

cisMuton

- Prep filters: mapping-quality and base-quality filters



- Variant extraction: Fisher's exact test
 - P -value, proportion ratio (~odds ratio), FG count



- Noise filter set 1
 - Misalignment filter
 - Strand-bias filter
 - Within-long homopolymer filter
 - MQ0 filter
 - Read-end-call filter
 - Surrounded-by-dust filter
 - Abnormal-BQ-drop filter (for Ion indels only)

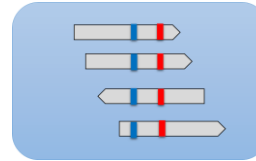


- Noise filter set 2
 - Second Fisher filter
 - Erroneous-read filter and trimming filter

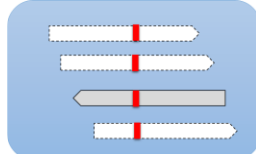


- Noise filter set 3
 - VAF-lees filter

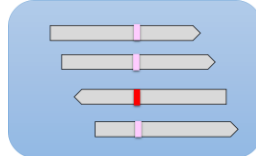
Misalignment filter



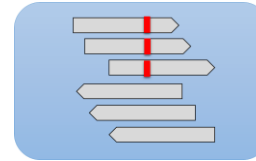
MQ0 filter



Abnormal-BQ-drop filter



Strand-bias filter



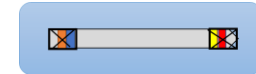
Read-end-call filter



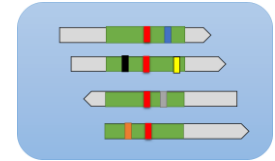
Mismatch filter



Trim filter



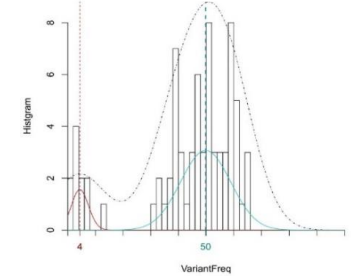
Within-long homopolymer filter



Surrounded-by-dust filter



VAF-lees filter



(Kato et al, 2018, *Genome Medicine*)