SnpEff: Variant analysis

Contents

Summary

Genome	reference_db
Date	2025-12-06 23:25
SnpEff version	`SnpEff 5.2b (build 2023-11-28 15:56), by Pablo Cingolani`
Command line arguments	`SnpEff -stats results/snpEff/snpEff.html reference_db results/variants/filtered_variants.vcf`
Warnings	9
Errors	0
Number of lines (input file)	16
Number of variants (before filter)	16
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	16
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 annotations	133
Genome total length	32,772
Genome effective length	32,772
Variant rate	1 variant every 2,048 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
NG_017013.2	32,772	16	2,048
Total	**32,772**	**16**	**2,048**

Number variants by type

Type	Total
SNP	14
MNP	0
INS	1
DEL	1
MIXED	0
INV	0
DUP	0
BND	0
INTERVAL	0
Total	**16**

Number of effects by impact

Type (alphabetical order)	Count	Percent
MODIFIER	133	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**	**Type (alphabetical order)**	**Count**	**Percent**
5_prime_UTR_variant	4	3.008%	**DOWNSTREAM**	32	24.06%
downstream_gene_variant	32	24.06%	**INTERGENIC**	4	3.008%
intergenic_region	4	3.008%	**INTRON**	83	62.406%
intron_variant	83	62.406%	**UPSTREAM**	10	7.519%
upstream_gene_variant	10	7.519%	**UTR_5_PRIME**	4	3.008%

Quality:

Min	68
Max	150
Mean	89.562
Median	78
Standard deviation	28.1
Values	68,70,73,78,79,82,141,146,150
Count	1,1,1,8,1,1,1,1,1

Insertions and deletions length:

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

Base changes (SNPs)

	A	C	G	T
A	0	0	2	0
C	0	0	2	4
G	4	0	0	0
T	0	0	2	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	18
Transversions	6
Ts/Tv ratio	3

All variants:

```
Sample ,sample1,Total
Transitions ,18,18
Transversions ,6,6
Ts/Tv ,3.000,3.000
```

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	87.5
Median	100
Standard deviation	22.361
Values	50,100
Count	4,12

Allele Count

Min	1
Max	2
Mean	1.75
Median	2
Standard deviation	0.447
Values	1,2
Count	4,12

Hom/Het per sample

```
Sample_names , sample1
Reference , 0
Het , 4
Hom , 12
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_017013.2, Position,0,1000,2000,3000,4000,5000,6000,7000,8000,9000,10000,11000,12000,13000,14000,15000,16000,17000,18000,19000,20000,21000,22000,23000,24000,25000,26000,27000,28000,29000,30000,31000,32000
NG_017013.2,Count,0,0,0,0,0,0,0,1,0,0,0,0,0,0,2,2,2,0,4,1,0,0,0,0,0,4,0,0,0,0
```

Details by gene

Here you can find a tab-separated table.