

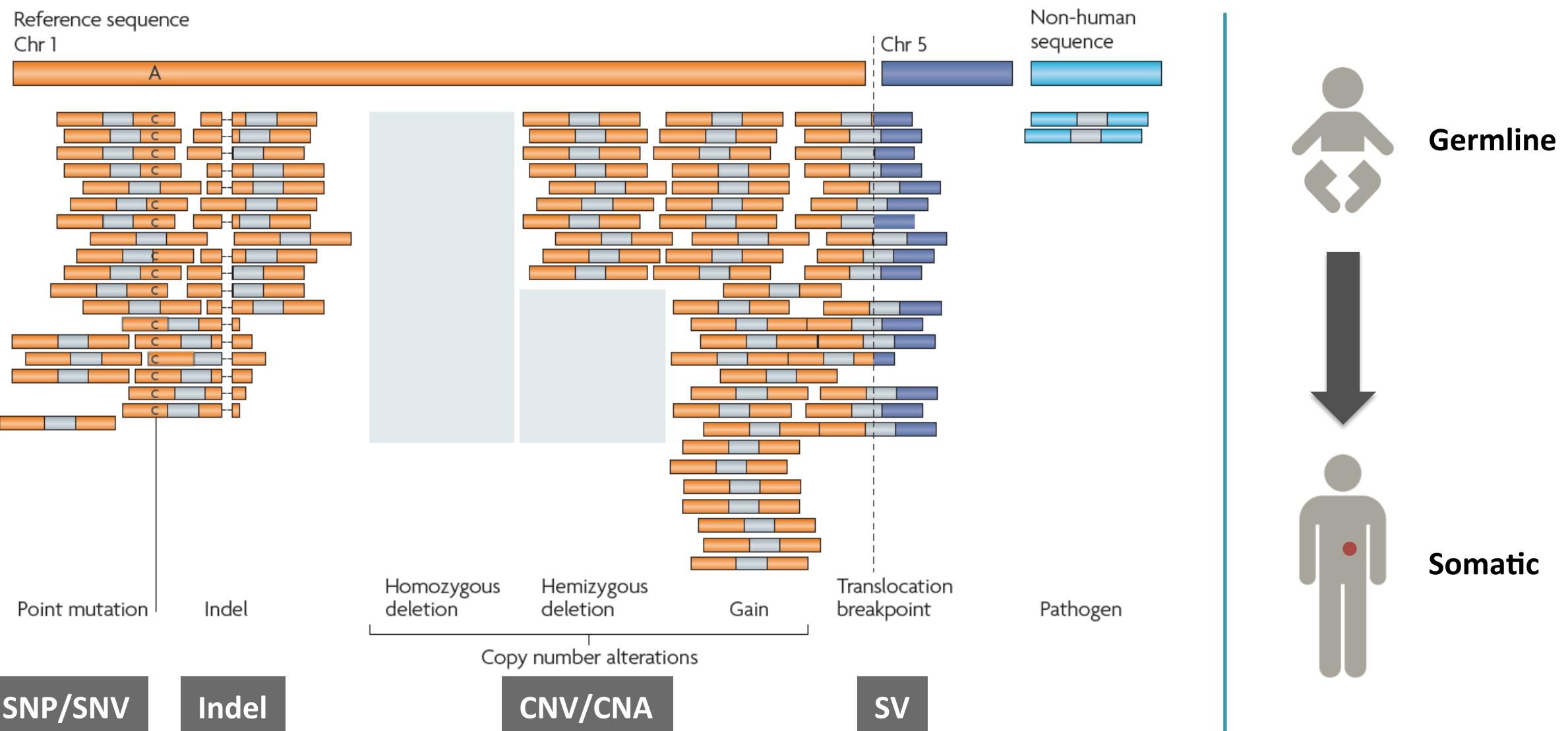


# GATK Best Practices for Variant Discovery

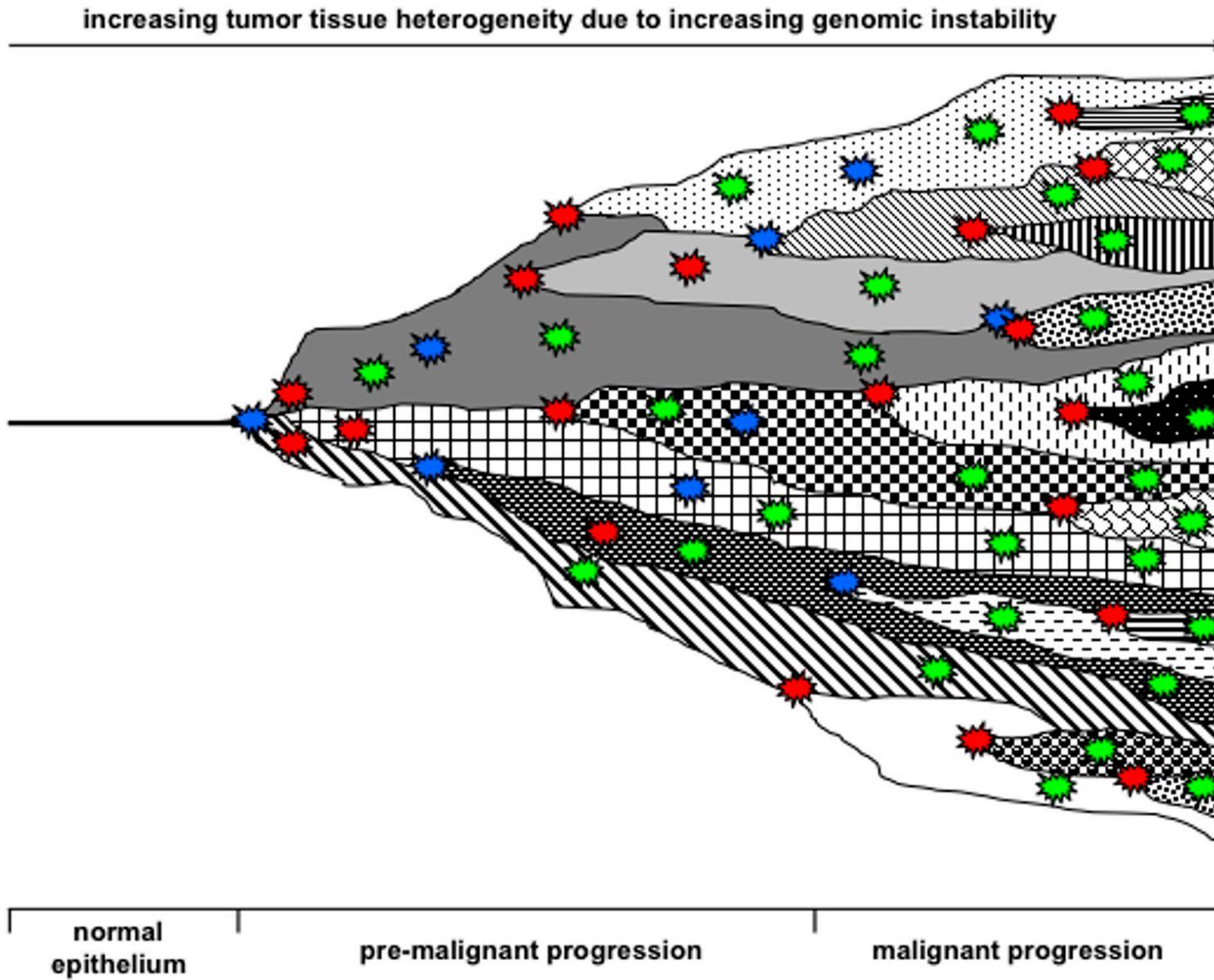


## Basics of Somatic Variant Discovery

# Different types of variants



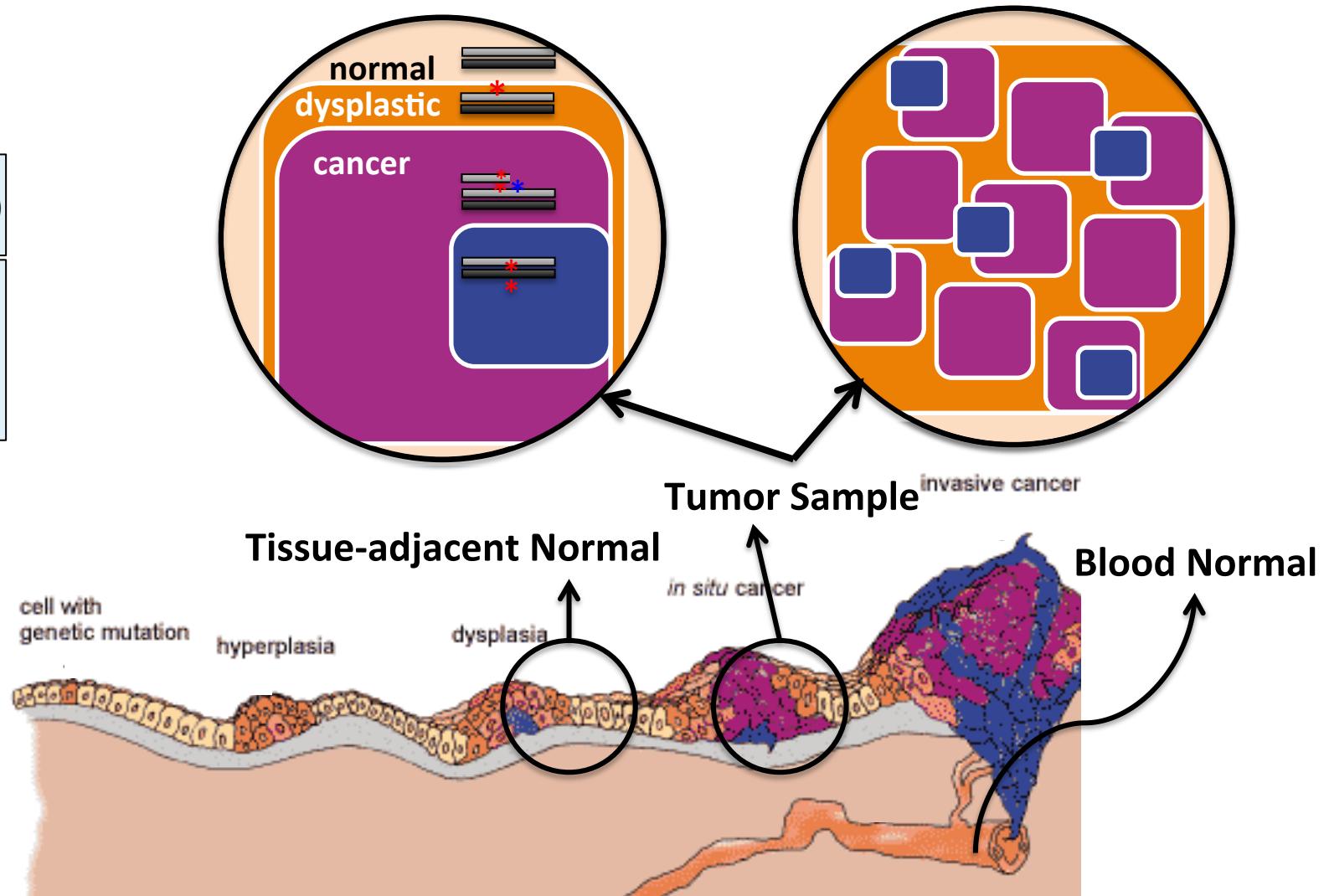
# Role of mutation events in tumor progression



# Tumor and normal contamination and heterogeneity

**Tumor purity** =  $\frac{\text{(tumor cells)}}{\text{(normal + tumor cells)}}$

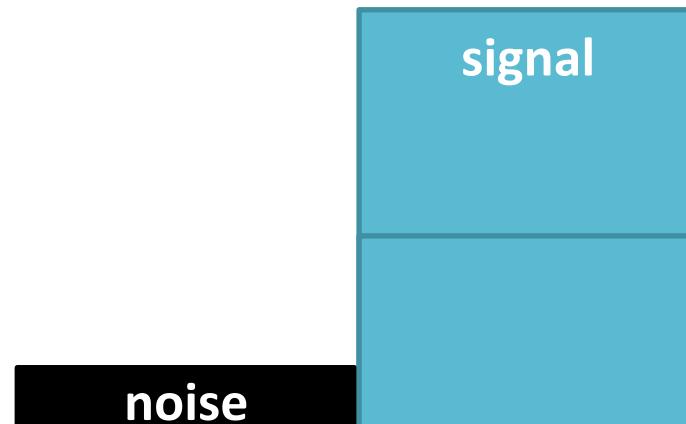
Tumor **heterogeneity** is based on polygenic populations, segregated or intermixed, due to ongoing subclonal evolution.



# Amount of signal may be comparable to noise

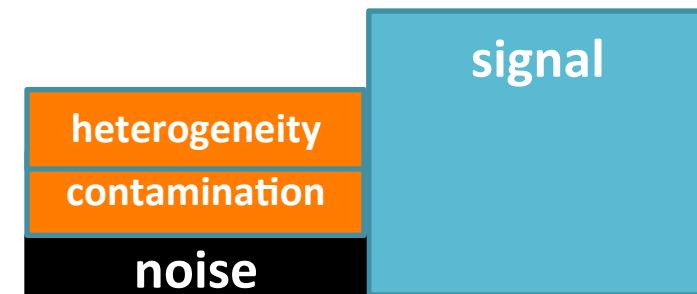
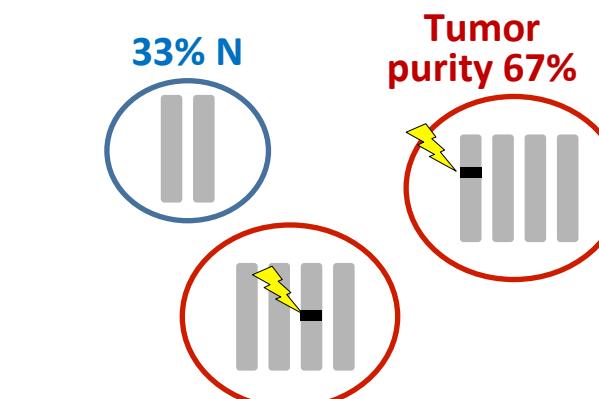


## Expectation for germline variants



+ AF expected to follow ploidy

## Expectation for somatic variants

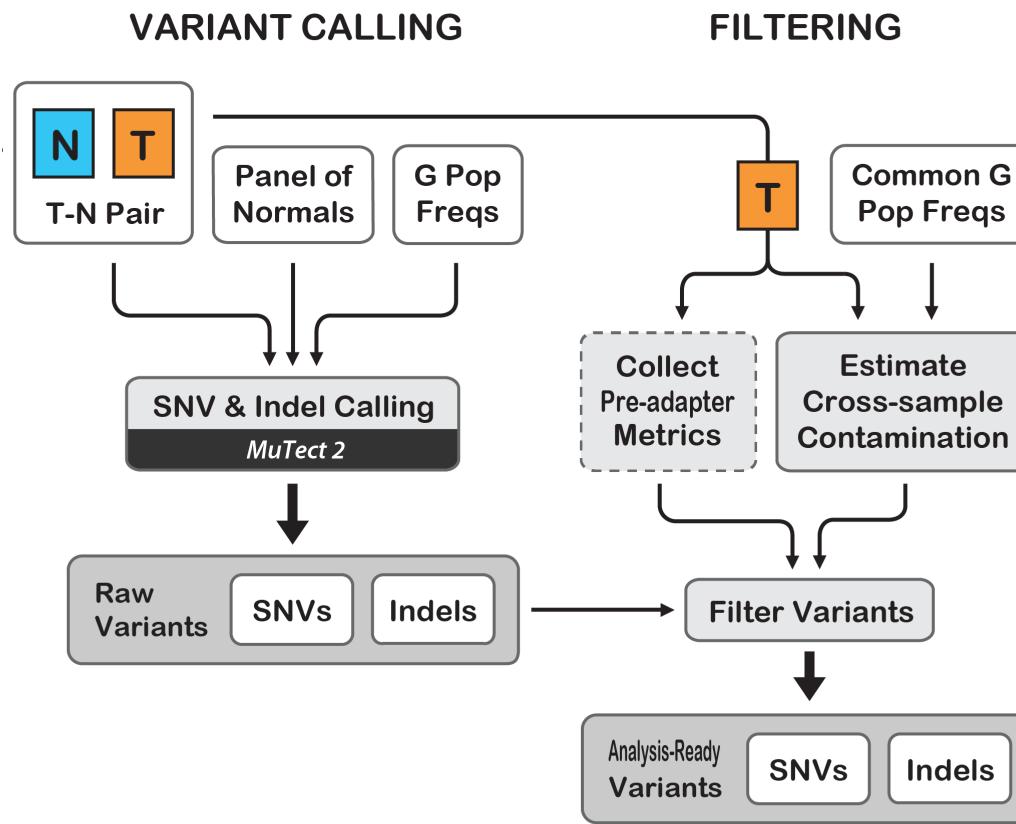


+ no reliance on ploidy for AF

# Somatic variant discovery workflows in GATK4



## Somatic SNV and Indel Discovery



## Somatic CNV Discovery

