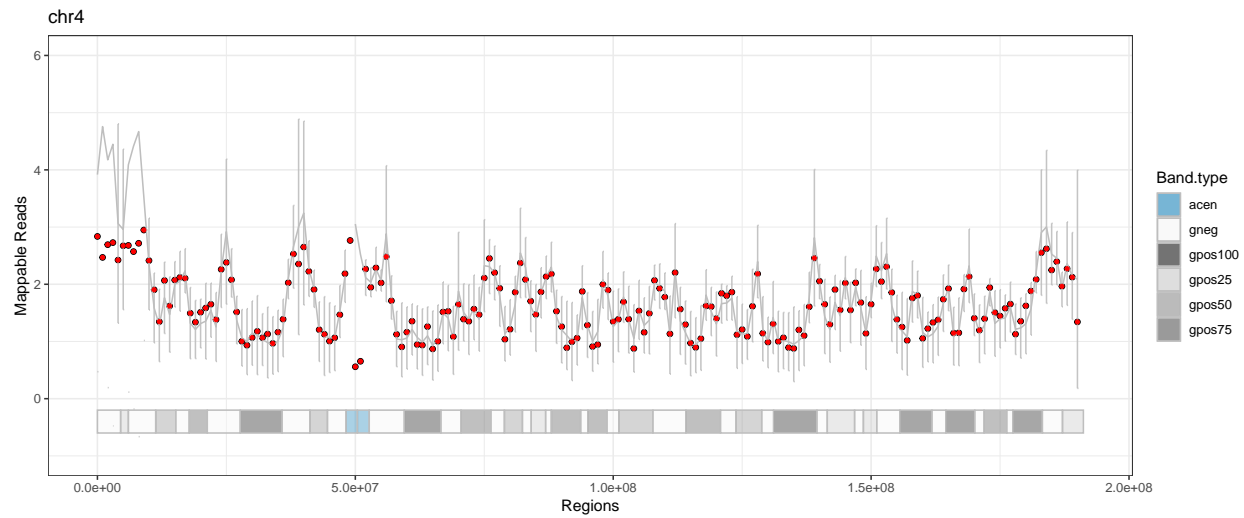
Papaemmanuil et al. (2016): Genomic Classification and Prognosis in Acute Myeloid Leukemia. The New England journal of medicine 374 (23), S. 2209–2221. DOI:10.1056/NEJMoa1516192.

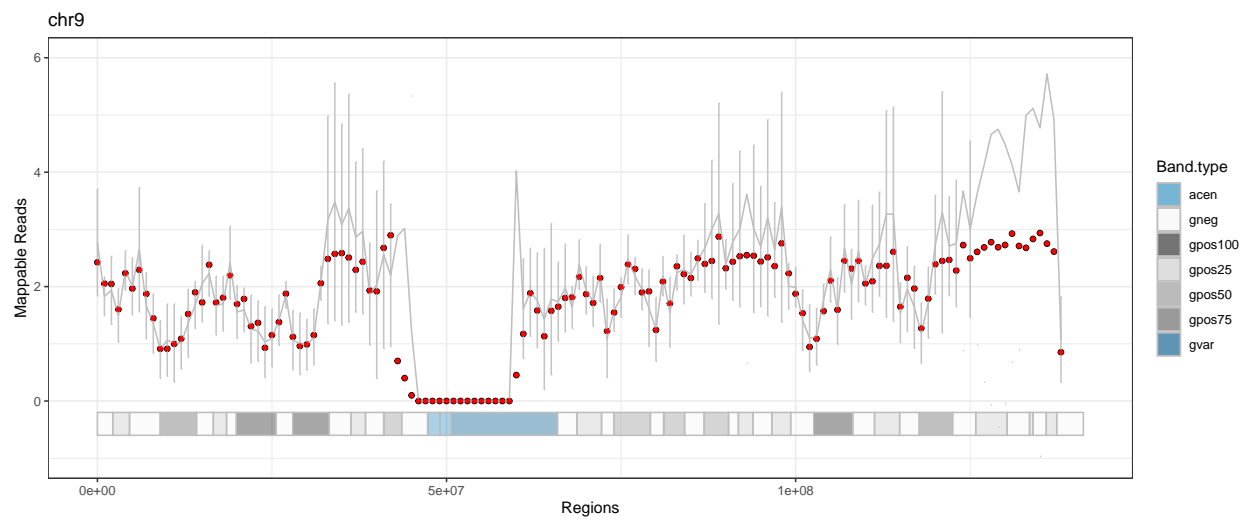
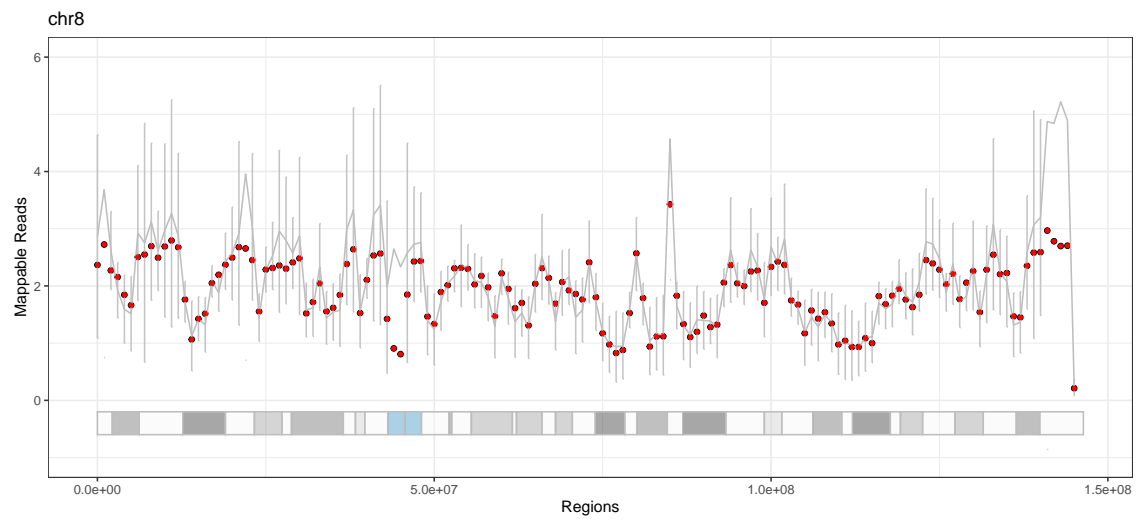
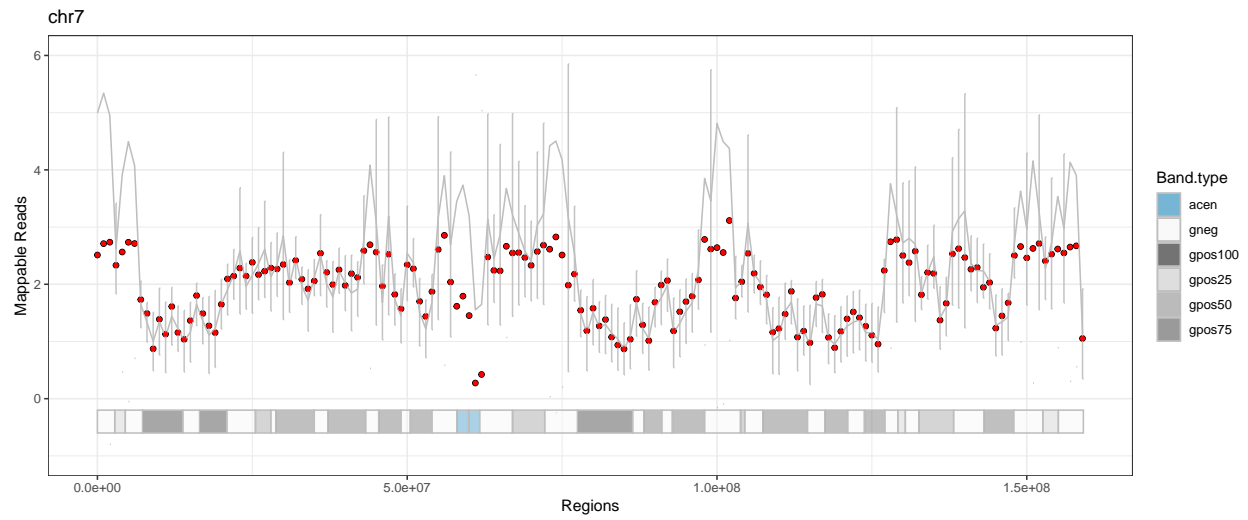
## Karyotype overview:

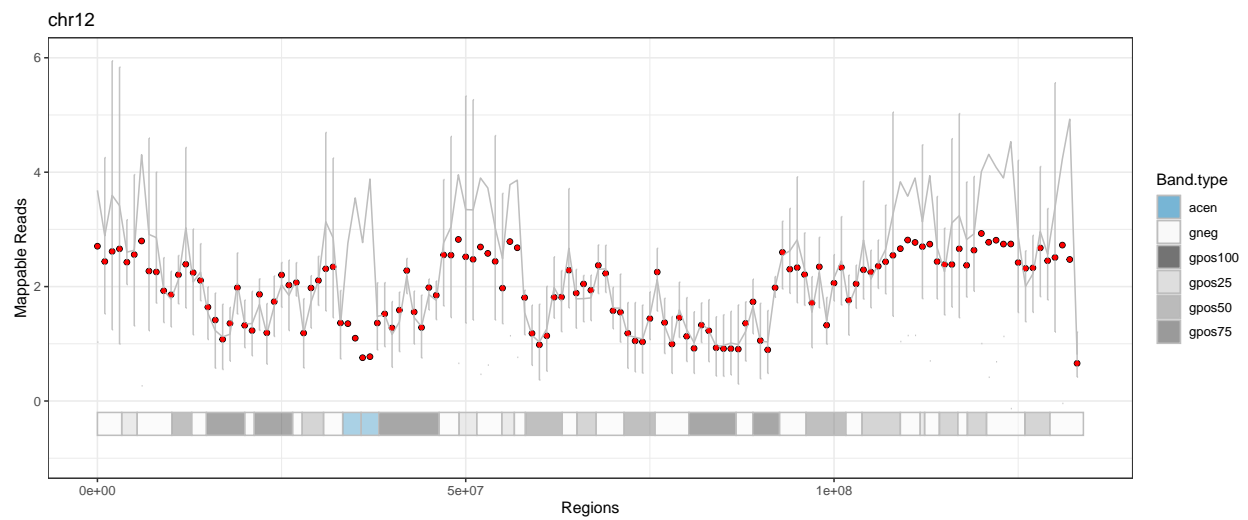
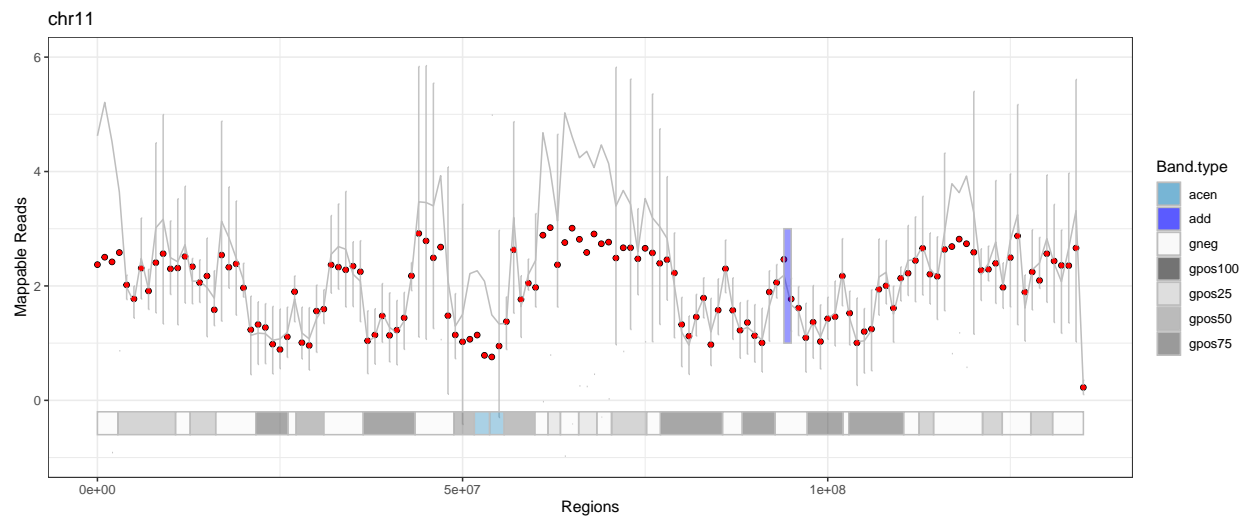
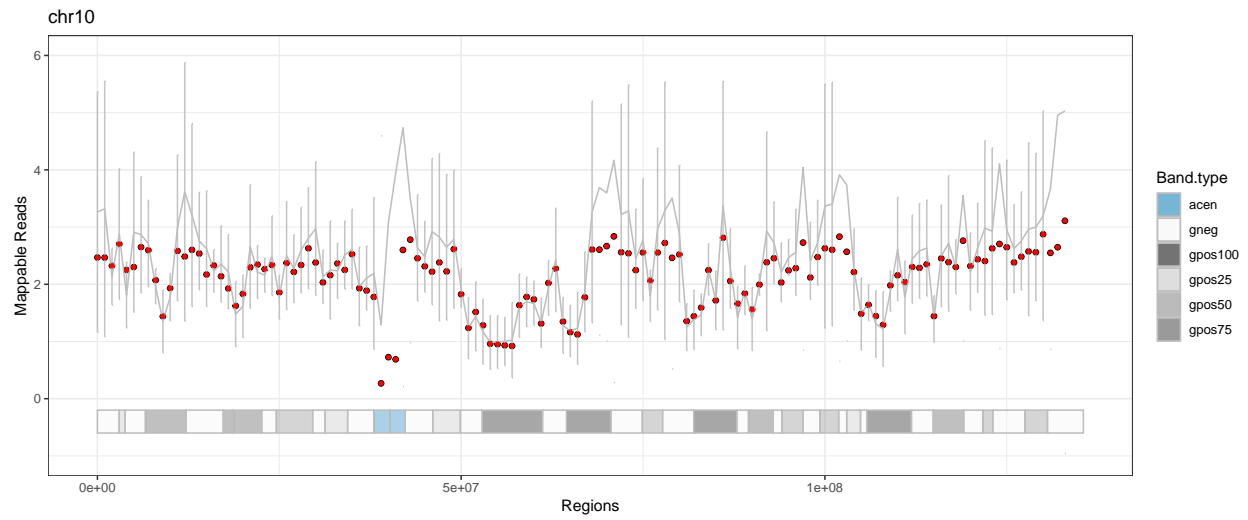


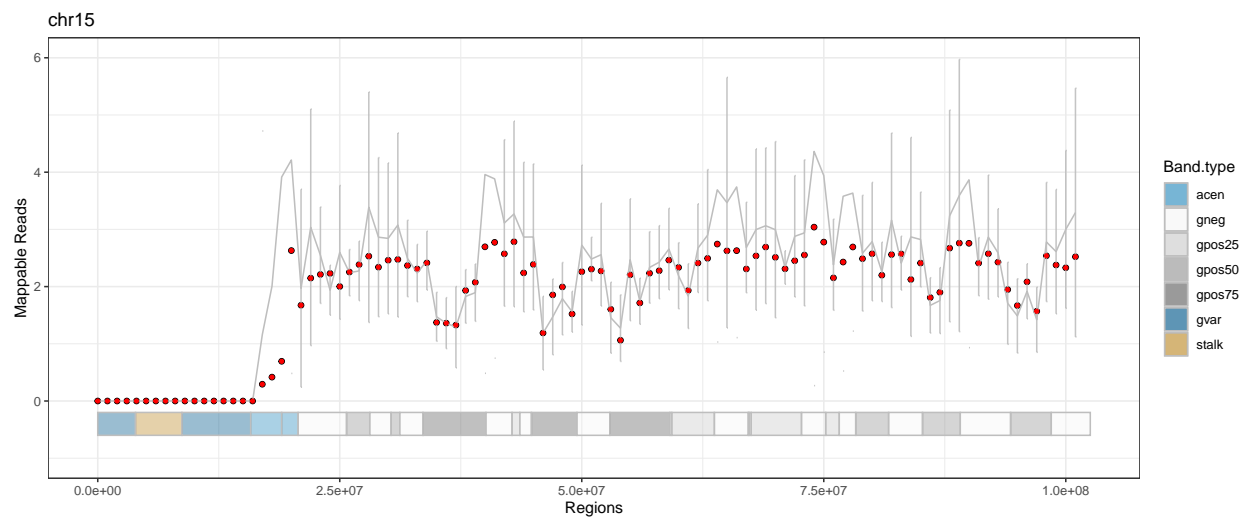
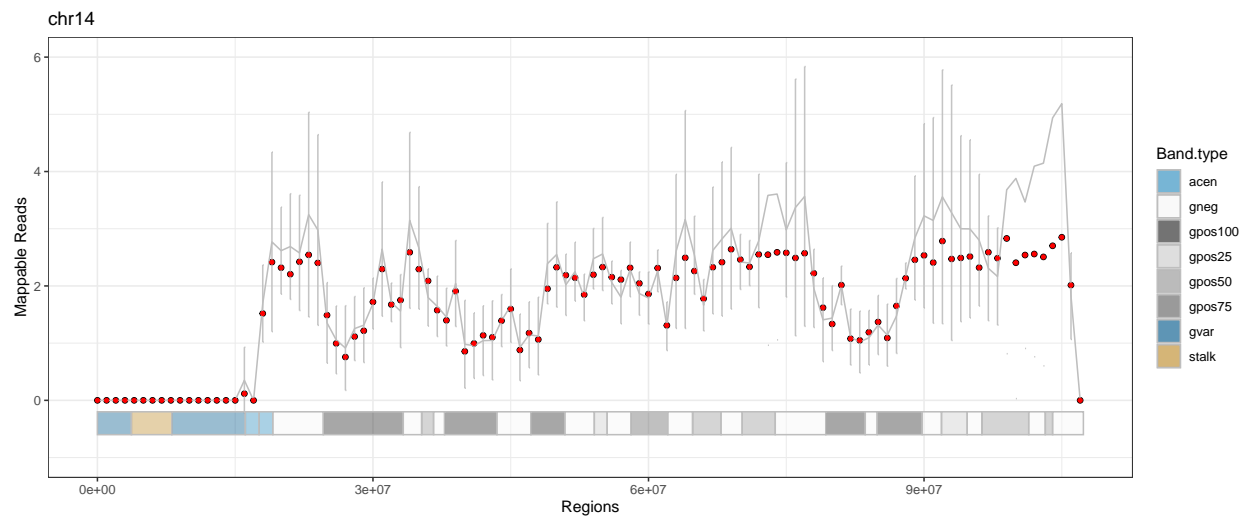
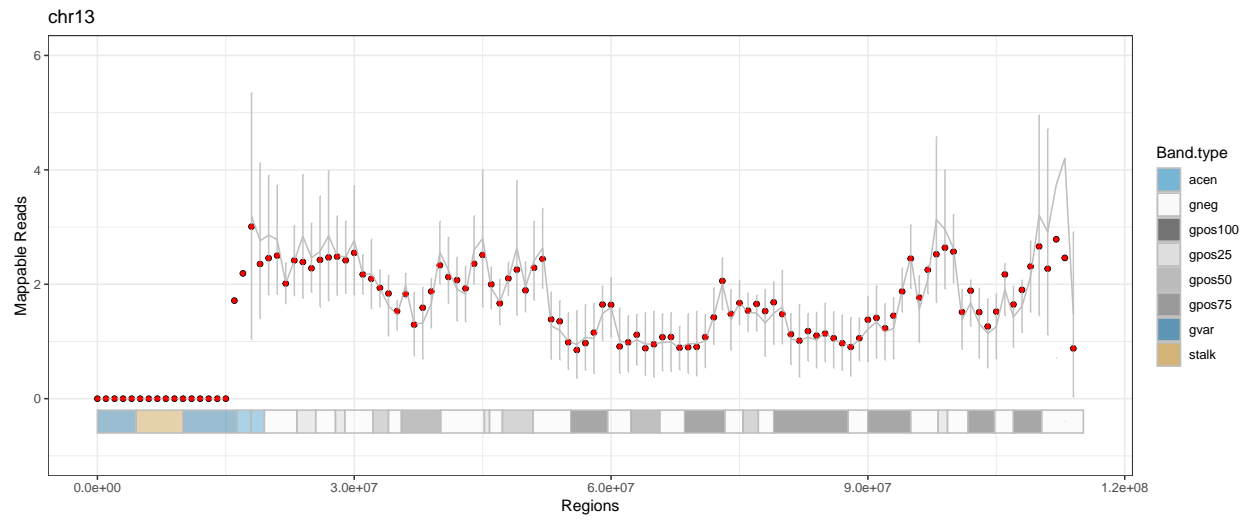
Chromosome Plots:

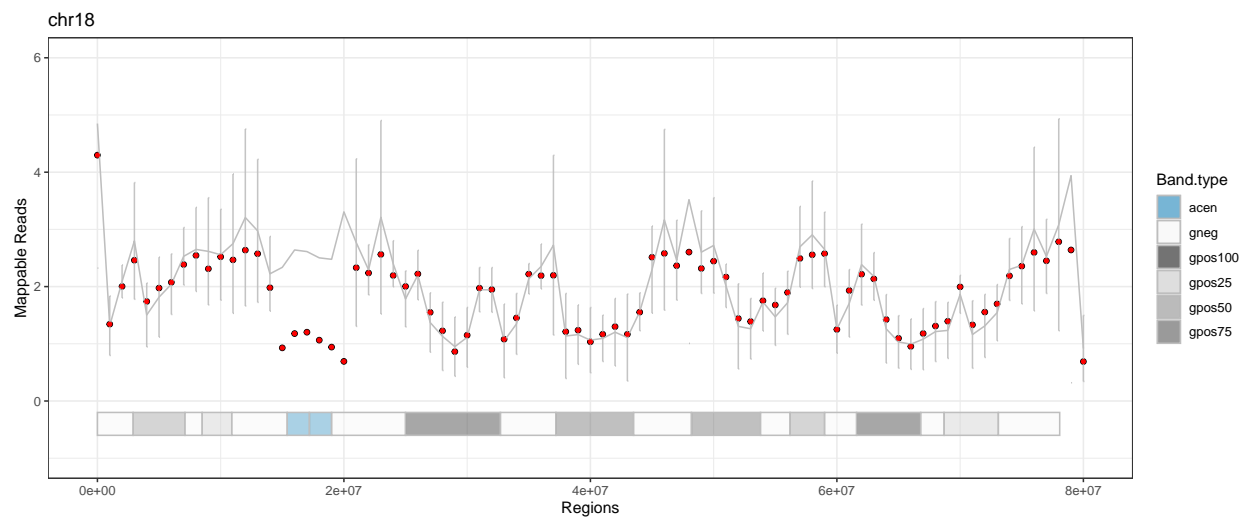
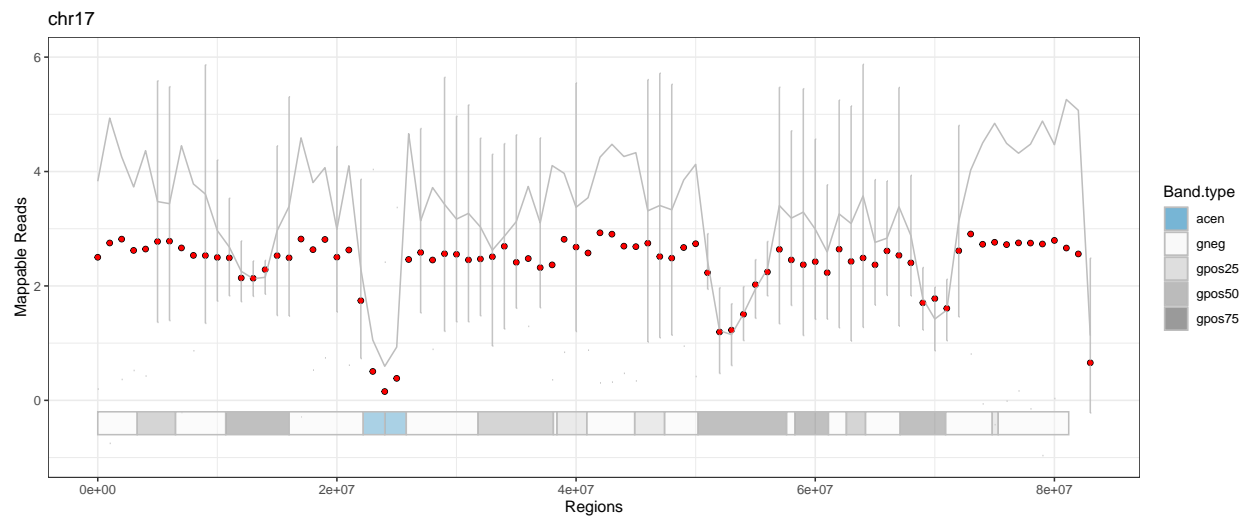
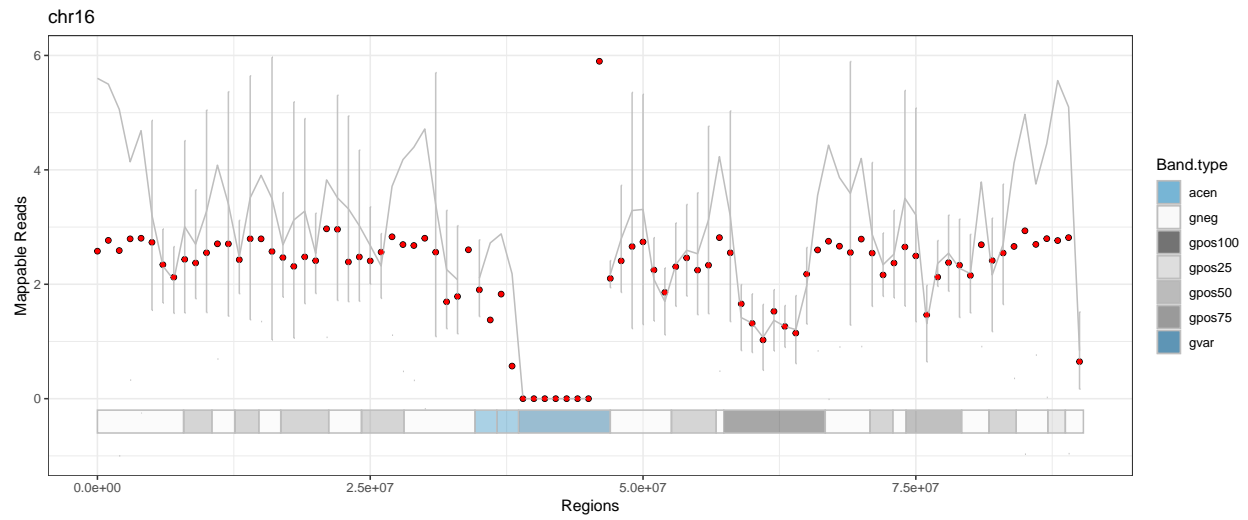




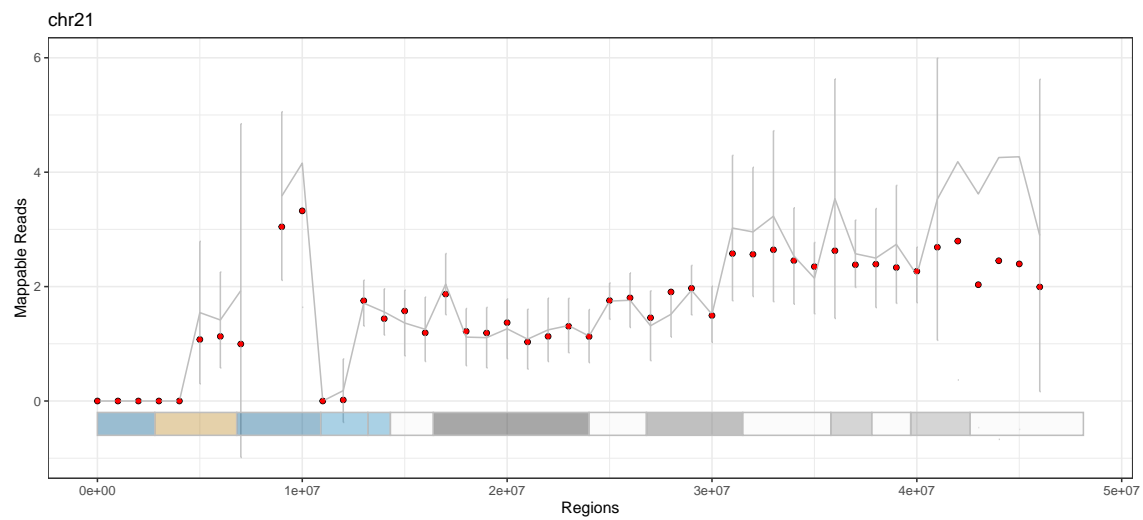
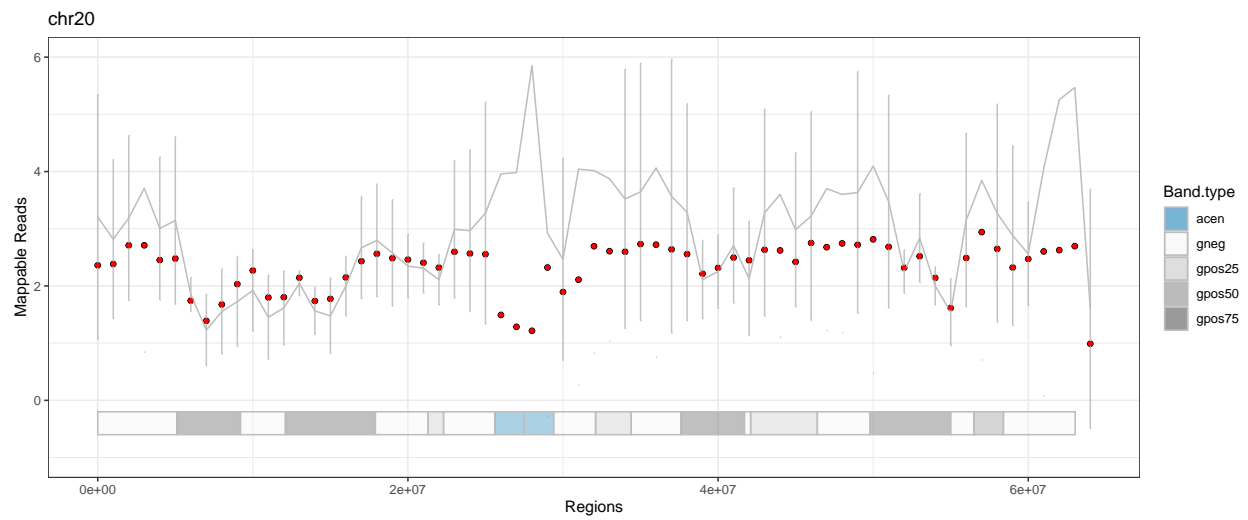
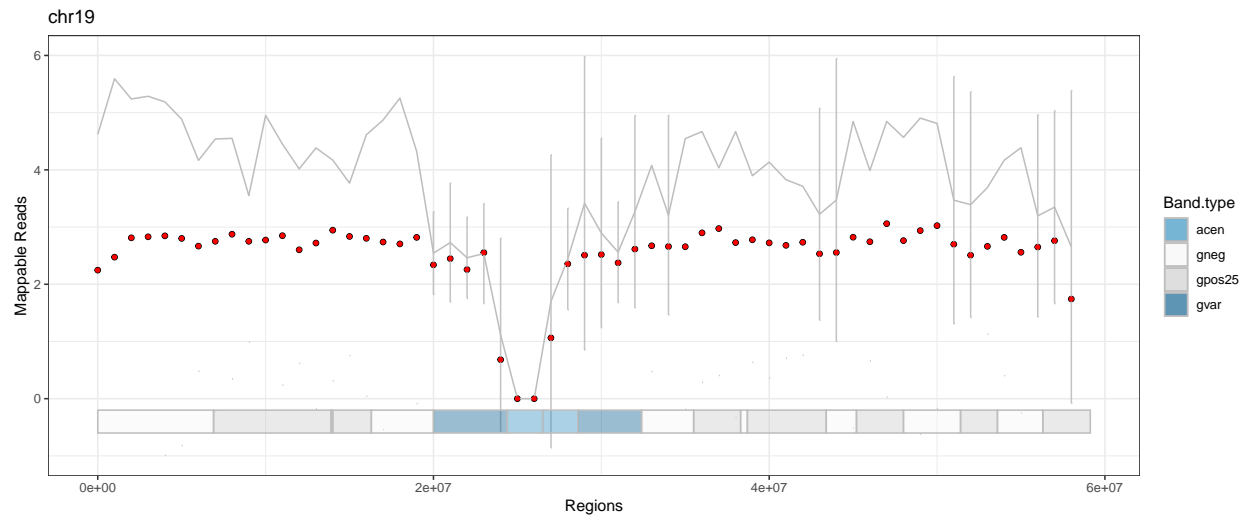


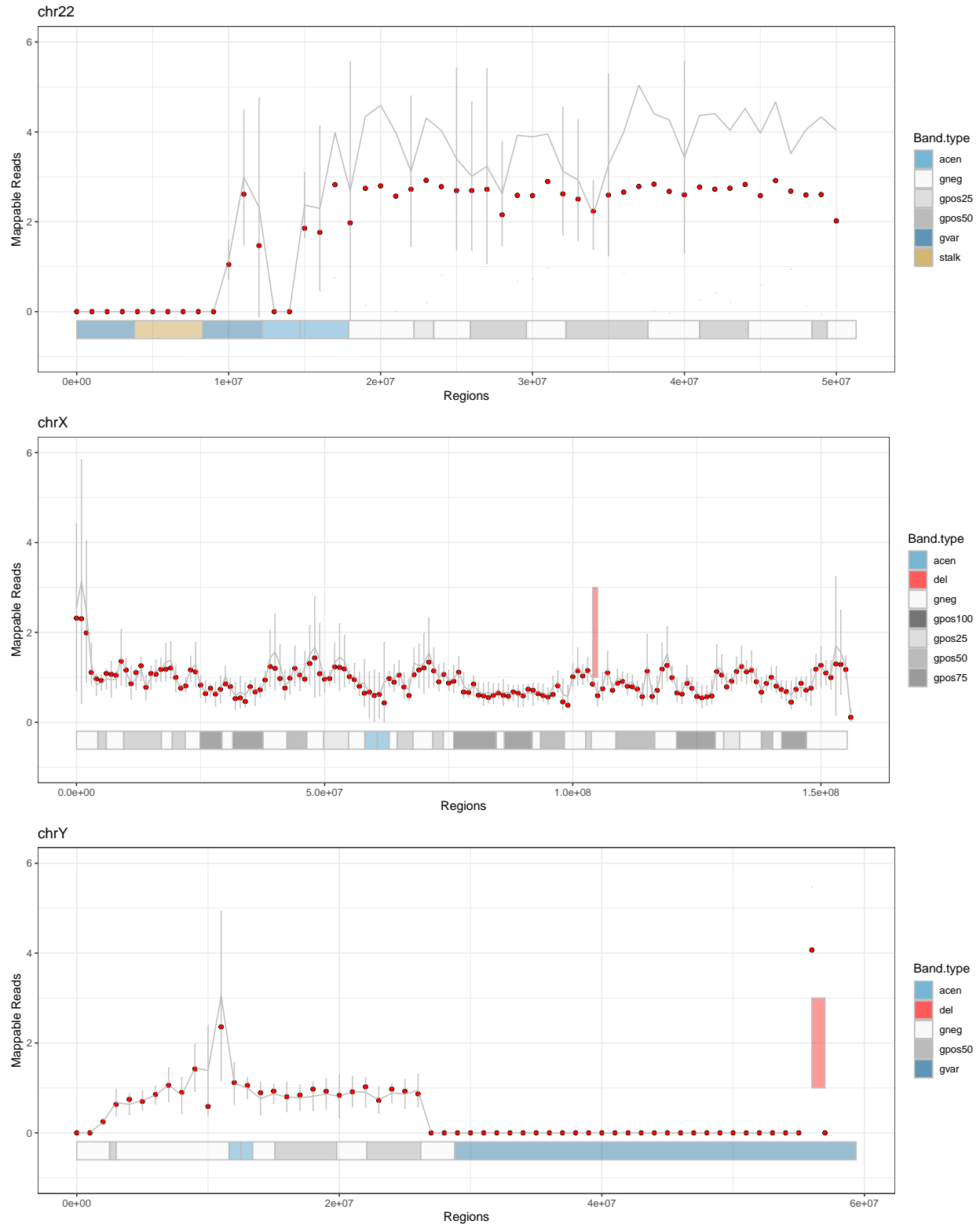












The legend contains two characteristics:

1. Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen,

- gvar, stalk.
2. The abnormal regions (add or del).