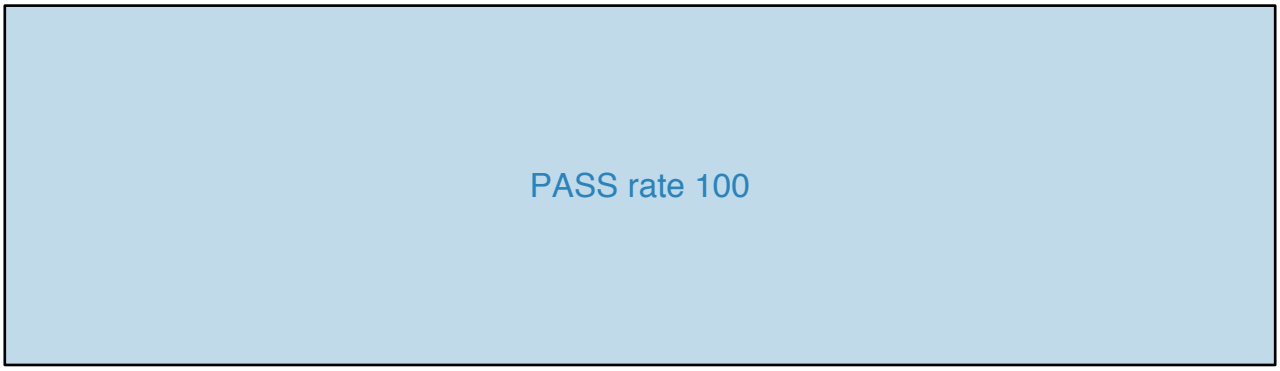
MyPAT00XX1

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



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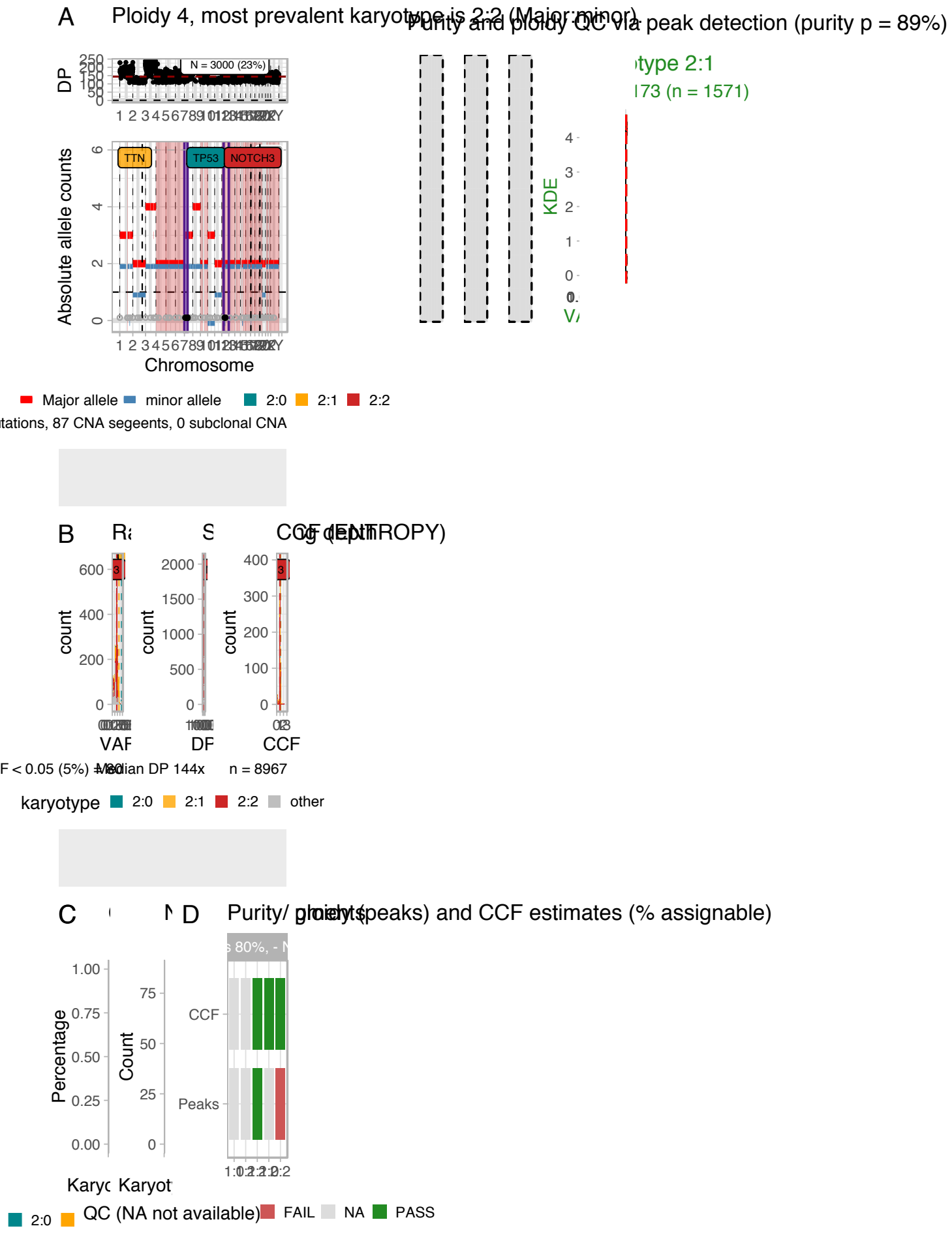
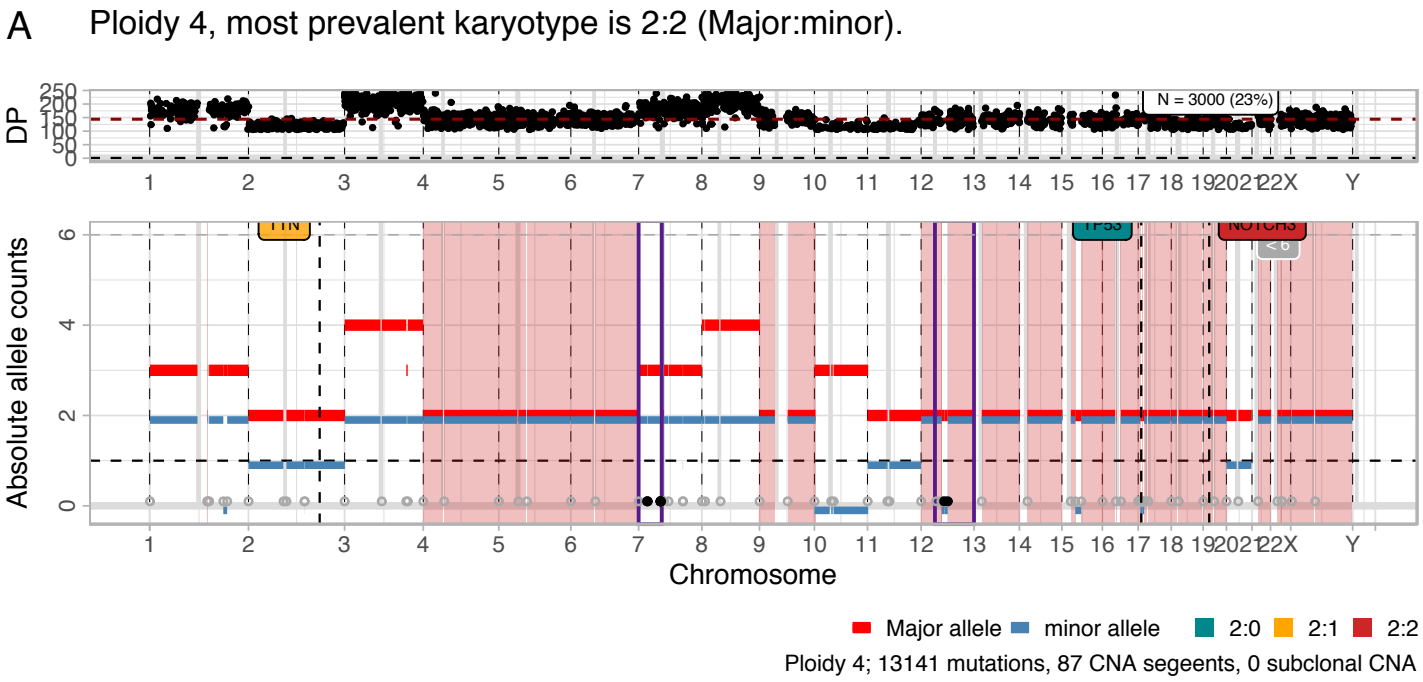
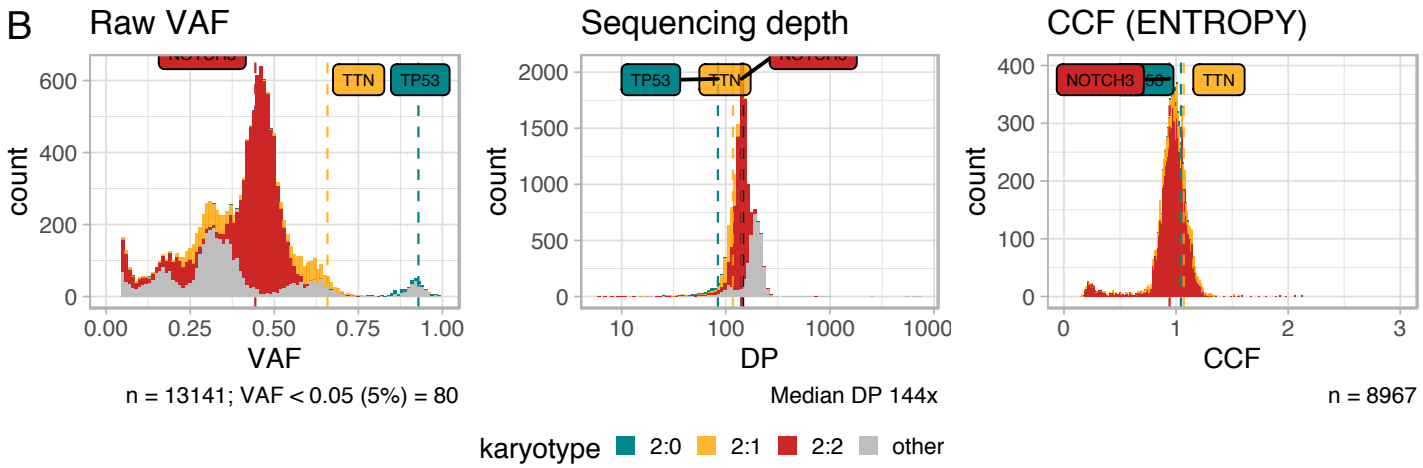
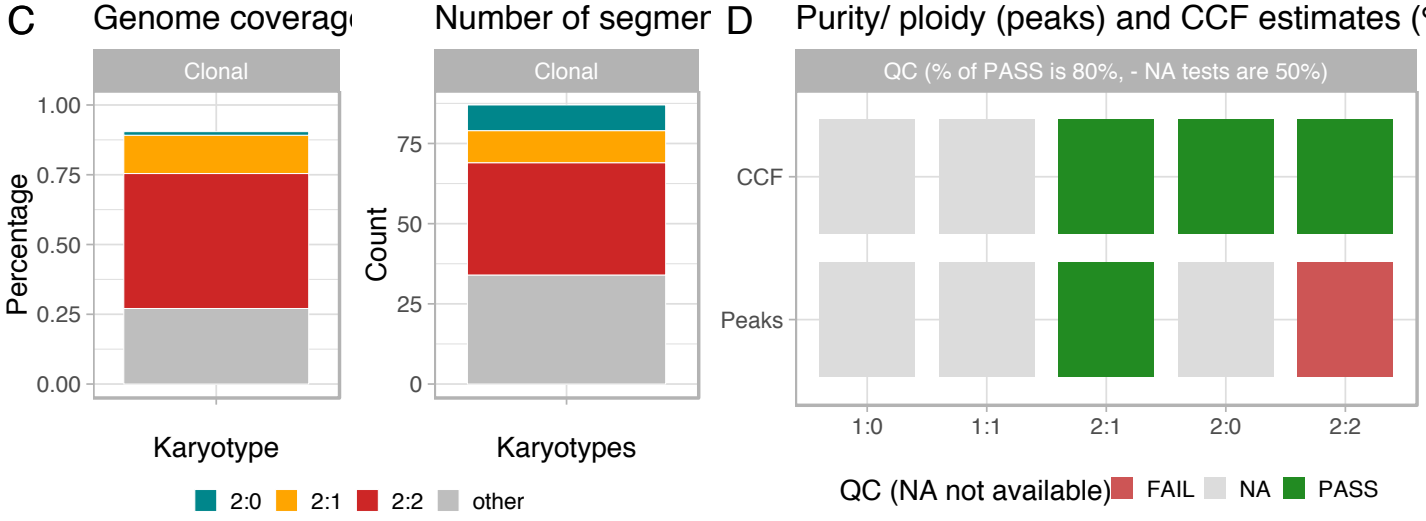
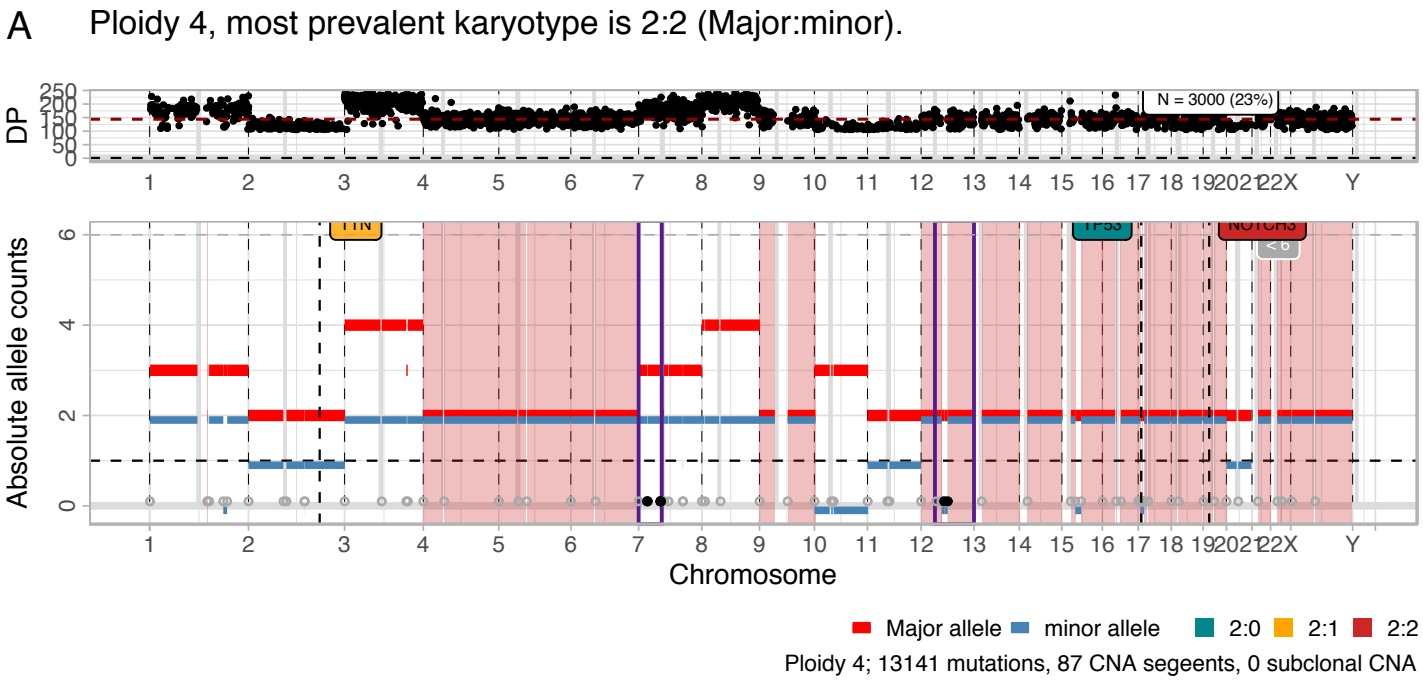



A
Ploidy 4, most prevalent karyotype is 2:2 (Major:minor).
DP
N = 3000 (23%)
Absolute allele counts
Chromosome
Major allele
minor allele
2:0
2:1
2:2
Ploidy 4; 13141 mutations, 87 CNA segeents, 0 subclonal CNA


B
Raw VAF
TTN
TP53
count
VAF
n = 13141; VAF < 0.05 (5%) = 80
Sequencing depth
DP
Median DP 144x
CCF (ENTROPY)
NOTCH3
CCF
n = 8967
karyotype
2:0
2:1
2:2
other


C
Genome coverag
Number of segmer
Clonal
Percentage
Count
Karyotype
Karyotypes
2:0
2:1
2:2
other
D
Purity/ ploidy (peaks) and CCF estimates (% ass
QC (% of PASS is 80%, - NA tests are 50%)
CCF
Peaks
1:0
1:1
2:1
2:0
2:2
QC (NA not available)
FAIL
NA
PASS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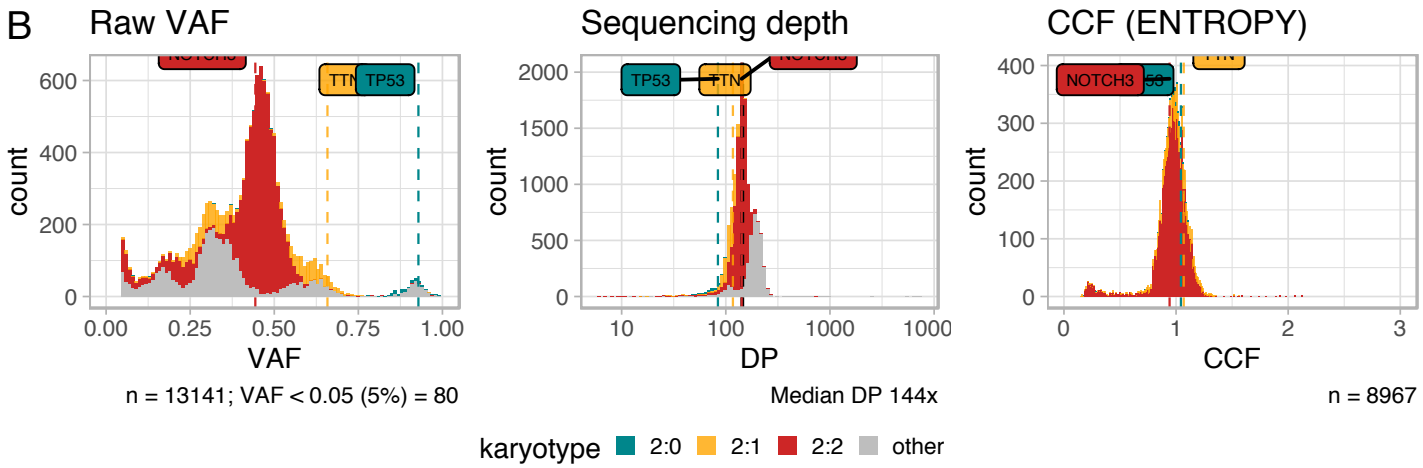
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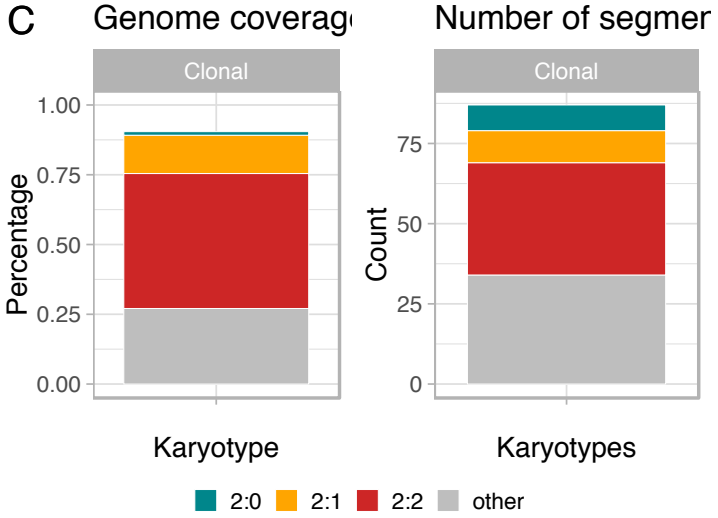
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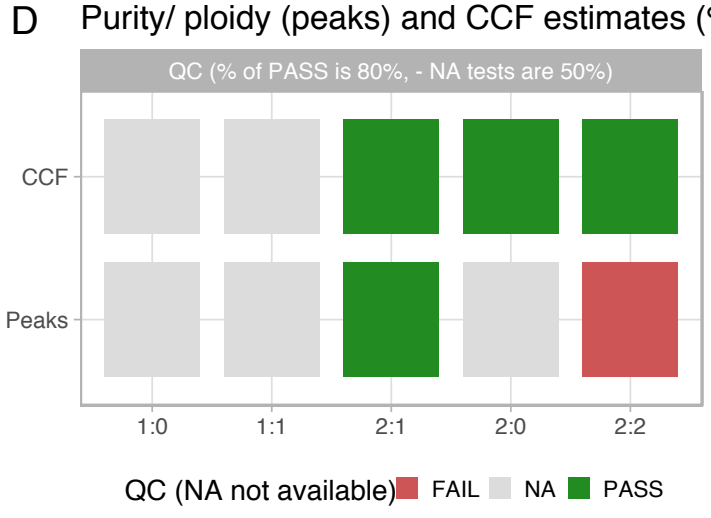
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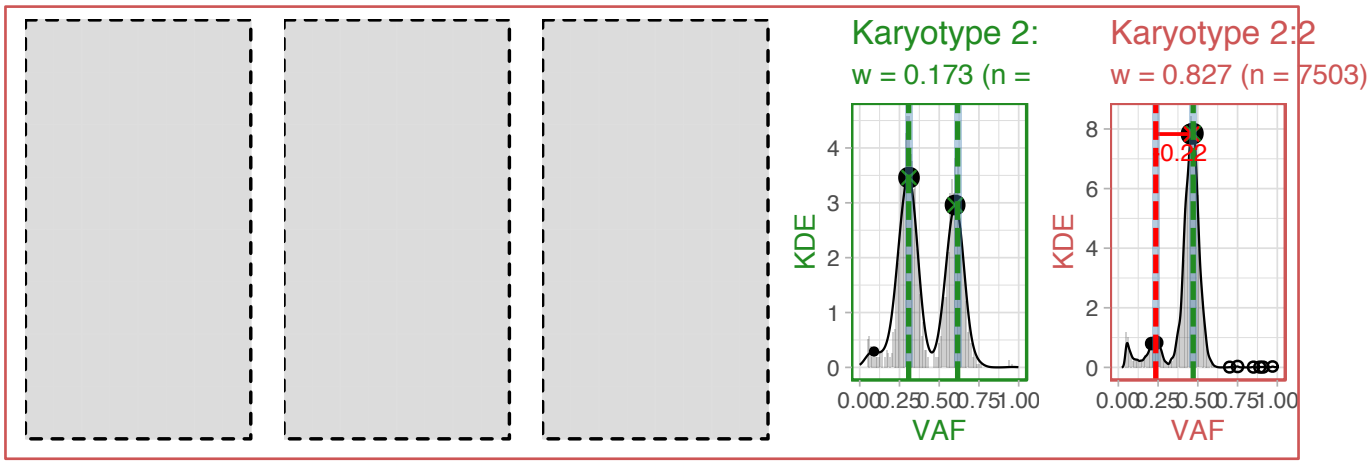
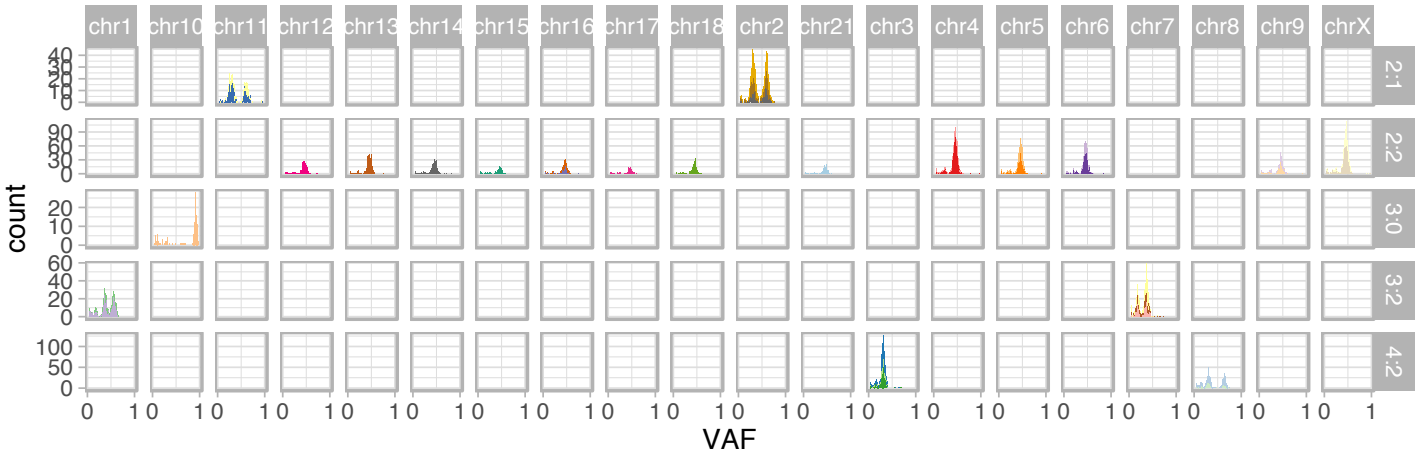
QC (% of PASS is 80%, - NA tests are 50%)
CCF
Peaks
1:0
1:1
2:1
2:0
2:2
QC (NA not available)
FAIL
NA
PASS

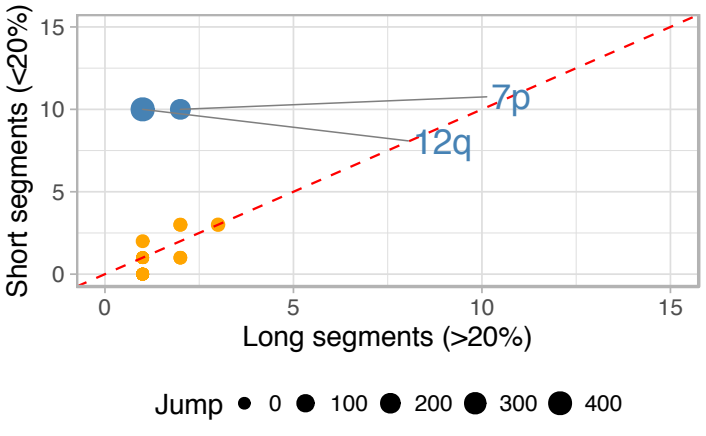
A Purity and ploidy QC via peak detection (purity p = 89%)



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

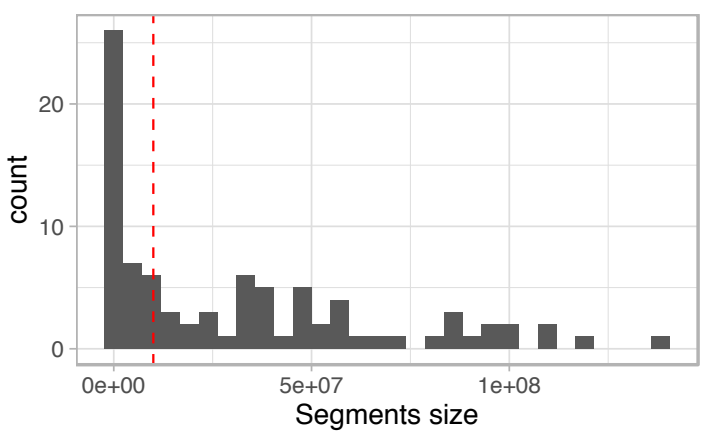


C Arm-level segments fragmentation (% relati



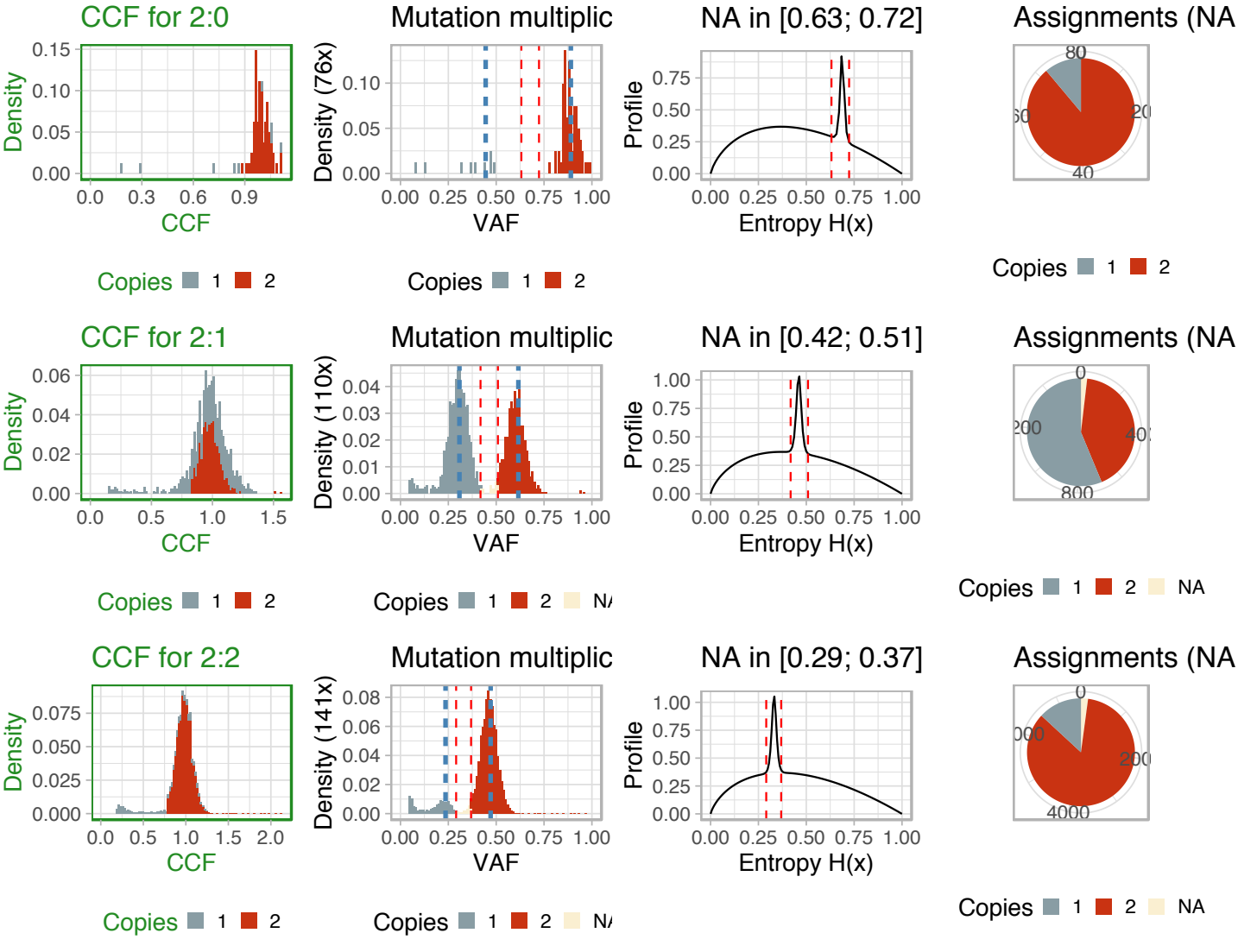
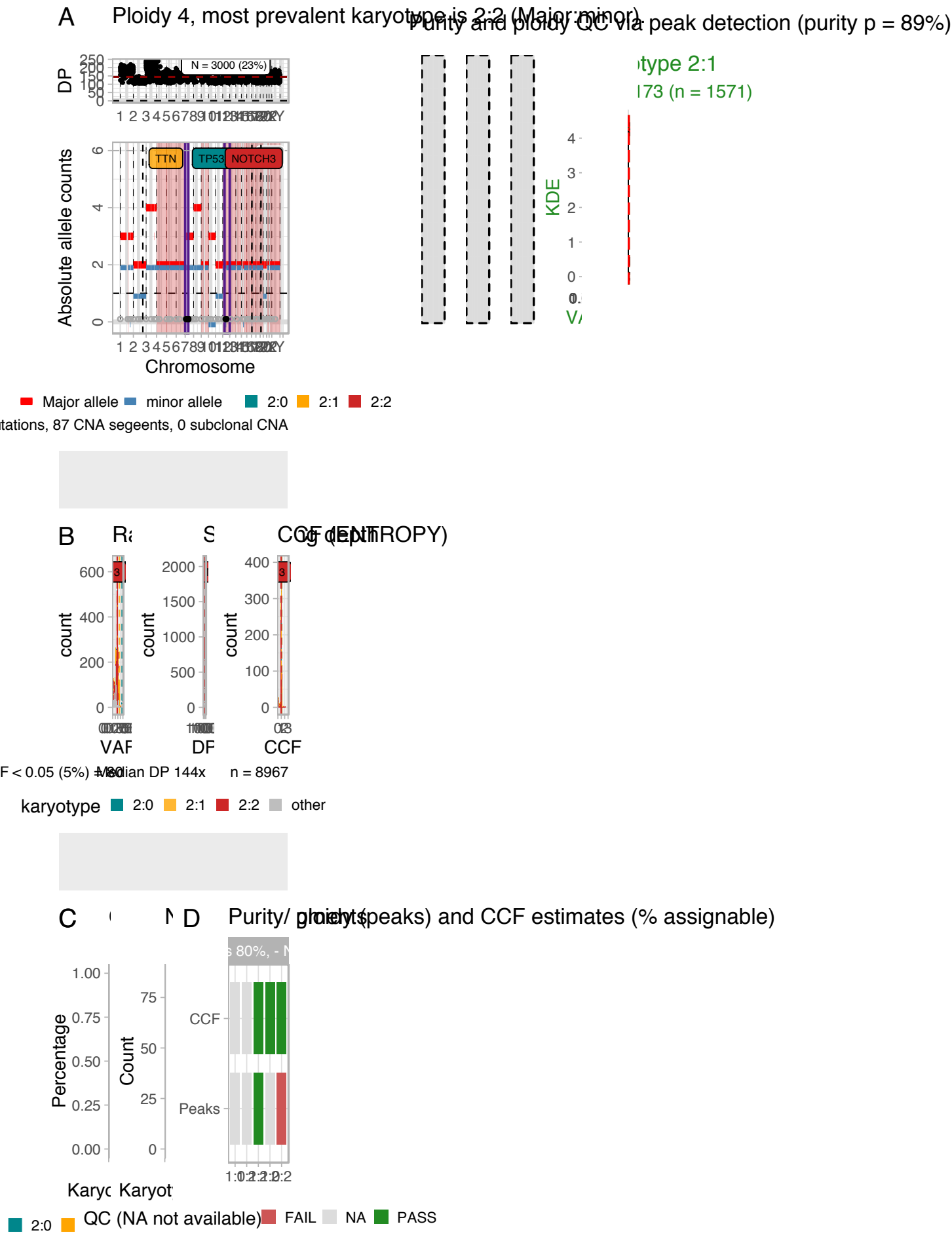
Bonferroni adjusted alpha = 0.005~ 2 significant tests.

Segments size distribution



Dashed line: 1e+07

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