Variants Calling

Task Name: snp

Call variants for an input assembly and a reference sequence using SAMtools mpileup and bcftool

Parameters:

bam - Input sorted BAM file(s) [Url datasets]

ref - Input reference sequence [Url datasets]

wout - Out file with variations [String]

bN - A/C/G/T only [Boolean]

bI - List of sites [String]

ml - BED or position list file [String]

bg - Per-sample genotypes [Boolean]

mC - Mapping quality downgrading coefficient [Number]

bT - Pair/trio calling [String]

mB - Disable BAQ computation [Boolean]

me - Gap extension error [Number]

mE - Extended BAQ computation [Boolean]

bF - Indicate PL [Boolean]

vw - Gap size [Number]

m6 - Illumina-1.3+ encoding [Boolean]

bi - INDEL-to-SNP Ratio [Number]

bA - Retain all possible alternate [Boolean]

vD - Max number of reads per input BAM [Number]

md - Max number of reads per input BAM [Number]

mL - Max INDEL depth [Number]

va - Alternate bases [Number]

v2 - BaseQ bias [String]

vd - Minimum read depth [Number]

v4 - End distance bias [Number]

v3 - MapQ bias [Number]

Q - Minimum RMS quality [Number]

v1 - Strand bias [Number]

mQ - Minimum base quality [Number]

mq - Minimum mapping quality [Number]

bd - Min samples fraction [Number]

b1 - N group-1 samples [Number]

bU - N permutations [Number]

bG - No genotype information [Boolean]

mI - No INDELs [Boolean]

mo - Gap open error [Number]

mP - List of platforms for indels [String]

vp - Log filtered [Boolean]

bP - Prior allele frequency spectrum. [String]

bQ - QCALL likelihood [Boolean]

mr - Pileup region [String]

bs - List of samples [String]

mh - Homopolymer errors coefficient [Number]

bt - Mutation rate [Number]

mA - Count anomalous read pairs [Boolean]

vW - A/C/G/T only [Number]

Example:

```
ugene snp --bam=test.bam --ref=test_ref.fa --wout=test_out.vcf
```