sample1

called ... null

Fraction cancer nuclei($\hat{\alpha}$)

Ploidy($\hat{\tau}$)

Model−based evaluation

Log−likelihood

SCNAs ... karyotype ... combined
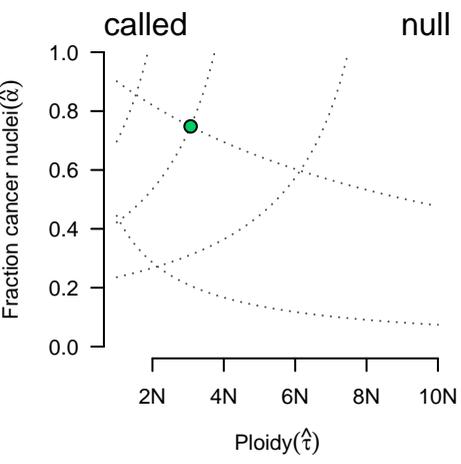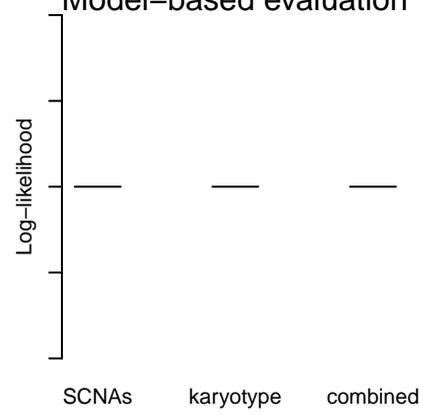
purity($\hat{\alpha}$) = 0.75, ploidy: $\hat{\tau}$ = 3.07, $\hat{\tau}_g$ = 3.09
$\hat{\sigma}_H$ = 0.008, $\hat{\theta}_Z$ = 0, %Het = 0.13
SCNAs = 470.68, Kar = −46.23, SSNVs = NA

Genomic fraction

Copy ratio