

SnpEff: Variant analysis

Contents

[Summary](#)
[Variant rate by chromosome](#)
[Variants by type](#)
[Number of variants by impact](#)
[Number of variants by functional class](#)
[Number of variants by effect](#)
[Quality histogram](#)
[InDel length histogram](#)
[Base variant table](#)
[Transition vs transversions \(ts/tv\)](#)
[Allele frequency](#)
[Allele Count](#)
[Codon change table](#)
[Amino acid change table](#)
[Chromosome variants plots](#)
[Details by gene](#)

Summary

Genome	Plasmodium_falciparum
Date	2021-08-13 19:46
SnpEff version	SnpEff 5.0e (build 2021-03-09 06:01), by Pablo Cingolani
Command line arguments	SnpEff Plasmodium_falciparum raw_variants.vcf
Warnings	0
Errors	49,978
Number of lines (input file)	49,441
Number of variants (before filter)	50,421
Number of not variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	49,978
Number of known variants (i.e. non-empty ID)	0 (0%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	980
Number of effects	49,978
Genome total length	23,292,637
Genome effective length	15
Variant rate	1 variant every 0 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
Pf3D7_01_v3	1	0	0
Pf3D7_02_v3	1	0	0
Pf3D7_03_v3	1	0	0
Pf3D7_04_v3	1	0	0
Pf3D7_05_v3	1	0	0
Pf3D7_06_v3	1	0	0
Pf3D7_07_v3	1	0	0
Pf3D7_08_v3	1	0	0
Pf3D7_09_v3	1	0	0
Pf3D7_10_v3	1	0	0
Pf3D7_11_v3	1	0	0
Pf3D7_12_v3	1	0	0
Pf3D7_13_v3	1	0	0
Pf3D7_14_v3	1	0	0
Pf3D7_MIT_v3	1	0	0
Total	15	49,978	0

Number variants by type

Type	Total
SNP	35,228
MNP	0
INS	7,037
DEL	7,713
MIXED	0
INV	0
DUP	0
BND	0
INTERVAL	0
Total	49,978

Number of effects by impact

Type (alphabetical order)	Count	Percent
---------------------------	-------	---------

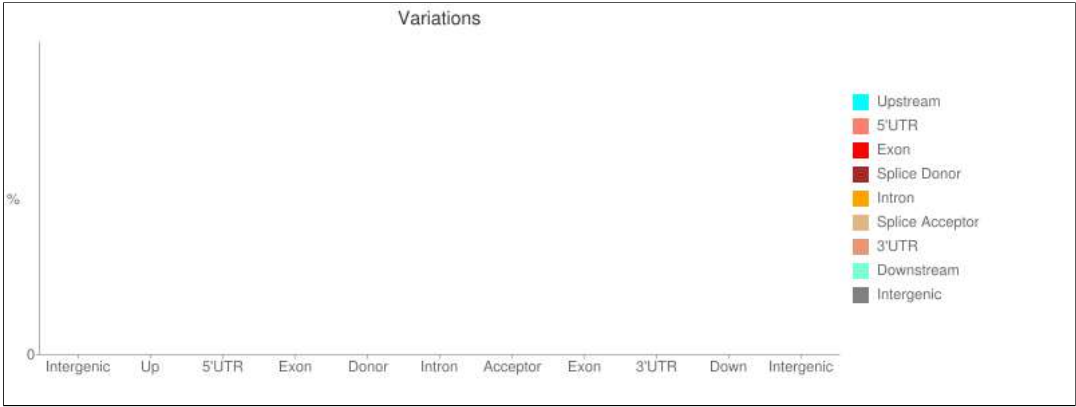
Number of effects by functional class

Type (alphabetical order)	Count	Percent
---------------------------	-------	---------

Missense / Silent ratio: 0

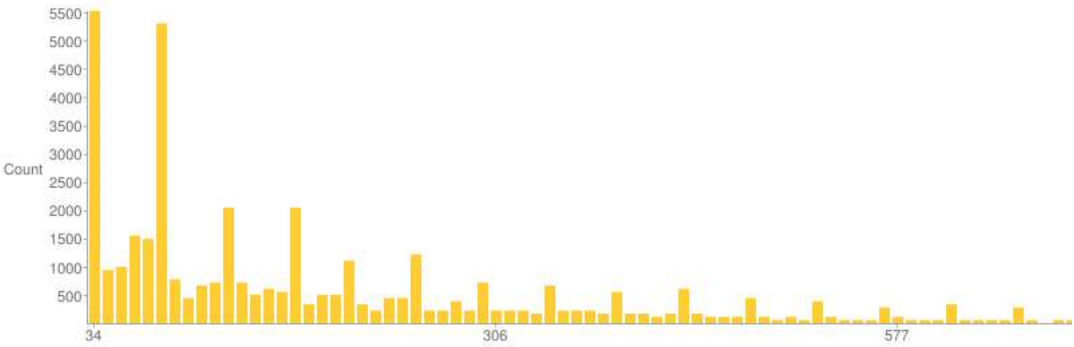
Number of effects by type and region

Type			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent



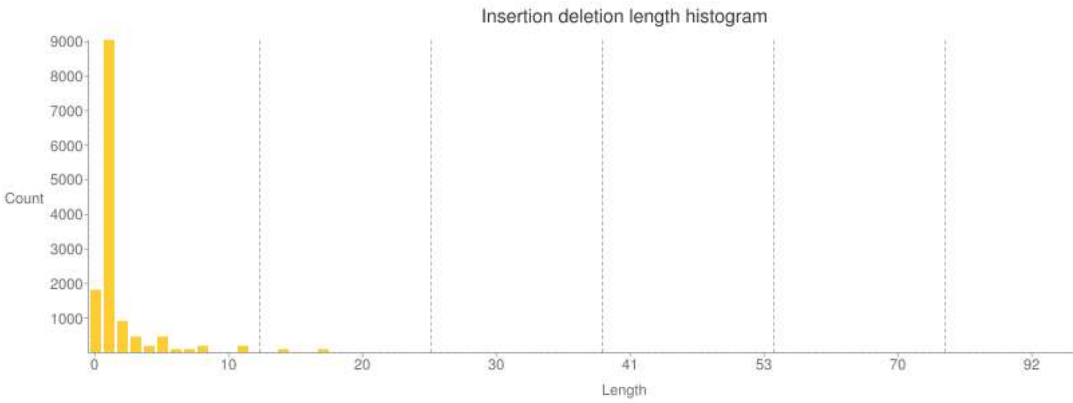
Quality:

Min	30
Max	97,717
Mean	406.551
Median	166
Standard deviation	814.774
Values	30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77
Count	154,431,200,103,176,2369,330,1571,129,62,173,107,80,161,117,88,187,39,39,205,57,56,190,52,69,195,66,118,316,156,123,269,114,151,323,71,60,



Insertions and deletions length:

Min	0
Max	167
Mean	3.161
Median	1
Standard deviation	7.682
Values	0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,40,41,42,43,44,46,47,48,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77
Count	1842,9030,937,502,219,498,107,148,261,68,26,237,27,24,129,27,15,142,3,17,68,9,2,86,3,8,33,5,4,47,8,6,9,2,1,50,3,2,7,1,13,1,3,12,2,15,1,5,3,1,13,



Base changes (SNPs)

	A	C	G	T
A	0	1,930	4,219	3,468
C	1,974	0	1,755	4,107
G	4,097	1,877	0	2,025
T	3,399	4,325	2,052	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	27,876
Transversions	29,908
Ts/Tv ratio	0.9321

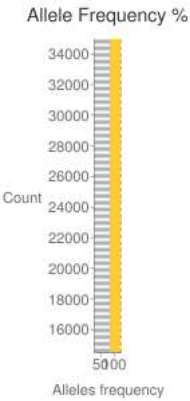
All variants:

Sample ,8G,Total
Transitions ,27876,27876
Transversions ,29908,29908
Ts/Tv ,0.932,0.932

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

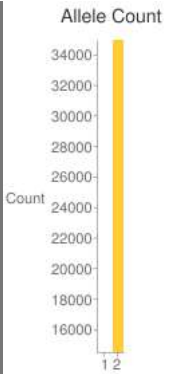
No results available (empty input?)

Allele frequency



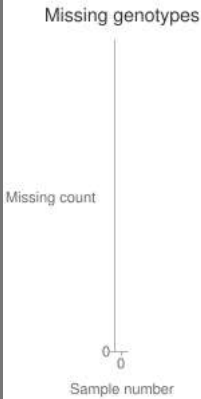
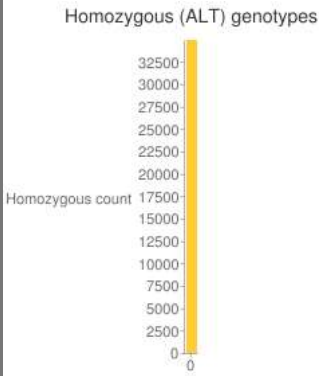
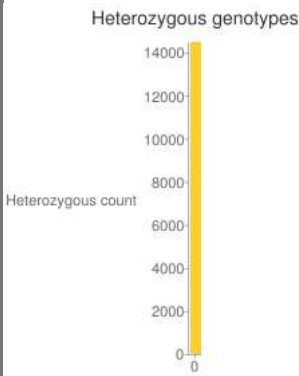
Min	50
Max	100
Mean	85.335
Median	100
Standard deviation	22.764
Values	50,100
Count	14501,34940

Allele Count



Min	1
Max	2
Mean	1.707
Median	2
Standard deviation	0.455
Values	1,2
Count	14501,34940

Hom/Het per sample



Sample_names , BG
Reference , 0
Het , 14501
Hom , 34940
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

variants histogram: Pf3D7_01_v3



Pf3D7_01_v3, Position,0,1
Pf3D7_01_v3,Count,0,0

variants histogram: Pf3D7_02_v3



Pf3D7_02_v3, Position,0,1
Pf3D7_02_v3,Count,0,0

variants histogram: Pf3D7_03_v3



Pf3D7_03_v3, Position,0,1
Pf3D7_03_v3,Count,0,0

iants histogram: Pf3D7_04_v3



Pf3D7_04_v3, Position,0,1
Pf3D7_04_v3,Count,0,0

iants histogram: Pf3D7_05_v3



Pf3D7_05_v3, Position,0,1
Pf3D7_05_v3,Count,0,0

iants histogram: Pf3D7_06_v3



Pf3D7_06_v3, Position,0,1
Pf3D7_06_v3,Count,0,0

iants histogram: Pf3D7_07_v3



Pf3D7_07_v3, Position,0,1
Pf3D7_07_v3,Count,0,0

iants histogram: Pf3D7_08_v3



Pf3D7_08_v3, Position,0,1
Pf3D7_08_v3,Count,0,0

iants histogram: Pf3D7_09_v3



Pf3D7_09_v3, Position,0,1
Pf3D7_09_v3,Count,0,0

iants histogram: Pf3D7_10_v3



Pf3D7_10_v3, Position,0,1
Pf3D7_10_v3,Count,0,0

iants histogram: Pf3D7_11_v3



Pf3D7_11_v3, Position,0,1
Pf3D7_11_v3,Count,0,0

ants histogram: Pf3D7_12_v3



Pf3D7_12_v3, Position,0,1
Pf3D7_12_v3,Count,0,0

ants histogram: Pf3D7_13_v3



Pf3D7_13_v3, Position,0,1
Pf3D7_13_v3,Count,0,0

ants histogram: Pf3D7_14_v3



Pf3D7_14_v3, Position,0,1
Pf3D7_14_v3,Count,0,0

ants histogram: Pf3D7_MIT_v3



Pf3D7_MIT_v3, Position,0,1
Pf3D7_MIT_v3,Count,0,0

Details by gene

[Here](#) you can find a tab-separated table.