

A

Simulated coverage: 50

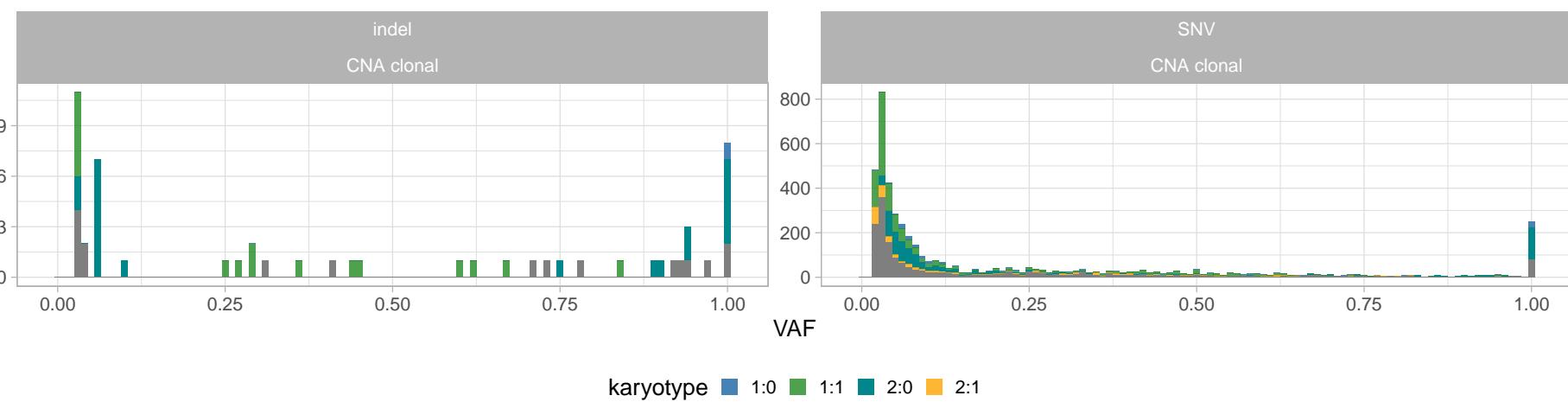
Simulated purity: 0.9

Sequencing Error rate: 0.004

Tumour type: LUAD

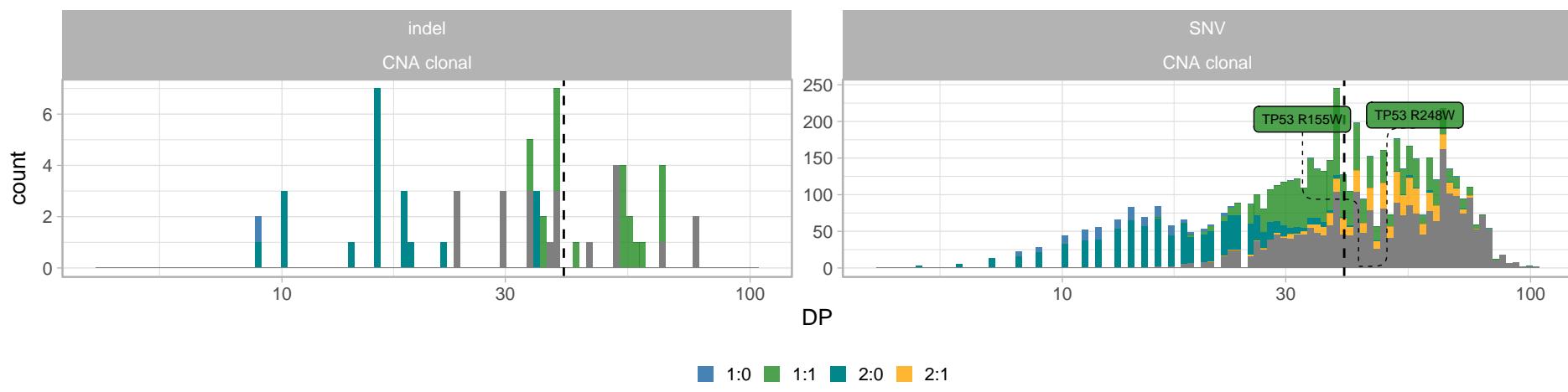
Germline subject :default

VAF



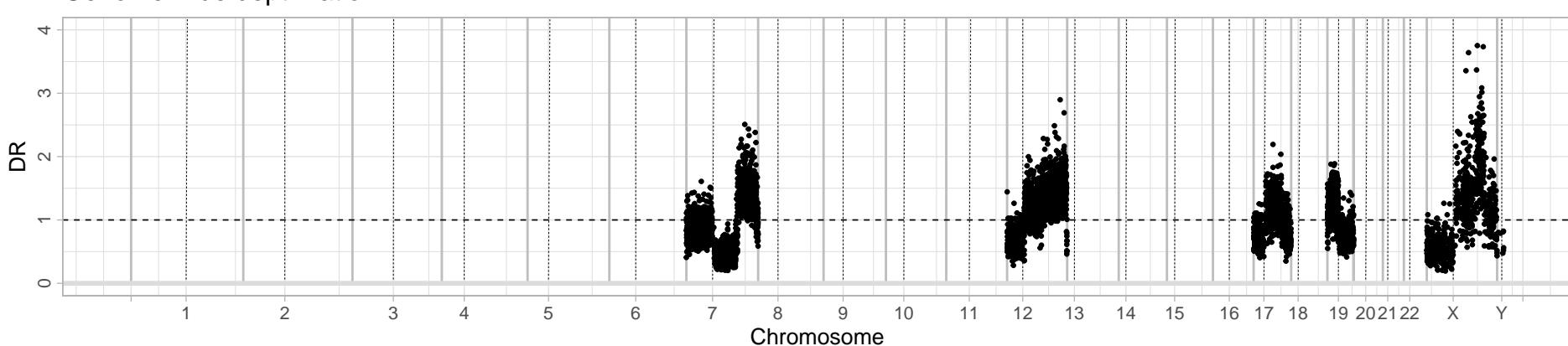
n = 4718; VAF < 0.02 = 977

Sequencing depth

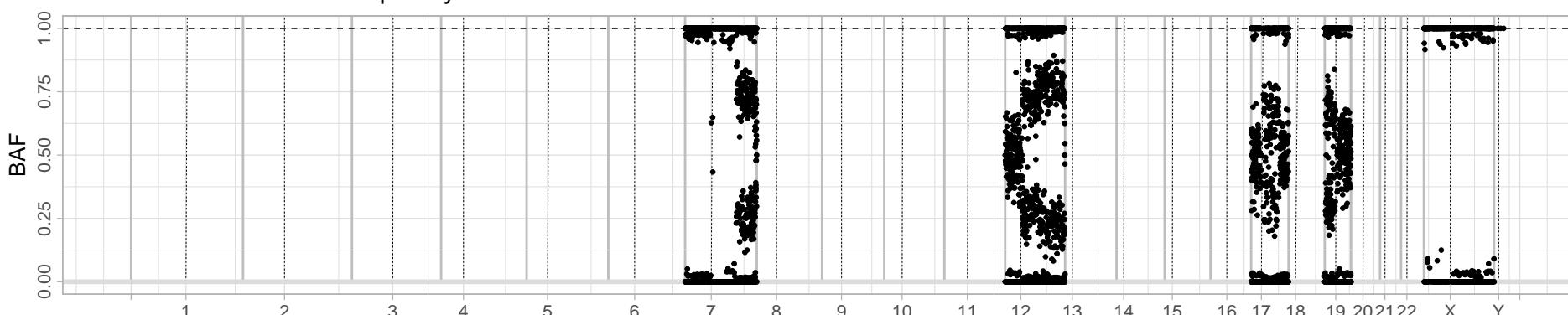


Median DP 40x

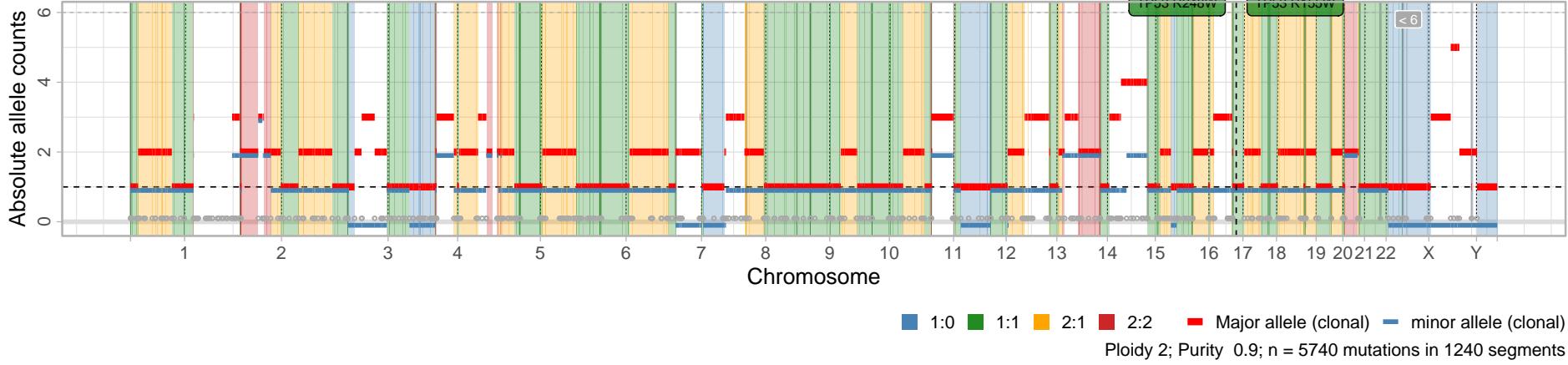
Genome wide depth ratio



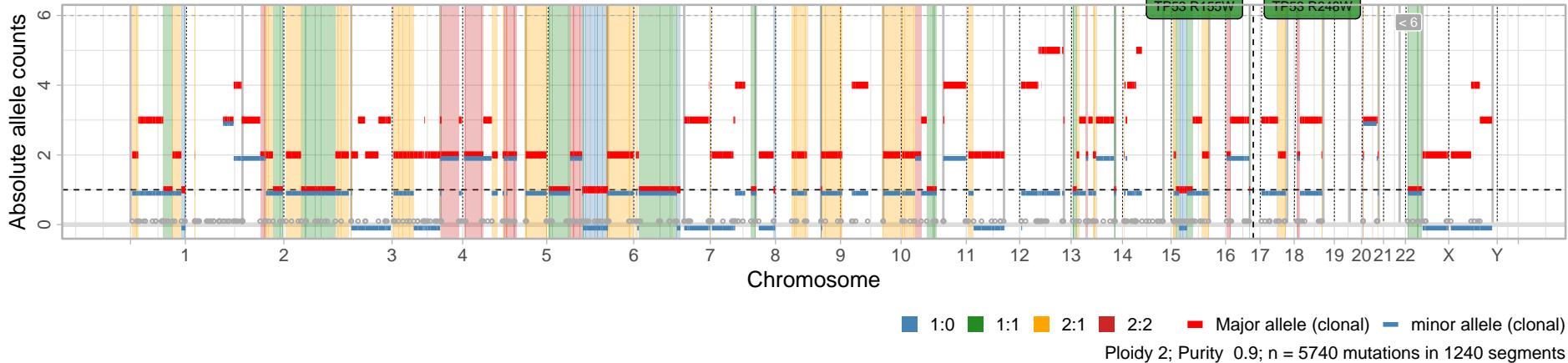
Genome wide B-allele frequency



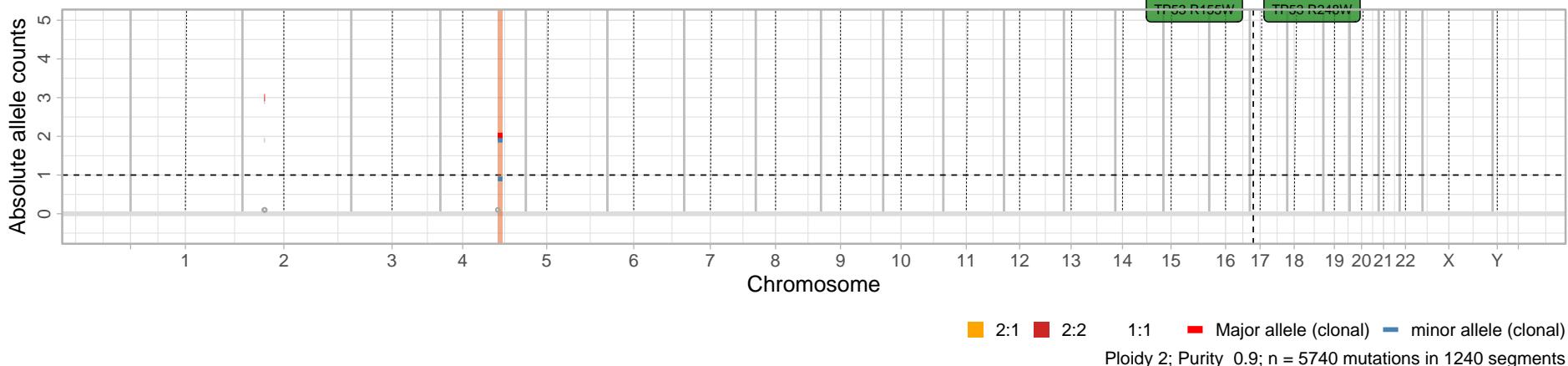
Median fraction of tumour cells: 0.72



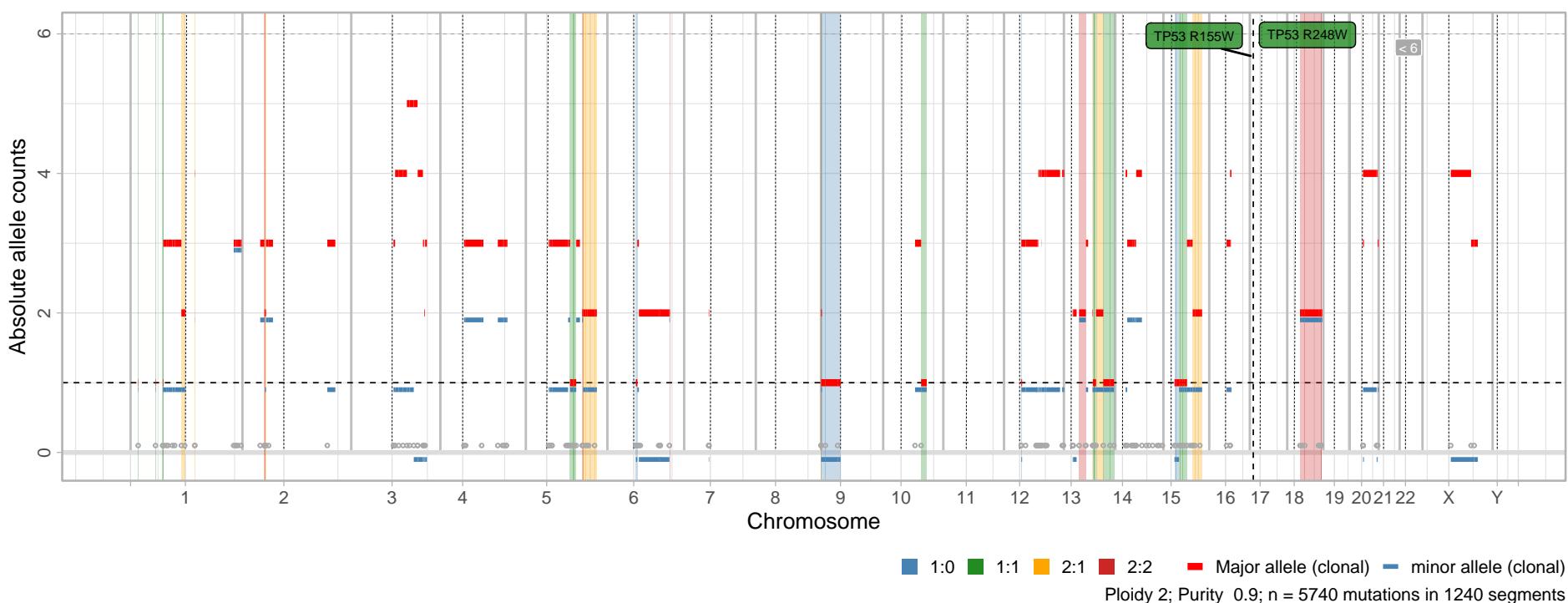
Median fraction of tumour cells: 0.2



Median fraction of tumour cells: 0.31



Median fraction of tumour cells: 0.14



B

Simulated coverage: 50

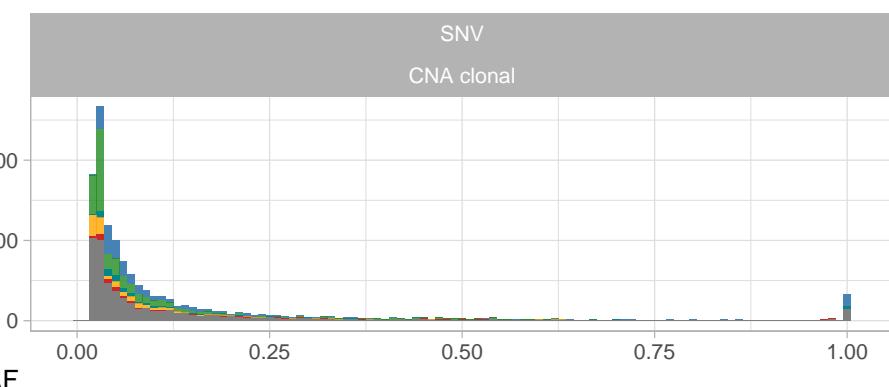
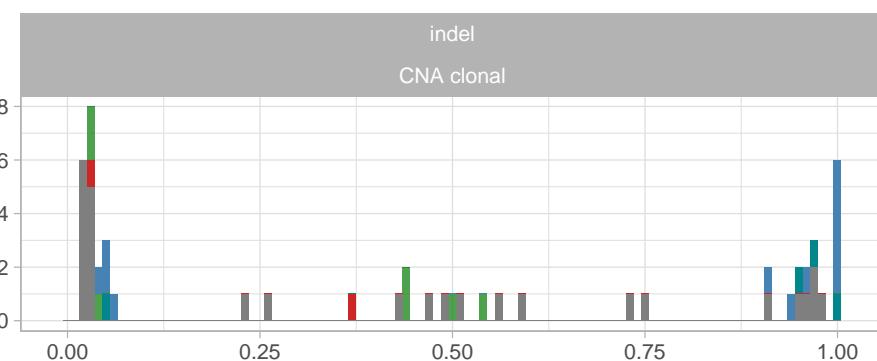
Simulated purity: 0.9

Sequencing Error rate: 0.004

Tumour type: LUAD

Germline subject :default

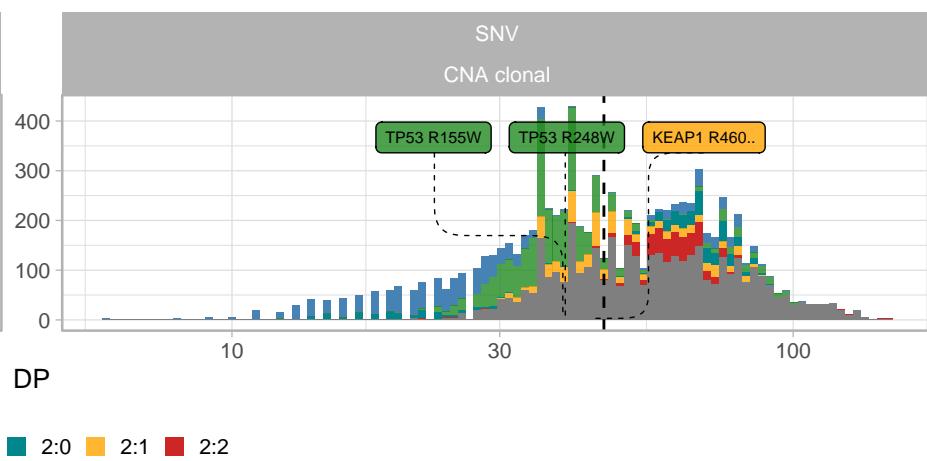
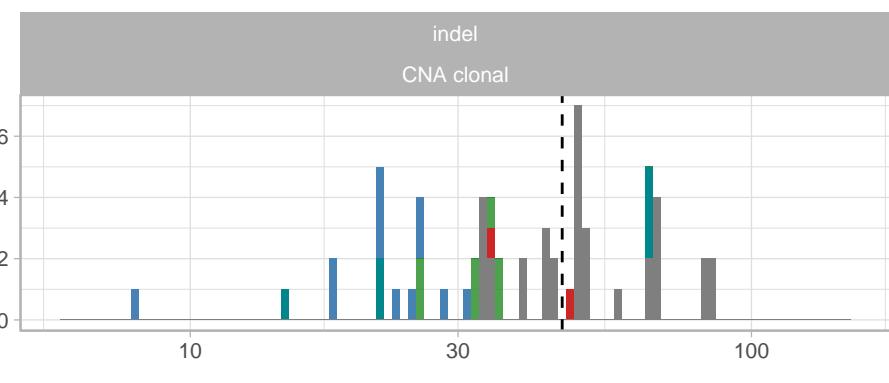
VAF



karyotype ■ 1:0 ■ 1:1 ■ 2:0 ■ 2:1 ■ 2:2

n = 6598; VAF < 0.02 = 2094

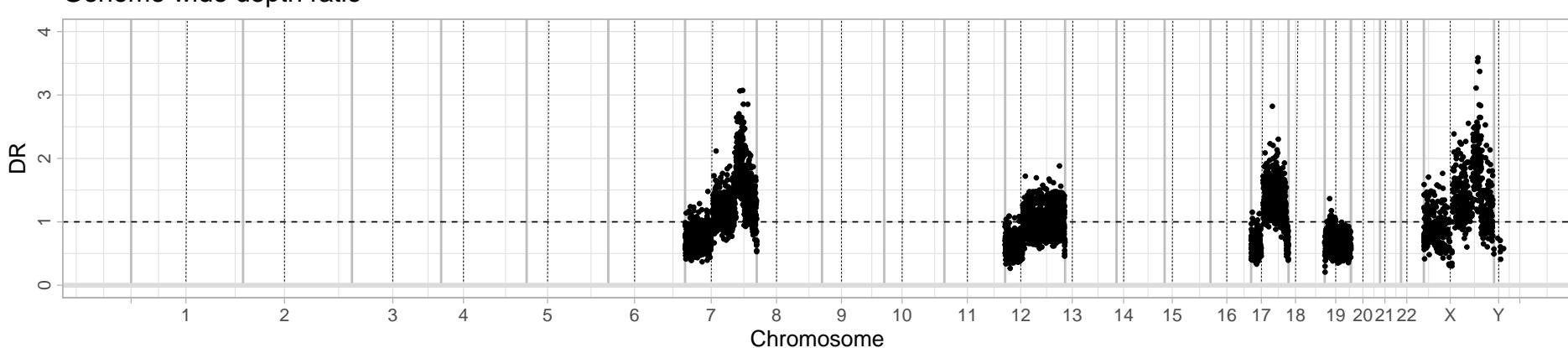
Sequencing depth



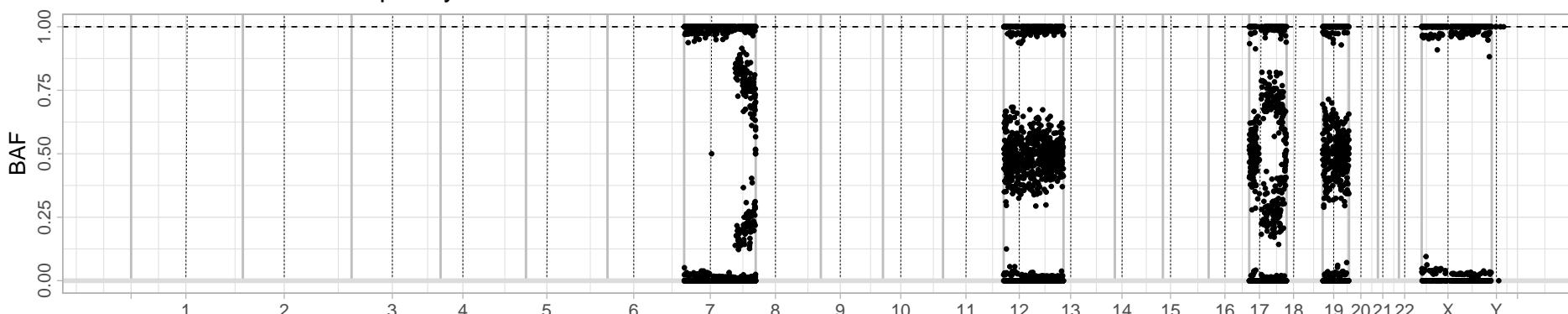
■ 1:0 ■ 1:1 ■ 2:0 ■ 2:1 ■ 2:2

Median DP 46x

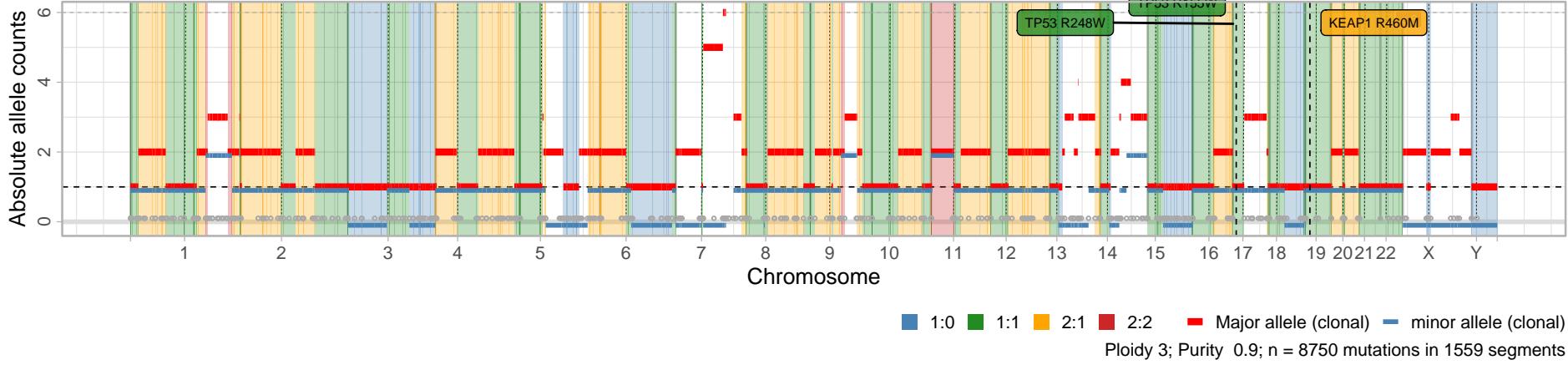
Genome wide depth ratio



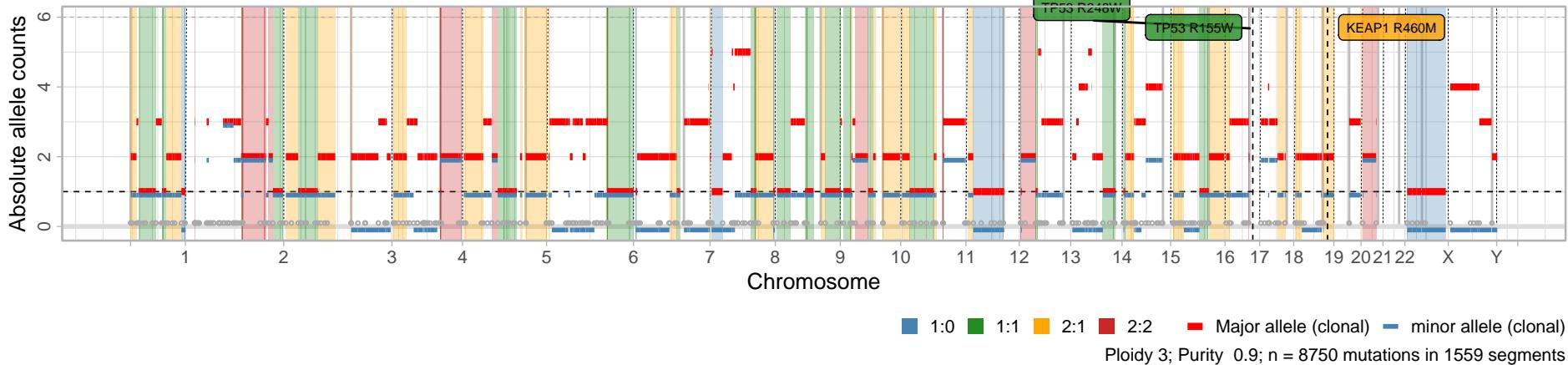
Genome wide B-allele frequency



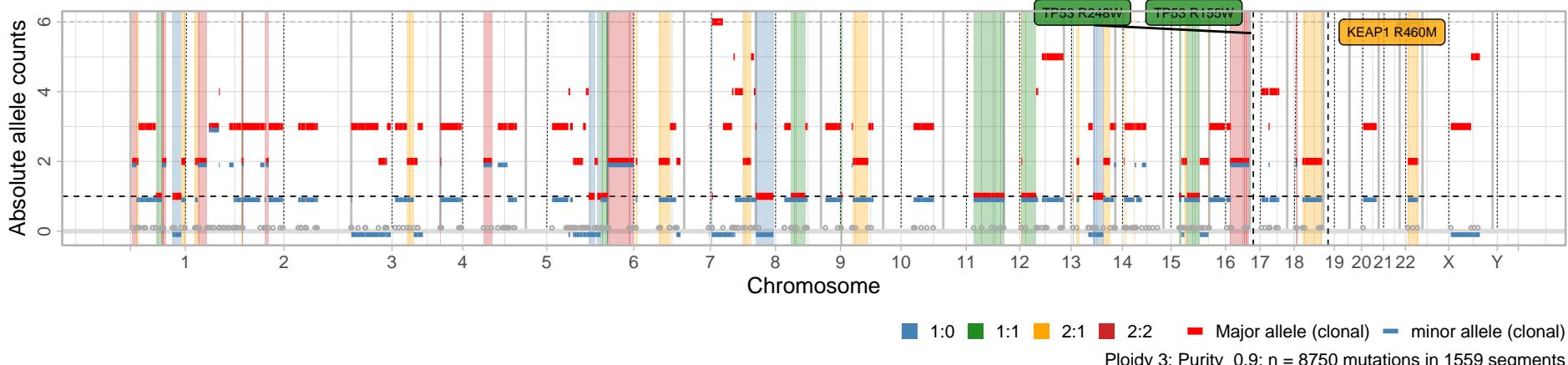
Median fraction of tumour cells: 0.58



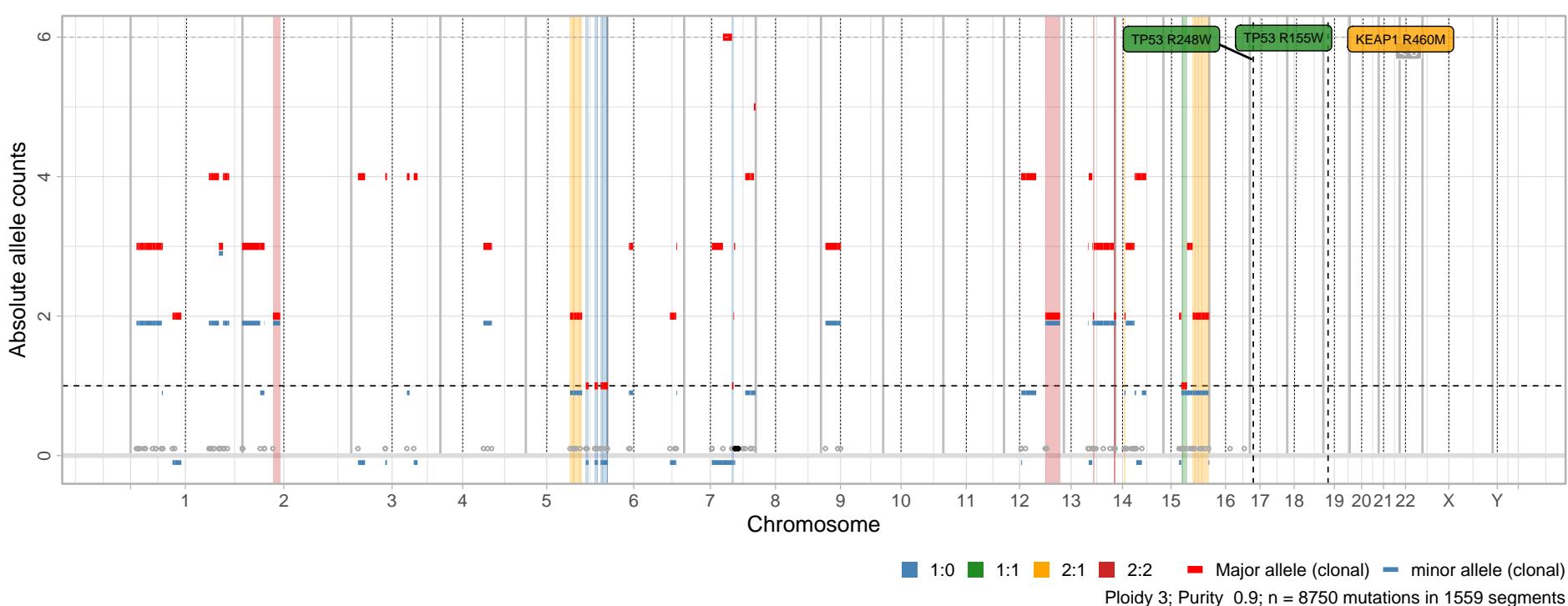
Median fraction of tumour cells: 0.22



Median fraction of tumour cells: 0.14



Median fraction of tumour cells: 0.11



C

Simulated coverage: 50

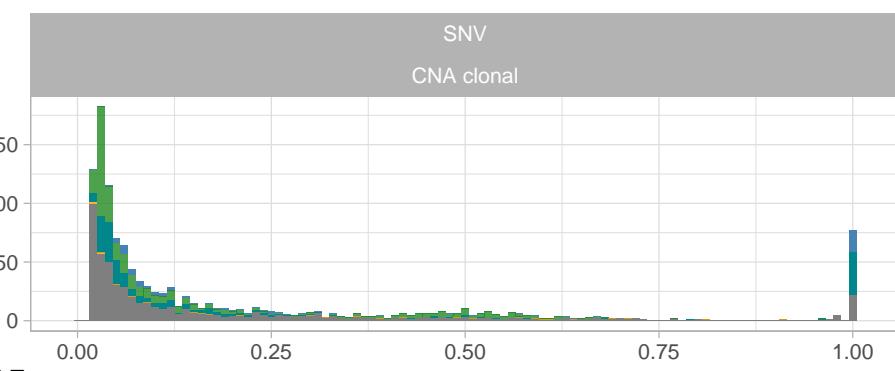
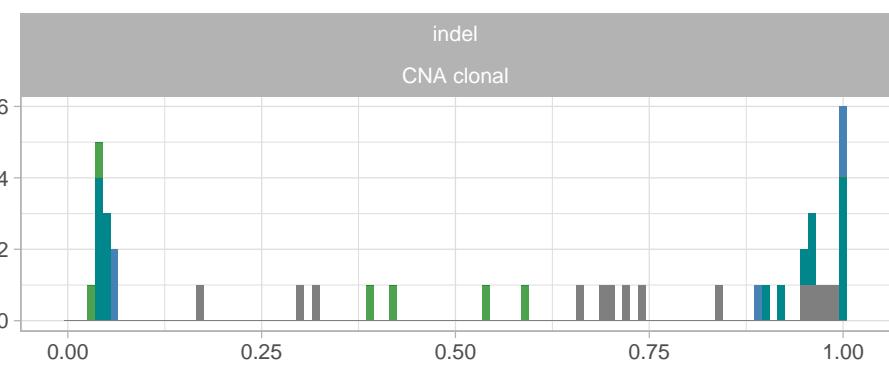
Simulated purity: 0.9

Sequencing Error rate: 0.004

Tumour type: LUAD

Germline subject :default

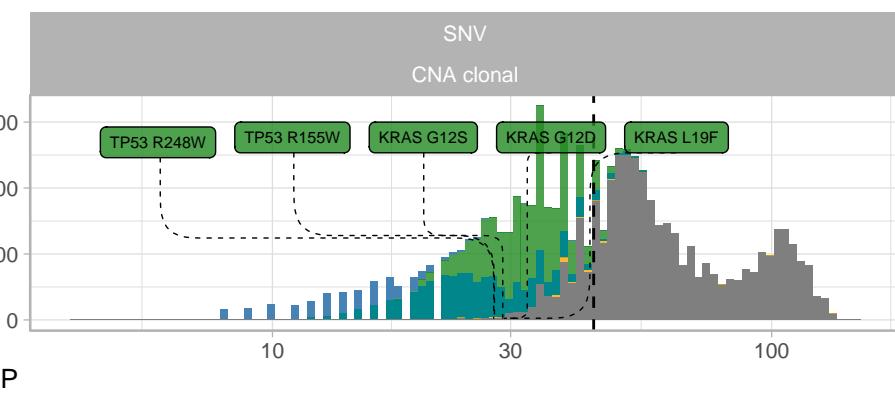
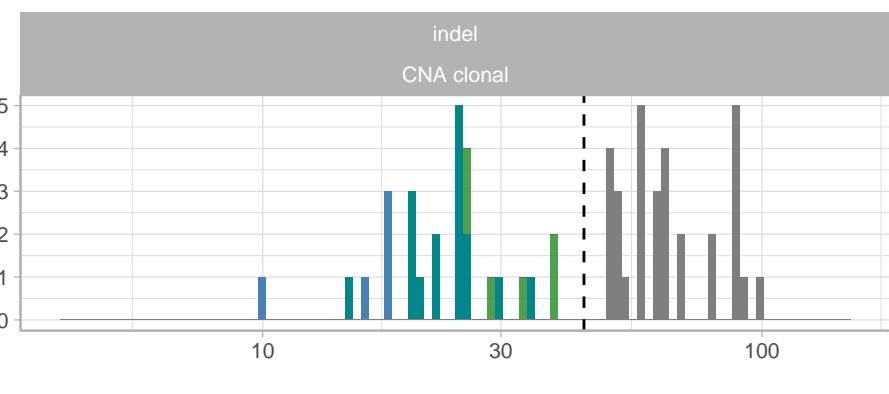
VAF



karyotype ■ 1:0 ■ 1:1 ■ 2:0 ■ 2:1

n = 6097; VAF < 0.02 = 1412

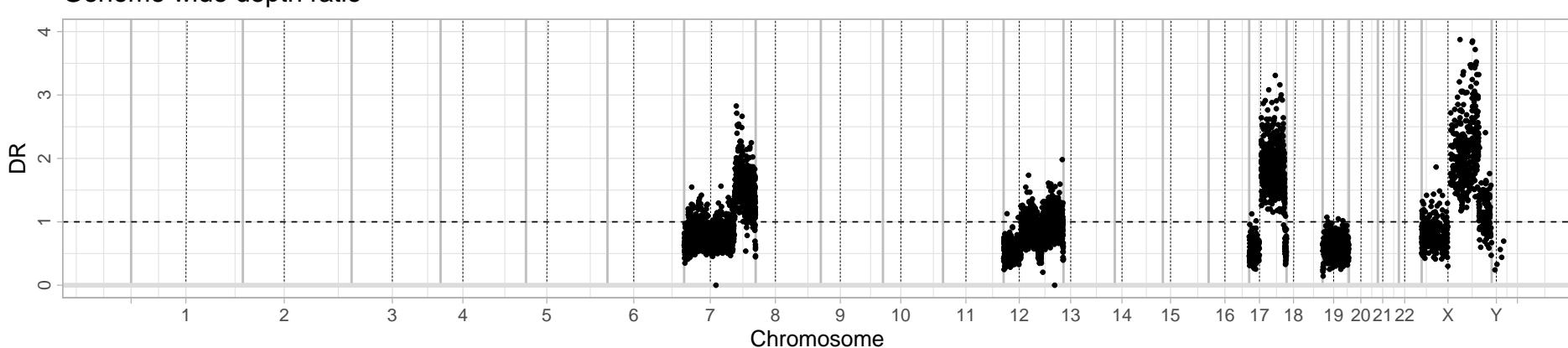
Sequencing depth



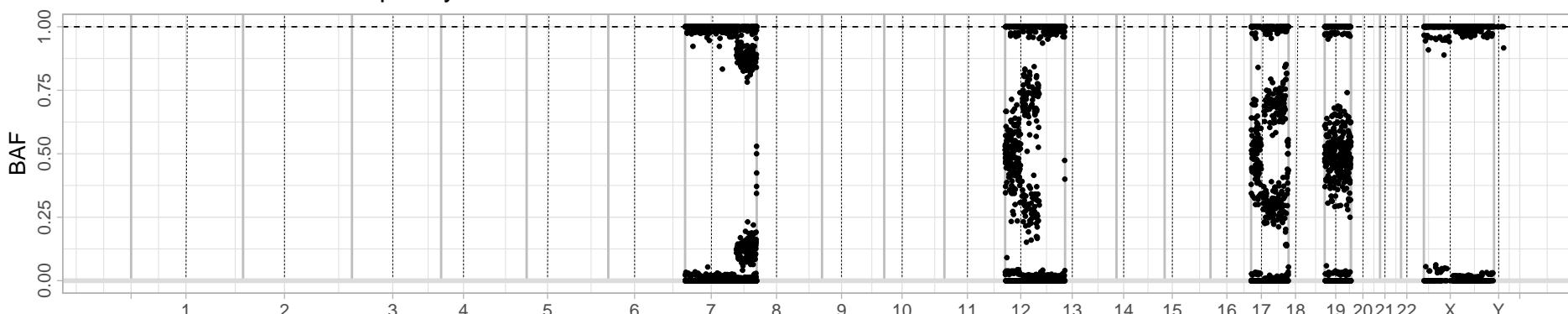
■ 1:0 ■ 1:1 ■ 2:0 ■ 2:1

Median DP 44x

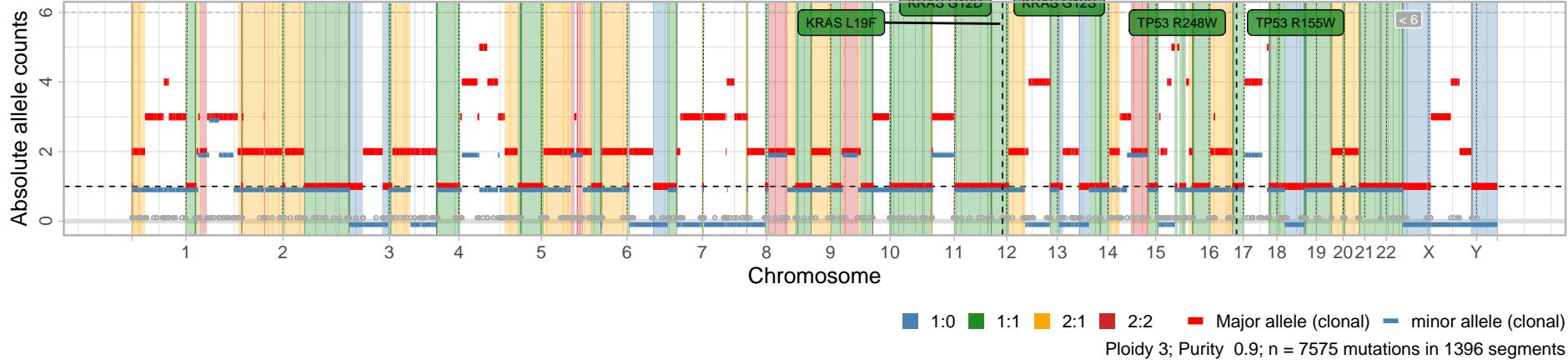
Genome wide depth ratio



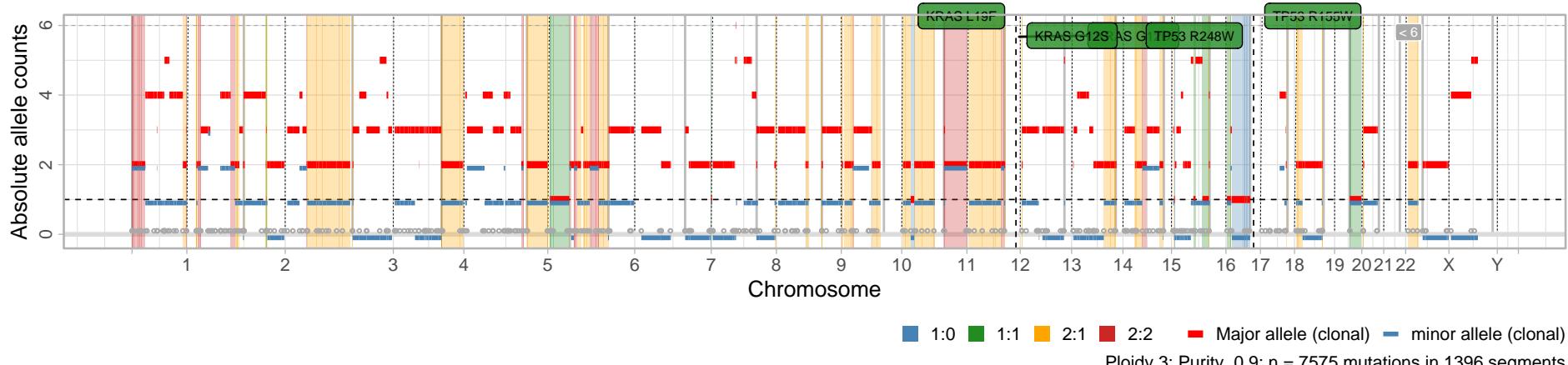
Genome wide B-allele frequency



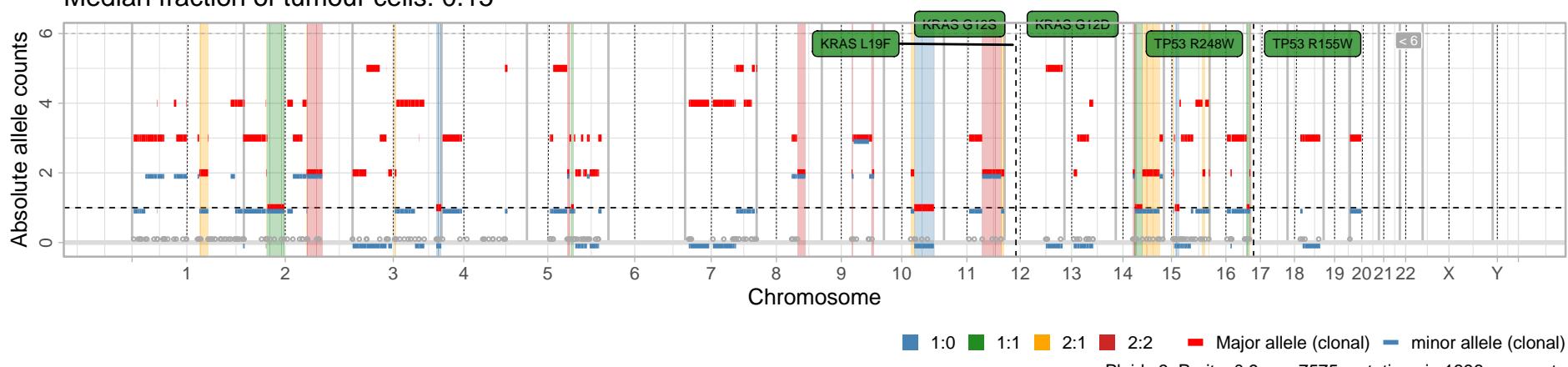
Median fraction of tumour cells: 0.62



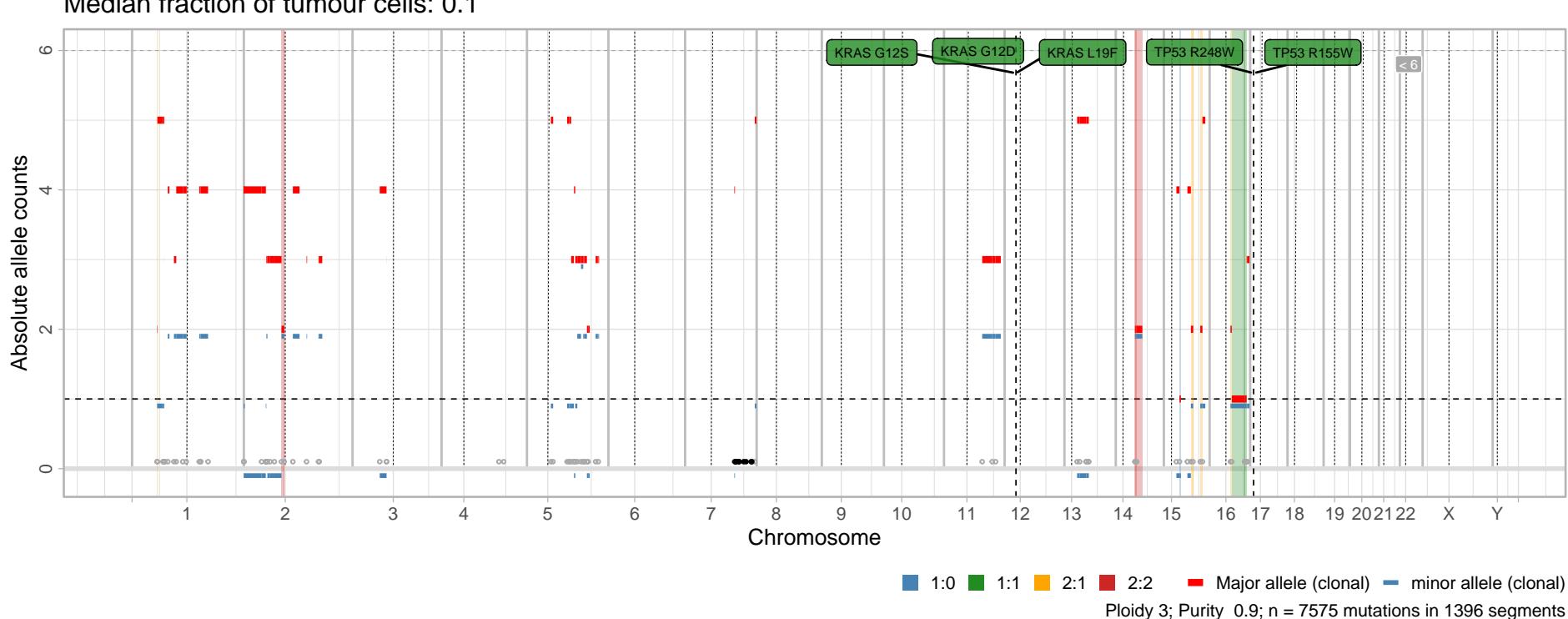
Median fraction of tumour cells: 0.26



Median fraction of tumour cells: 0.15



Median fraction of tumour cells: 0.1



D

Simulated coverage: 50

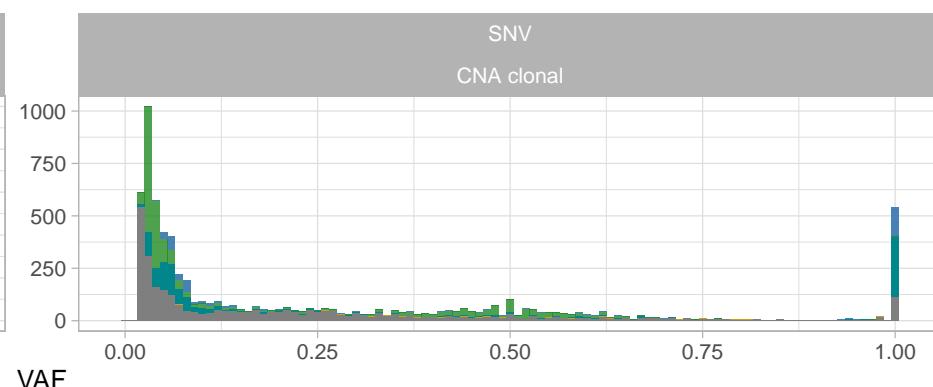
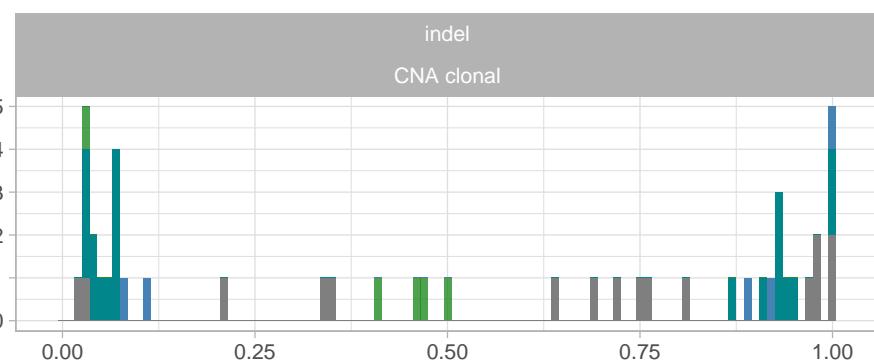
Simulated purity: 0.9

Sequencing Error rate: 0.004

Tumour type: LUAD

Germline subject :default

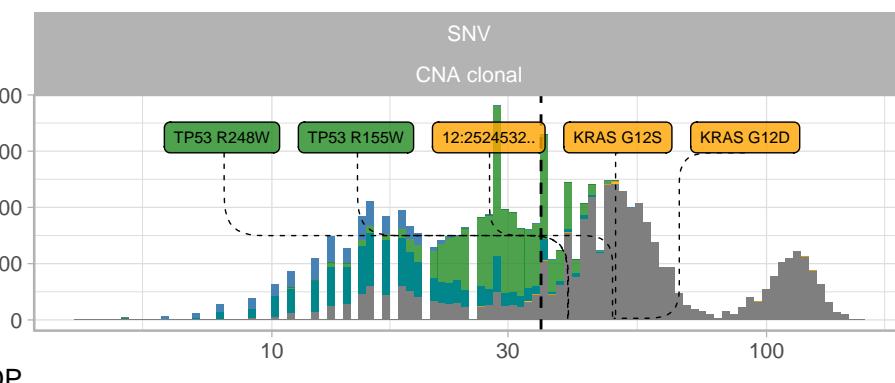
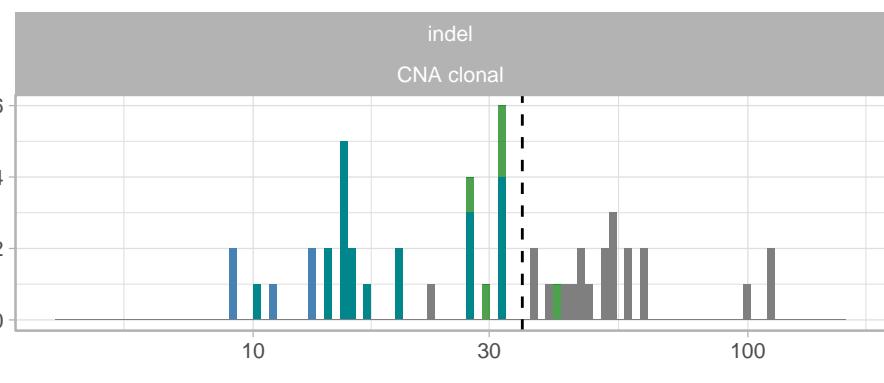
VAF



karyotype ■ 1:0 ■ 1:1 ■ 2:0 ■ 2:1

n = 7012; VAF < 0.02 = 1204

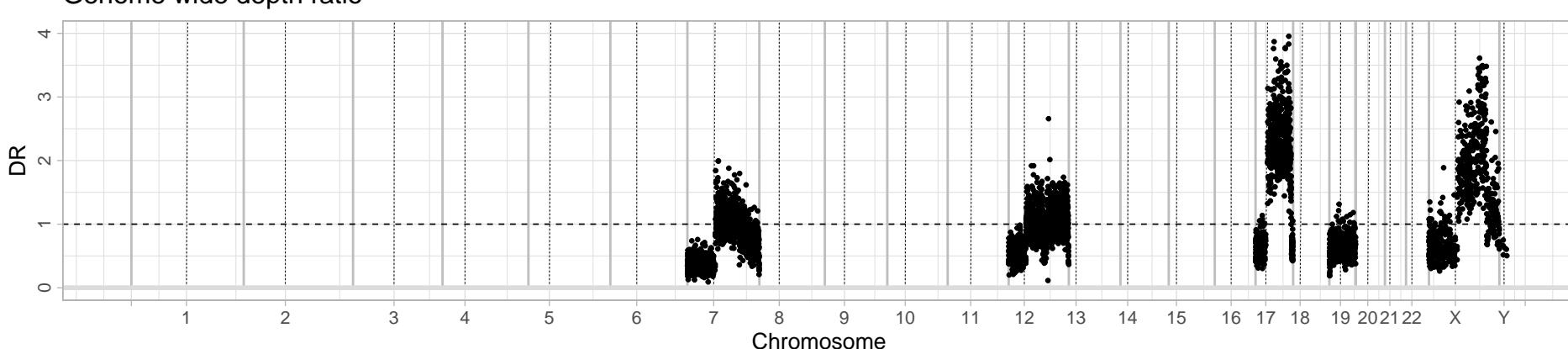
Sequencing depth



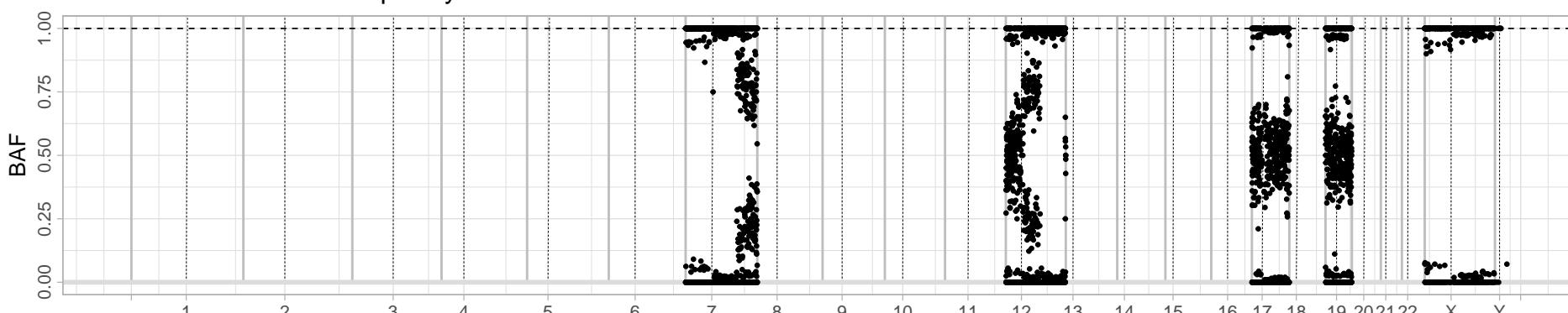
■ 1:0 ■ 1:1 ■ 2:0 ■ 2:1

Median DP 35x

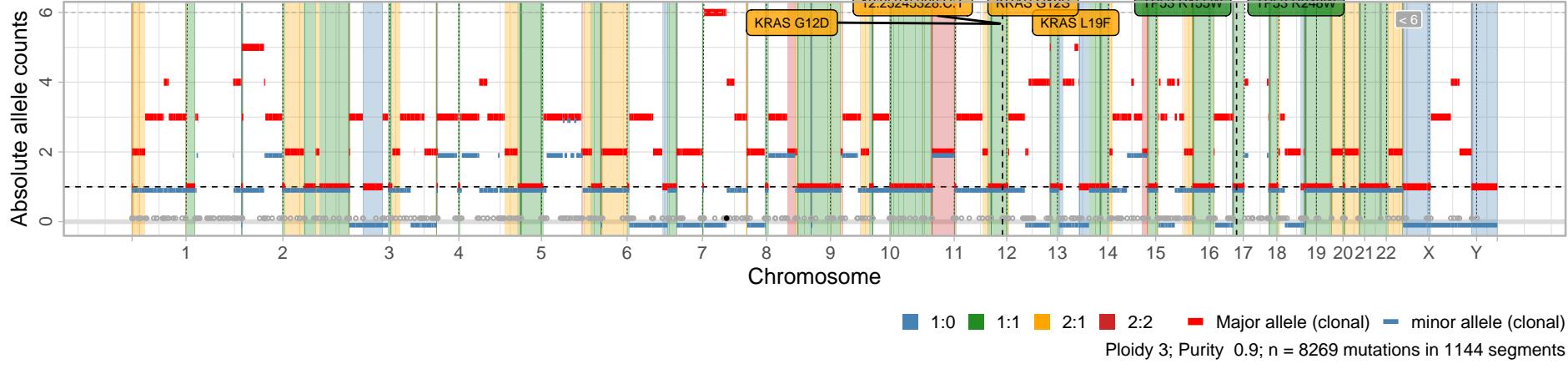
Genome wide depth ratio



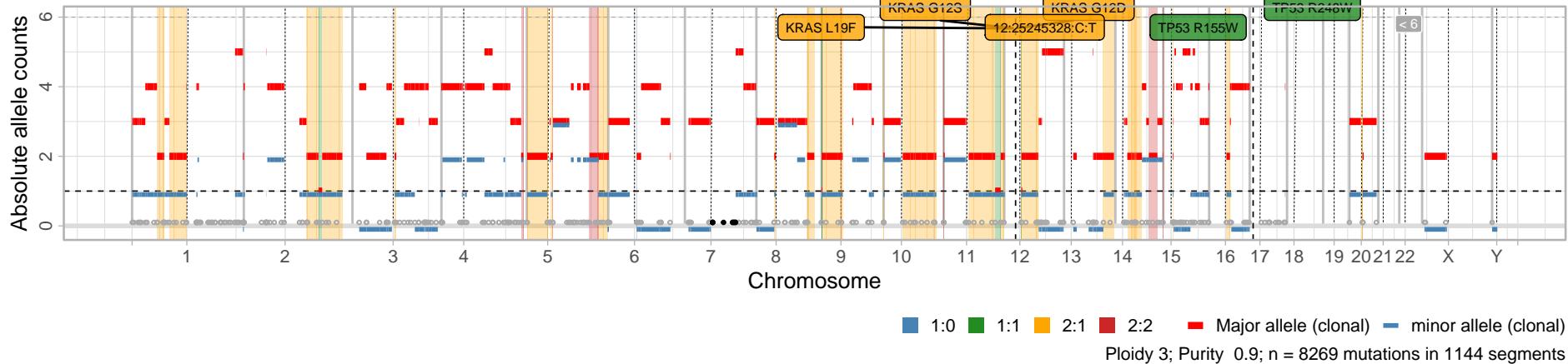
Genome wide B-allele frequency



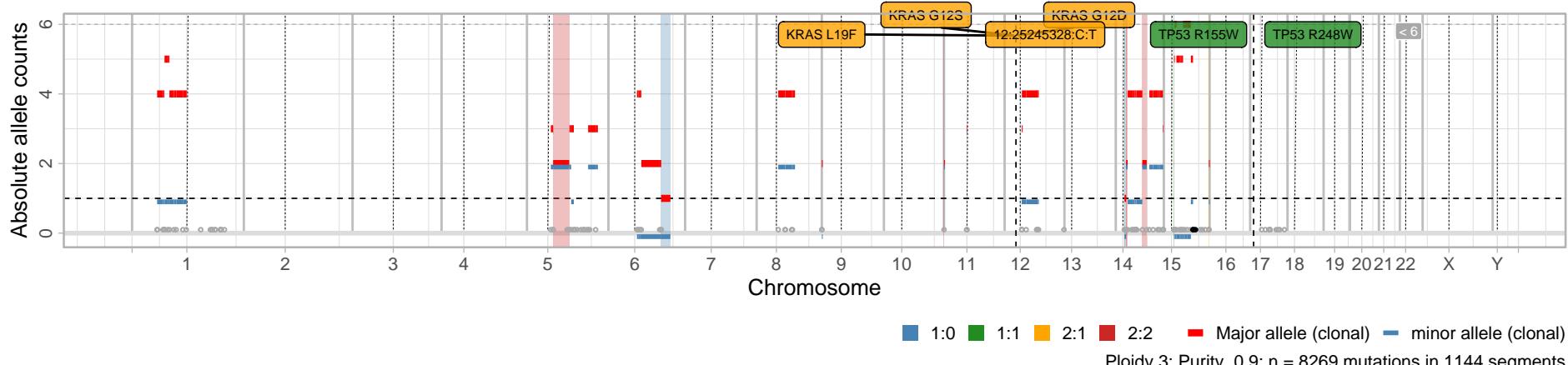
Median fraction of tumour cells: 0.77



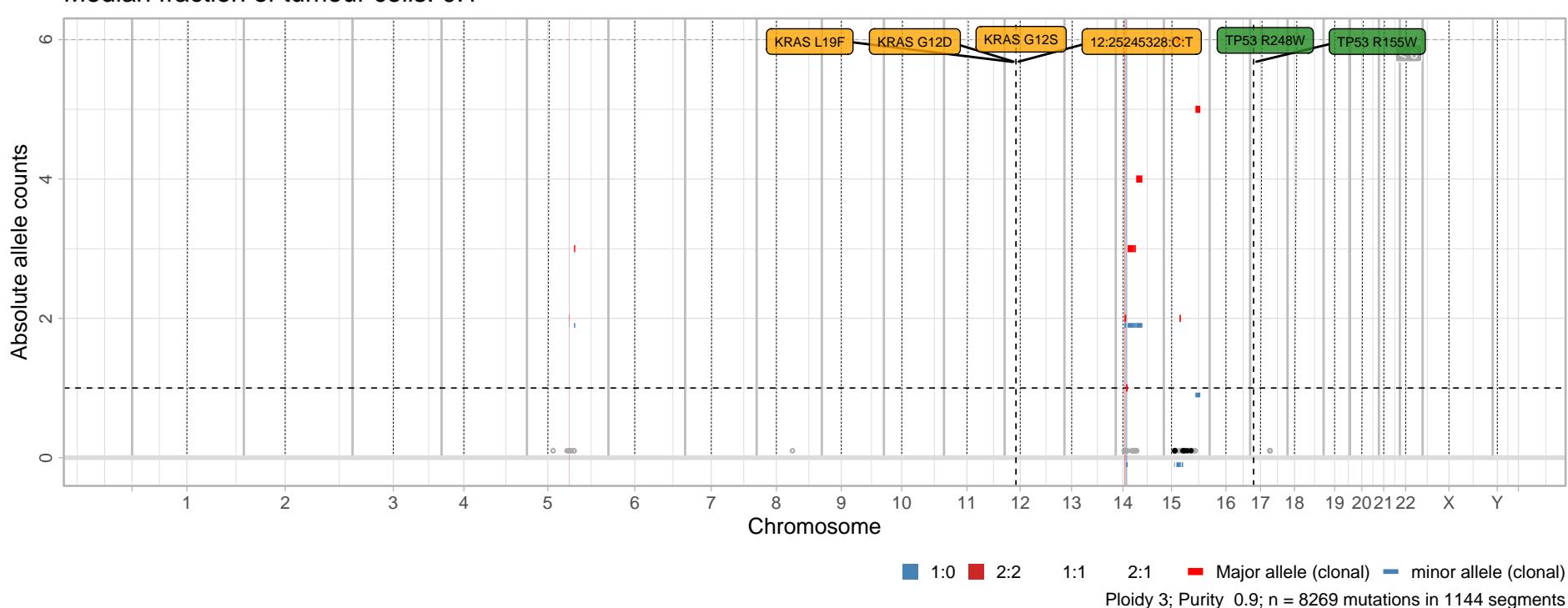
Median fraction of tumour cells: 0.19



Median fraction of tumour cells: 0.12



Median fraction of tumour cells: 0.1



E

Simulated coverage: 50

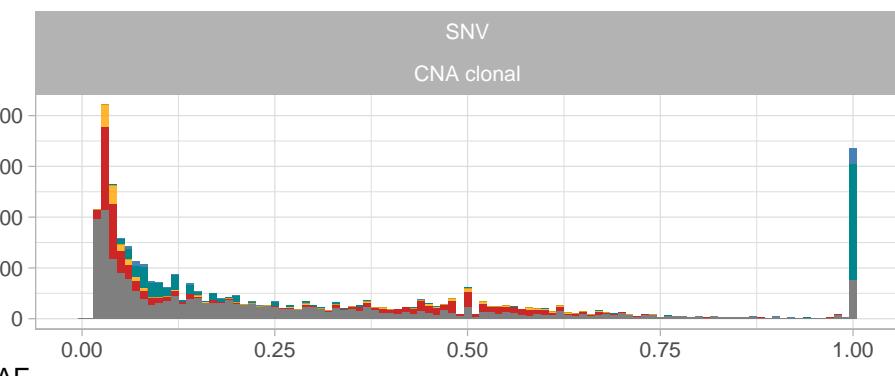
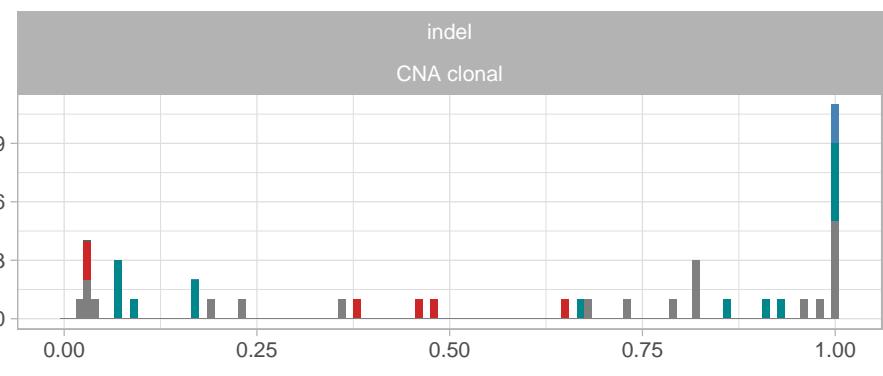
Simulated purity: 0.9

Sequencing Error rate: 0.004

Tumour type: LUAD

Germline subject :default

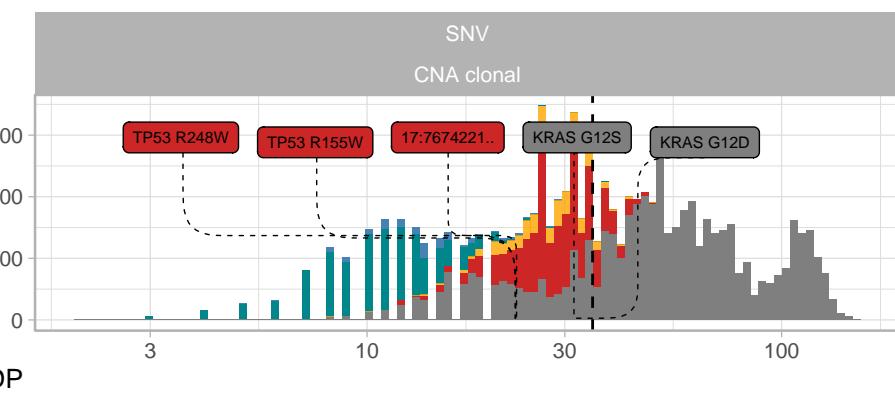
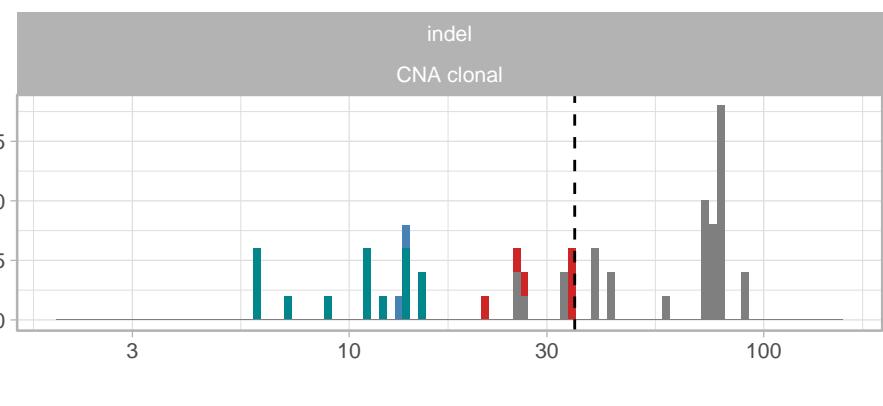
VAF



karyotype ■ 1:0 ■ 2:0 ■ 2:1 ■ 2:2

n = 7430; VAF < 0.02 = 1224

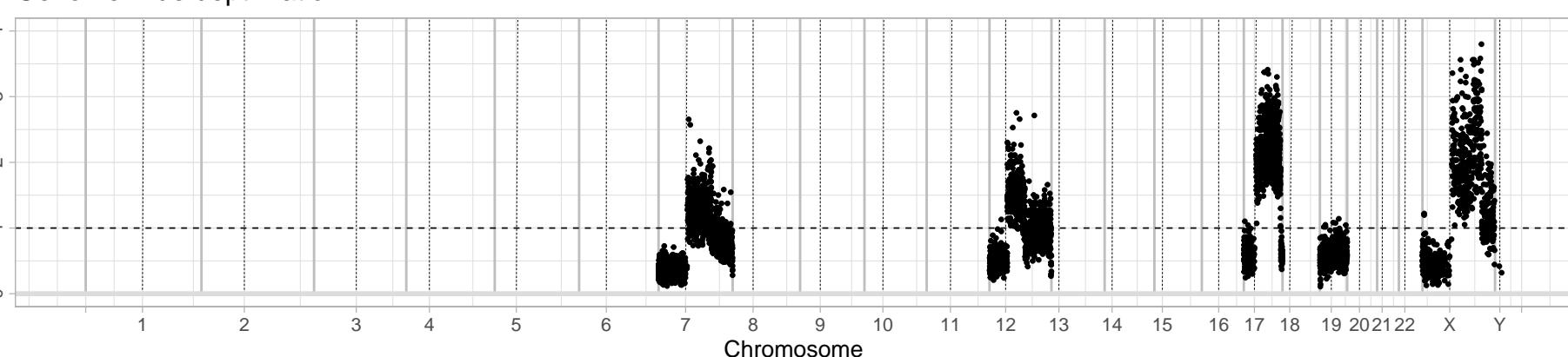
Sequencing depth



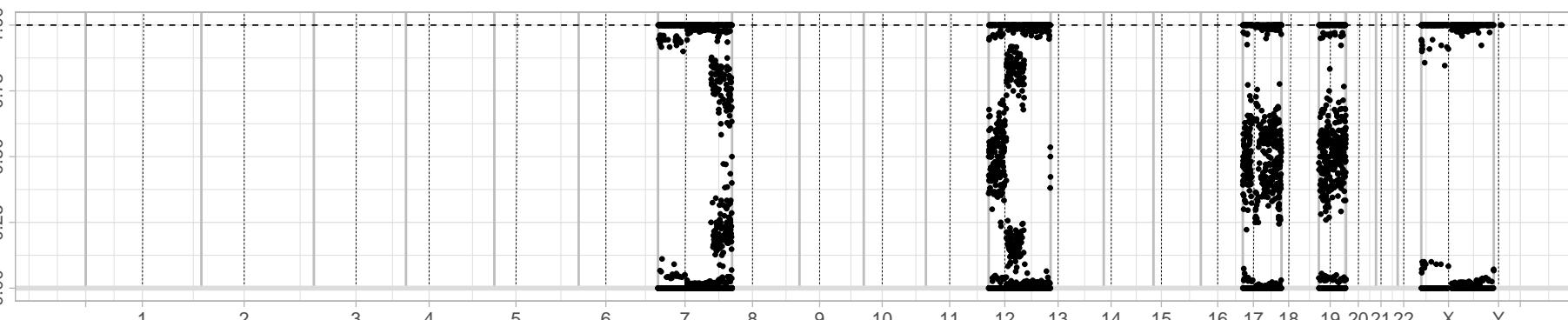
■ 1:0 ■ 2:0 ■ 2:1 ■ 2:2

Median DP 35x

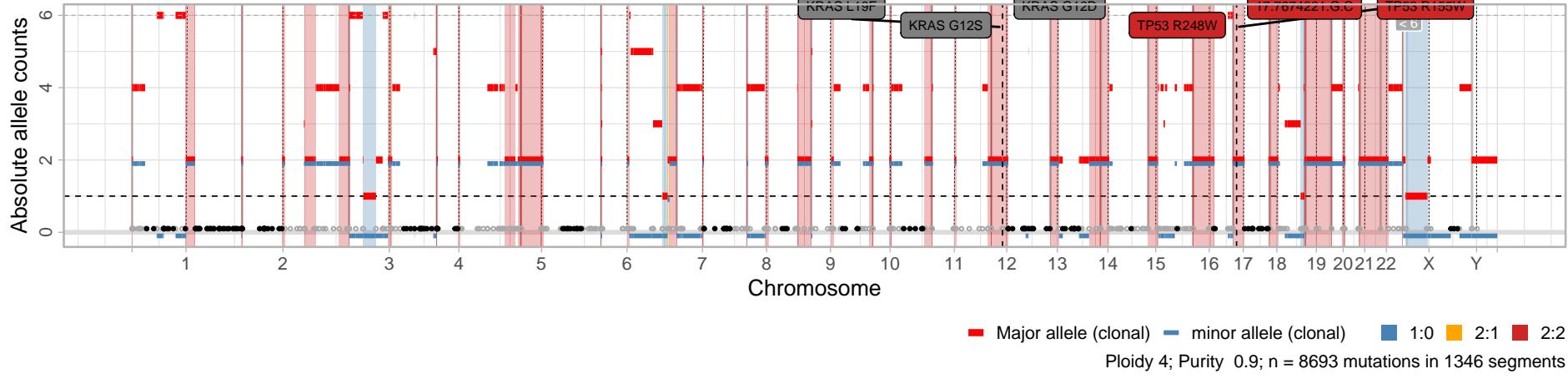
Genome wide depth ratio



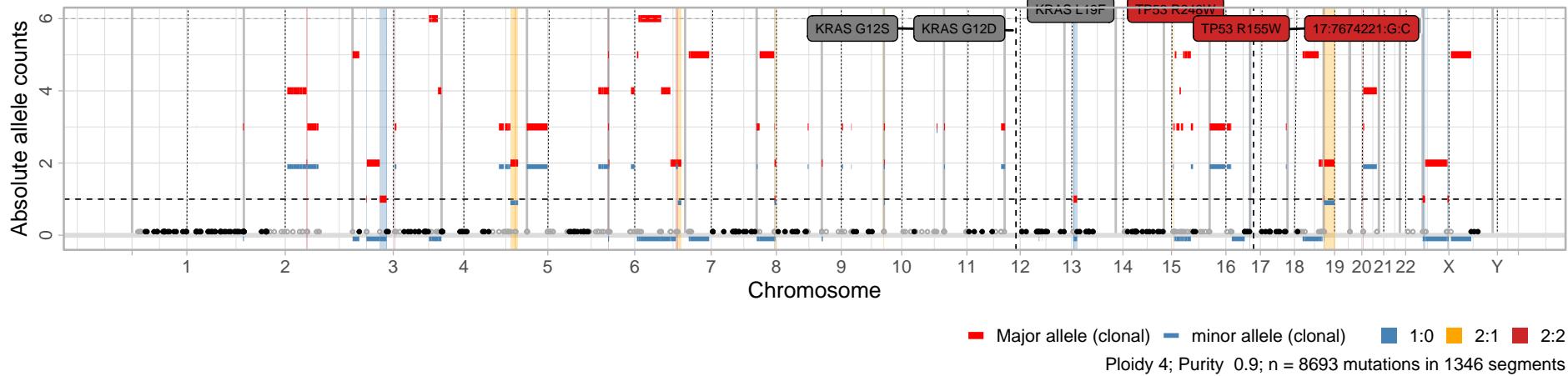
Genome wide B-allele frequency



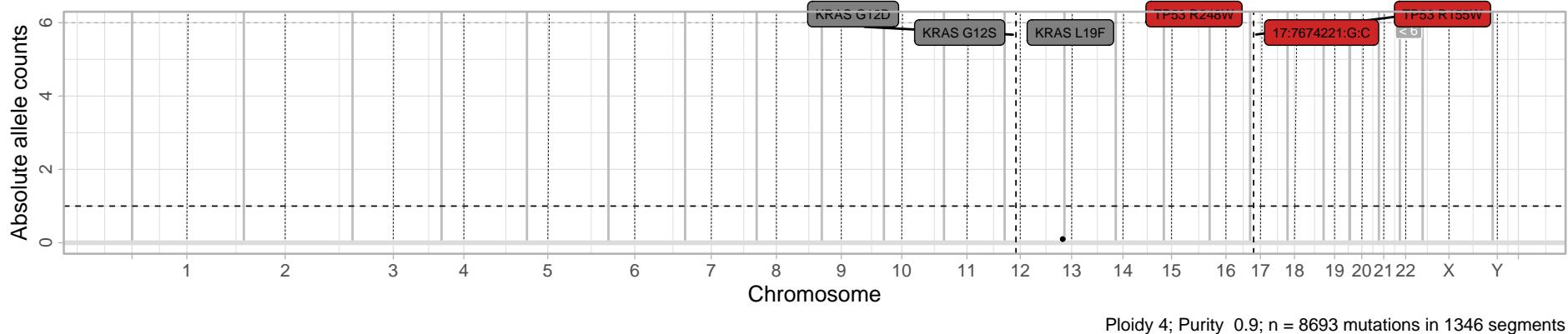
Median fraction of tumour cells: 0.61



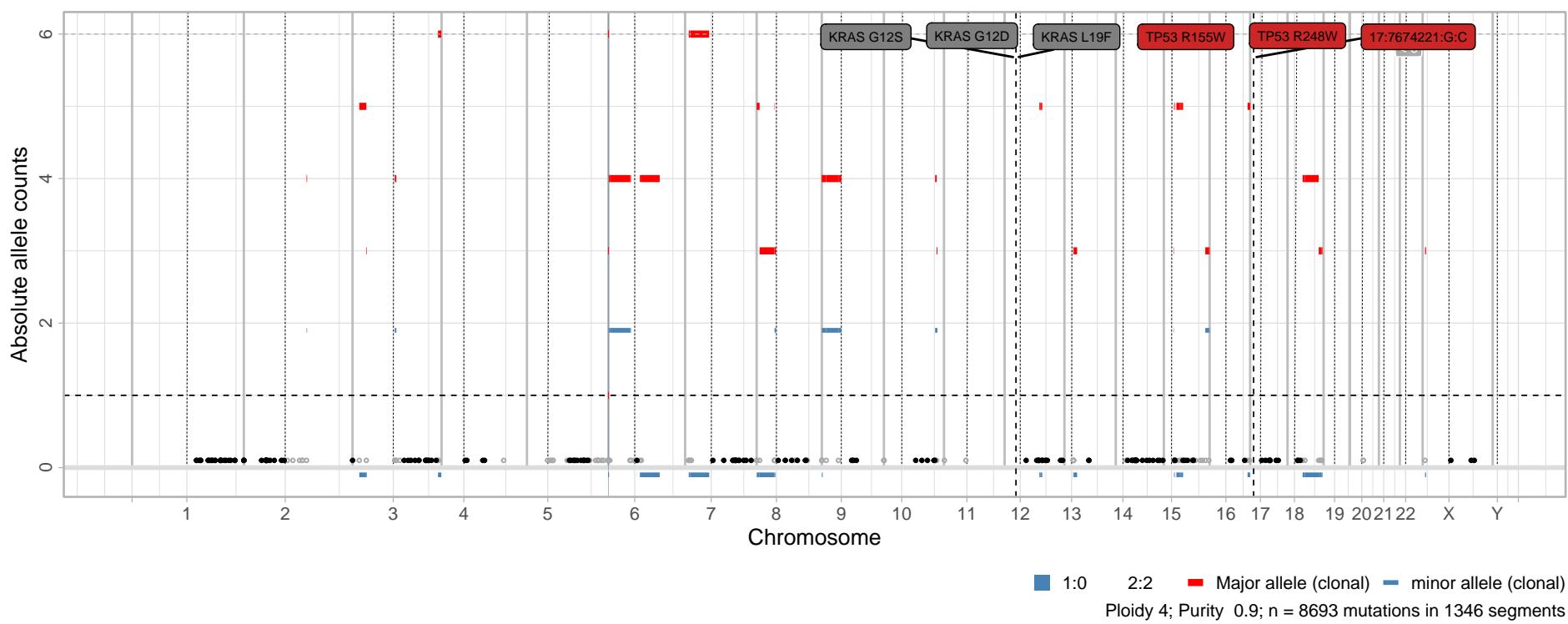
Median fraction of tumour cells: 0.25



Median fraction of tumour cells: 0.4



Median fraction of tumour cells: 0.14



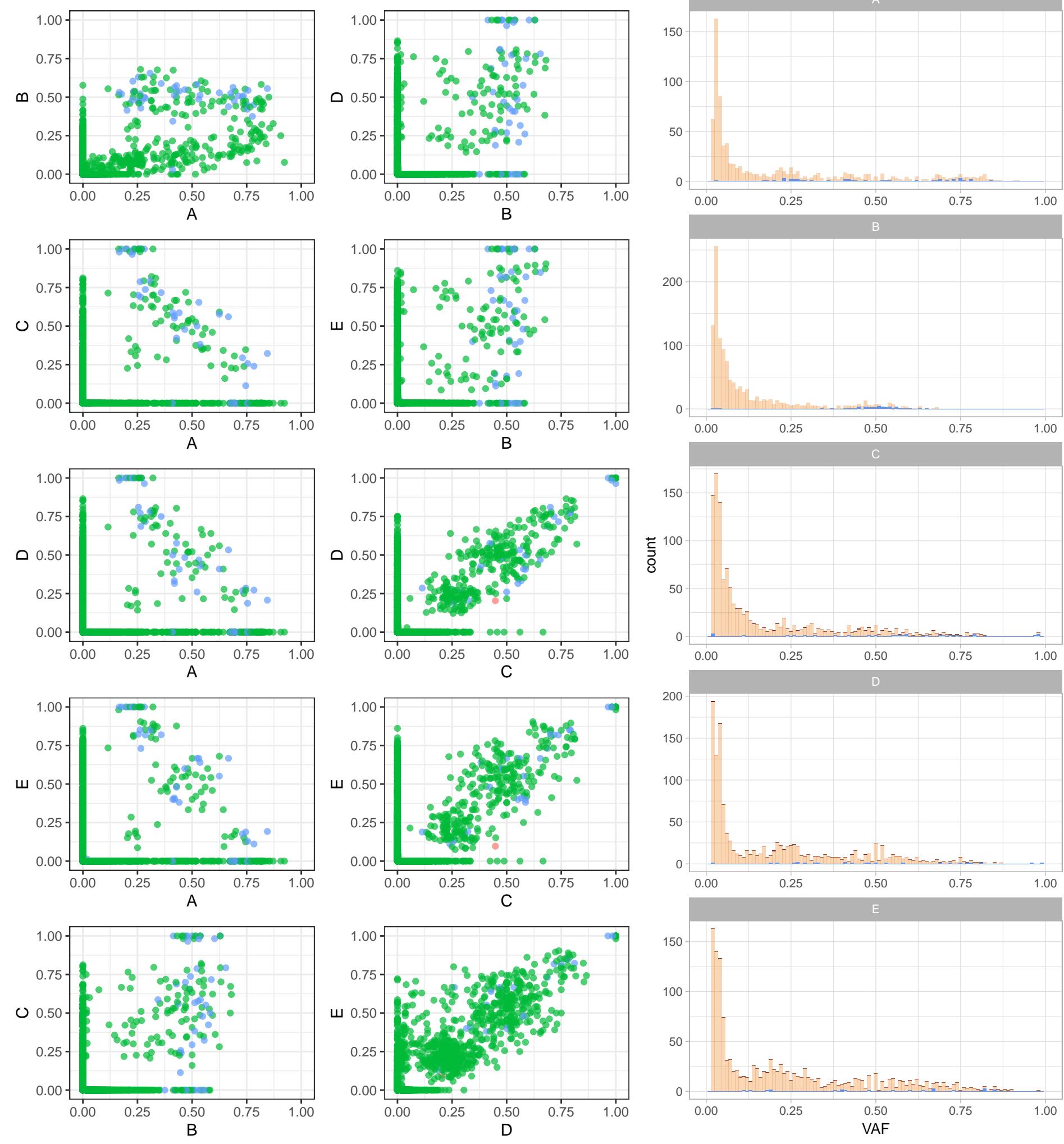
Chromosome 7

Chromosome 7



Chromosome 12

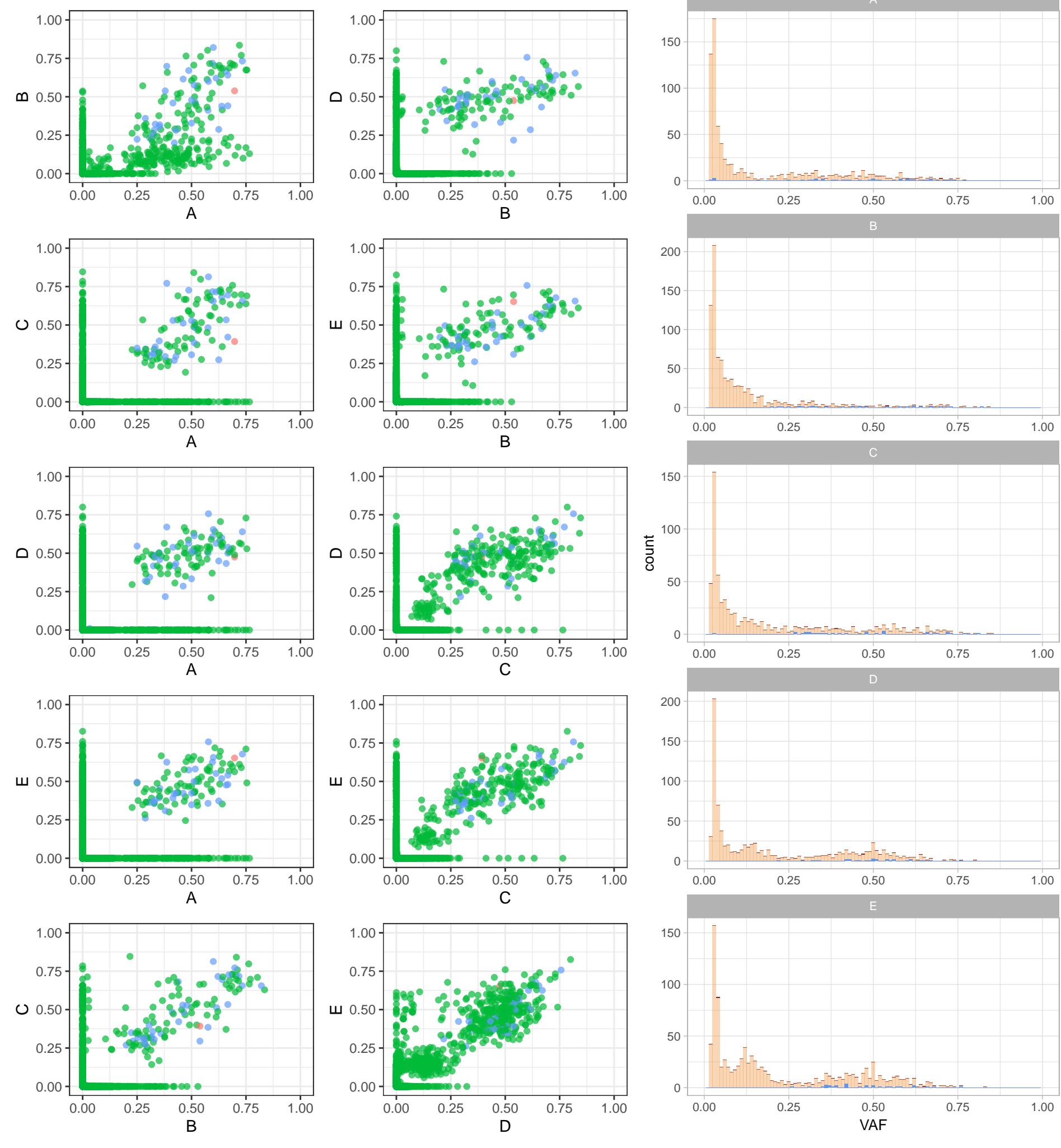
Chromosome 12



labels ● driver ● passenger ● pre-neoplastic classes ■ driver ■ passenger ■ pre-neoplastic

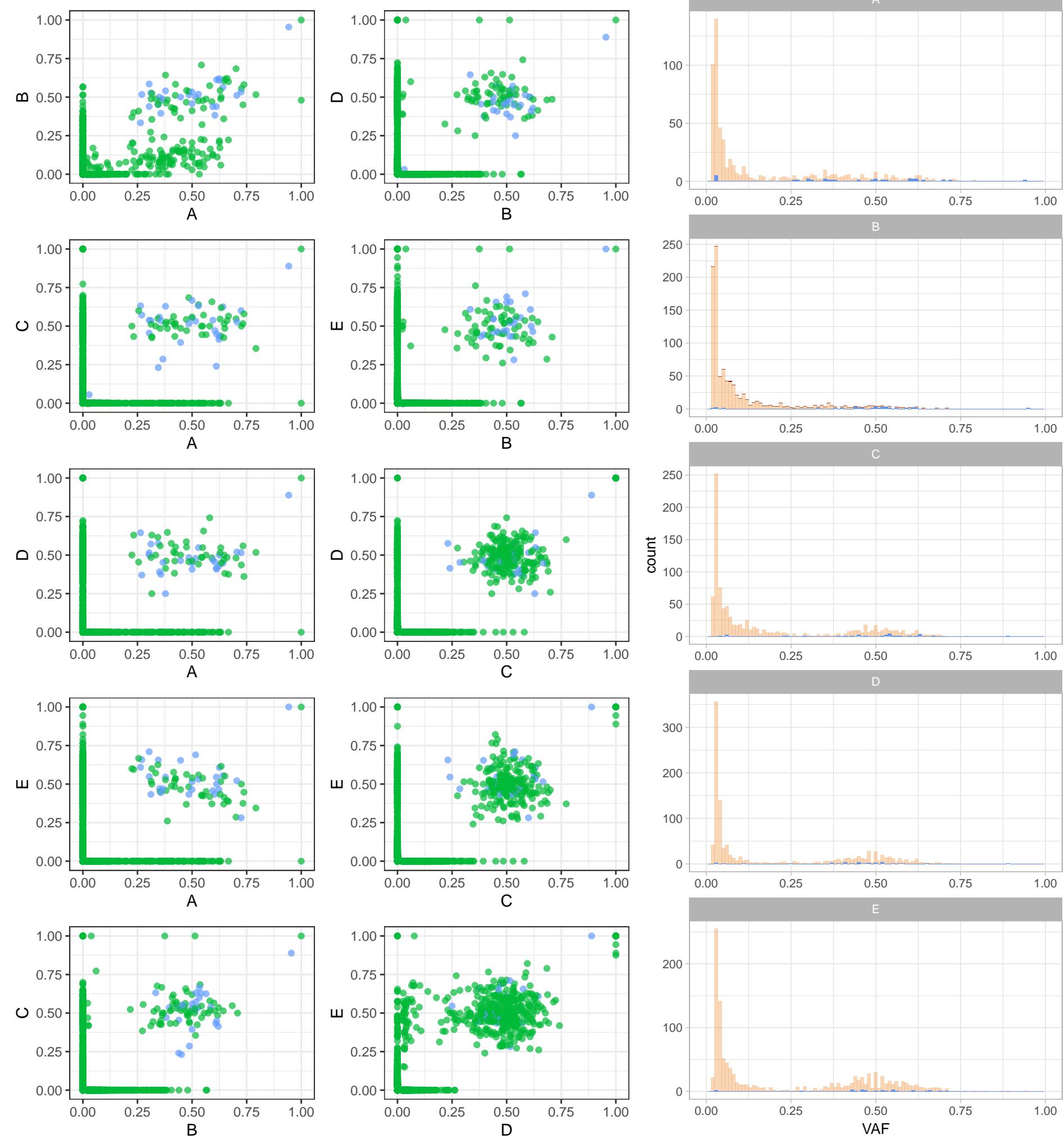
Chromosome 17

Chromosome 17



Chromosome 19

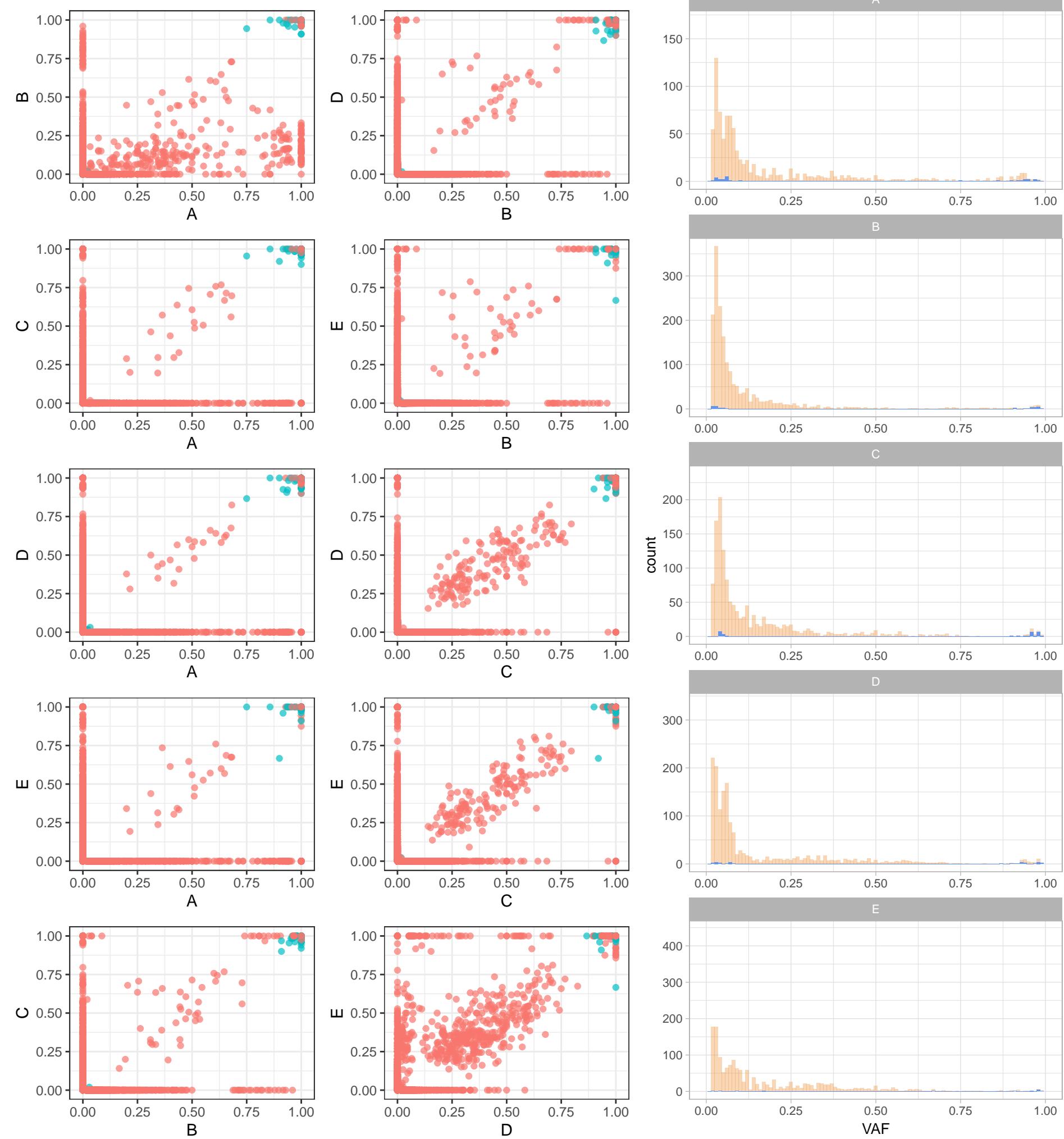
Chromosome 19



labels driver passenger pre-neoplastic classes driver passenger pre-neoplastic

Chromosome X

Chromosome X

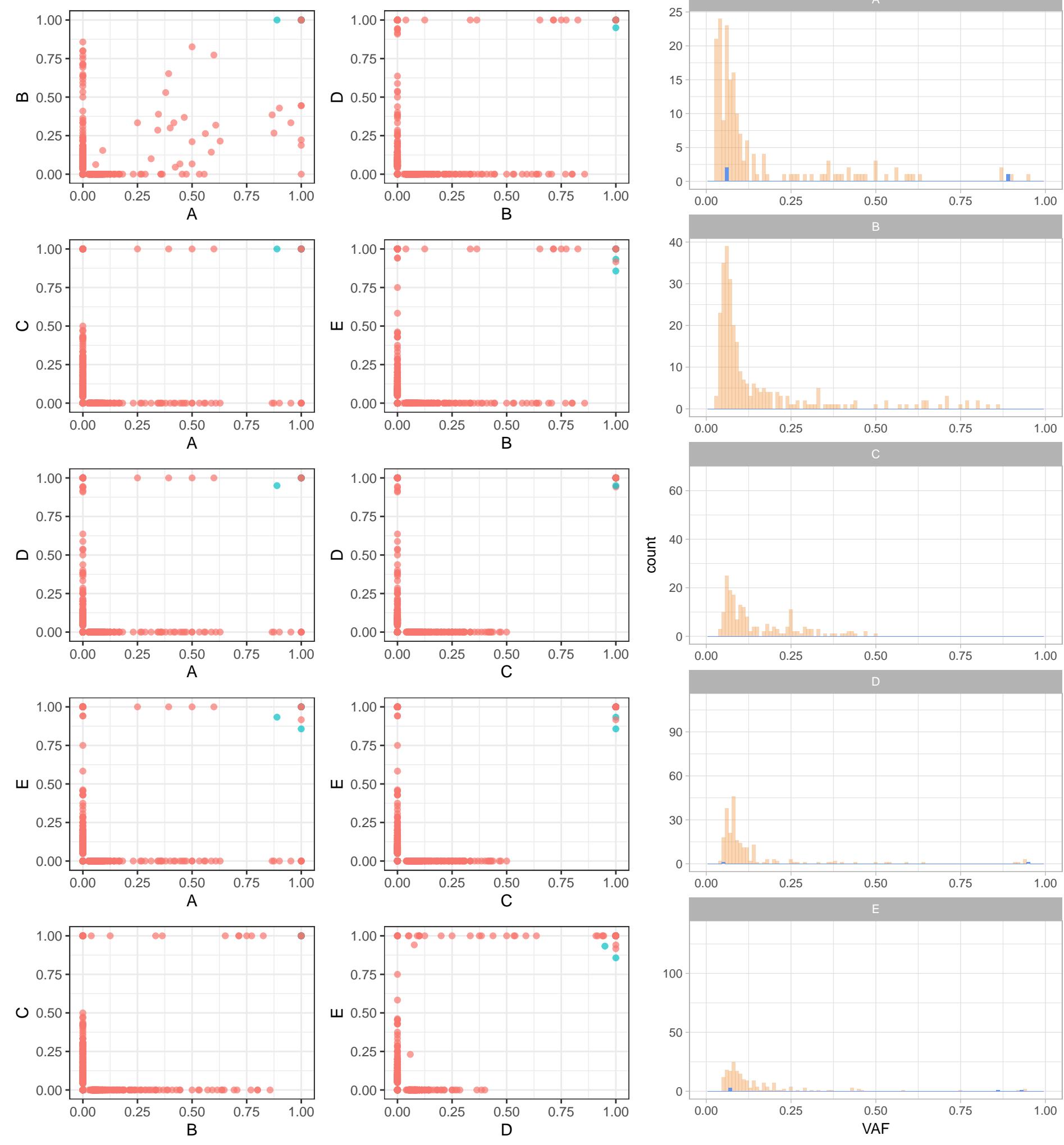


labels ● passenger ● pre-neoplastic

classes orange passenger blue pre-neoplastic

Chromosome Y

Chromosome Y



labels

● passenger ● pre-neoplastic

classes

● passenger ● pre-neoplastic

Mutational signatures

