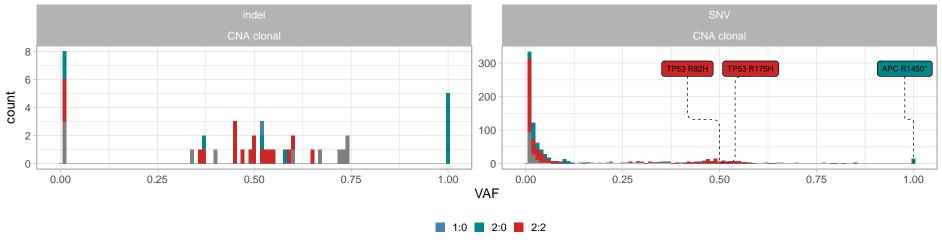
Sample_A

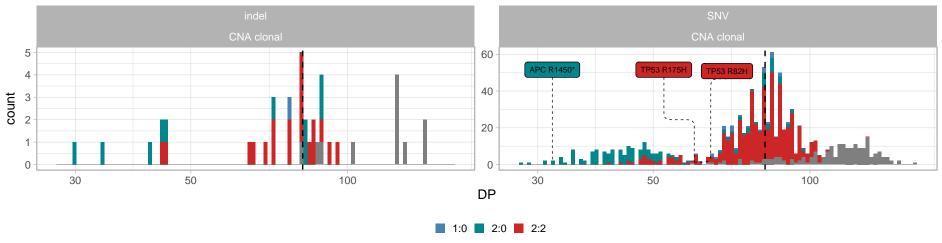
Simulated coverage: 80 Simulated purity: 1 Sequencing Errore rate: 0.001 Tumour type: COAD Germline subject :default

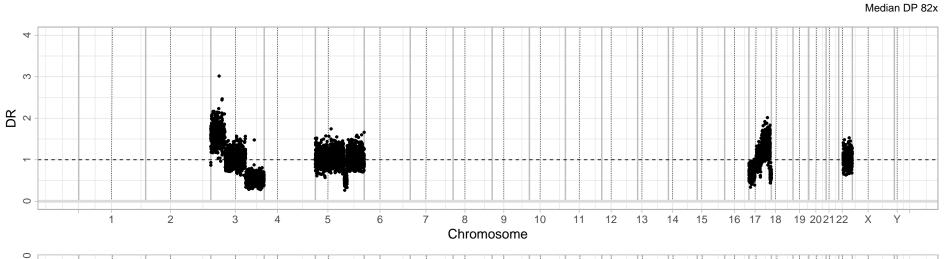
VAF

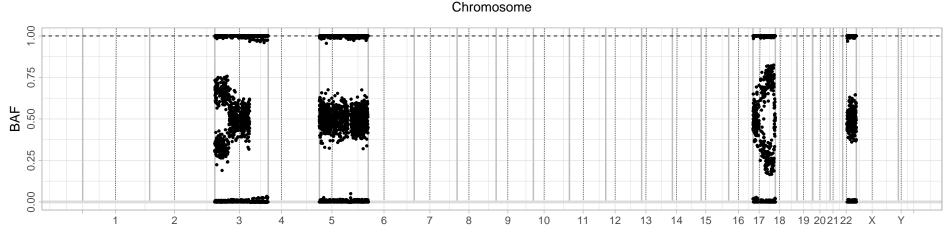


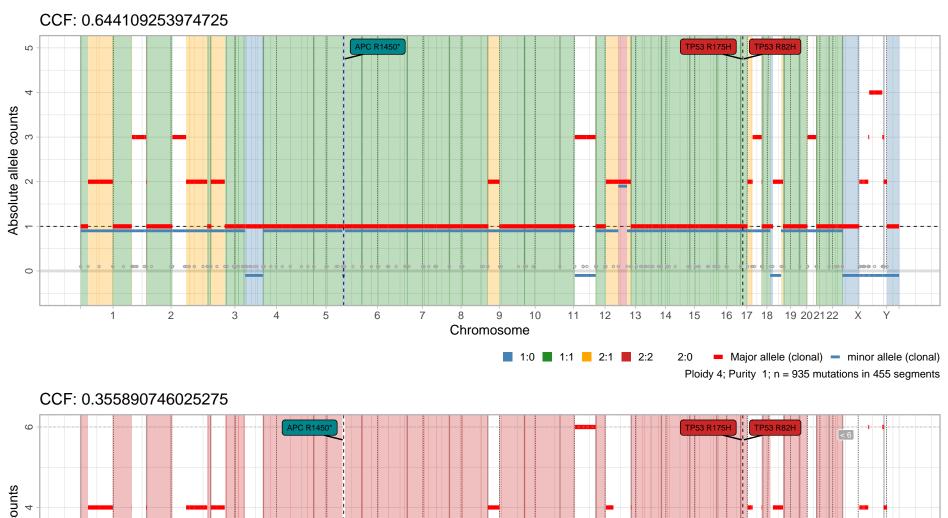
n = 935; VAF < 0.05 (5%) = 582

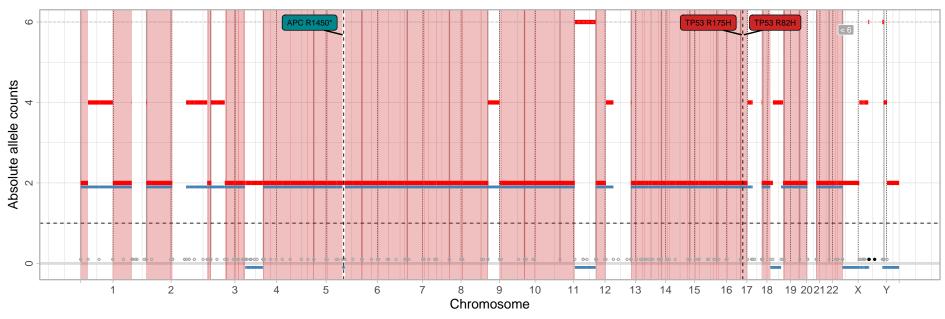
Sequencing depth



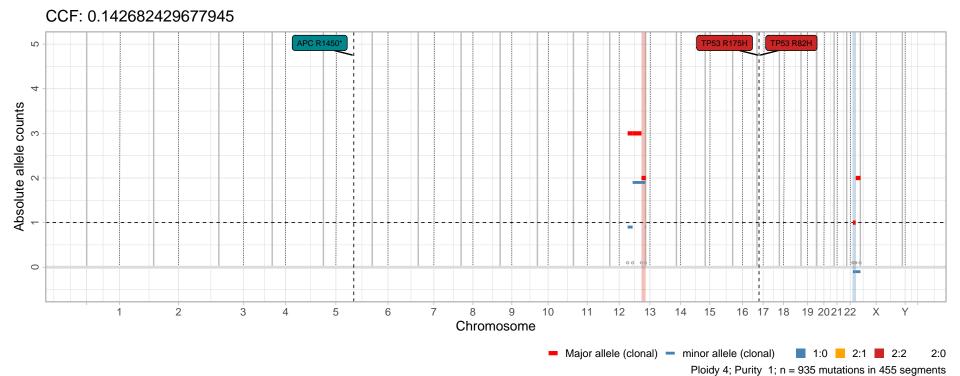








■ Major allele (clonal) ■ minor allele (clonal) ■ 2:2 2:0
Ploidy 4; Purity 1; n = 935 mutations in 455 segments

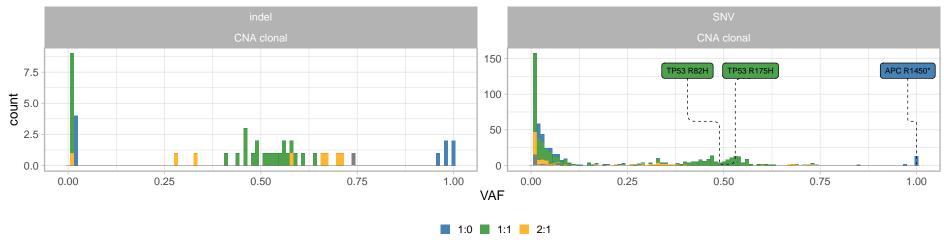


Sample_B

Simulated coverage: 80 Simulated purity: 1

Sequencing Errore rate: 0.001
Tumour type: COAD
Germline subject :default

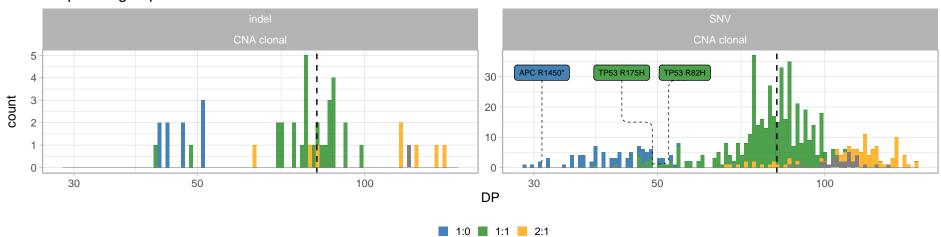
VAF

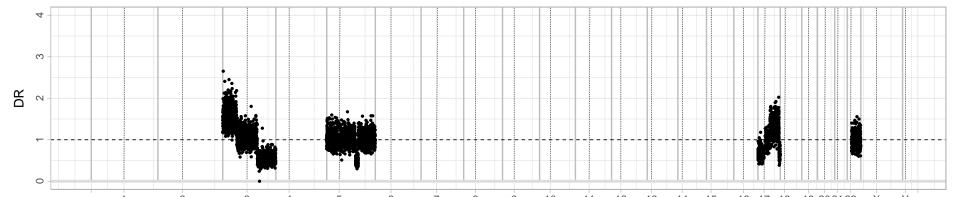


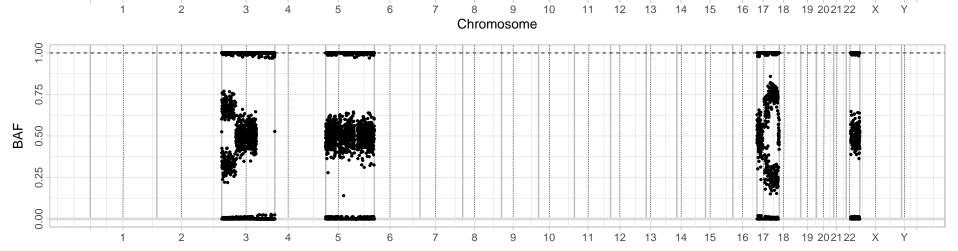
n = 634; VAF < 0.05 (5%) = 304

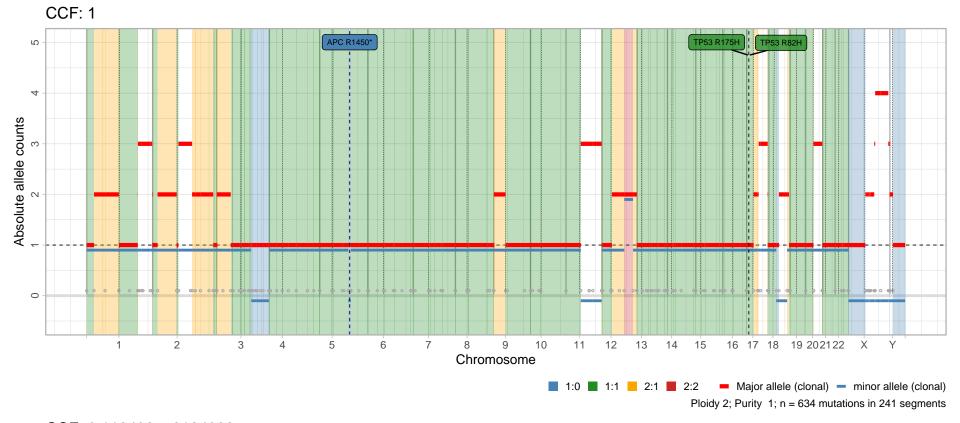
Median DP 82x

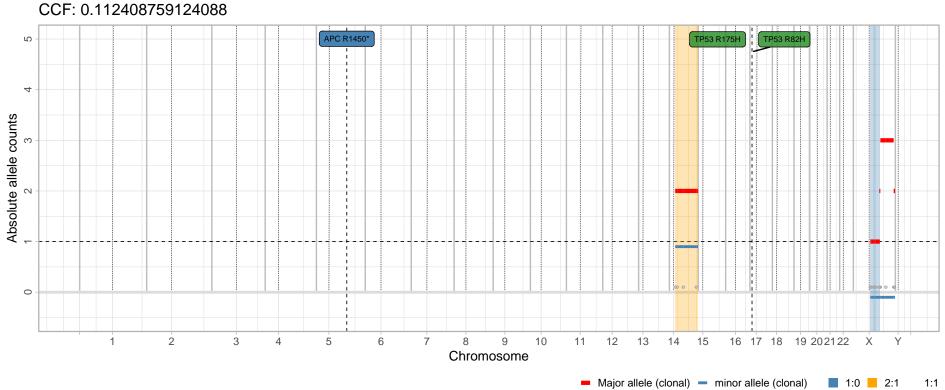
Sequencing depth









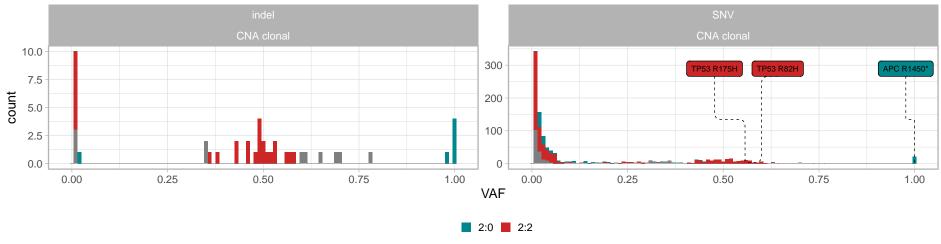


Ploidy 2; Purity 1; n = 634 mutations in 241 segments

Sample_C

Simulated coverage: 80 Simulated purity: 1 Sequencing Errore rate: 0.001 Tumour type: COAD Germline subject :default

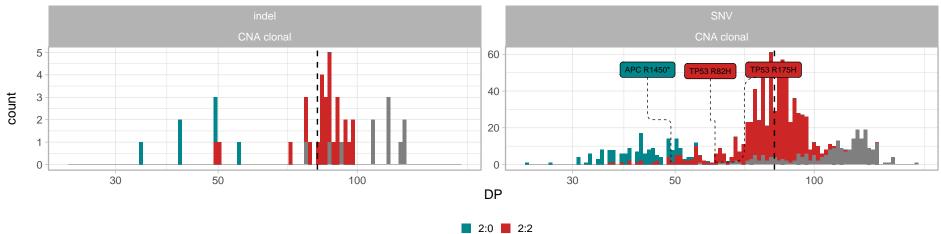
VAF

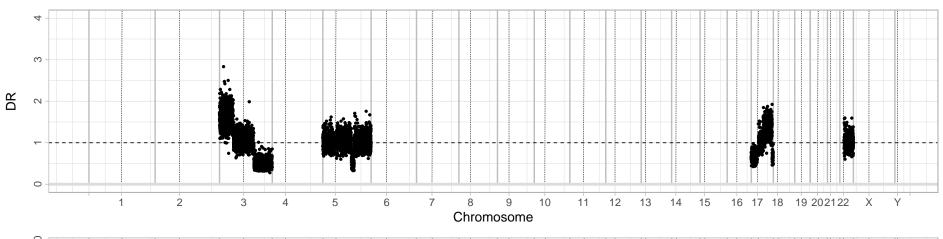


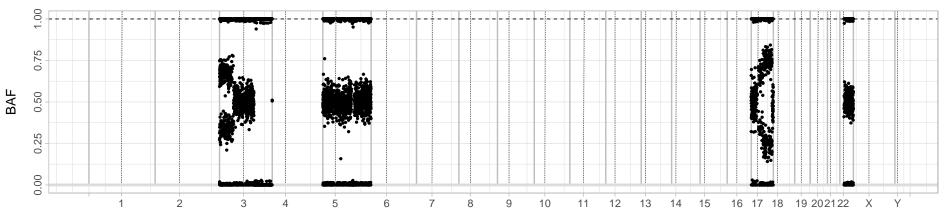
n = 1079; VAF < 0.05 (5%) = 662

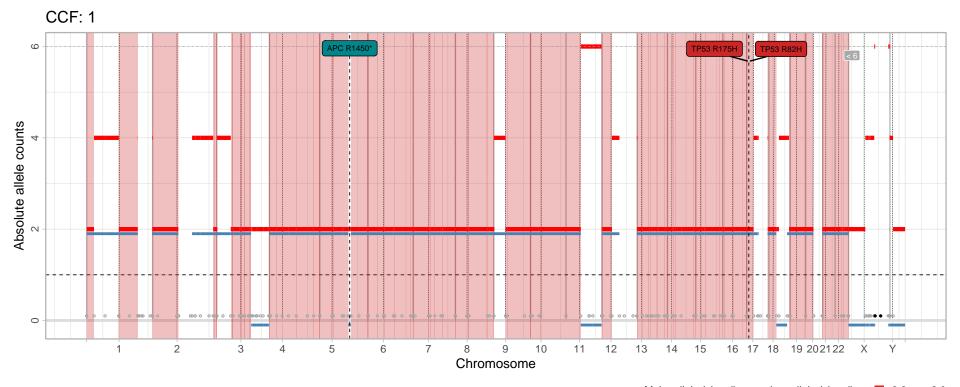
Median DP 82x

Sequencing depth

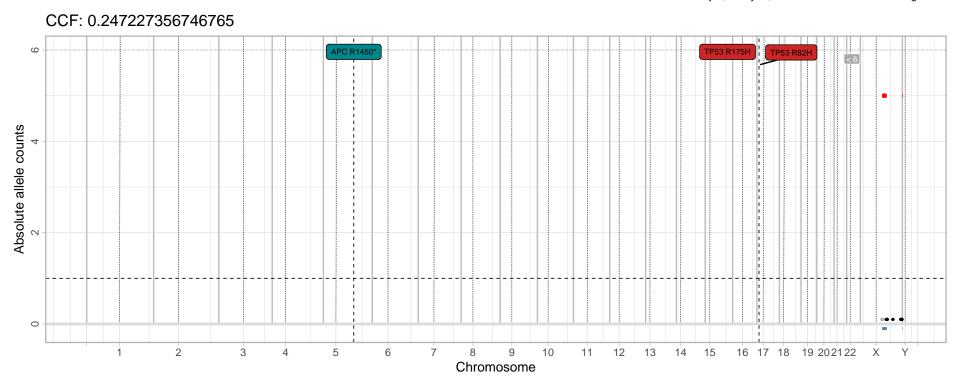








■ Major allele (clonal) ■ minor allele (clonal) ■ 2:2 2:0
Ploidy 4; Purity 1; n = 1079 mutations in 235 segments



Major allele (clonal) — minor allele (clonal)
 Ploidy 4; Purity 1; n = 1079 mutations in 235 segments