Mutation and polymorphism calling settings

θ_1 --consensus-frequency-cutoff
     (DEFAULT = consensus mode, 0.8; polymorphism mode, 0.95)

θ_c --polymorphism-frequency-cutoff
     (DEFAULT = consensus mode, 0.2; polymorphism mode, 0.05)

S_1 --consensus-score-cutoff
     (DEFAULT= 10)

S_θ --polymorphism-score-cutoff
     (DEFAULT = consensus mode, 10; polymorphism mode, 2)

C_1 --consensus-minimum-coverage-each-strand
     (DEFAULT = 0)

C_θ --polymorphism-minimum-coverage-each-strand
     (DEFAULT = consensus mode, 0; polymorphism mode, 2)

α_c --polymorphism-bias-cutoff
     (DEFAULT = OFF)

Indel / homopolymer settings

--polymorphism-no-indels
     (DEFAULT = FALSE)

--polymorphism-reject-indel-homopolymer-length
     (DEFAULT = OFF; polymorphism mode, 3)

--polymorphism-reject-surrounding-homopolymer-length
     (DEFAULT = OFF; polymorphism mode, 2)

Read Alignment (RA) evidence attributes

A_R Reference allele

A_1 Major allele

A_θ Minor allele

θ Frequency of major allele

Consensus score

E_1 E-value of posterior probability of consensus model (θ_{test} = 100%)

Polymorphism score

E_θ E-value of LRT of polymorphic model with ($\theta_{test} = \theta$) versus the consensus model

$C_{1,top}/C_{1,bot}$ Reads with major allele on top/bottom strand

$C_{\theta,top}/C_{\theta,bot}$ Reads with variant allele on top/bottom strand

p_s Read strand bias (Fisher's exact test)

p_q Base quality bias (Kolmogorov-Smirnov test)