SnpEff: Variant analysis

Contents

Summary

Genome	reference_db
Date	2025-12-06 23:21
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	0
Errors	0
Number of lines (input file)	13
Number of variants (before filter)	14
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	14
Number of known variants (i.e. non-empty ID)	0 (0%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	1
Number of annotations	16
Genome total length	13,455
Genome effective length	13,455
Variant rate	1 variant every 961 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
NG_007457.2	13,455	14	961
Total	**13,455**	**14**	**961**

Number variants by type

Type	Total
SNP	13
MNP	0
INS	0
DEL	1
MIXED	0
INV	0
DUP	0
BND	0
INTERVAL	0
Total	**14**

Number of effects by impact

Type (alphabetical order)	Count	Percent
MODERATE	1	6.25%
MODIFIER	15	93.75%

Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	1	100%

Missense / Silent ratio: 0

Number of annotaitons and region counts

Annotation			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
downstream_gene_variant	1	6.25%	DOWNSTREAM	1	6.25%
intergenic_region	1	6.25%	EXON	1	6.25%
intragenic_variant	1	6.25%	INTERGENIC	1	6.25%
intron_variant	11	68.75%	INTRON	11	68.75%
missense_variant	1	6.25%	TRANSCRIPT	1	6.25%
upstream_gene_variant	1	6.25%	UPSTREAM	1	6.25%

Quality:

Min	32
Max	295
Mean	98.615
Median	70
Standard deviation	67.778
Values	32,41,45,54,61,70,102,109,115,121,122,295
Count	1,1,1,1,1,1,1,1,2,1,1,1

Insertions and deletions length:

Min	1
Max	1
Mean	1
Median	0.5
Standard deviation	0
Values	1
Count	1

Base changes (SNPs)

	A	C	G	T
A	0	0	1	0
C	0	0	2	2
G	3	0	0	0
T	1	4	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	13
Transversions	4
Ts/Tv ratio	3.25

All variants:

```
Sample ,sample1,Total
Transitions ,13,13
Transversions ,4,4
Ts/Tv ,3.250,3.250
```

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	73.077
Median	50
Standard deviation	25.944
Values	50,100
Count	7,6

Allele Count

Min	1
Max	2
Mean	1.462
Median	1
Standard deviation	0.519
Values	1,2
Count	7,6

Hom/Het per sample

```
Sample_names , sample1
Reference , 0
Het , 7
Hom , 6
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).

	ACC	GCC
ACC		
GCC	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).

	A	T
A		1
T		

Variants by chromosome

```
            NG_007457.2, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,2200,2300,2400,2500,2600,2700,2800,2900,3000,3100,3200,3300,3400,3500,3600,3700,3800,3900,4000,4100,4200,4300,4400,4500,4600,4700,4800,4900,5000,5100,5200,5300,5400,5500,5600,
NG_007457.2,Count,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,8,3,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0
```

Details by gene

Here you can find a tab-separated table.