



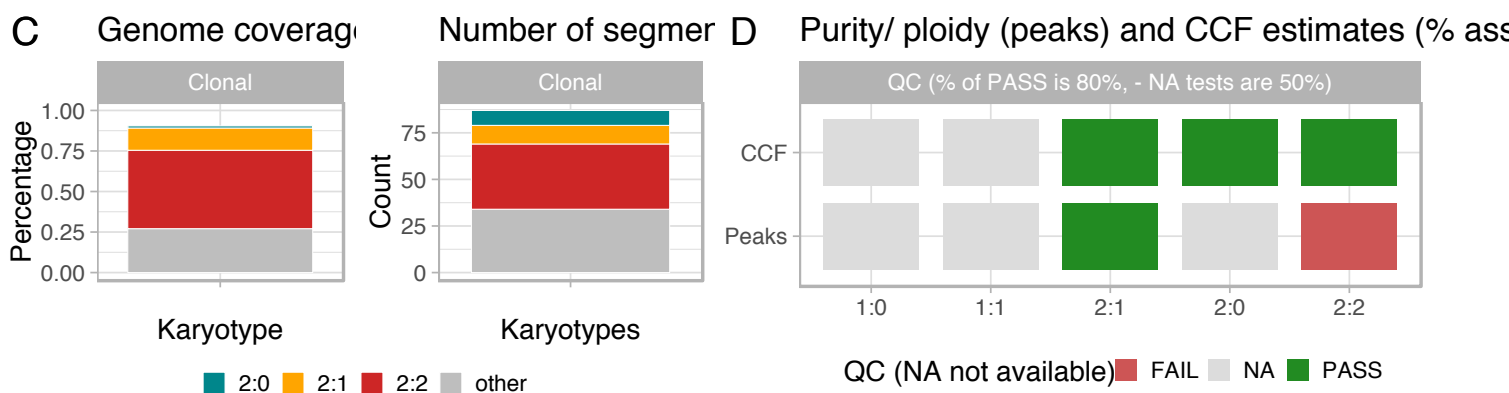
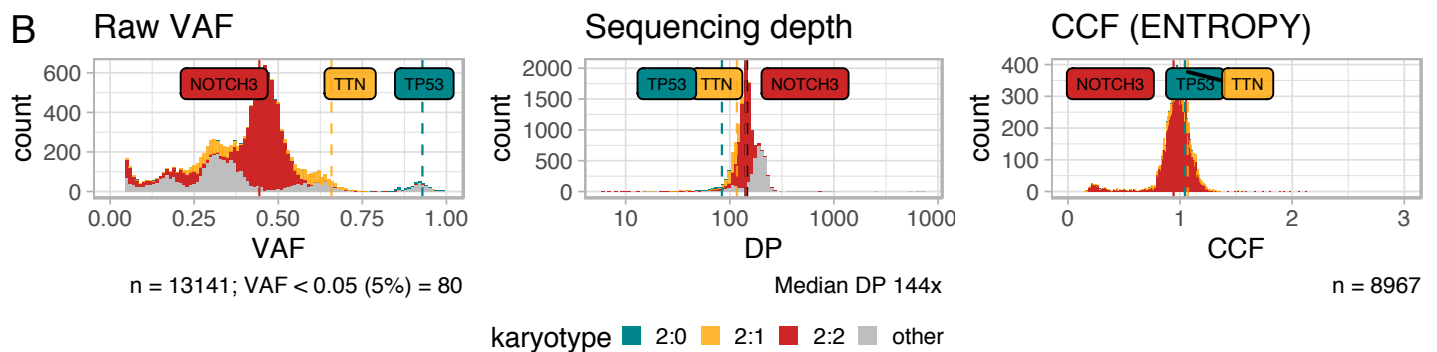
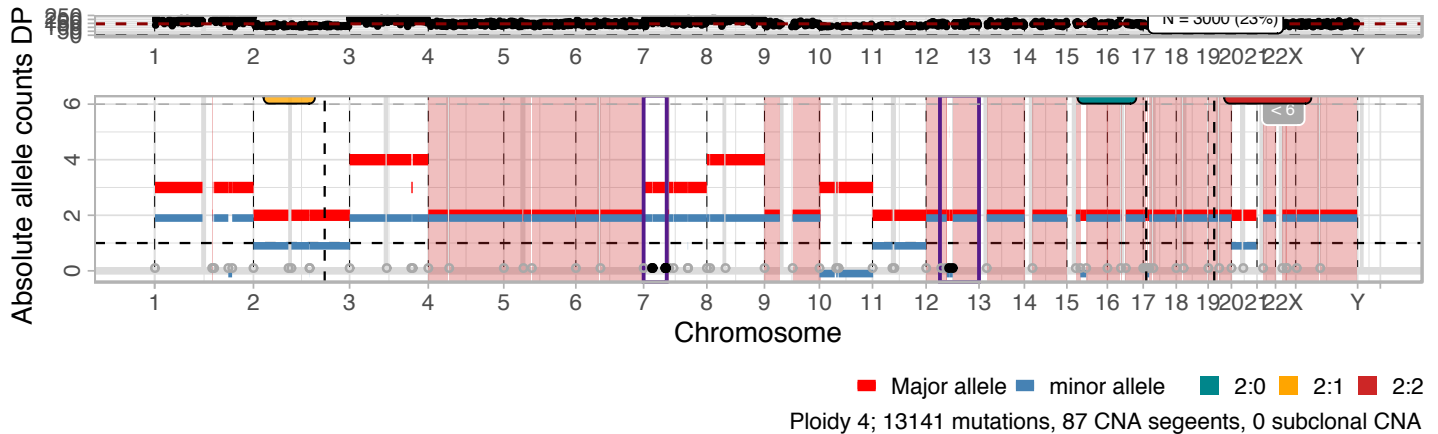
S

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



PASS rate 13

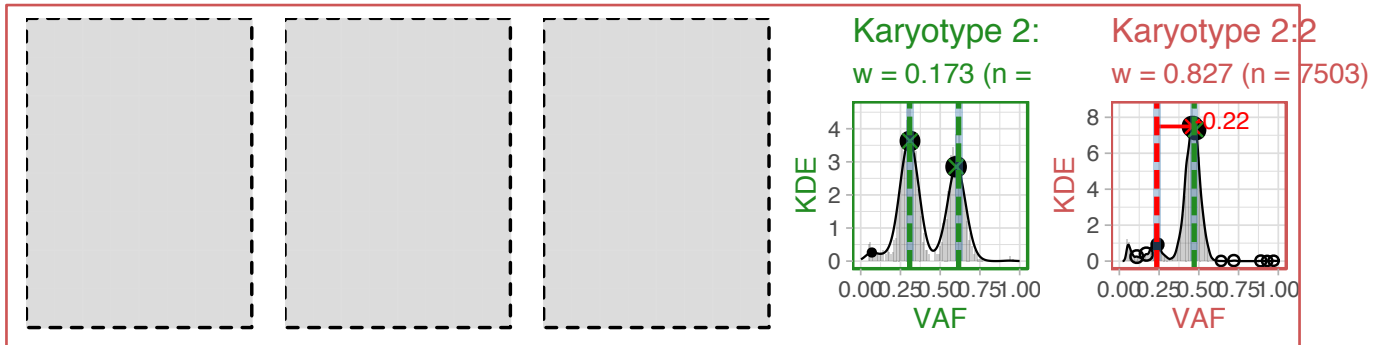
## A Ploidy 4, most prevalent karyotype is 2:2 (Major:minor).



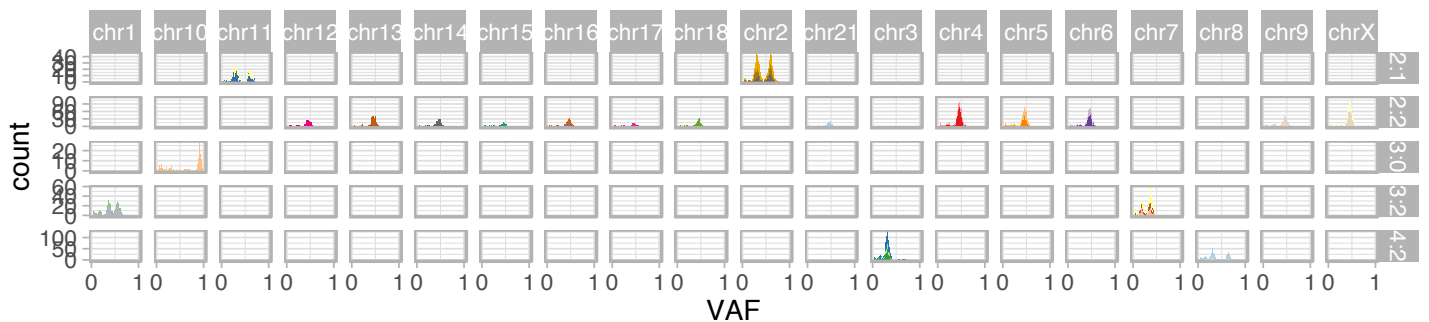
# S

Purity/ ploidy QC (A), data (B) and fragmentation (C).

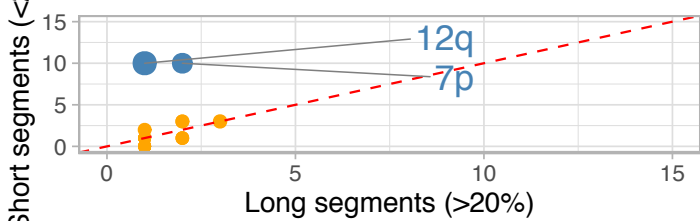
## A Purity and ploidy QC via peak detection (purity $p = 89\%$ )



## B Segments with $>131.41$ mutations (1% of total) and $>2129860$ bases (10% of median length)



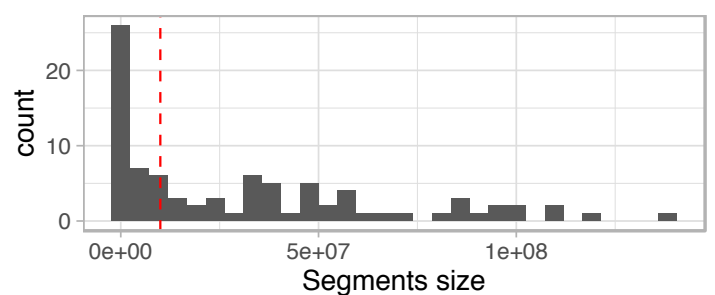
## Arm-level segments fragmentation (% relative)



Jump • 0 • 100 • 200 • 300 • 400

Bonferroni adjusted alpha = 0.005~ 2 significant tests.

## Segments size distribution



QC PASS (per karyotype) if we can assign >90% of mutation burden

