SnpEff: Variant analysis

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Summary

Genome	reference_db
Date	2025-12-07 17:12
SnpEff version	`SnpEff 5.4a (build 2025-11-25 12:22), by Pablo Cingolani`
Command line arguments	`SnpEff  -stats results/snpEff/snpEff.html reference_db results/variants/filtered_variants.vcf`
Warnings	5
Errors	0
Number of lines (input file)	182
Number of variants (before filter)	184
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	184
Number of known variants (i.e. non-empty ID)	0 (0%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	2
Number of annotations	184
Genome total length	112,164
Genome effective length	112,164
Variant rate	1 variant every 609 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
NG_053114.1	112,164	184	609
Total	**112,164**	**184**	**609**

Number variants by type

Type	Total
SNP	177
MNP	0
INS	7
DEL	0
MIXED	0
INV	0
DUP	0
CNV	0
BND	0
INTERVAL	0
Total	**184**

Number of effects by impact

Type (alphabetical order)	Count	Percent
MODIFIER	184	100%

Number of effects by functional class

Type (alphabetical order)	Count	Percent

Missense / Silent ratio: 0

Number of annotaitons and region counts

Annotation

Type (alphabetical order)	Count	Percent
intron_variant	184	100%

Region

Type (alphabetical order)	Count	Percent
INTRON	184	100%

Quality:

Min	30
Max	2,911
Mean	647.56
Median	358
Standard deviation	728.009
Values	30,31,35,37,38,46,48,51,52,53,55,58,59,64,73,78,82,85,104,105,112,121,127,134,136,165,166,172,181,194,206,210,226,232,233,242,244,276,281,298,301,302,319,327,346,370,3[illegible]
Count	2,7,13,1,1,2,2,2,1,2,1,2,1,2,3,14,1,1,1,1,1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,3,1,1,1,4,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,4,1,1,2,1,1,2,3,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,

Insertions and deletions length:

Min	0
Max	2
Mean	0.571
Median	0
Standard deviation	0.787
Values	0,1,2
Count	4,2,1

Base changes (SNPs)

	A	C	G	T
A	0	3	35	9
C	5	0	4	30
G	24	11	0	6
T	16	28	6	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	184
Transversions	102
Ts/Tv ratio	1.8039

All variants:

```
Sample ,sample1,Total
Transitions ,184,184
Transversions ,102,102
Ts/Tv ,1.804,1.804
```

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	83.516
Median	100
Standard deviation	23.57
Values	50,100
Count	60,122

Allele Count

Min	1
Max	2
Mean	1.67
Median	2
Standard deviation	0.471
Values	1,2
Count	60,122

Hom/Het per sample

```
Sample_names , sample1
Reference , 0
Het , 60
Hom , 122
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).

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

```
                NG_053114.1, 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_053114.1,Count,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,8,2,0,0,0,0,0,0,0,0,0,7,0,0,0,0,4,36,61,17,6,0,0,0,0,0,0,14,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
```

Details by gene

Here you can find a tab-separated table.