

Genome	hg19
Date	2021-08-18 08:18
Snpeff version	Snpeff 4.3t (build 2017-11-24 10:18), by Pablo Cingolani
Command line arguments	Snpeff -i vcf -o vcf -formatEff -classic -sequenceOntology -noShiftHgvs -noHgvs -geneId -oicr -lof -noLoF -cancer -stats /data/dnb03/galaxy_db/job_working_directory/027/360/27360542/outputs/galaxy_dataset_0402a81d-20c0-4dc0-a9af-a741ef965b68.dat hg19 /data/dnb03/galaxy_db/files/2/a/0/dataset_2a0b52c8-c45f-40d5-af4a-9f9f34745587.dat
Warnings	31
Errors	0
Number of lines (input file)	10,671
Number of variants (before filter)	10,671
Number of not variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	10,671
Number of known variants (i.e. non-empty ID)	0 ( 0% )
Number of multi-allelic VCF entries (i.e. more than two alleles)	0
Number of effects	12,825
Genome total length	3,137,161,265
Genome effective length	3,038,627,131
Variant rate	1 variant every 284,755 bases

## Variations

