

**Mutation and polymorphism calling settings**

- $\theta_1$  --consensus-frequency-cutoff  
(DEFAULT = consensus mode, 0.8; polymorphism mode, 0.95)
- $\theta_c$  --polymorphism-frequency-cutoff  
(DEFAULT = consensus mode, 0.1; polymorphism mode, 0.0)
- $S_1$  --consensus-score-cutoff  
(DEFAULT= 10)
- $S_\theta$  --polymorphism-score-cutoff  
(DEFAULT = consensus mode, 10; polymorphism mode, 2)
- $C_1$  --consensus-minimum-coverage-each-strand  
(DEFAULT = 0)
- $C_\theta$  --polymorphism-minimum-coverage-each-strand  
(DEFAULT = consensus mode, 0; polymorphism mode, 2)
- $\alpha_c$  --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
- $A_\theta$  Minor allele
- $\theta$  Frequency of major allele
- Consensus score**
  - $E_1$  E-value of posterior probability of consensus model ( $\theta_{\text{test}} = 100\%$ )
- Polymorphism score**
  - $E_\theta$  E-value of LRT of polymorphic model with ( $\theta_{\text{test}} = \theta$ ) 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)