SnpEff: Variant analysis

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Summary

Genome	GRCh38.99
Date	2025-01-02 05:11
SnpEff version	`SnpEff 5.2e (build 2024-10-04 18:09), by Pablo Cingolani`
Command line arguments	`SnpEff -no-upstream -no-downstream -no-utr -o vcf GRCh38.99 rs7903146_normalized.vcf`
Warnings	2
Errors	0
Number of lines (input file)	2
Number of variants (before filter)	2
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	2
Number of known variants (i.e. non-empty ID)	2 (100%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	0
Number of annotations	28
Genome total length	63,147,197,748
Genome effective length	133,797,422
Variant rate	1 variant every 66,898,711 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
10	133,797,422	2	66,898,711
Total	**133,797,422**	**2**	**66,898,711**

Number variants by type

Type	Total
SNP	2
MNP	0
INS	0
DEL	0
MIXED	0
INV	0
DUP	0
CNV	0
BND	0
INTERVAL	0
Total	**2**

Number of effects by impact

Type (alphabetical order)	Count	Percent
MODIFIER	28	100%

Number of effects by functional class

Type (alphabetical order)	Count	Percent

Missense / Silent ratio: 0

Number of annotaitons and region counts

Annotation	Region

Type (alphabetical order)	Count	Percent
intron_variant	28	100%

Type (alphabetical order)	Count	Percent
INTRON	28	100%

Quality:

Insertions and deletions length:

Base changes (SNPs)

	A	C	G	T
A	0	0	0	0
C	0	0	1	1
G	0	0	0	0
T	0	0	0	0

Ts/Tv (transitions / transversions)

Note: Only SNPs are used for this statistic.
Note: This Ts/Tv ratio is a 'raw' ratio (ratio of observed events).

Transitions	1
Transversions	1
Ts/Tv ratio	1

All variants:

```
Sample ,Total
Transitions ,1,1
Transversions ,1,1
Ts/Tv ,1.000,1.000
```

Only known variants (i.e. the ones having a non-empty ID field):

```
Sample ,Total
Transitions ,1,1
Transversions ,1,1
Ts/Tv ,1.000,1.000
```

Allele frequency

Allele Count

Min	1
Max	1
Mean	1
Median	1
Standard deviation	0
Values	1
Count	2

Hom/Het per sample

```
Sample_names
Reference
Het
Hom
Missing
```

Codon changes

How to read this table:
- Rows are reference codons and columns are changed codons. E.g. Row 'AAA' column 'TAA' indicates how many 'AAA' codons have been replaced by 'TAA' codons.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

Amino acid changes

How to read this table:
- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

Variants by chromosome

10, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000,13000000,1400000
10,Count,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0

Details by gene

Here you can find a tab-separated table.