

Golden_C_DB

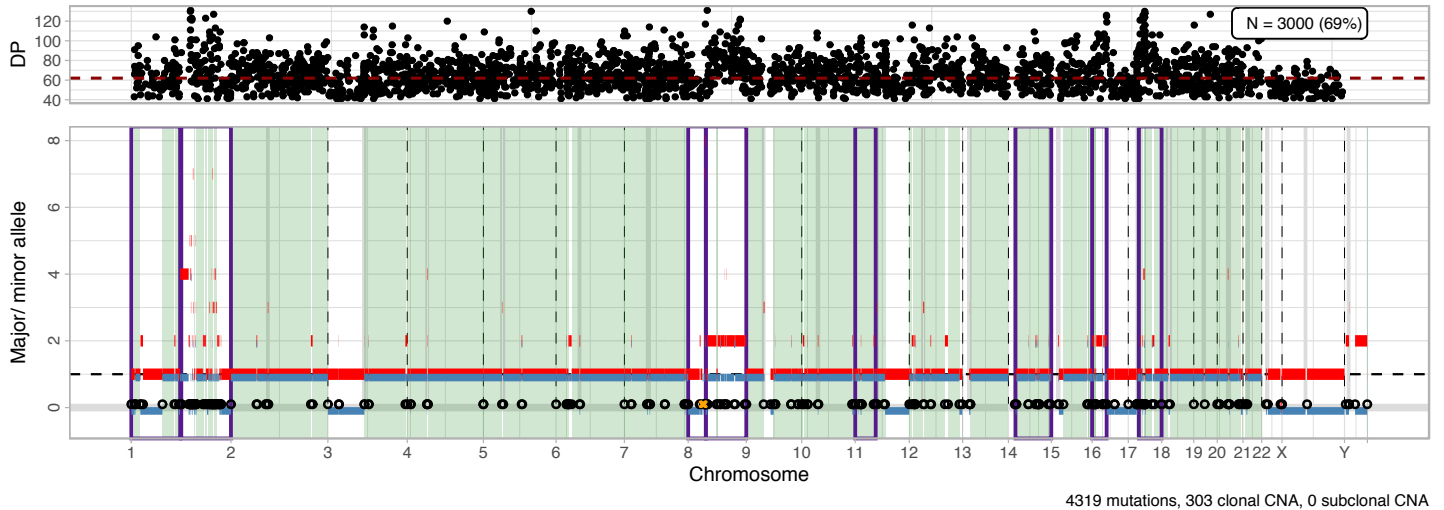
Data quality check (QC) from matched Copy Number and mutation data.

PASS rate 50

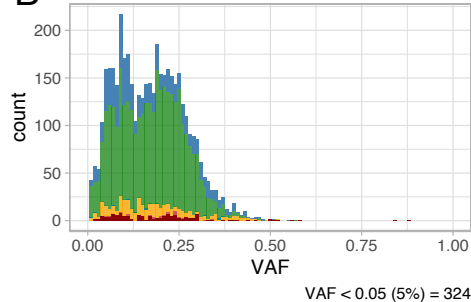
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CNA Segments (A), mutations (B), genome coverage (C) and QC (D).

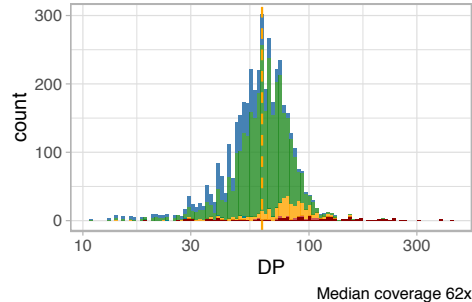
A Ploidy 2, most prevalent karyotype is 1:1 (Major:minor).



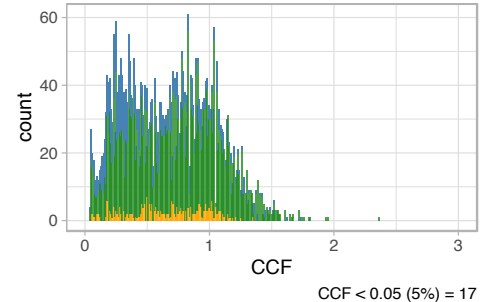
B Raw VAF



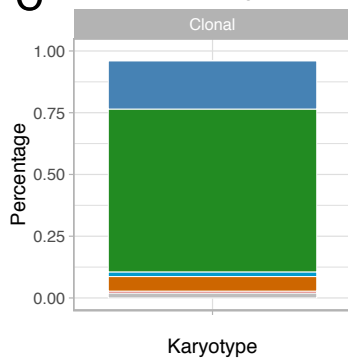
Sequencing depth (coverage)



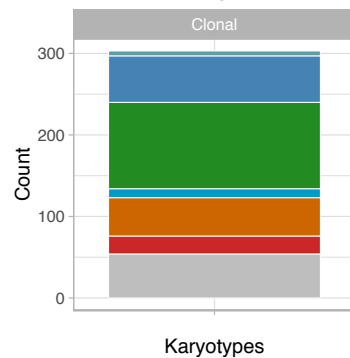
CCF values



C Genome coverage



Number of segments



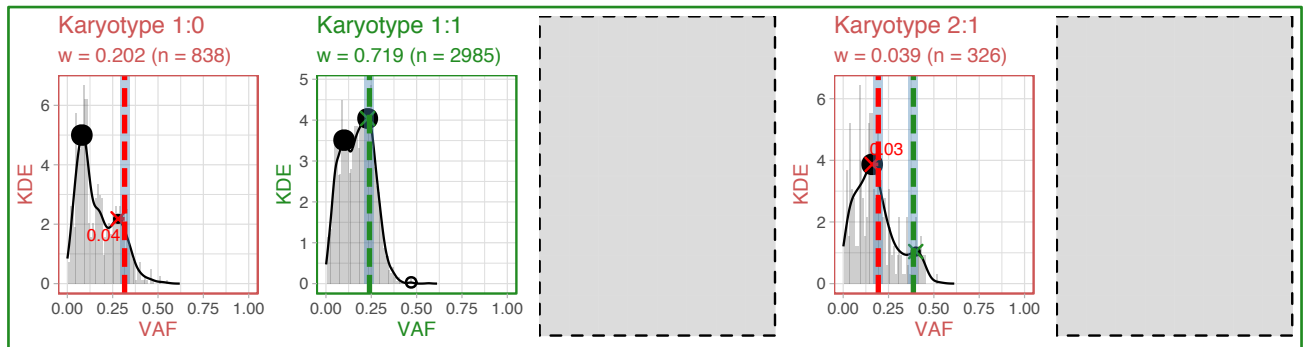
D Purity/ ploidy (peaks) and CCF estimates (% assignable)



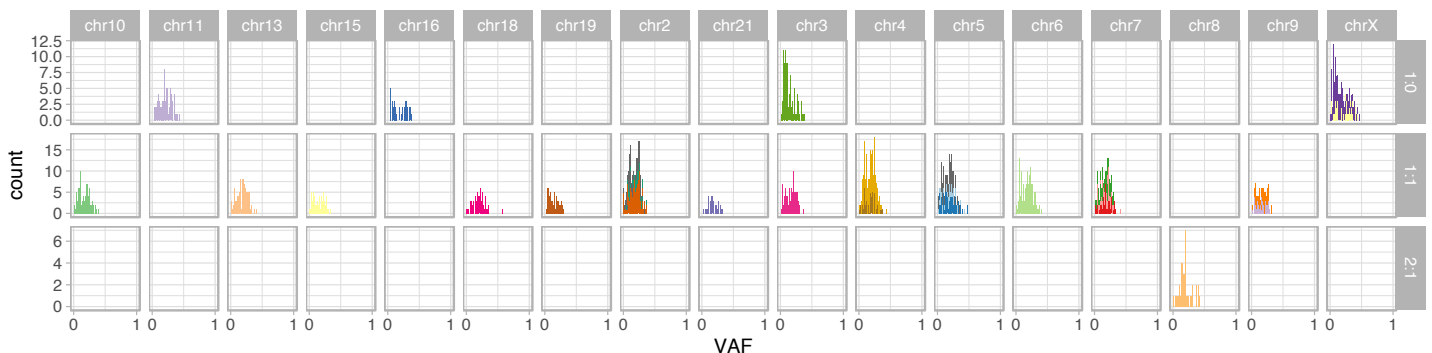
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Purity/ ploidy QC (A), data (B) and fragmentation (C).

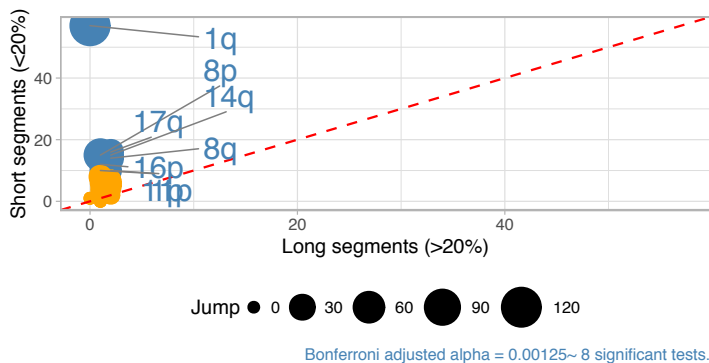
A Purity and ploidy QC via peak detection (purity $p = 48\%$)



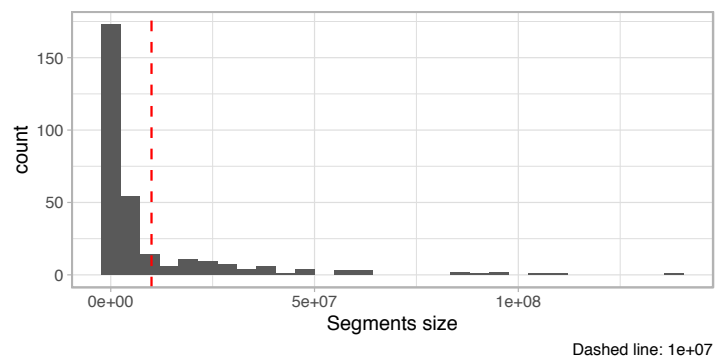
B Segments with >43.19 mutations (1% of total) and >167394.9 bases (10% of median length)



C Arm-level segments fragmentation (% relative to arm length)



Segments size distribution



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Cancer Cell Fractions estimation and QC.

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

