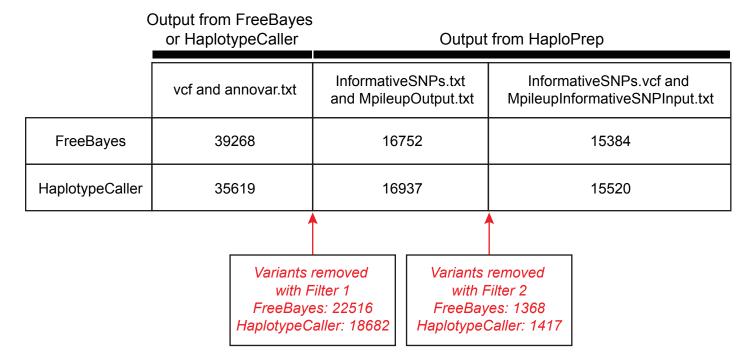
## Variant Caller Benchmark Test

## **Variant Count:**



**Filter 1:** Filters for SNPs with a population allele frequency ≥ 1% in the 1000 Genomes database and read allele frequency between 30-70% (heterozygous).

**Filter 2:** Filters SNPs based on actual read data; filters for variants with read allele frequency between 40-60% and read depth  $\geq 10$ .

## InformativeSNPs.vcf comparison:

	Total SNPs Found	Duplicates	Duplicates Removed	Overlapping SNPs	Unique SNPs	% Overlap	% Unique
FreeBayes	15384	17	15367	15176	191	98.76%	1.24%
HaplotypeCaller	15520	0	15520	15176	344	97.78%	2.22%