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## 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/gatk_snps_filtered.vcf.gz --offline --output_file ../NGS_nextflow/results/vep_gatk3.txt --species gallus_gallus
Start time	2025-12-13 20:10:29
End time	2025-12-13 20:29:03
Run time	1114 seconds
Input file	../NGS_nextflow/results/gatk_snps_filtered.vcf.gz
Output file	../NGS_nextflow/results/vep_gatk3.txt

## Data version

assembly	bGalGal1.mat.broiler.GRCg7b
dbSNP	150
genebuild	
regbuild	1.0
sift	sift

## General statistics

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Lines of input read 2279796

Variants processed 2279796

Variants filtered out 0

Novel / existing variants -

Overlapped genes 24628

Overlapped transcripts 62433

Overlapped regulatory features -

## Variant classes

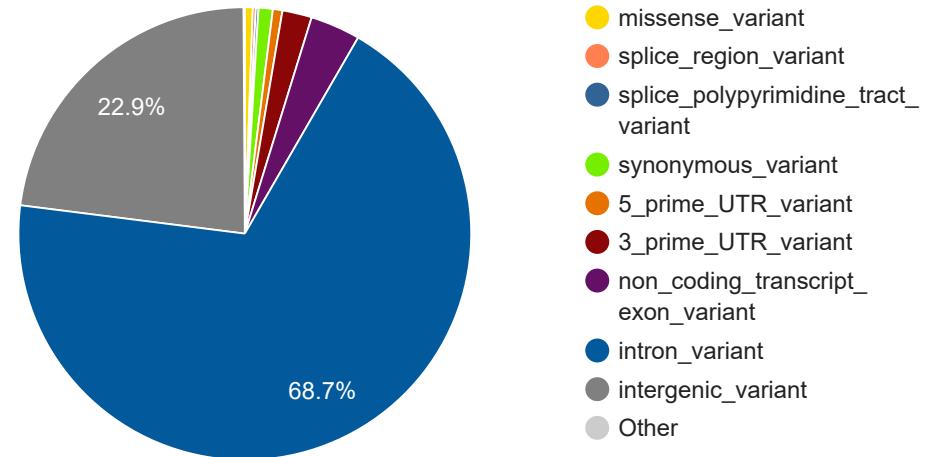


Variant class	Count
SNV	2,279,796

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## Consequences (most severe)

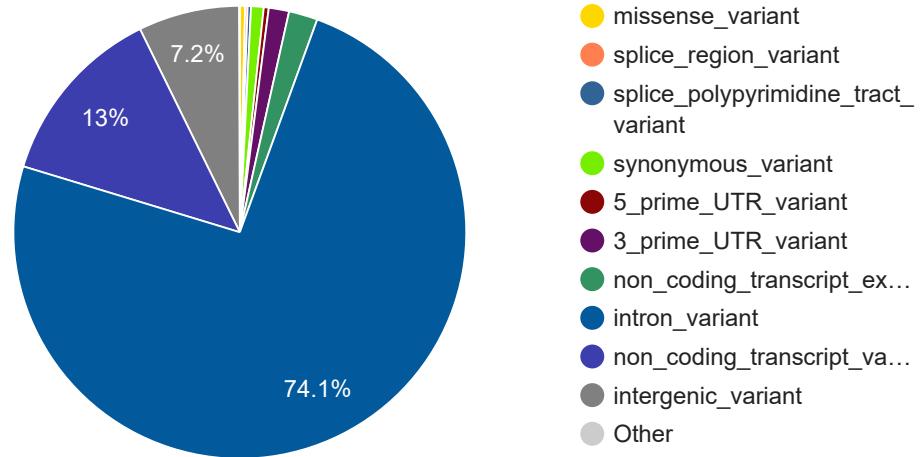


Consequence type	Count
splice_acceptor_variant	179
splice_donor_variant	274
stop_gained	186
stop_lost	35
start_lost	139
missense_variant	12,918
splice_donor_5th_base_variant	336
splice_region_variant	4,862

## Consequences (all)

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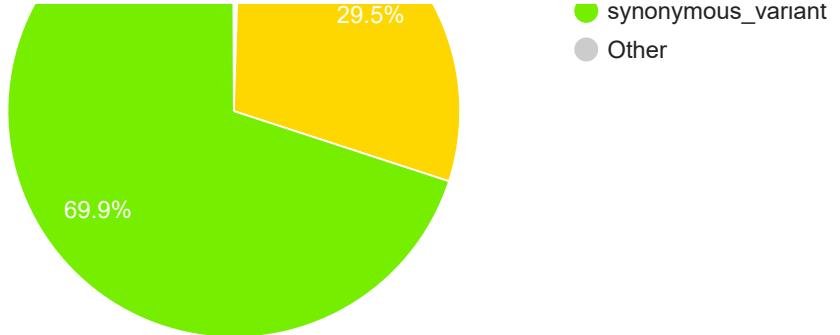
splice_acceptor_variant	234
splice_donor_variant	353
stop_gained	293
stop_lost	42
start_lost	160
missense_variant	27,434
splice_donor_5th_base_variant	701
splice_region_variant	12,455

## Coding consequences



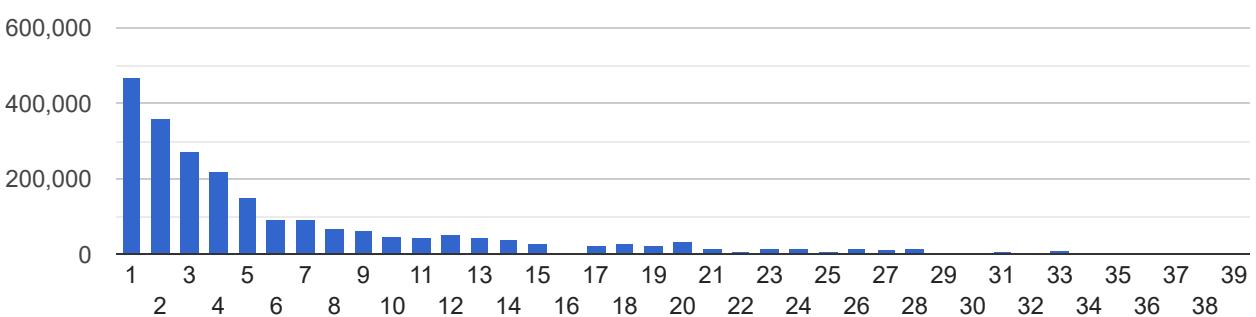
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Consequence type	Count
stop_gained	293
stop_lost	42
start_lost	160
missense_variant	27,434
start_retained_variant	2
stop_retained_variant	15
synonymous_variant	64,961
coding_sequence_variant	1

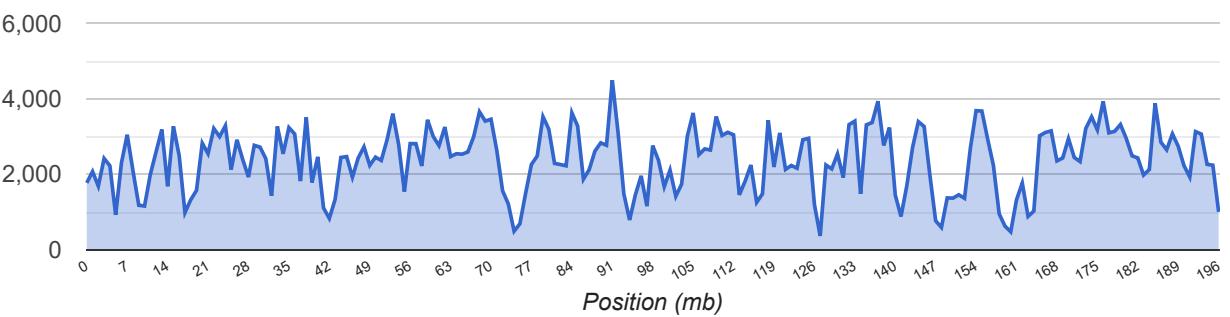
## Variants by chromosome



Links
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Chromosome	Count
1	468,059
2	360,273
3	273,550
4	219,039
5	150,926
6	92,678
7	93,831
8	68,063
9	62,409

### Distribution of variants on chromosome 1



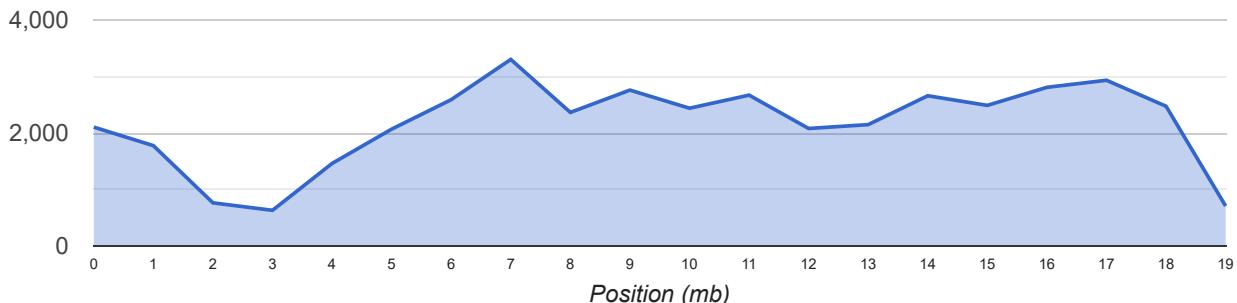
### Distribution of variants on chromosome 10



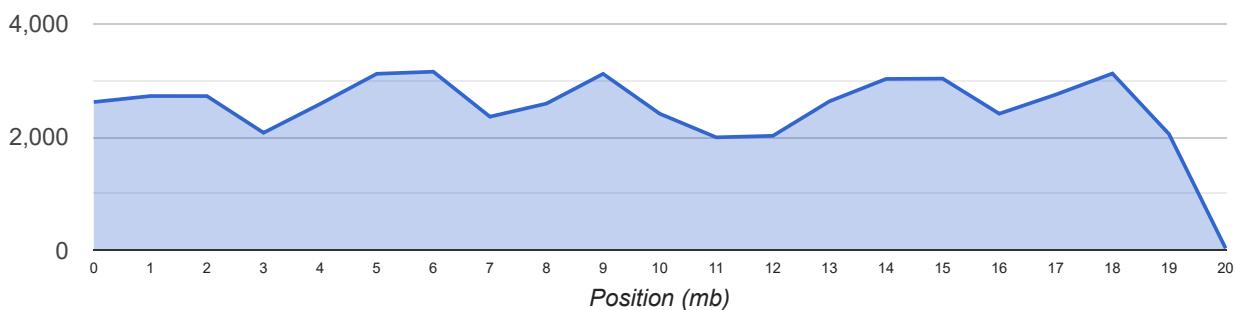
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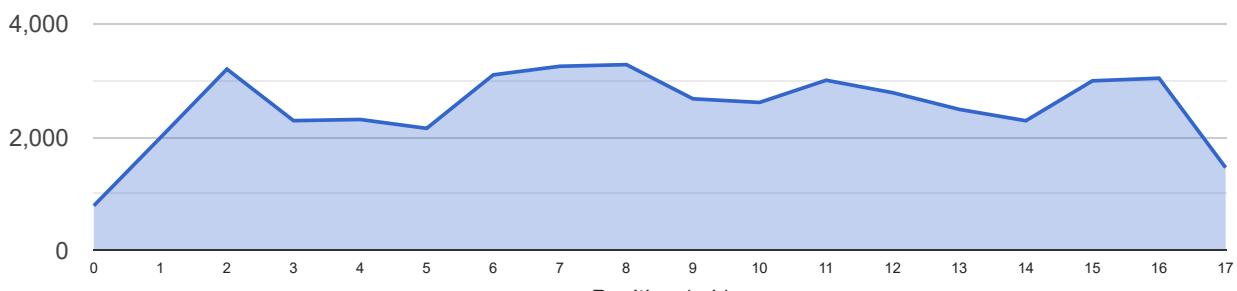
## Distribution of variants on chromosome 11



## Distribution of variants on chromosome 12

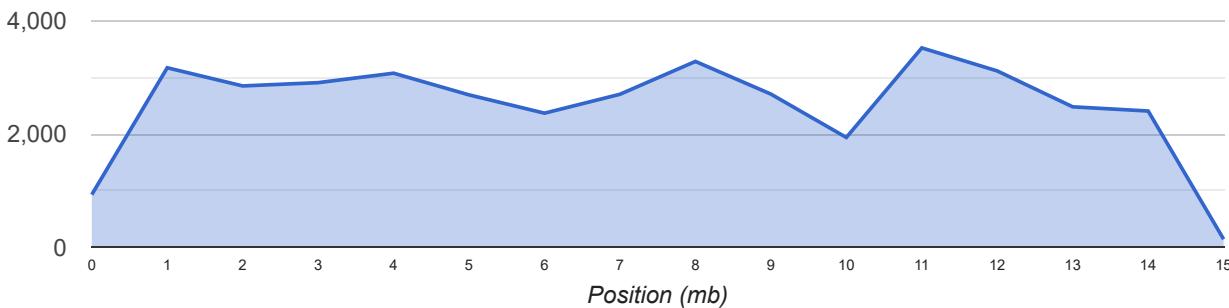
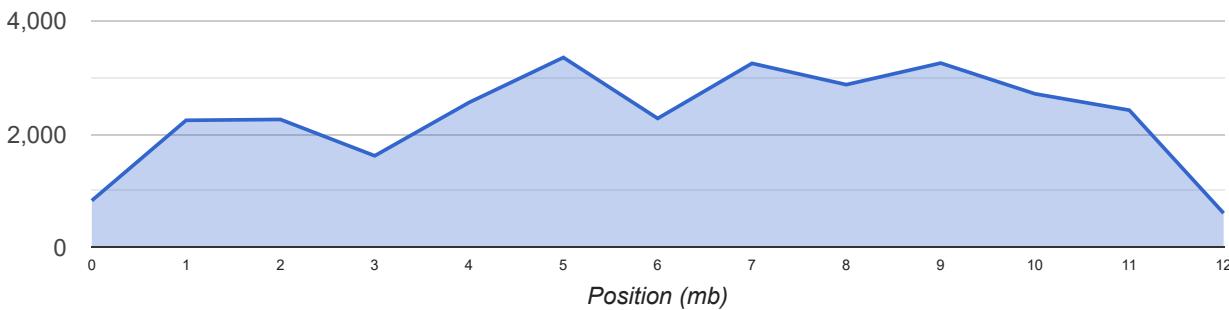
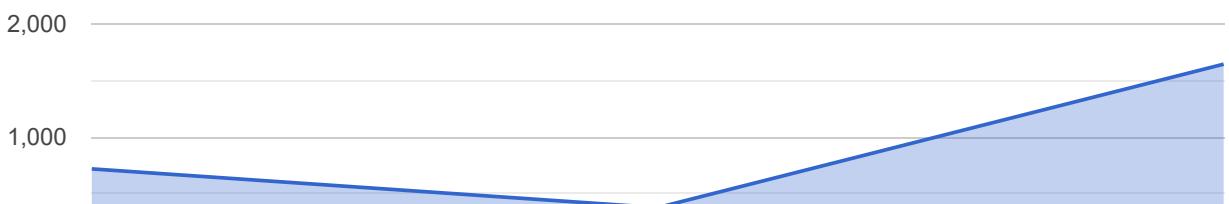


## Distribution of variants on chromosome 13



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

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0

Position (mb)

2

**Distribution of variants on chromosome 17**

4,000

0

Position (mb)

**Distribution of variants on chromosome 18**

4,000

0

Position (mb)

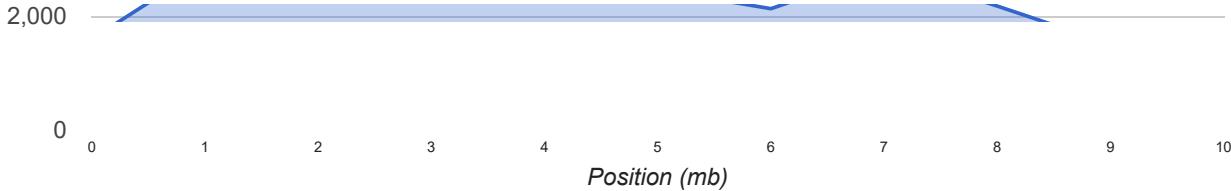
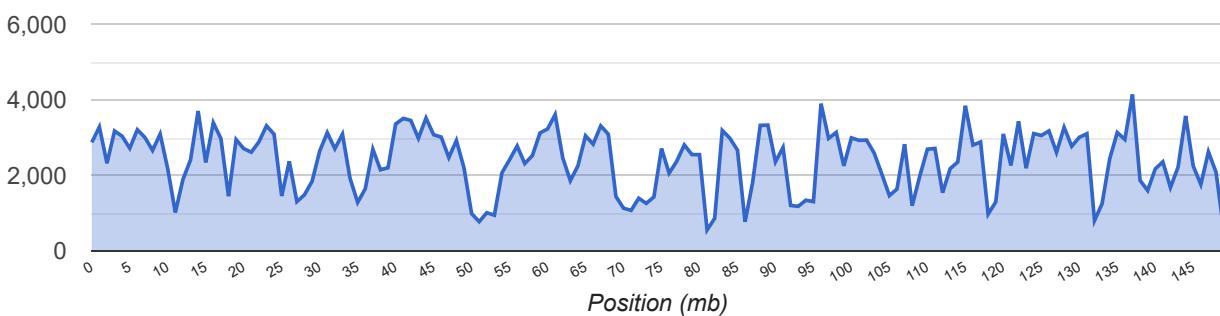
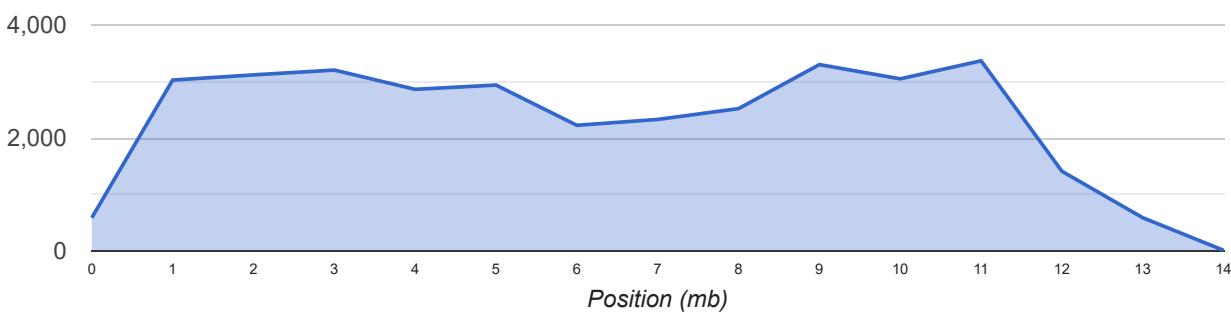
**Distribution of variants on chromosome 19**

4,000



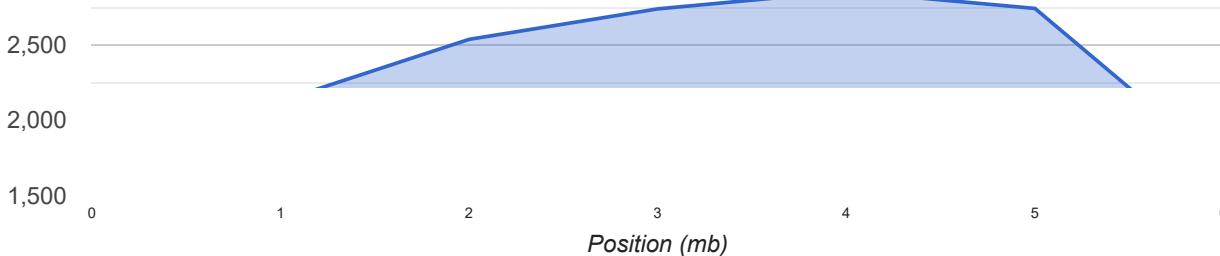
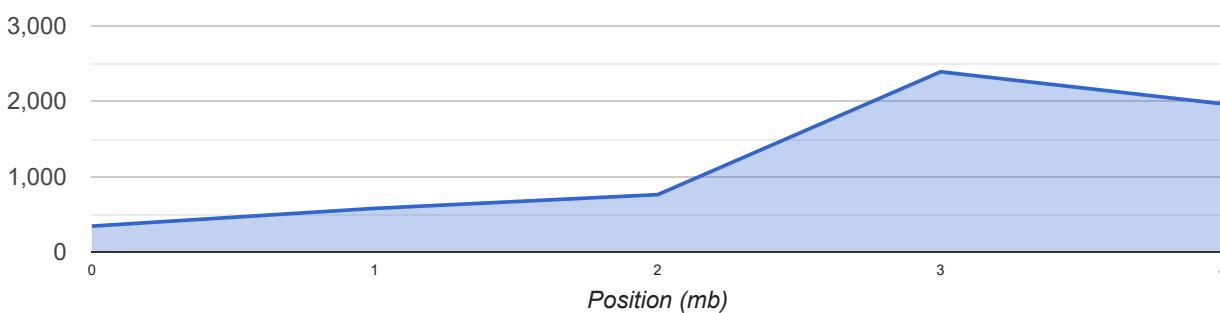
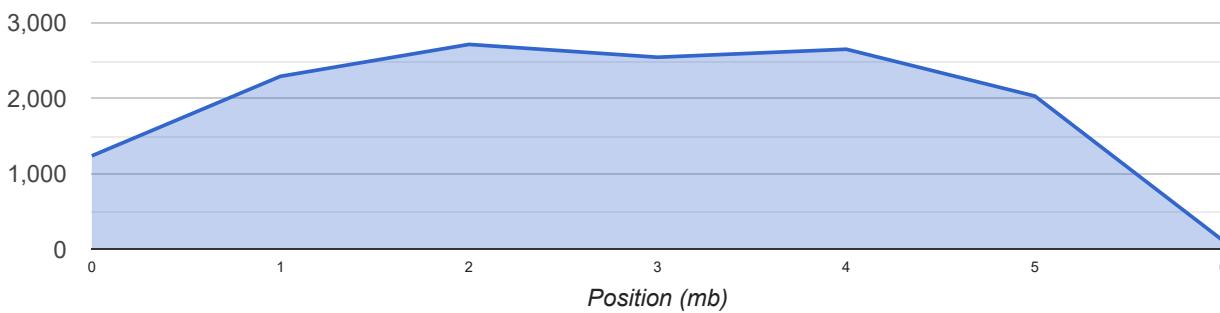
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**Distribution of variants on chromosome 2****Distribution of variants on chromosome 20****Distribution of variants on chromosome 21**

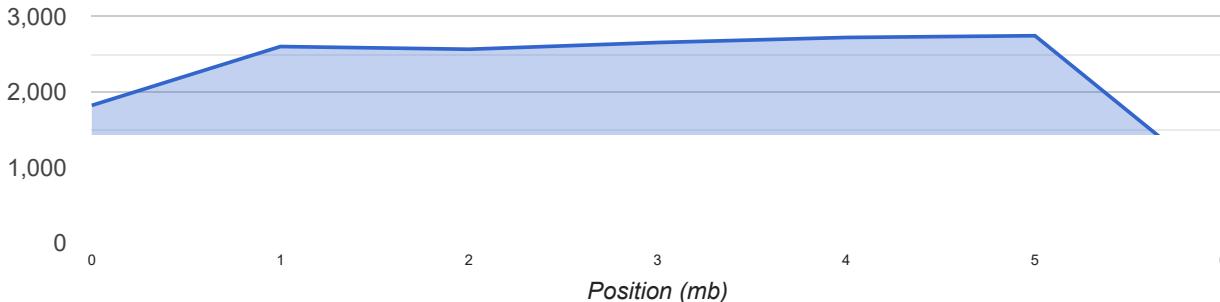
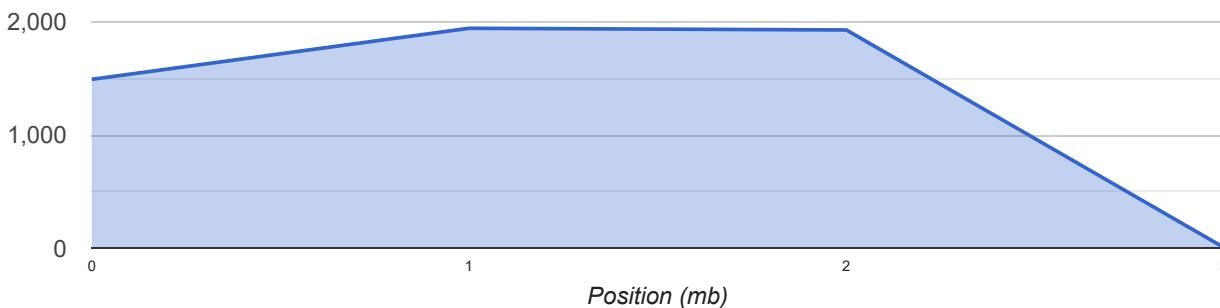
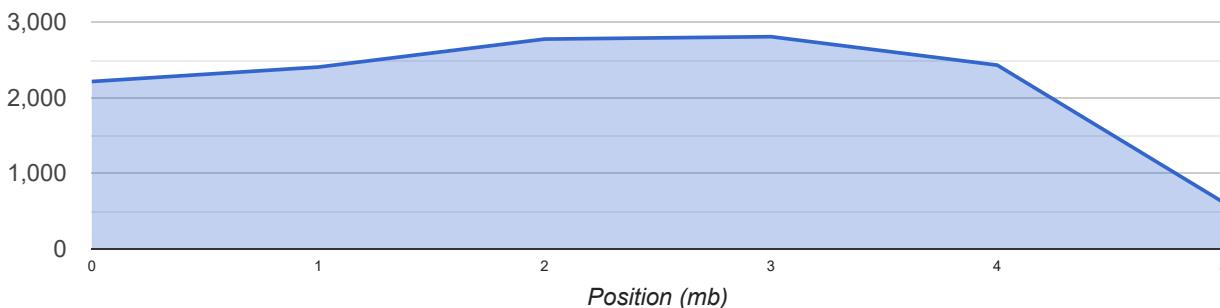
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**Distribution of variants on chromosome 22****Distribution of variants on chromosome 23****Distribution of variants on chromosome 24**

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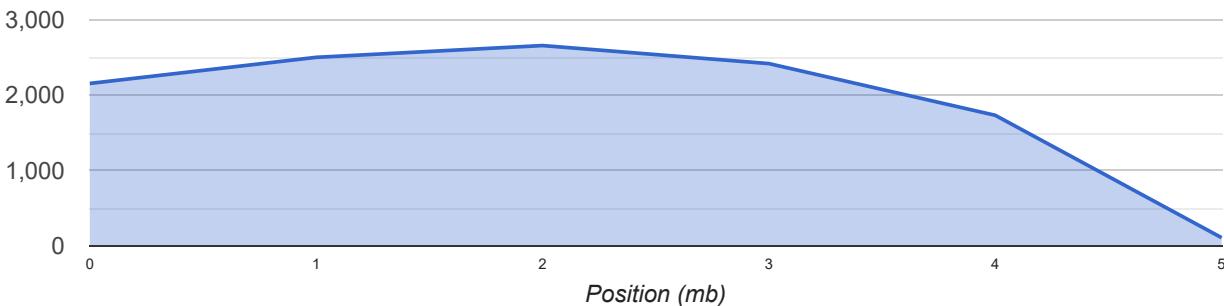
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**Distribution of variants on chromosome 25****Distribution of variants on chromosome 26**

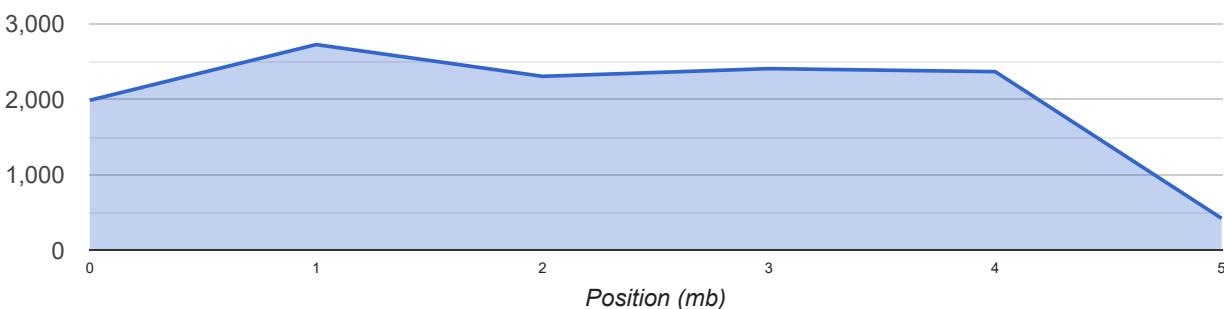
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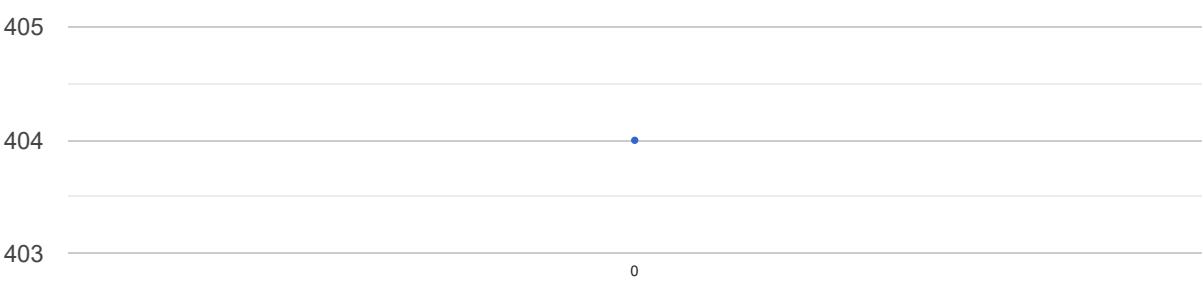
## Distribution of variants on chromosome 27



## Distribution of variants on chromosome 28

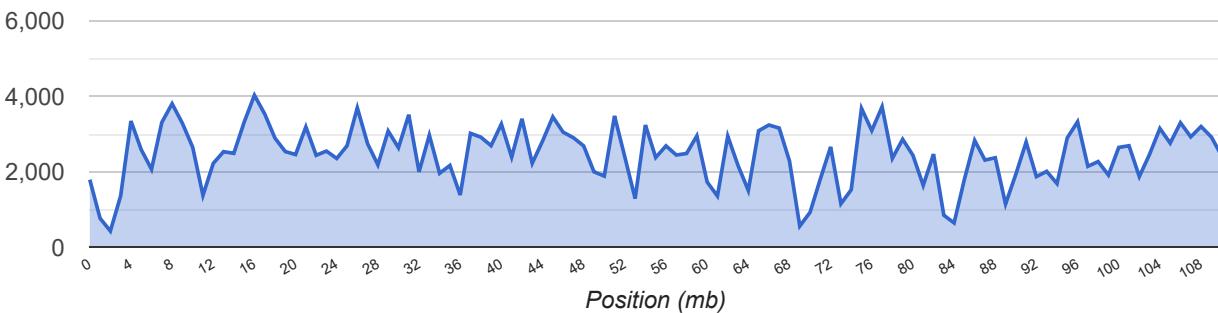
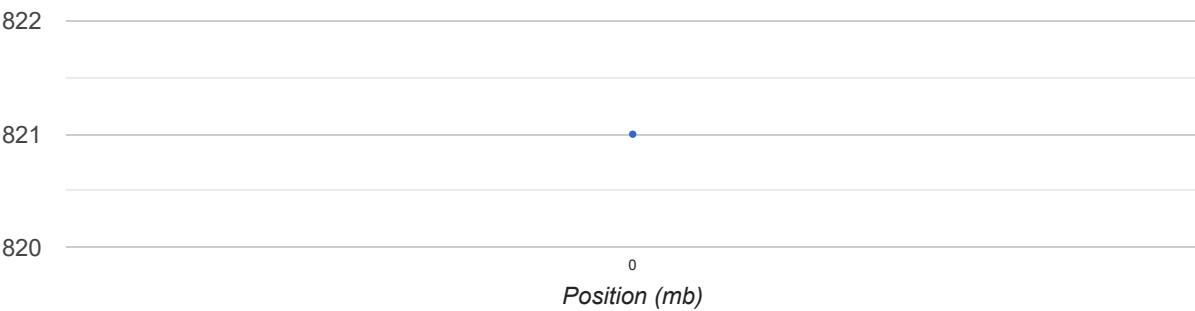


## Distribution of variants on chromosome 29



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

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0

Position (mb)

2

440

439

438

Position (mb)

### Distribution of variants on chromosome 32

0

Position (mb)

3

### Distribution of variants on chromosome 33

4,000

2,000

0

1

2

3

Position (mb)

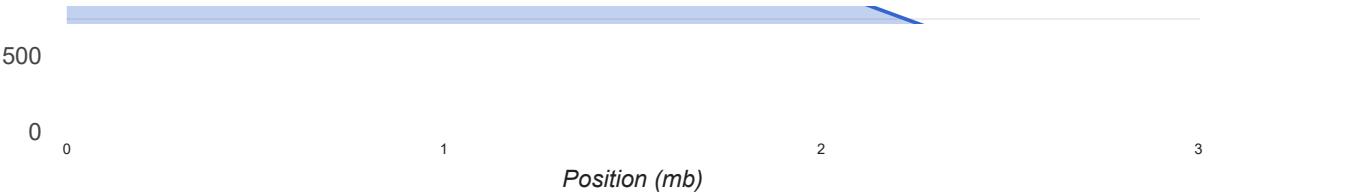
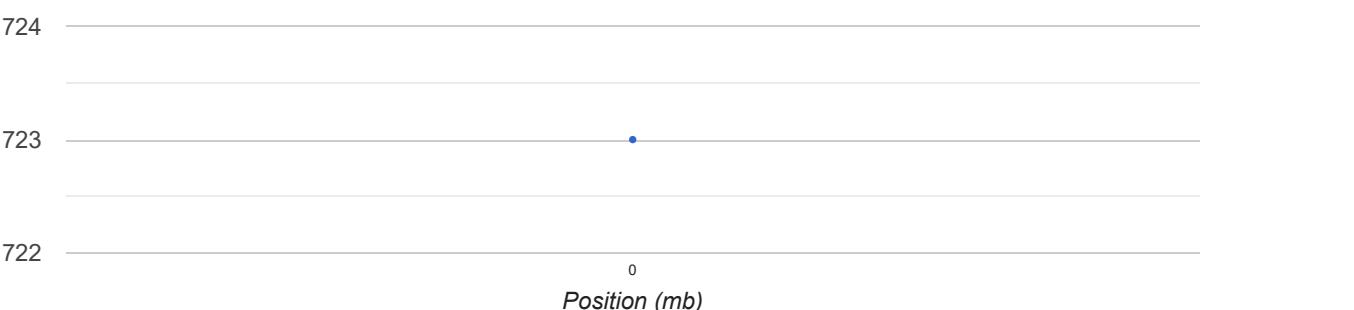
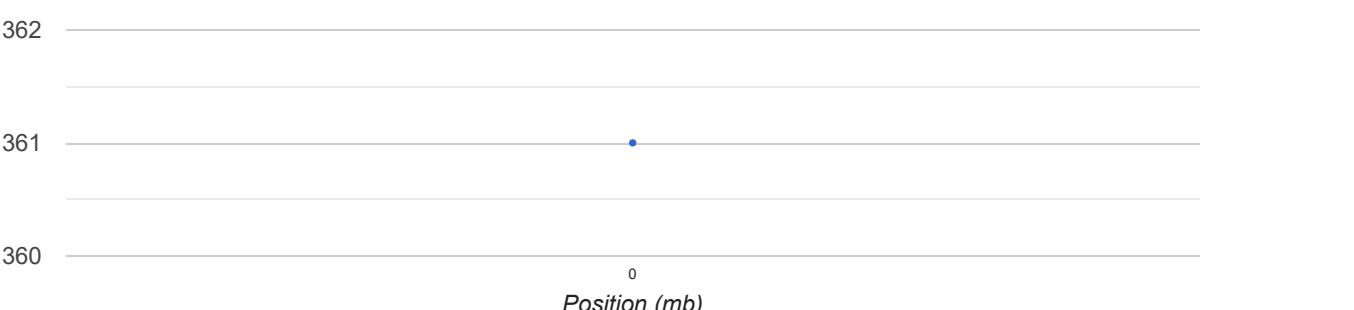
### Distribution of variants on chromosome 34

1,500

1,000

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

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511

.

510

0

*Position (mb)***Distribution of variants on chromosome 38**

485

.

484

.

483

0

*Position (mb)***Distribution of variants on chromosome 39**

214

.

213

.

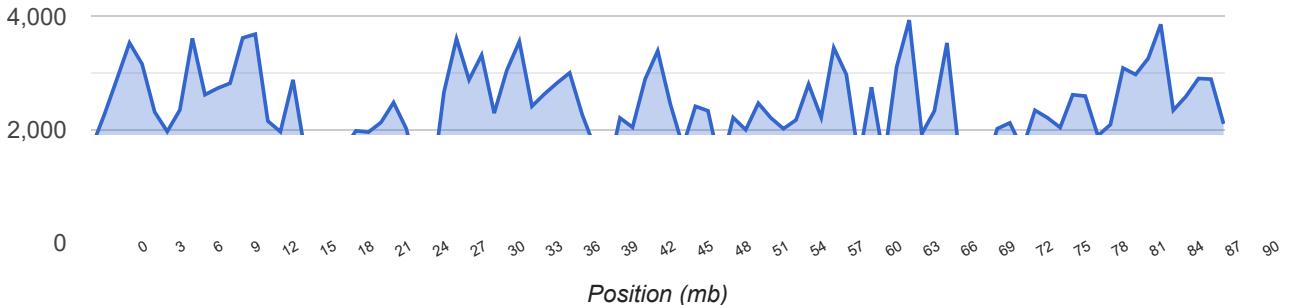
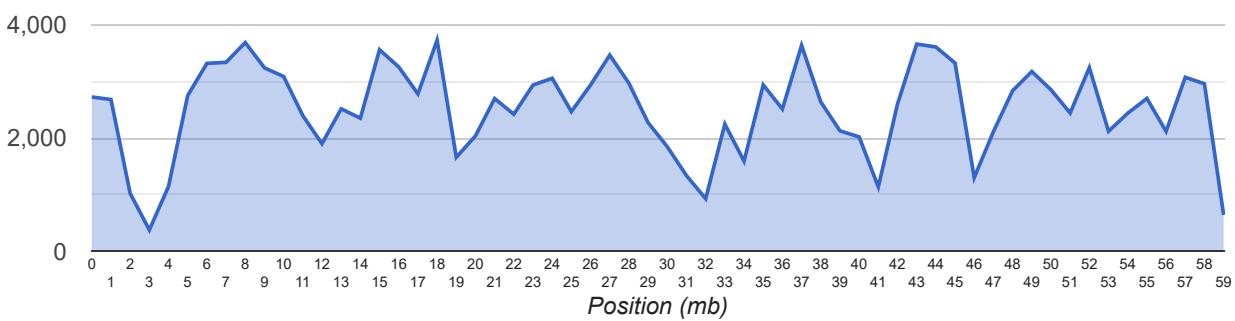
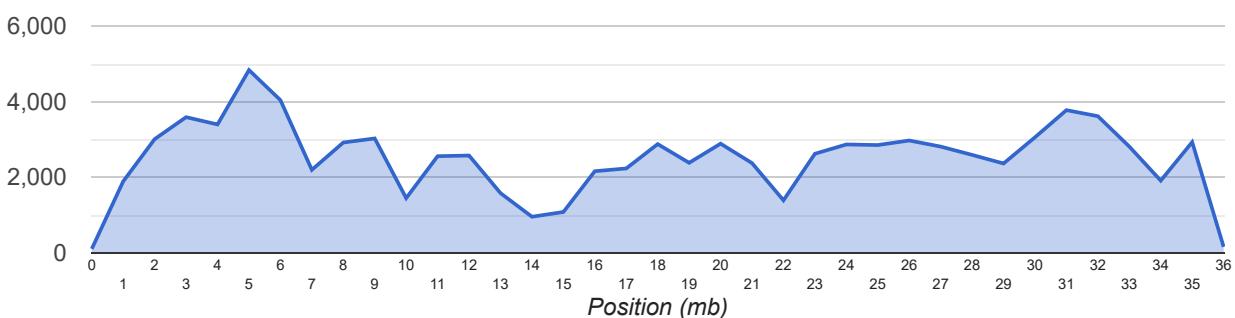
212

0

*Position (mb)***Distribution of variants on chromosome 4**

**Links**

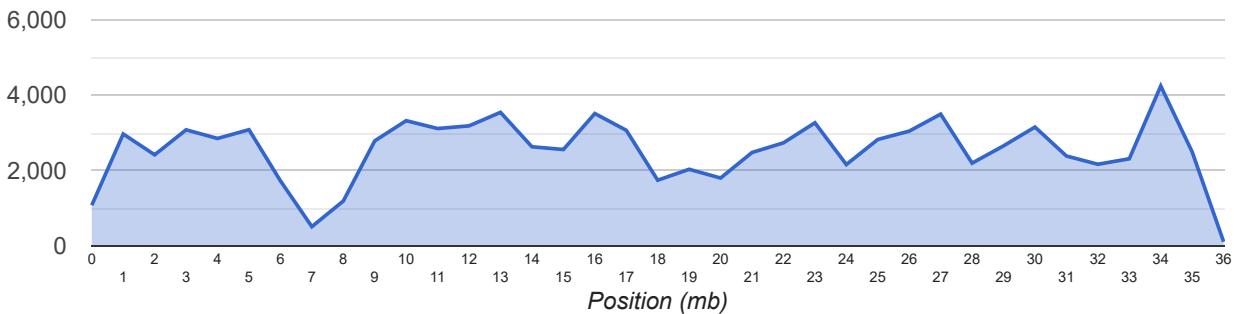
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**Distribution of variants on chromosome 5****Distribution of variants on chromosome 6**

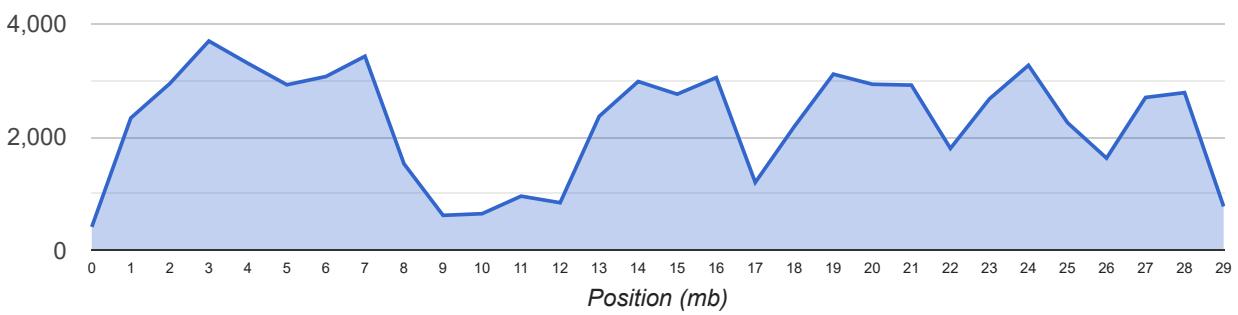
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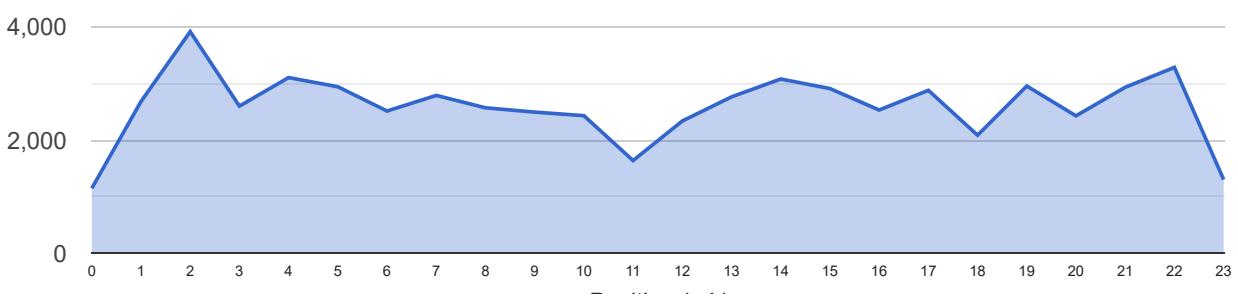
## Distribution of variants on chromosome 7



## Distribution of variants on chromosome 8



## Distribution of variants on chromosome 9



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