SnpEff: Variant analysis

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Summary

Genome	reference_db
Date	2025-12-06 00:56
SnpEff version	SnpEff 5.1d (build 2022-04-19 15:49), by Pablo Cingolani
Command line arguments	SnpEff -stats results/snpEff/snpEff.html reference_db results/variants/filtered_variants.vcf
Warnings	1
Errors	0
Number of lines (input file)	30
Number of variants (before filter)	30
Number of not variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	30
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	30
Genome total length	67,646
Genome effective length	67,646
Variant rate	1 variant every 2,254 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
NG_013302.2	67,646	30	2,254
Total	**67,646**	**30**	**2,254**

Number variants by type

Type	Total
SNP	26
MNP	0
INS	2
DEL	2
MIXED	0
INV	0
DUP	0
BND	0
INTERVAL	0
Total	**30**

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	1	3.333%
LOW	2	6.667%
MODIFIER	27	90%

Number of effects by functional class

Type (alphabetical order)	Count	Percent
NONSENSE	1	33.333%
SILENT	2	66.667%

Missense / Silent ratio: 0

Number of effects by type and region

Type

Type (alphabetical order)	Count	Percent
intergenic_region	10	33.333%
intron_variant	17	56.667%
stop_gained	1	3.333%
synonymous_variant	2	6.667%

Region

Type (alphabetical order)	Count	Percent
EXON	3	10%
INTERGENIC	10	33.333%
INTRON	17	56.667%

Quality:

Min	30
Max	265
Mean	93.067
Median	78
Standard deviation	40.265

Values	30,54,63,70,72,73,77,78,109,116,120,121,123,265
Count	1,1,1,2,1,3,1,9,3,1,1,4,1,1

Insertions and deletions length:

Min	0
Max	1
Mean	0.5
Median	0.5
Standard deviation	0.577
Values	0,1
Count	2,2

Base changes (SNPs)

	A	C	G	T
A	0	1	4	1
C	0	0	1	4
G	5	0	0	2
T	0	7	1	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	30
Transversions	9
Ts/Tv ratio	3.3333

All variants:

```
Sample ,sample1,Total
Transitions ,30,30
Transversions ,9,9
Ts/Tv ,3.333,3.333
```

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

```
No results available (empty input?)
```

Allele frequency

Min	50
Max	100
Mean	76.667
Median	100
Standard deviation	25.371
Values	50,100
Count	14,16

Allele Count

Min	1
Max	2
Mean	1.533
Median	2
Standard deviation	0.507
Values	1,2
Count	14,16

Hom/Het per sample

```
Sample_names , sample1
Reference , 0
Het , 14
Hom , 16
Missing , 0
```

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).

	GAA	GAC	GAT	TAA	TCC	TCT
GAA				1		
GAC			1			
GAT						
TAA						
TCC						
TCT					1	

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).

	*	D	E	S
*				
D		1		
E	1			
S				1

Variants by chromosome

```
NG_013302.2, Position,0,1000,2000,3000,4000,5000,6000,7000,8000,9000,10000,11000,12000,13000,14000,15000,16000,17000,18000,19000,20000,21000,22000,23000,24000
NG_013302.2,Count,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,14,0,0,0,0,0,0,0,0,0,2,0,0,0,0,0,3,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,10,0,0,0,0,0,0,0
```

Details by gene

Here you can find a tab-separated table.