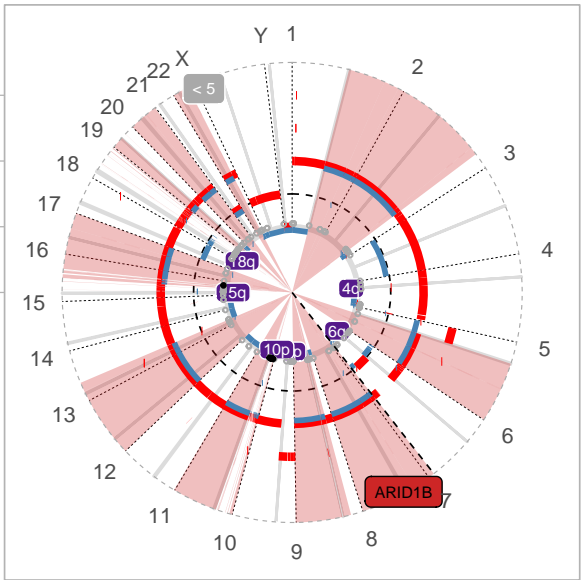


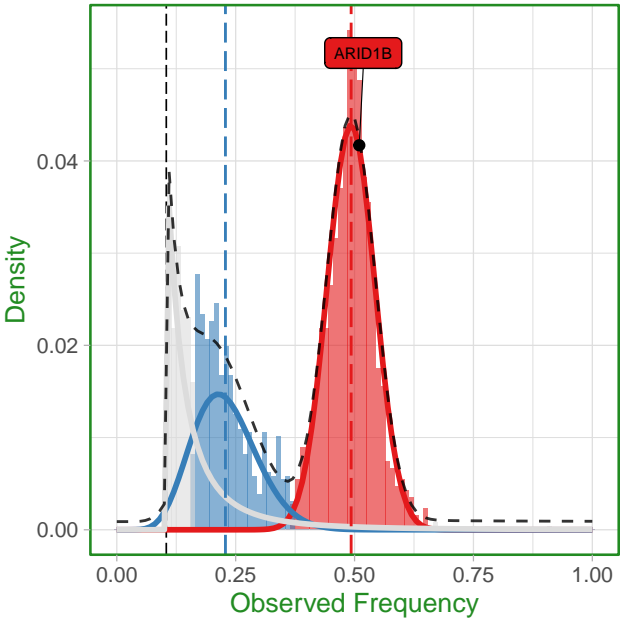
Example CCF deconvolution



■ 2:2 ■ Major allele ■ minor allele

ty 0.92; n = 2831 mutations in 221 segments; 10 fragmented arms

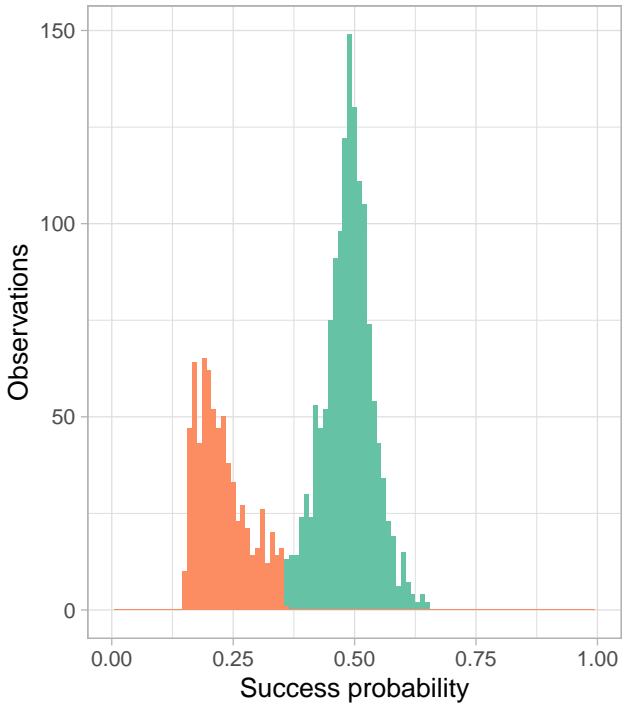
QC PASS  $p_{\text{PASS}} = 0.97$   
n = 2565; Tail 20.4%, C2 24.6%, C1 54.9%



Cluster ■ C1 ■ C2 ■ Tail

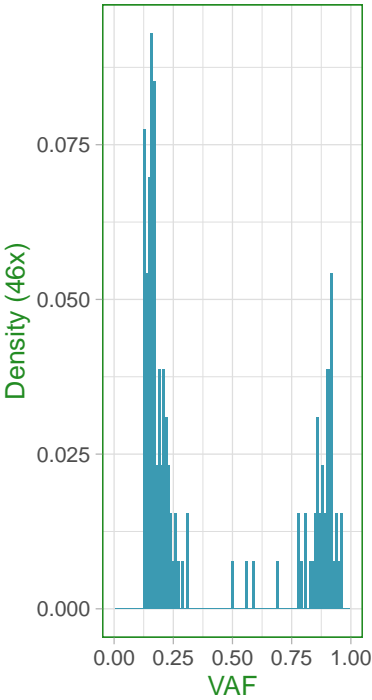
MM (100 steps;  $\epsilon = 2e-04$ ),  $z_{nk} > 0$

n = 2158, BBin 1 67%, BBin 2 33%



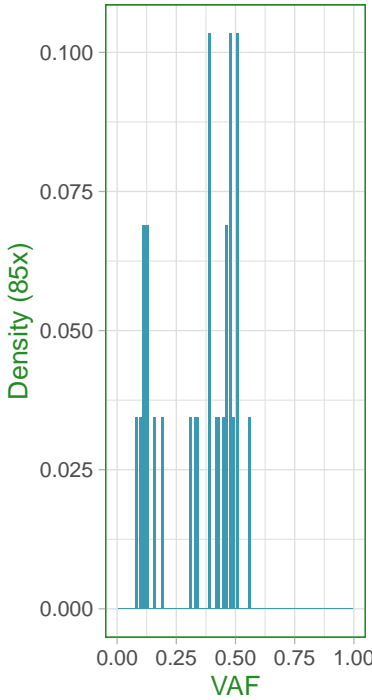
Cluster ■ BBin 1 ■ BBin 2

Mutation multiplicity



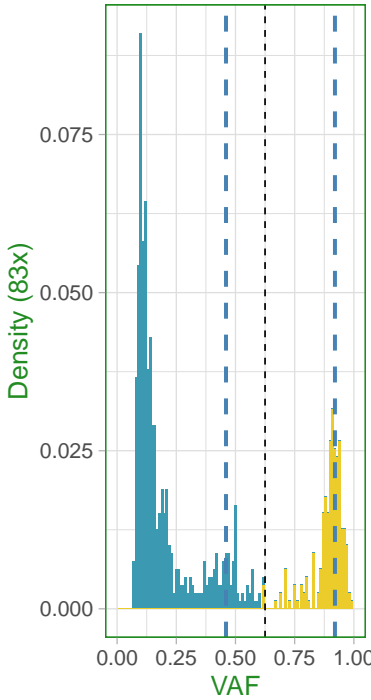
Copies ■ 1 ■ 2

Mutation multiplicity



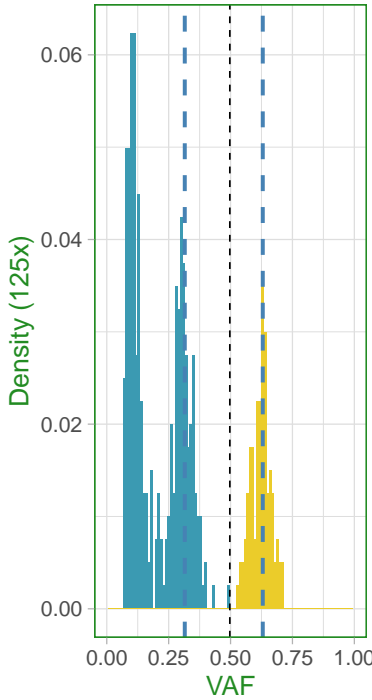
Copies ■ 1 ■ 2

Mutation multiplicity



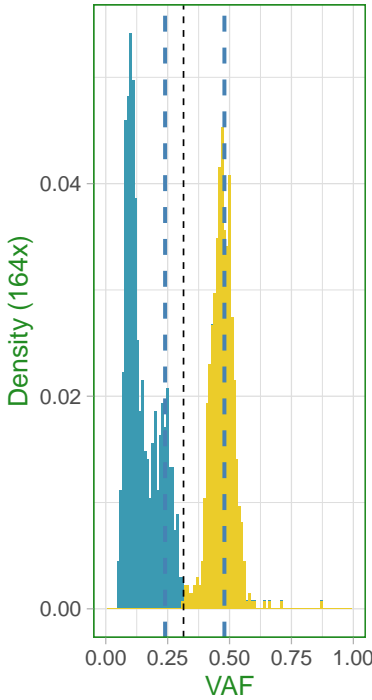
Copies ■ 1 ■ 2

Mutation multiplicity



Copies ■ 1 ■ 2

Mutation multiplicity



Copies ■ 1 ■ 2