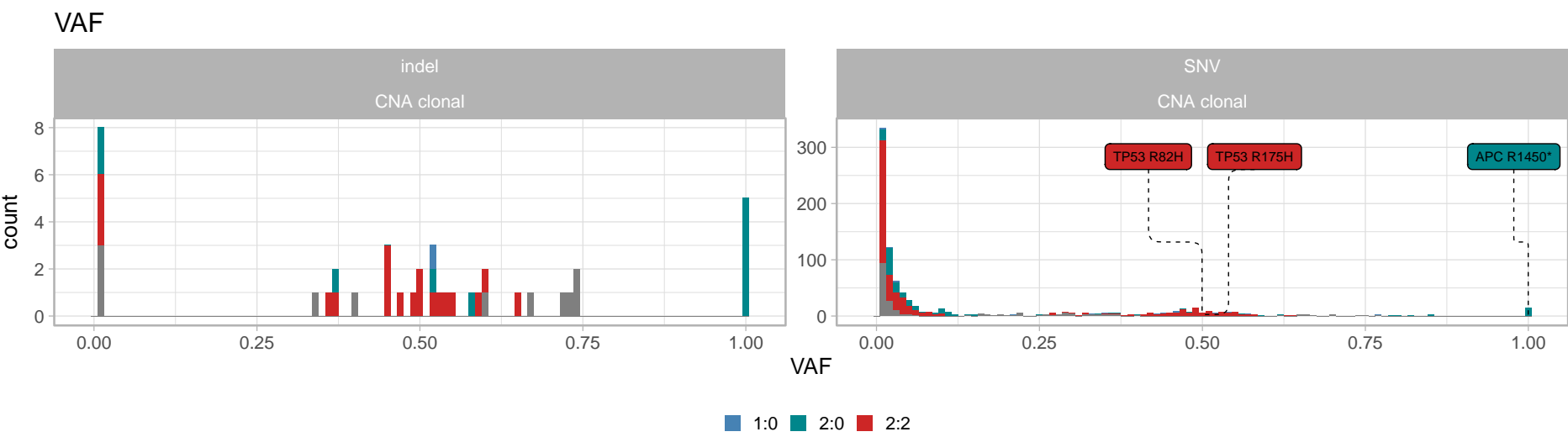
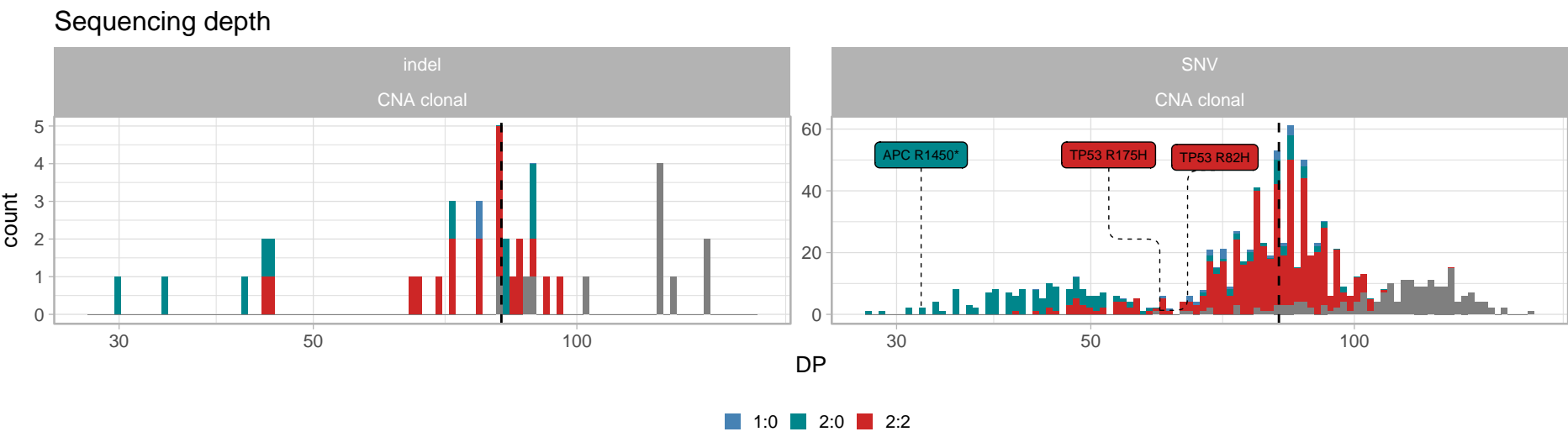


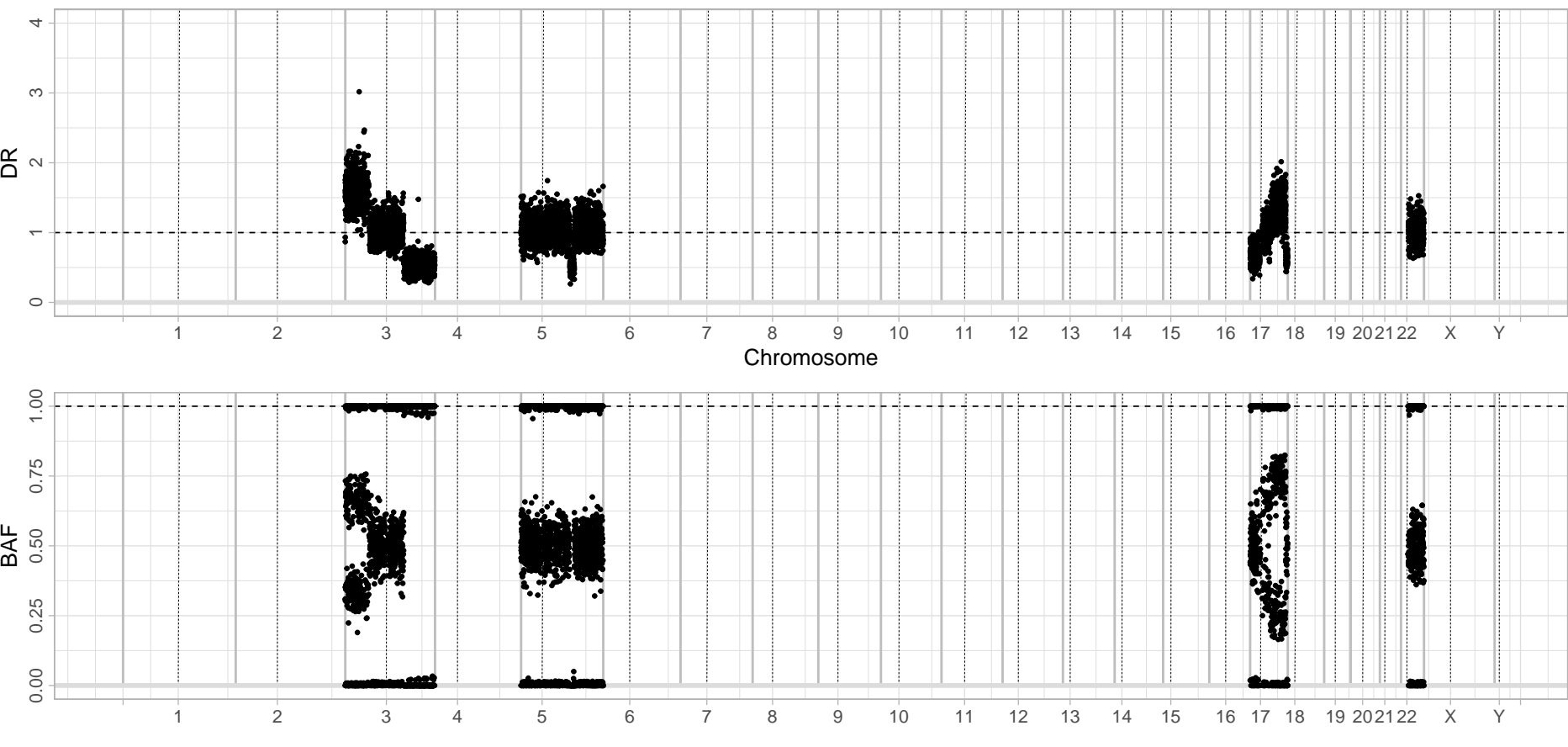
Sample_A
Simulated coverage: 80
Simulated purity: 1
Sequencing Error rate: 0.001
Tumour type: COAD
Germline subject :default



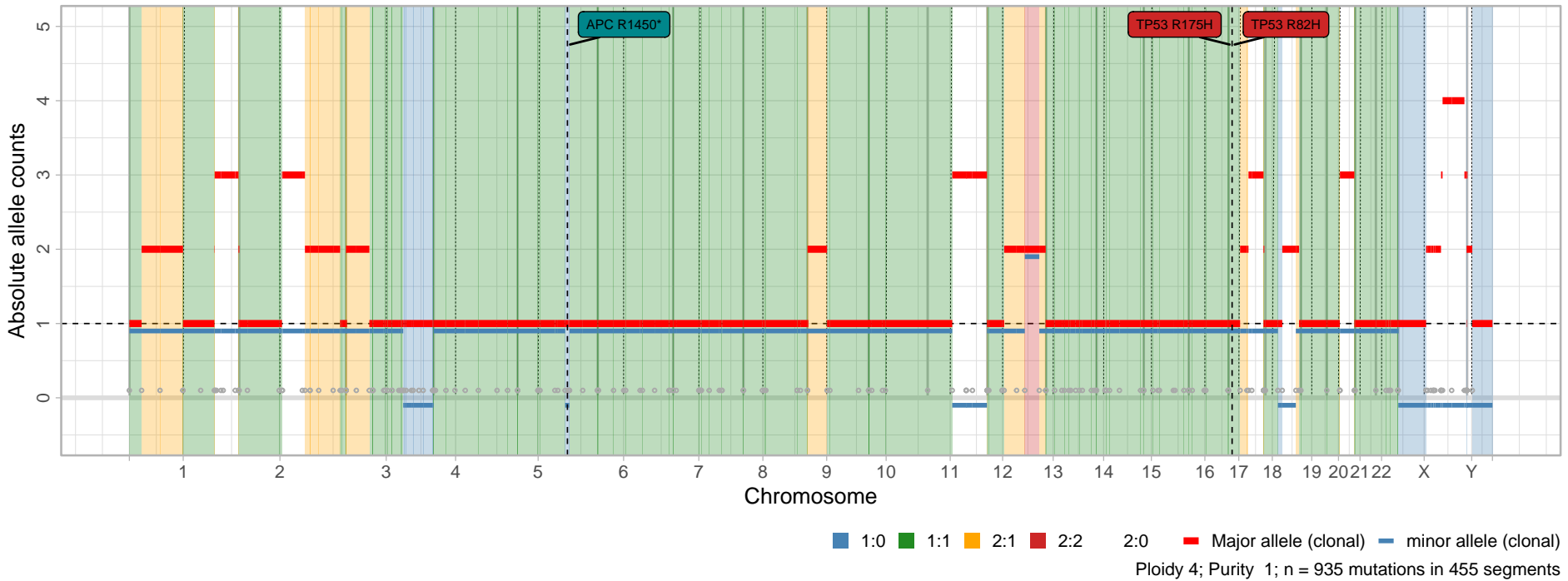
n = 935; VAF < 0.05 (5%) = 582



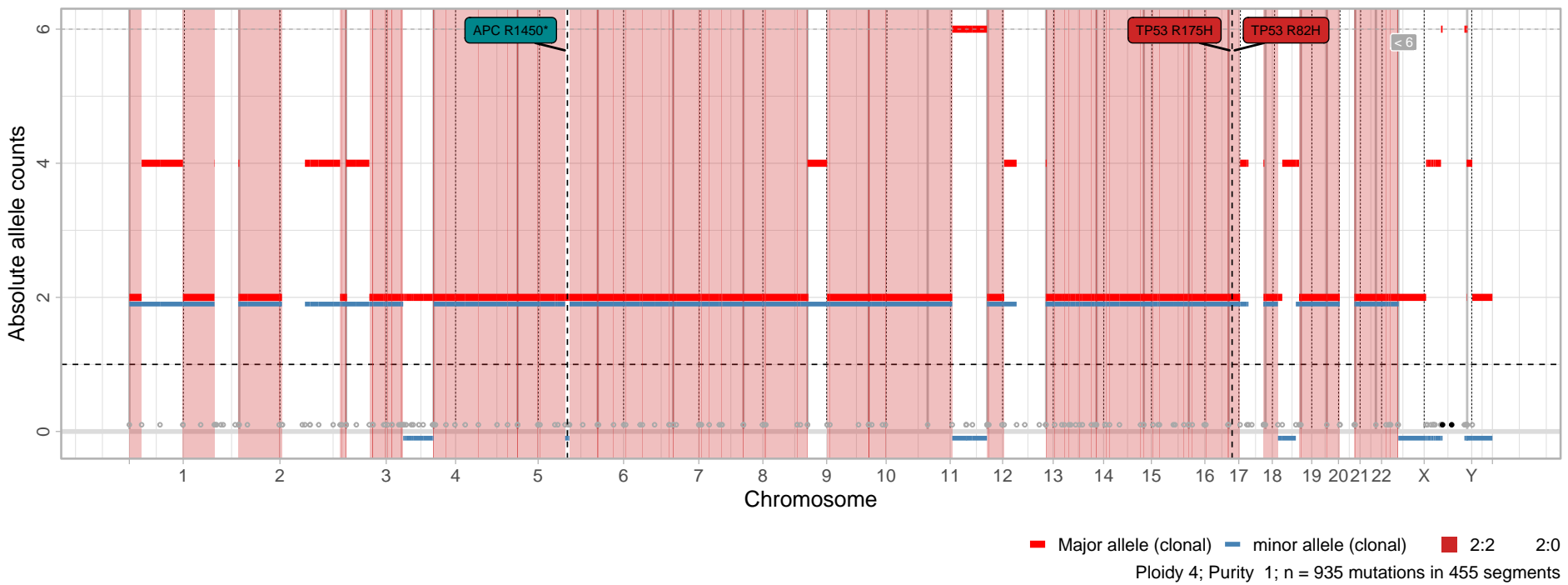
Median DP 82x



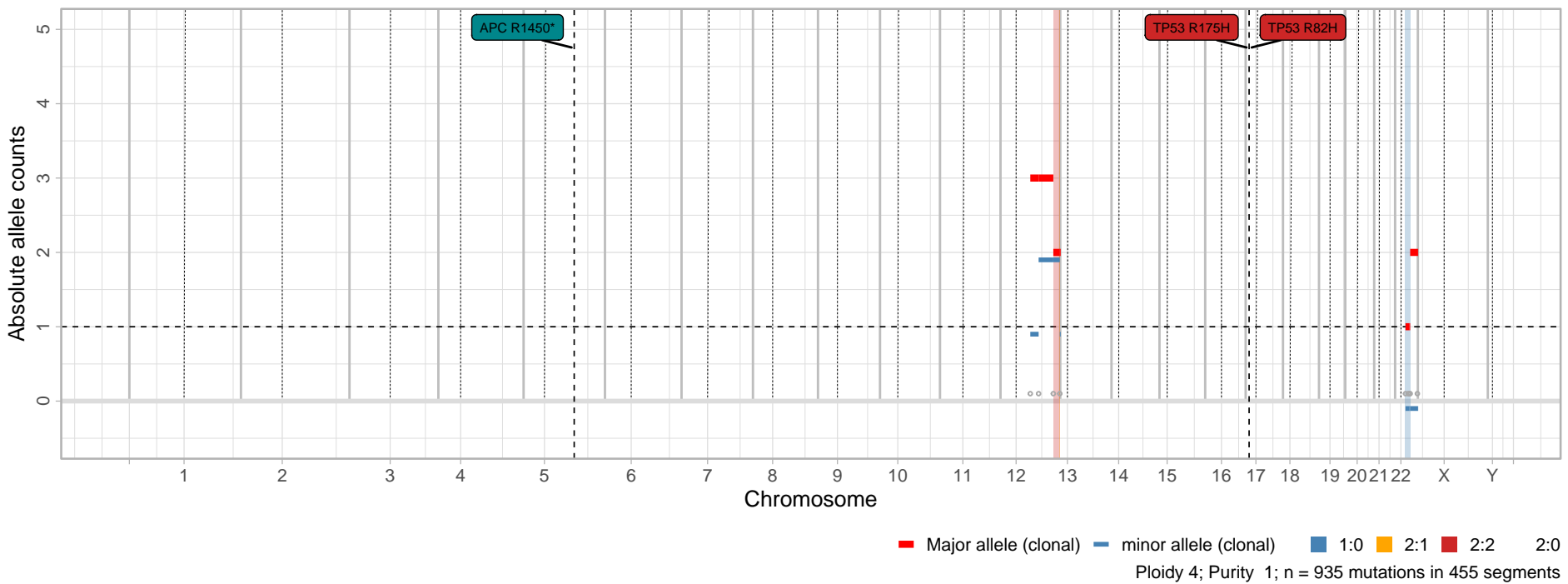
CCF: 0.644109253974725



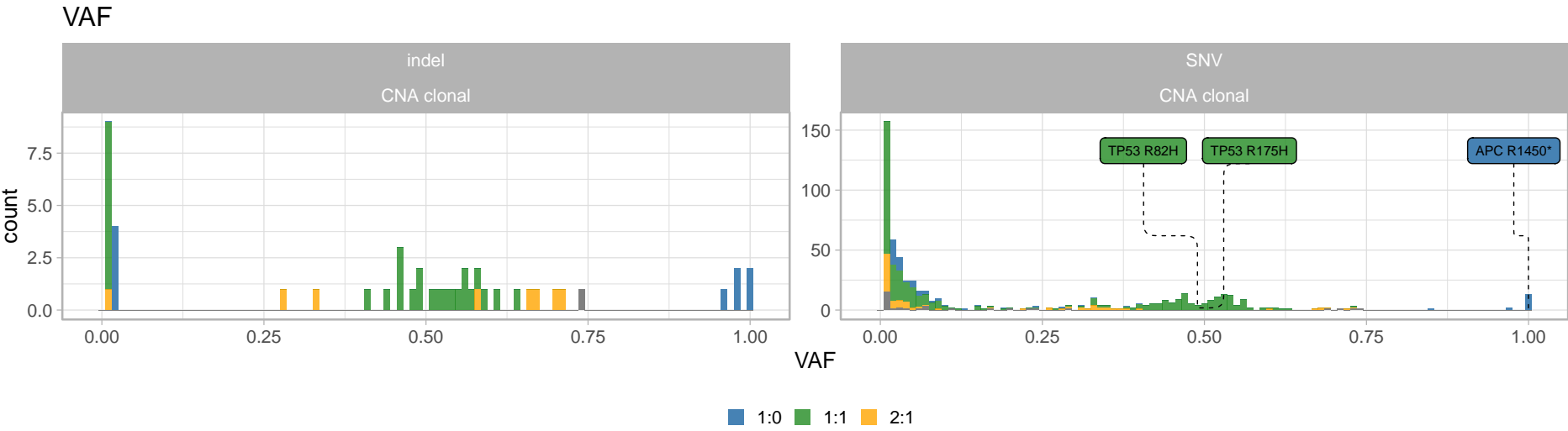
CCF: 0.355890746025275



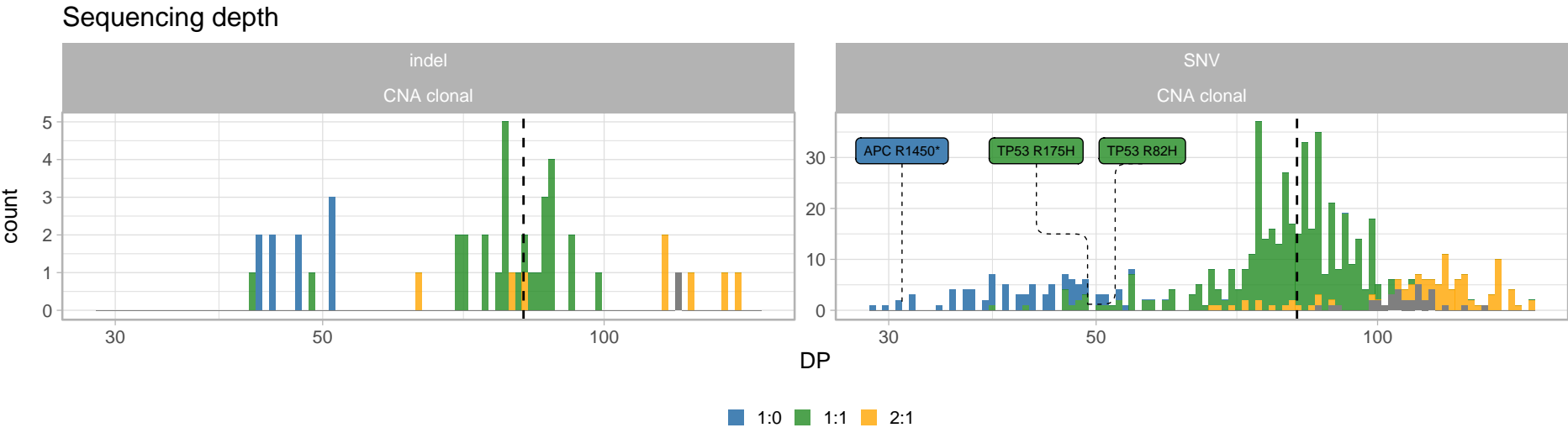
CCF: 0.142682429677945



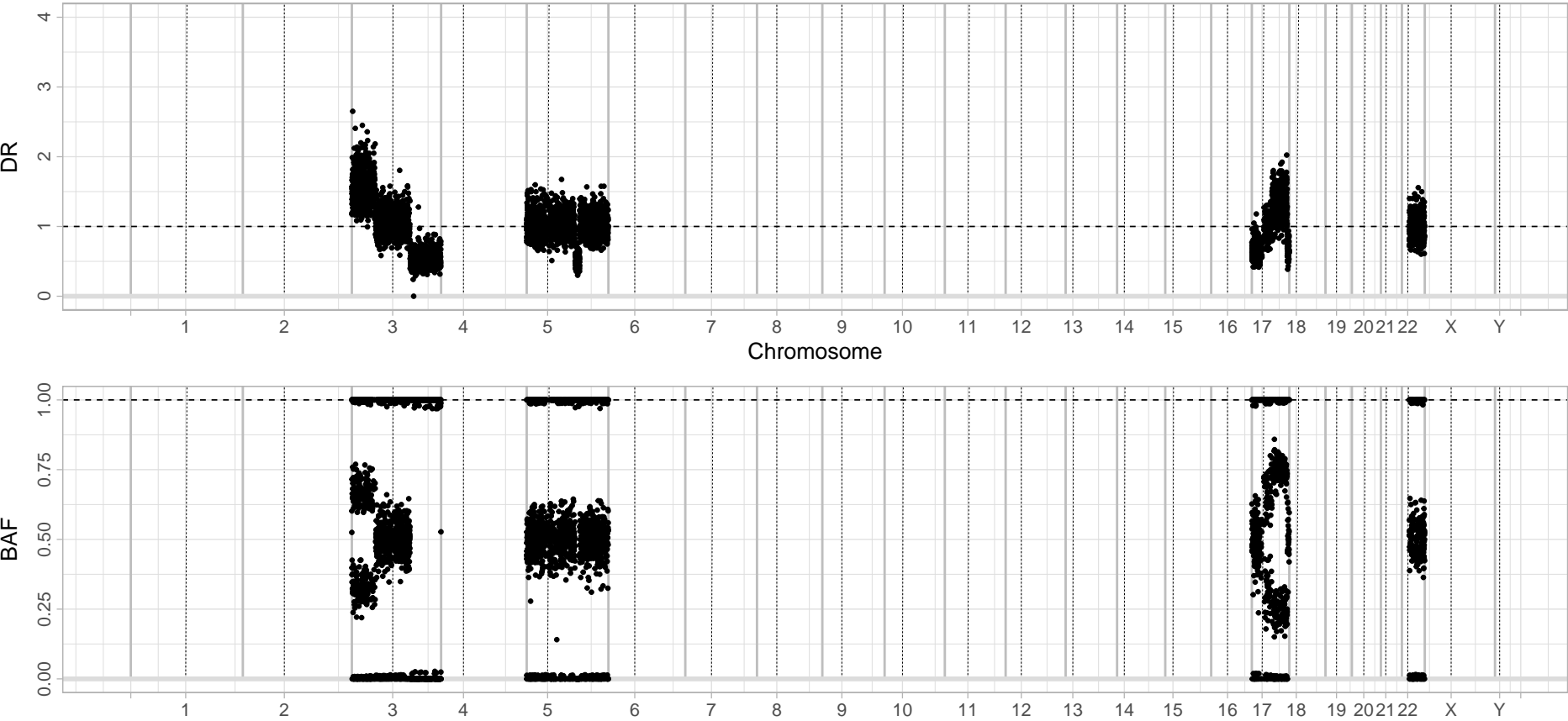
Sample_B
Simulated coverage: 80
Simulated purity: 1
Sequencing Error rate: 0.001
Tumour type: COAD
Germline subject :default



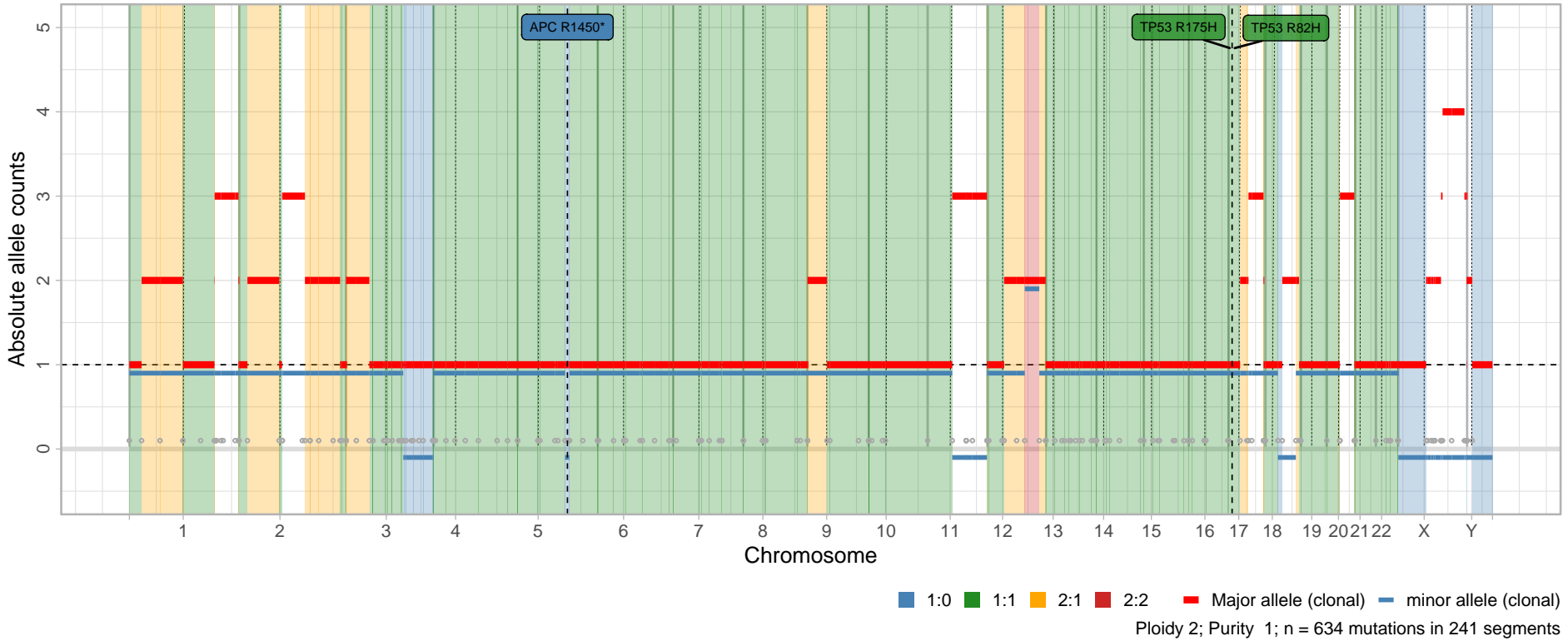
n = 634; VAF < 0.05 (5%) = 304



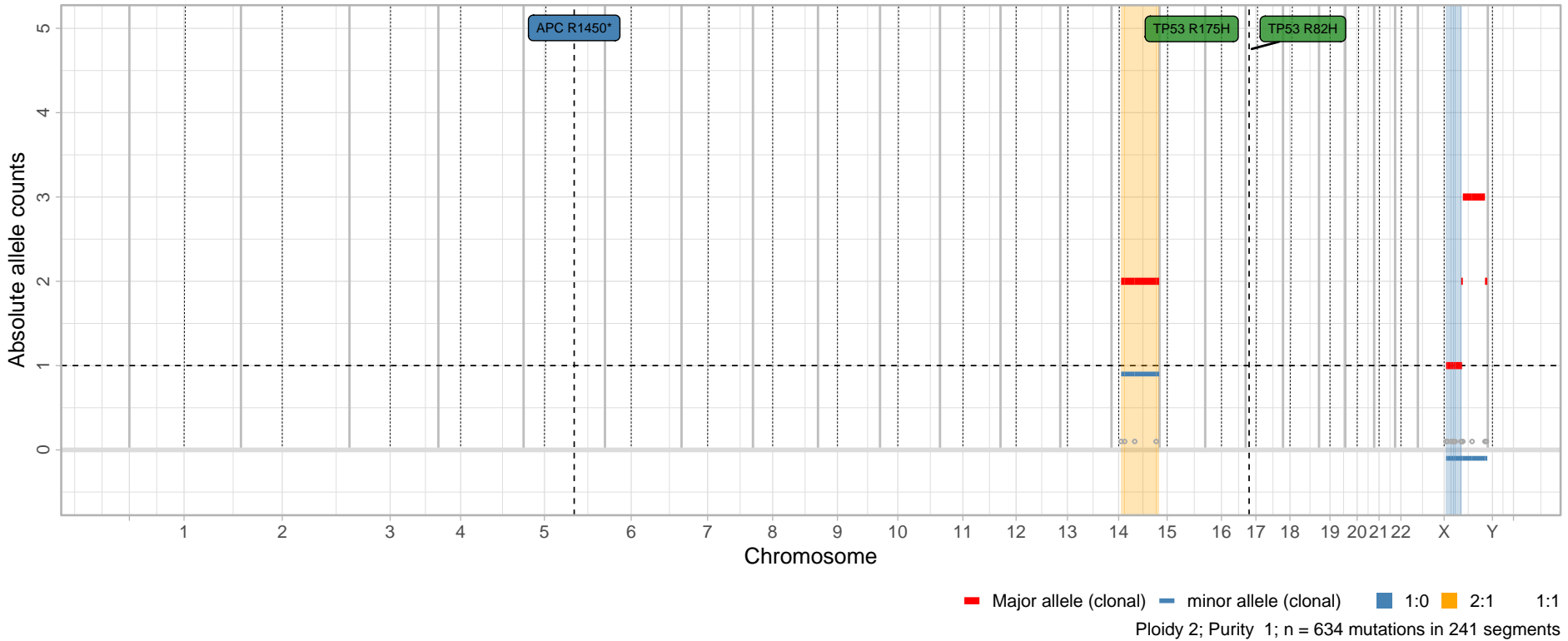
Median DP 82x



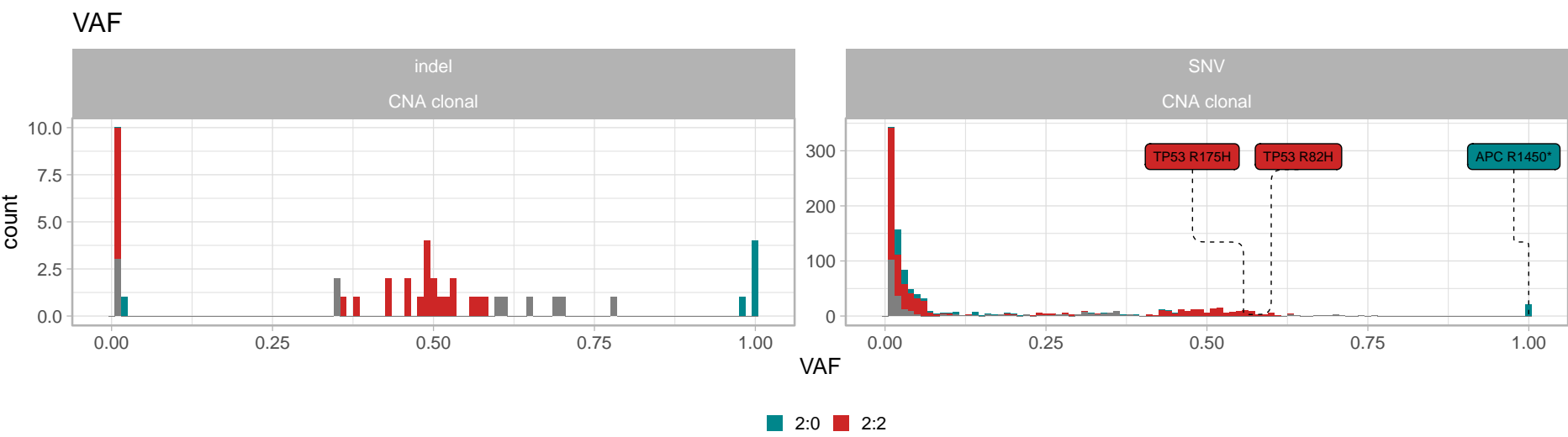
CCF: 1



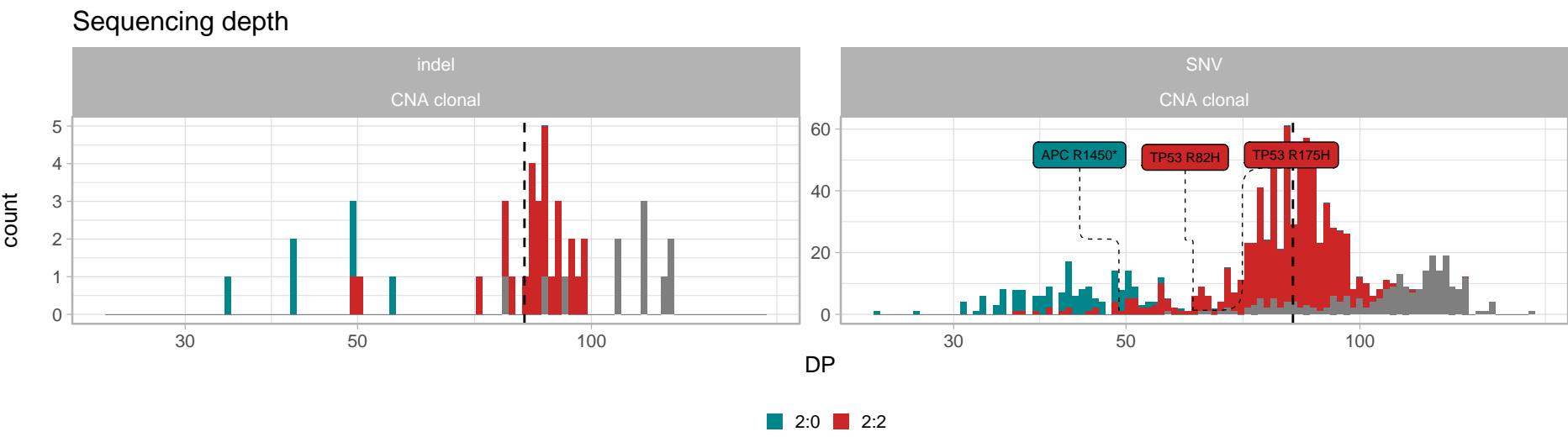
CCF: 0.112408759124088



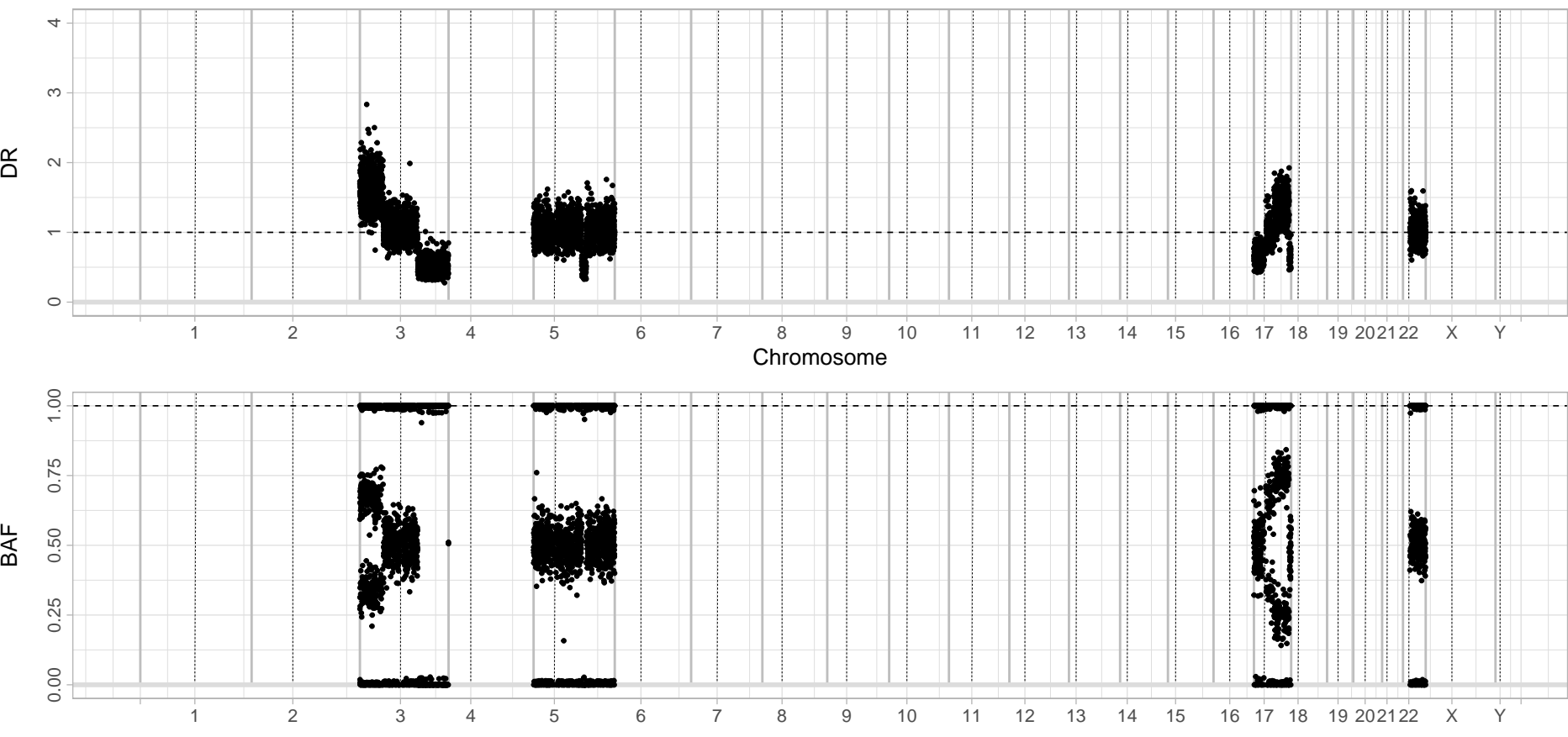
Sample_C
Simulated coverage: 80
Simulated purity: 1
Sequencing Error rate: 0.001
Tumour type: COAD
Germline subject :default



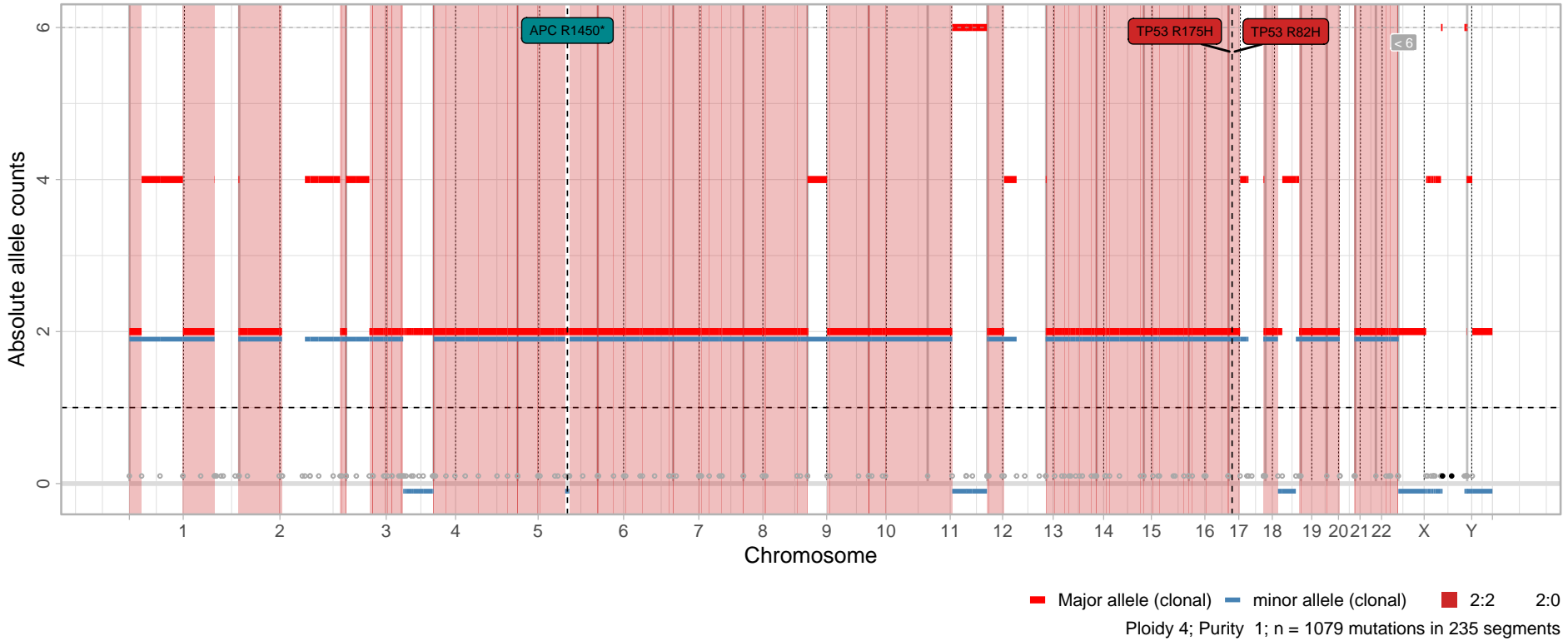
n = 1079; VAF < 0.05 (5%) = 662



Median DP 82x



CCF: 1



CCF: 0.247227356746765

