



Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

VEP run statistics

VEP version (API) 115.2 (115)

Annotation sources Cache: /home/adaso/.vep/gallus_gallus/115_bGalGal1.mat.broiler.GRCg7b

Species gallus_gallus

Command line options
--input_file ../NGS_nextflow/results/variants/bcftools_snps.vcf.gz --offline
--output_file ../NGS_nextflow/results/vep_bcftools2_1.txt --species gallus_gallus

Start time 2025-12-13 21:14:32

End time 2025-12-13 21:26:08

Run time 696 seconds

Input file ../NGS_nextflow/results/variants/bcftools_snps.vcf.gz

Output file ../NGS_nextflow/results/vep_bcftools2_1.txt

Data version

assembly bGalGal1.mat.broiler.GRCg7b

dbSNP 150

genebuild

regbuild 1.0

sift sift

General statistics

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

Lines of input read 1433423

Variants processed 1433423

Variants filtered out 0

Novel / existing variants -

Overlapped genes 23704

Overlapped transcripts 60574

Overlapped regulatory features -

Variant classes

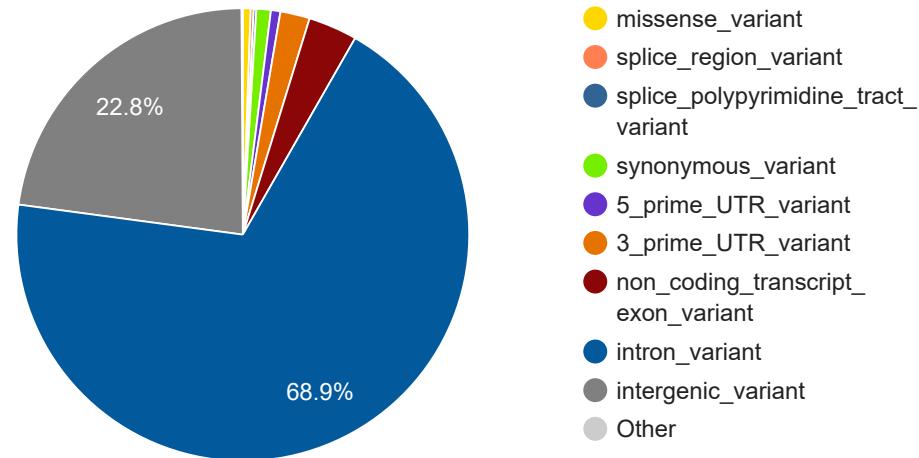


Variant class	Count
SNV	1,433,423

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

Consequences (most severe)

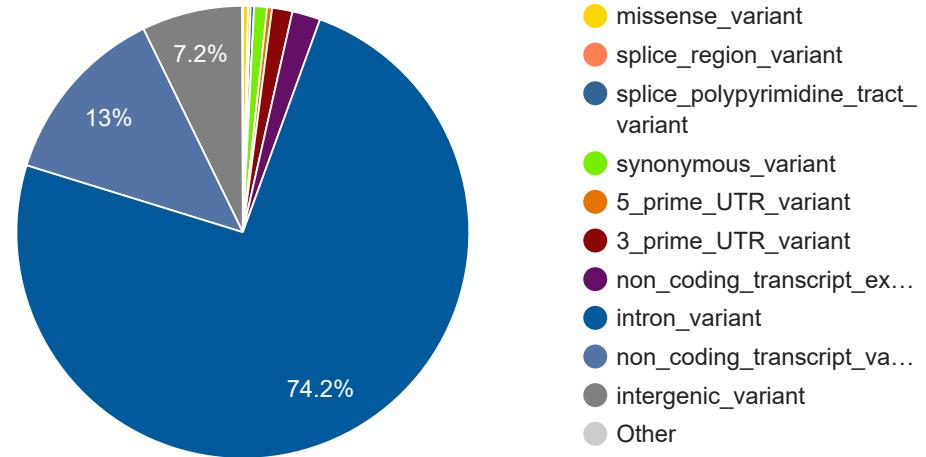


Consequence type	Count
splice_acceptor_variant	101
splice_donor_variant	179
stop_gained	113
stop_lost	18
start_lost	77
missense_variant	7,971
splice_donor_5th_base_variant	228
splice_region_variant	3,097

Consequences (all)

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)



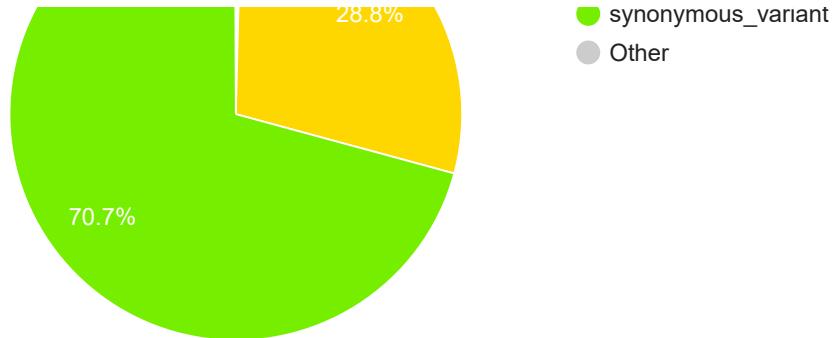
Consequence type	Count
splice_acceptor_variant	126
splice_donor_variant	241
stop_gained	152
stop_lost	23
start_lost	84
missense_variant	17,103
splice_donor_5th_base_variant	484
splice_region_variant	8,001

Coding consequences



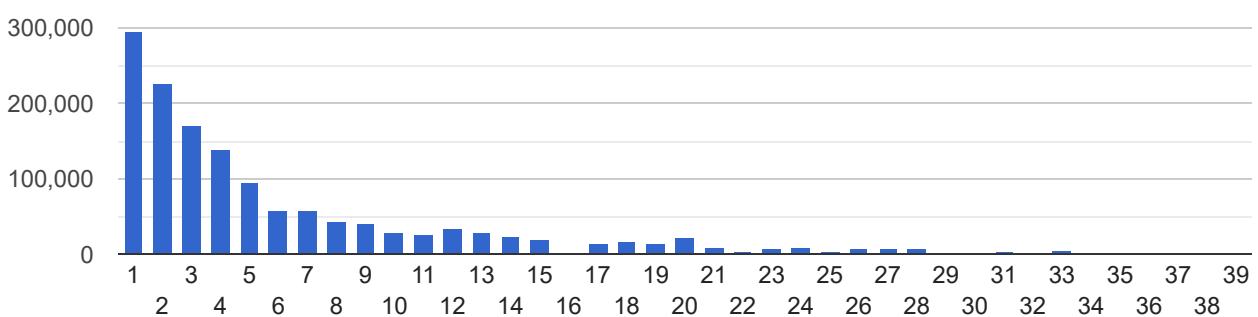
Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)



Consequence type	Count
stop_gained	152
stop_lost	23
start_lost	84
missense_variant	17,103
start_retained_variant	2
stop_retained_variant	16
synonymous_variant	41,957

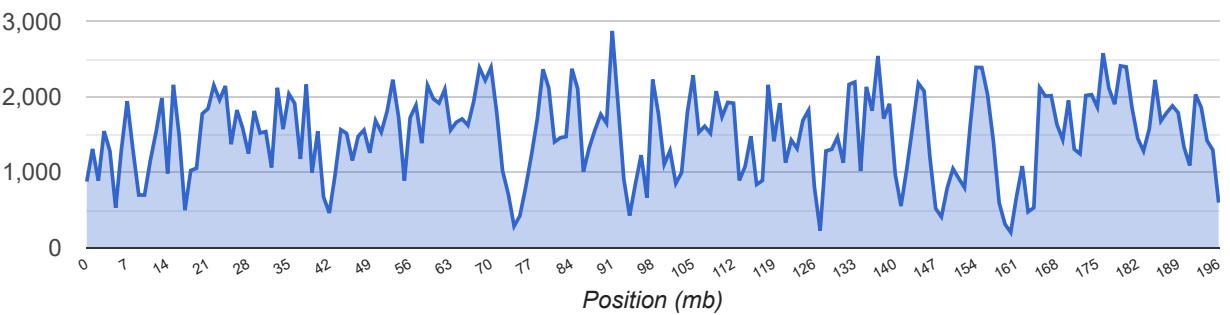
Variants by chromosome



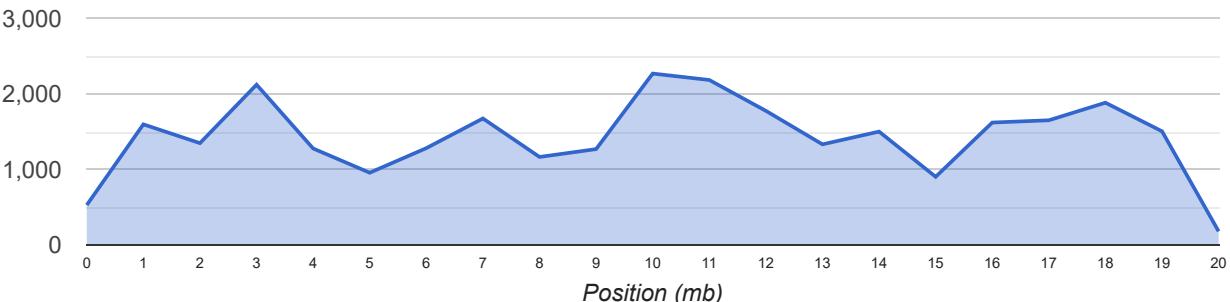
Links
<ul style="list-style-type: none">Top of pageVEP run statisticsData versionGeneral statisticsVariant classesConsequences (most severe)Consequences (all)Coding consequencesVariants by chromosomePosition in protein

Chromosome	Count
1	294,067
2	227,741
3	170,680
4	138,274
5	95,707
6	57,330
7	59,666
8	43,813
9	40,572

Distribution of variants on chromosome 1



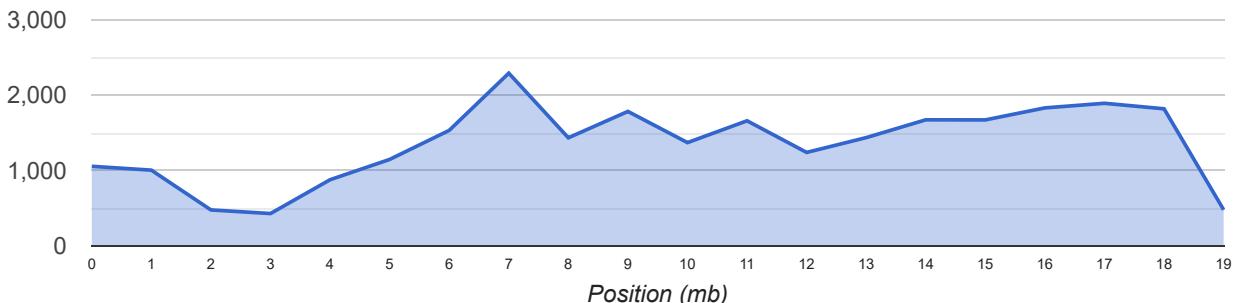
Distribution of variants on chromosome 10



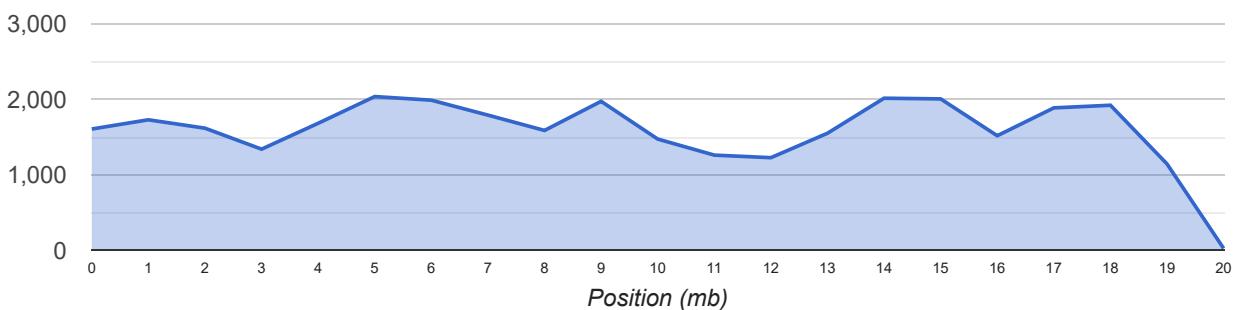
Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

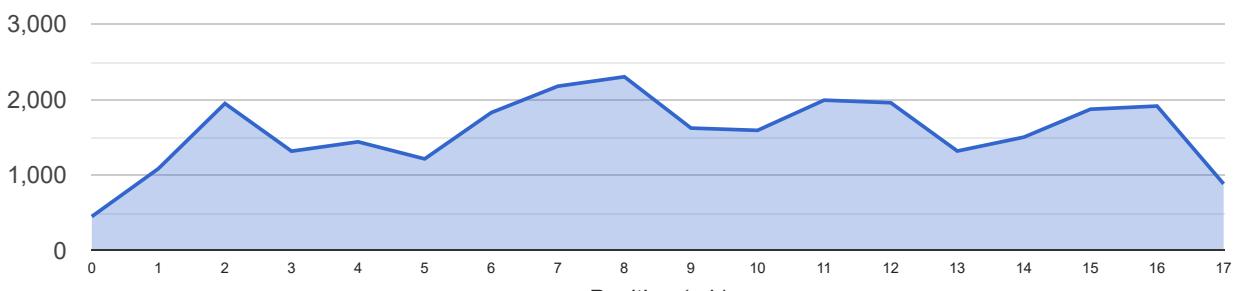
Distribution of variants on chromosome 11



Distribution of variants on chromosome 12

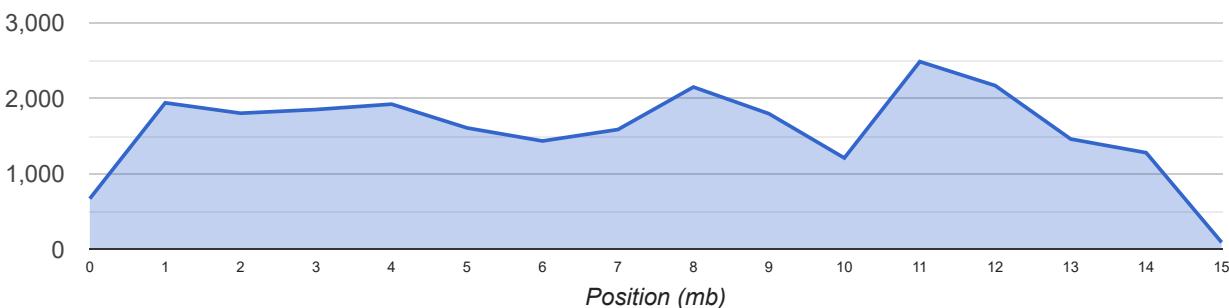
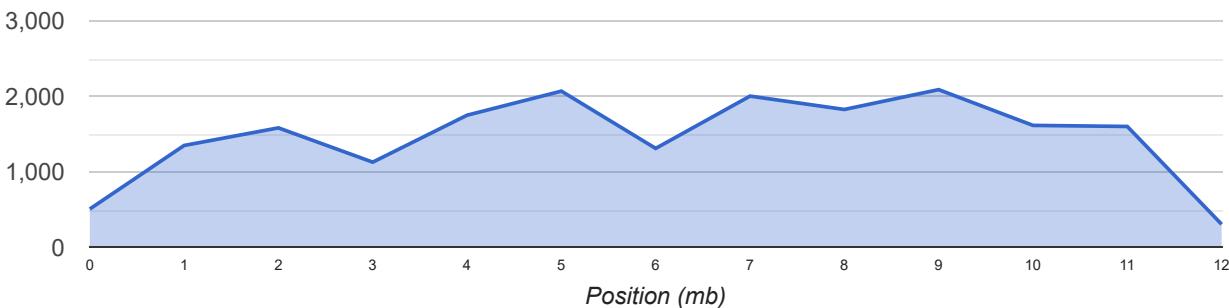
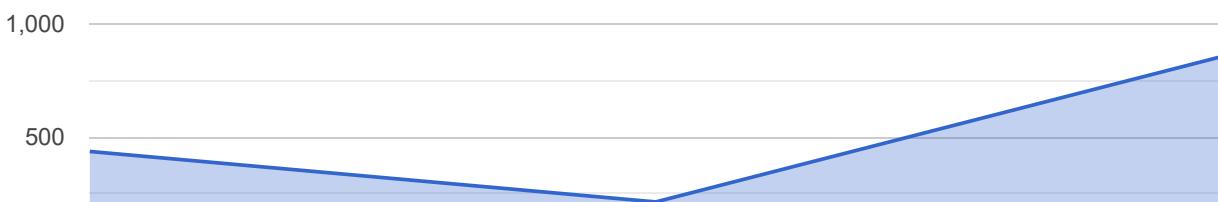


Distribution of variants on chromosome 13



Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

*Position (mb)***Distribution of variants on chromosome 14****Distribution of variants on chromosome 15****Distribution of variants on chromosome 16**

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

0

Position (mb)

2

Distribution of variants on chromosome 17

2,000

0

Position (mb)

10

1

11

2

3

4

5

6

7

8

9

10

11

Distribution of variants on chromosome 18

3,000

2,000

1,000

0

Position (mb)

10

1

11

2

3

4

5

6

7

8

9

10

11

Distribution of variants on chromosome 19

3,000

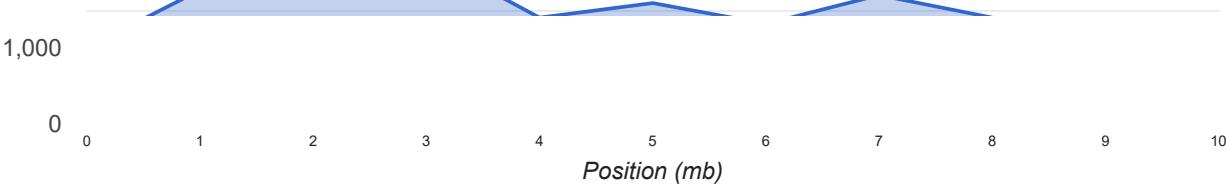
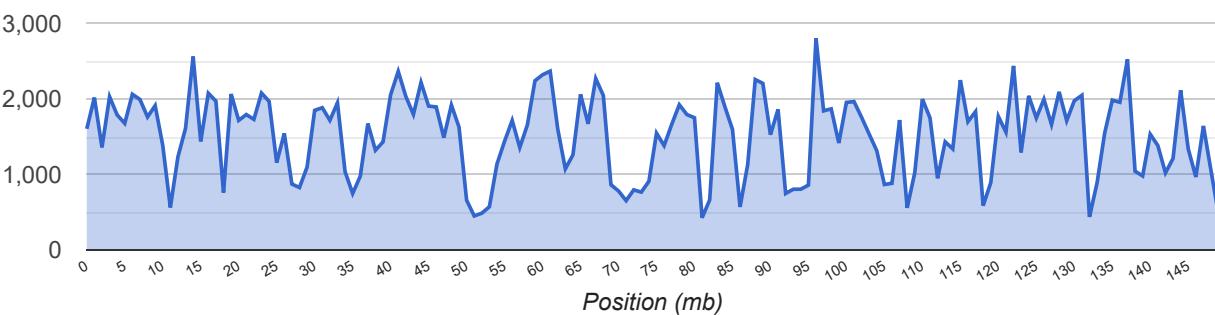
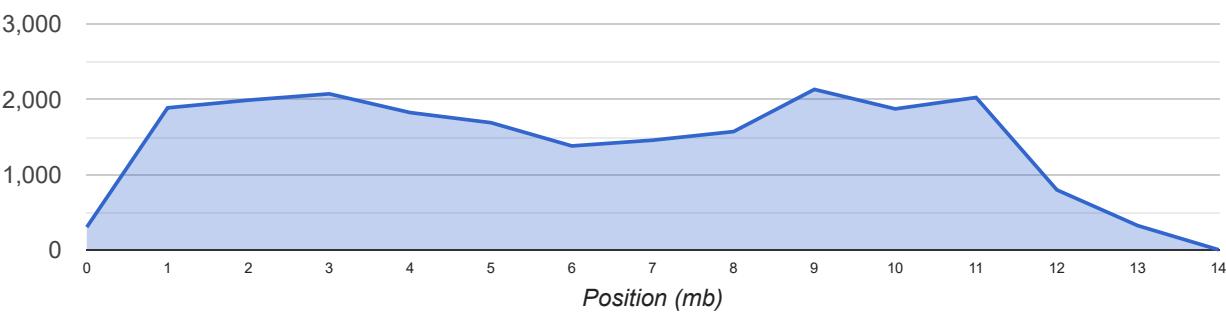
2,000

0

1

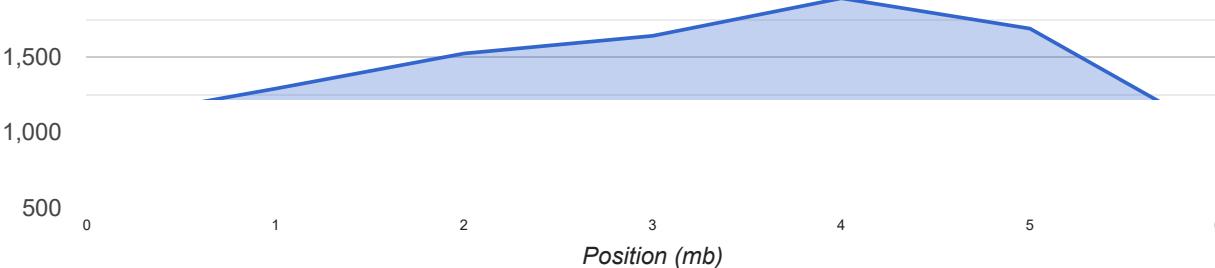
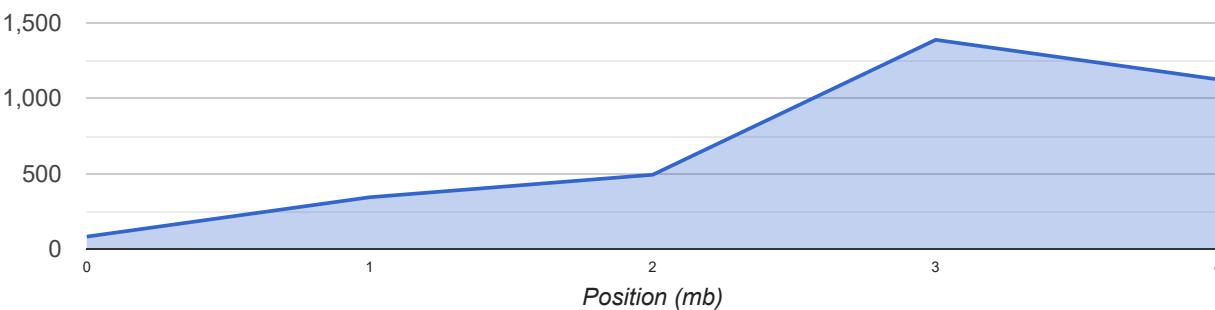
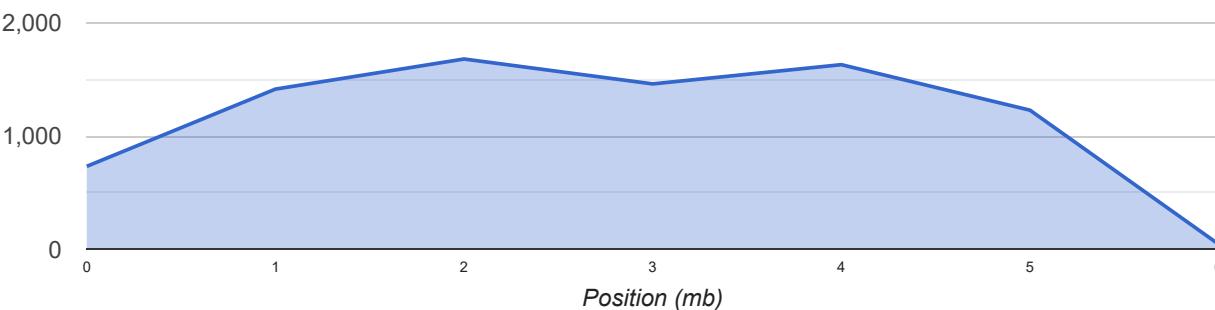
Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

**Distribution of variants on chromosome 2****Distribution of variants on chromosome 20****Distribution of variants on chromosome 21**

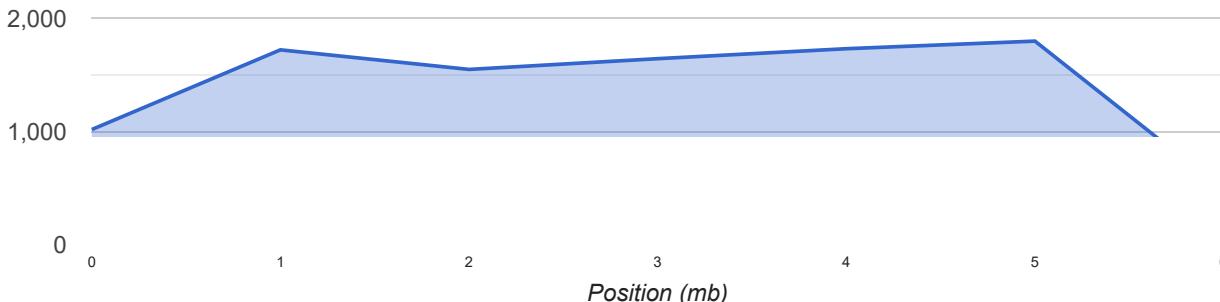
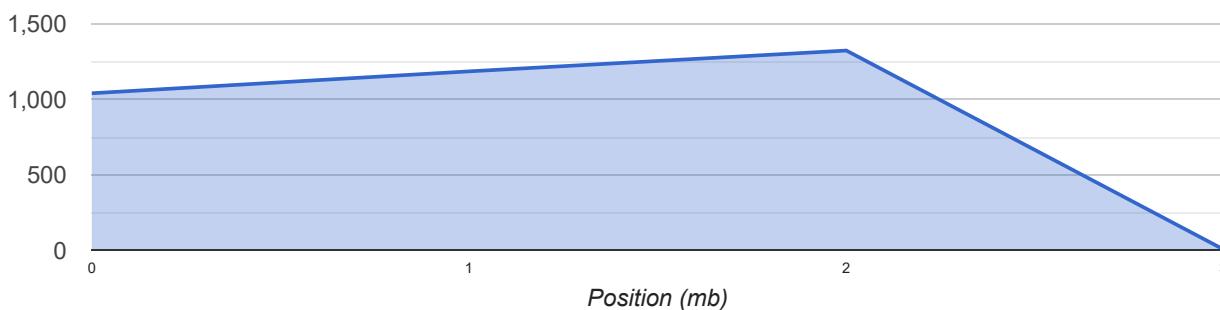
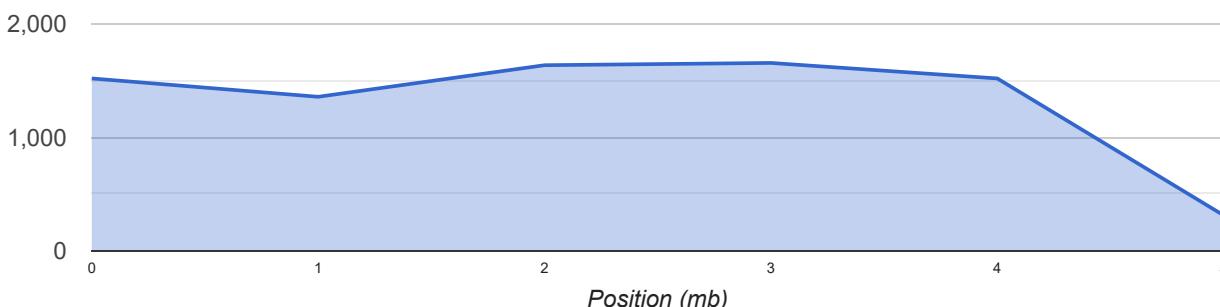
Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

**Distribution of variants on chromosome 22****Distribution of variants on chromosome 23****Distribution of variants on chromosome 24**

Links

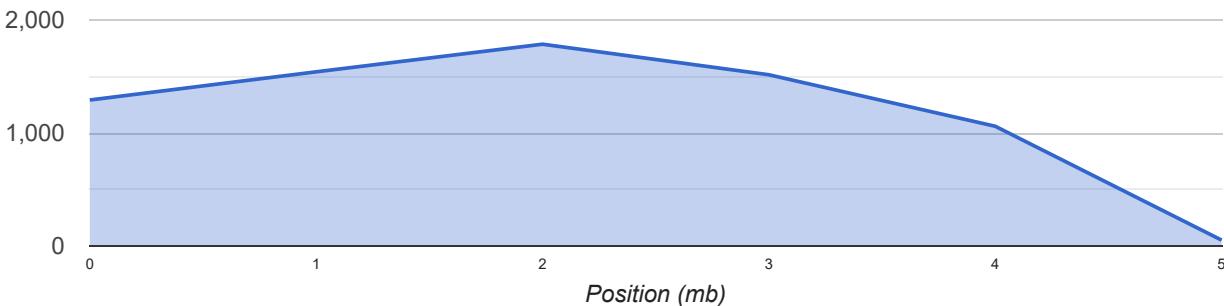
- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

**Distribution of variants on chromosome 25****Distribution of variants on chromosome 26**

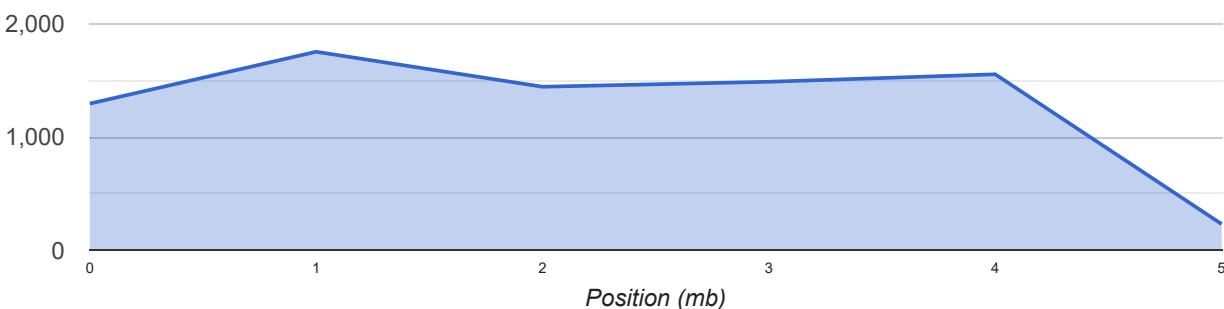
Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

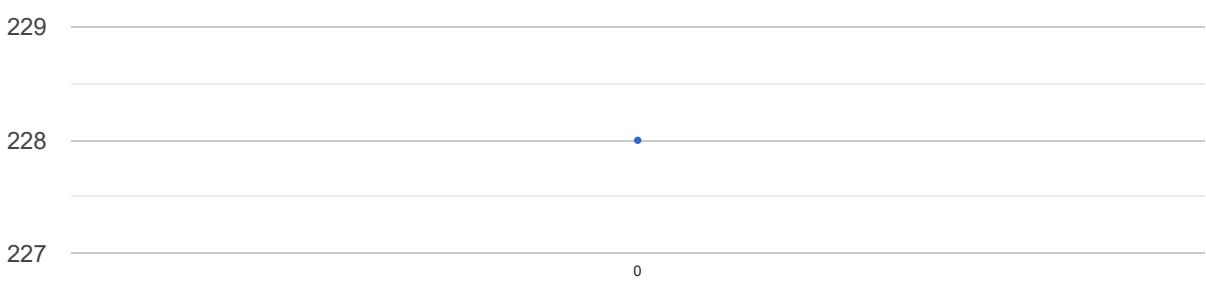
Distribution of variants on chromosome 27



Distribution of variants on chromosome 28

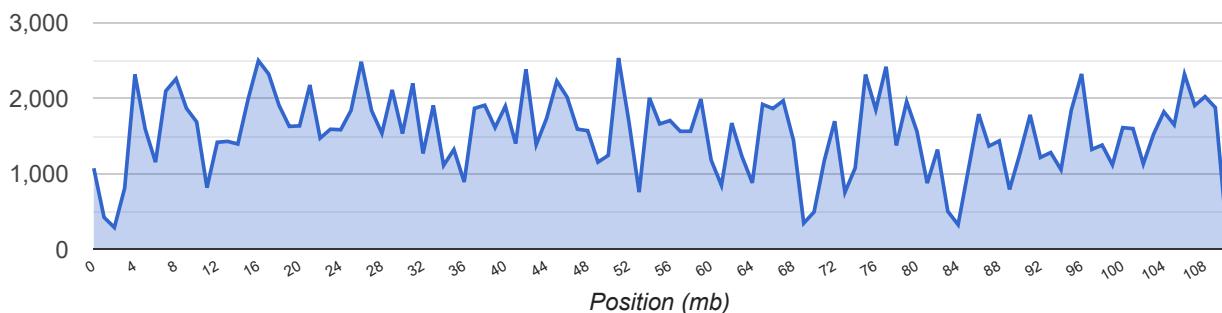
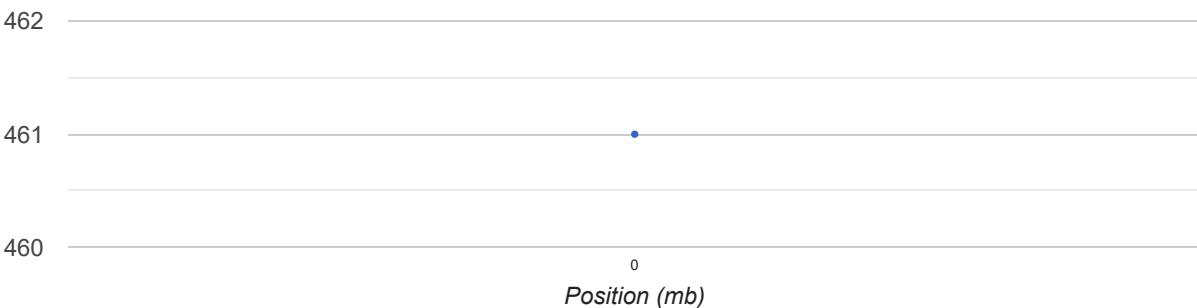


Distribution of variants on chromosome 29



Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

*Position (mb)***Distribution of variants on chromosome 3****Distribution of variants on chromosome 30****Distribution of variants on chromosome 31**

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

0

Position (mb)

2

191

190

189

0

Position (mb)

Distribution of variants on chromosome 32

3,000

2,000

1,000

0

0

1

2

3

Position (mb)

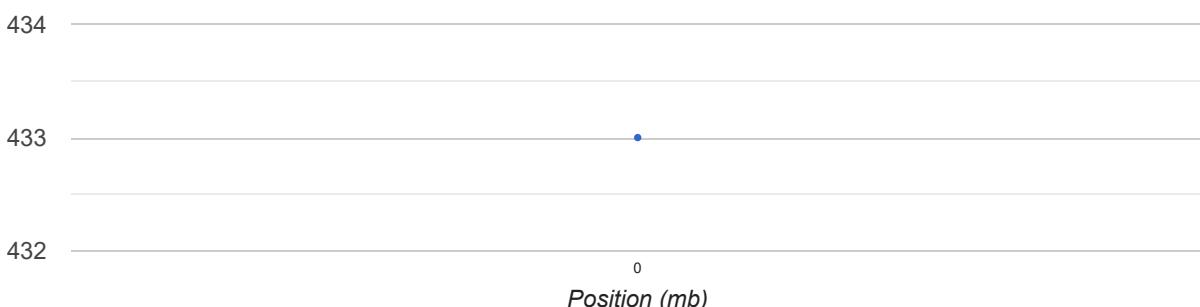
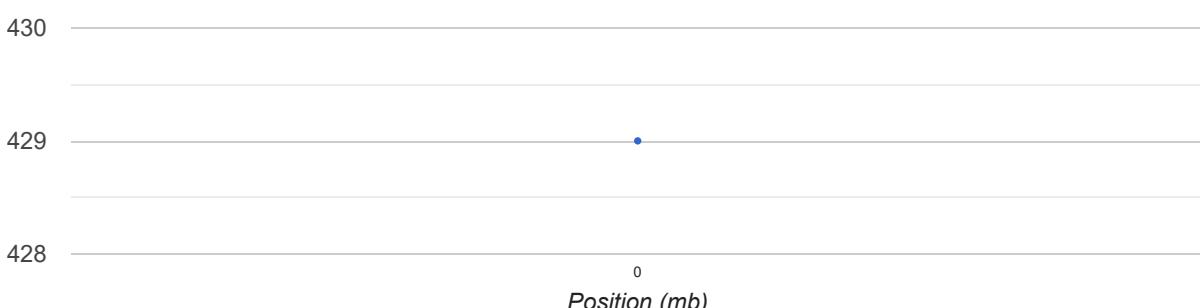
Distribution of variants on chromosome 33

Distribution of variants on chromosome 34

1,000

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

**Distribution of variants on chromosome 35****Distribution of variants on chromosome 36****Distribution of variants on chromosome 37**

Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

223



A dot plot showing the distribution of variants on chromosome 38. The y-axis is labeled '223' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

222



A dot plot showing the distribution of variants on chromosome 38. The y-axis is labeled '222' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

Distribution of variants on chromosome 38

266



A dot plot showing the distribution of variants on chromosome 39. The y-axis is labeled '266' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

265



A dot plot showing the distribution of variants on chromosome 39. The y-axis is labeled '265' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

264



A dot plot showing the distribution of variants on chromosome 39. The y-axis is labeled '264' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

0

Position (mb)

Distribution of variants on chromosome 39

97



A dot plot showing the distribution of variants on chromosome 4. The y-axis is labeled '97' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

96



A dot plot showing the distribution of variants on chromosome 4. The y-axis is labeled '96' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

95



A dot plot showing the distribution of variants on chromosome 4. The y-axis is labeled '95' and the x-axis is labeled 'Position (mb)' with '0' at the center. A single blue dot is positioned exactly at the 0 mb mark.

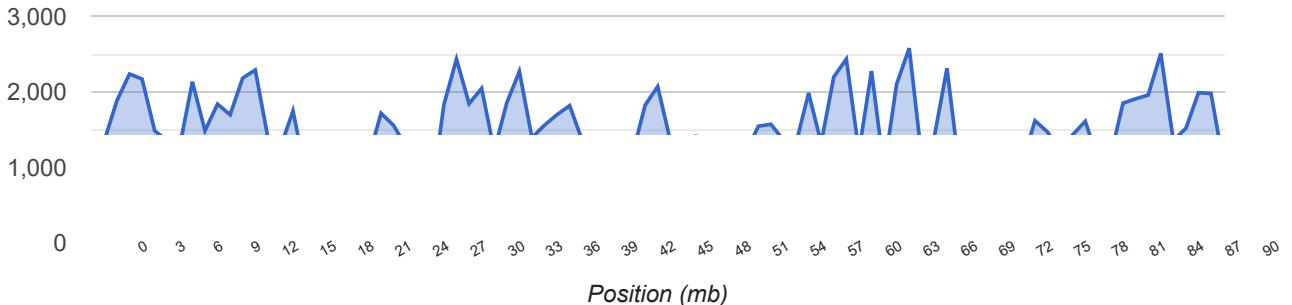
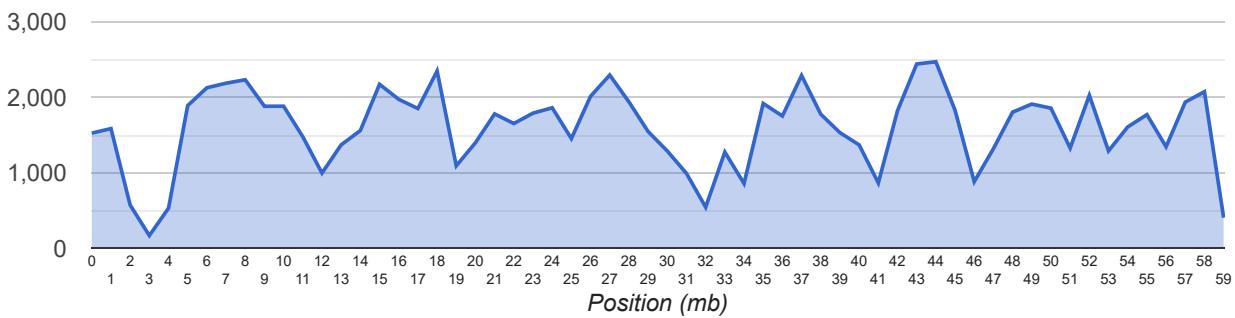
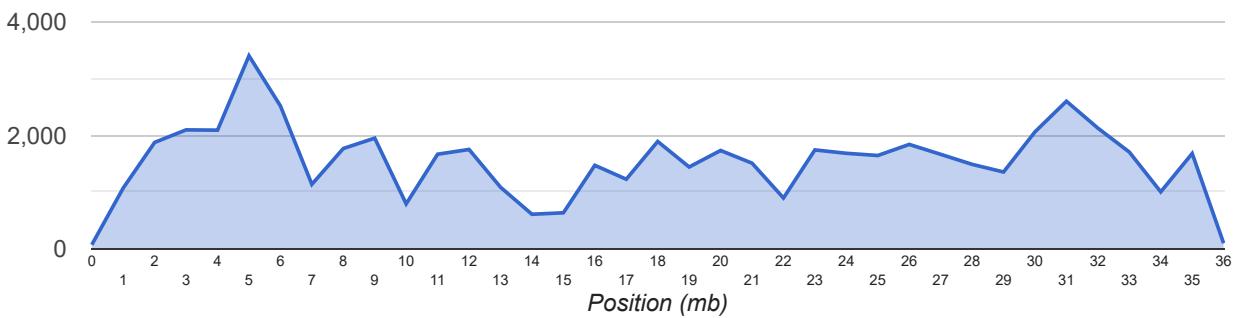
0

Position (mb)

Distribution of variants on chromosome 4

Links

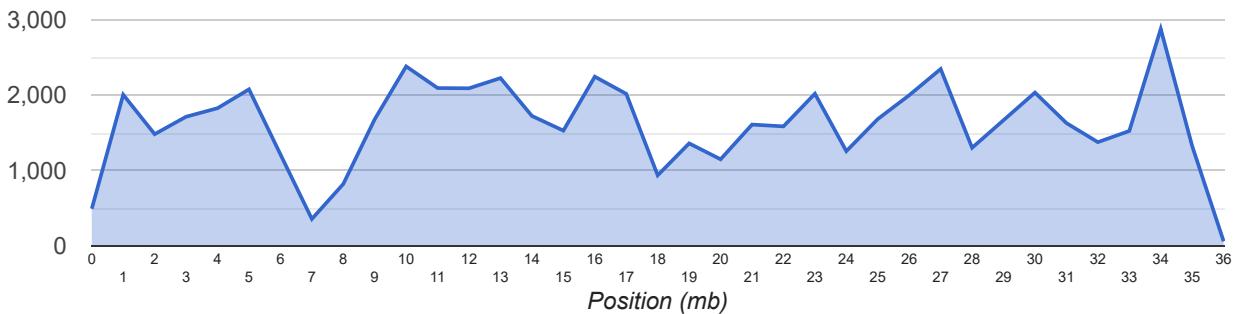
- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

**Distribution of variants on chromosome 5****Distribution of variants on chromosome 6**

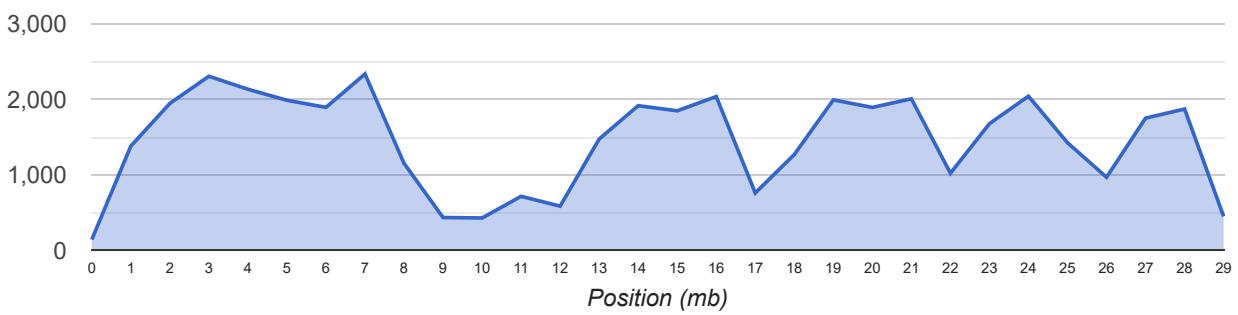
Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

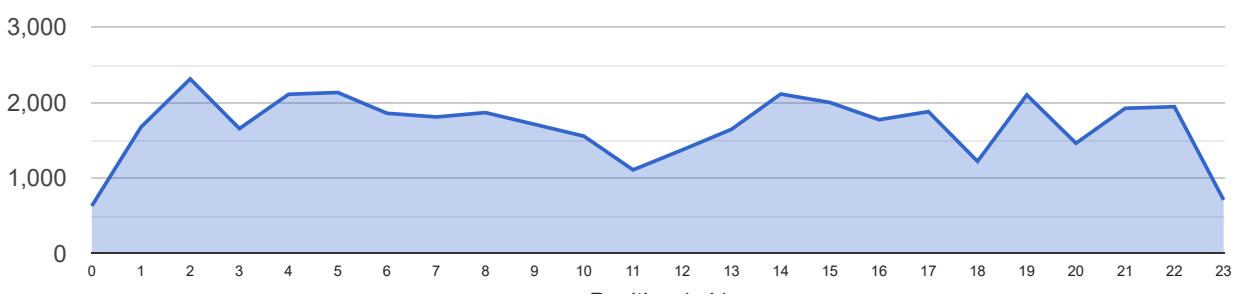
Distribution of variants on chromosome 7



Distribution of variants on chromosome 8



Distribution of variants on chromosome 9



Links

- [Top of page](#)
- [VEP run statistics](#)
- [Data version](#)
- [General statistics](#)
- [Variant classes](#)
- [Consequences \(most severe\)](#)
- [Consequences \(all\)](#)
- [Coding consequences](#)
- [Variants by chromosome](#)
- [Position in protein](#)

*Position (mb)***Position in protein**