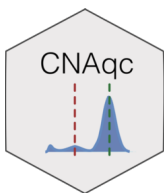


# My Sample

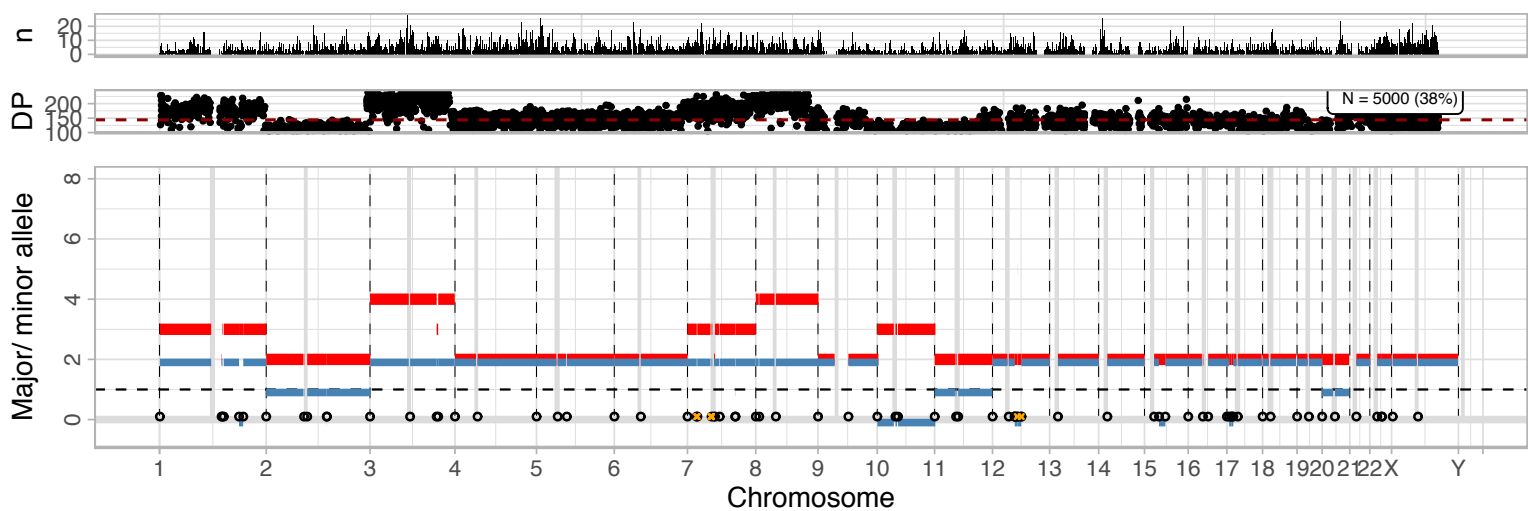
Data quality check (QC) from matched Copy Number and mutation data.

2020-02-19



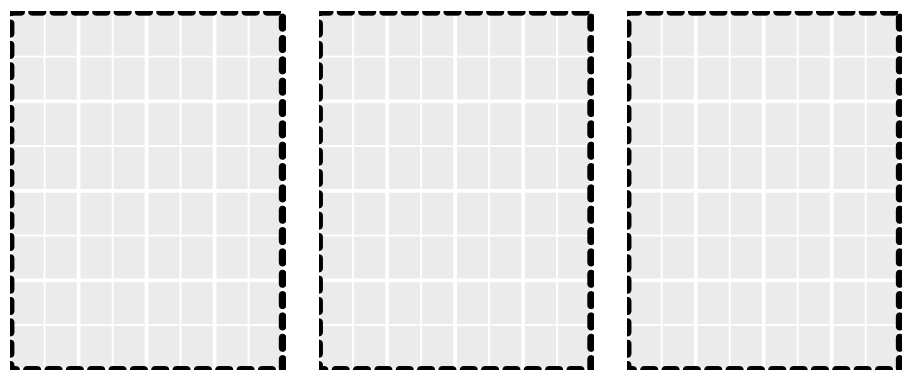
# My Sample

Segments data and purity/ ploidy QC.

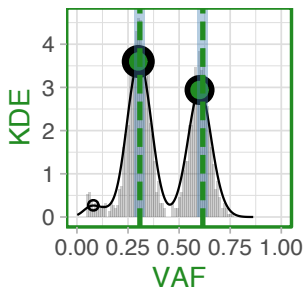


13141 mutations, 87 clonal CNA, 0 subclonal CNA

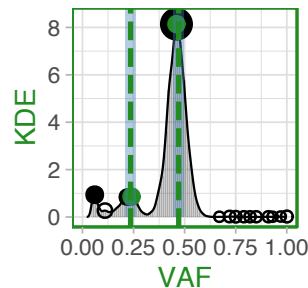
Peak detection for purity 89%



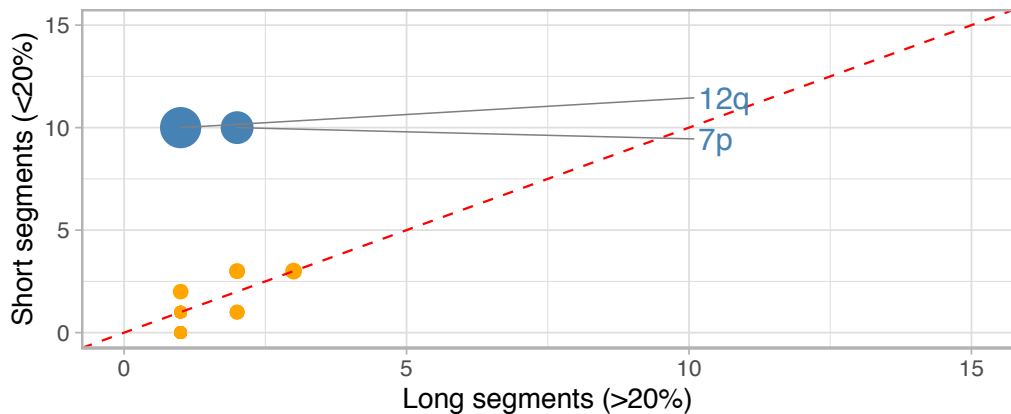
Karyotype 2:1  
w = 0.086 (n = 156)



Karyotype 2:2  
w = 0.414 (n = 7478)



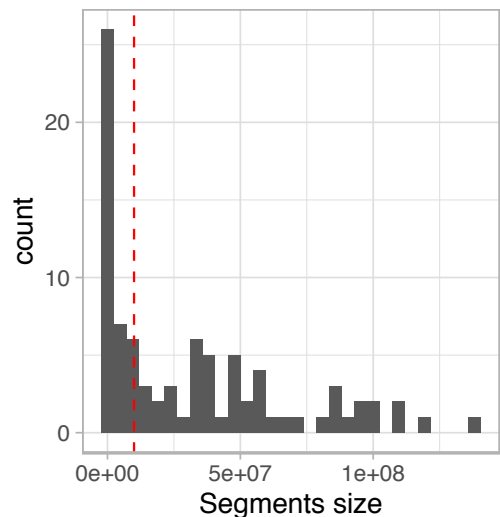
2 overfragmented arms at  $\alpha = 0.01$  with FWER



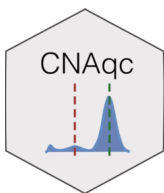
Jump • 0 100 200 300 400

Bonferroni adjusted alpha = 0.005~ 2 significant tests.

Segments size distribution



Dashed line: 1e+07



# My Sample

Cancer Cell Fractions data

Cancer Cell Fractions (estimated)

