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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

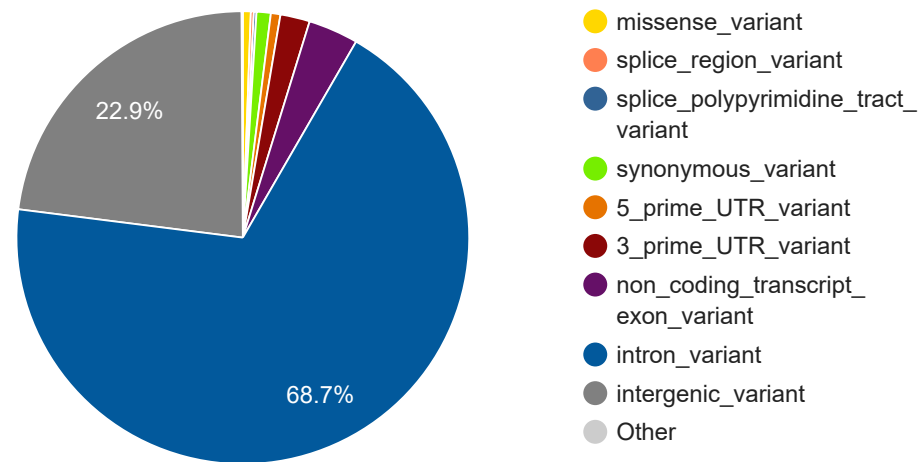


Variant class	Count
SNV	2,279,796

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Consequences (most severe)

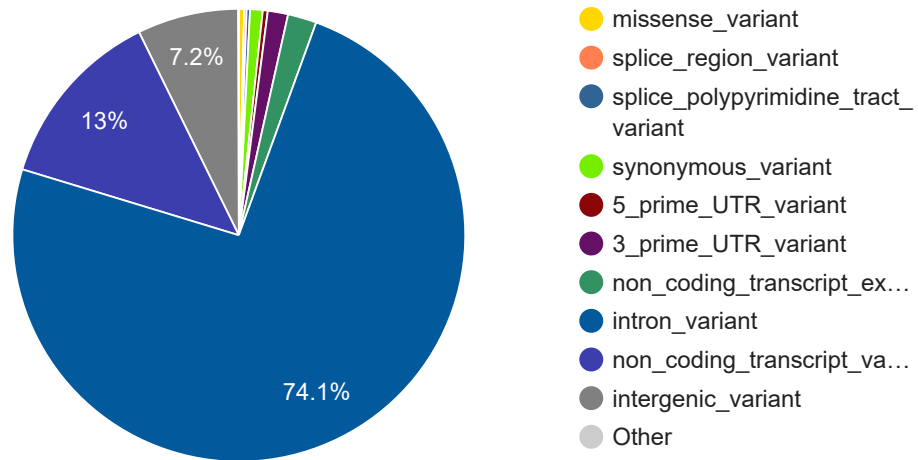


Consequence type	Count
splice_acceptor_variant	179
splice_donor_variant	274
stop_gained	186
stop_lost	35
start_lost	139
missense_variant	12,918
splice_donor_5th_base_variant	336
splice_region_variant	4,862

Consequences (all)

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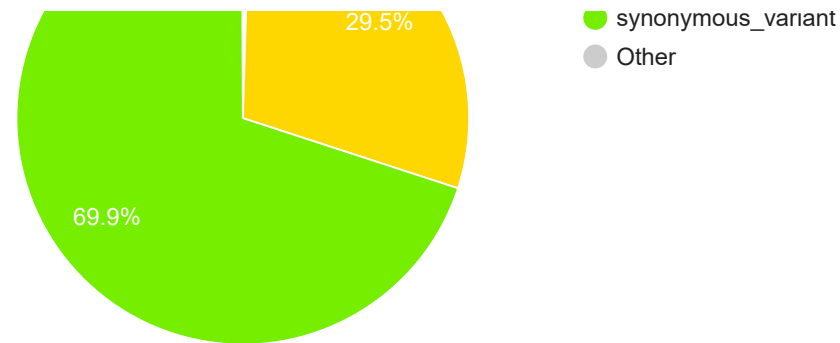
splice_acceptor_variant	234
splice_donor_variant	353
stop_gained	293
stop_lost	42
start_lost	160
missense_variant	27,434
splice_donor_5th_base_variant	701
splice_region_variant	12,455

Coding consequences



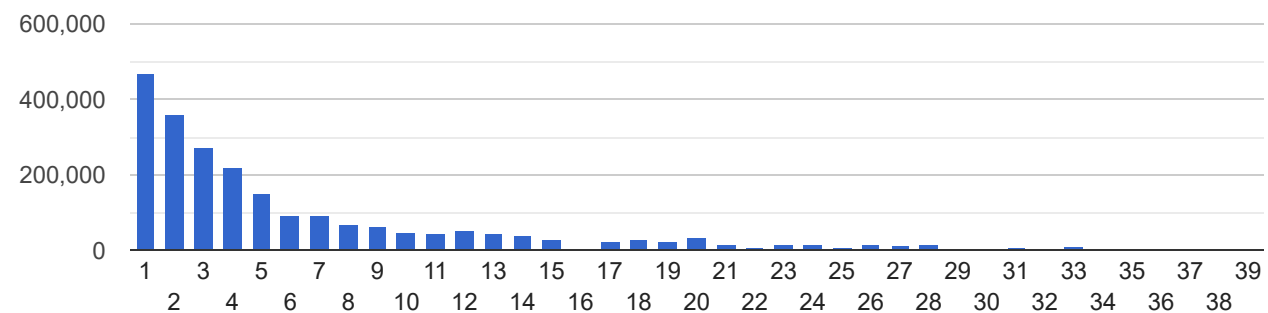
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Consequence type	Count
stop_gained	293
stop_lost	42
start_lost	160
missense_variant	27,434
start_retained_variant	2
stop_retained_variant	15
synonymous_variant	64,961
coding_sequence_variant	1

Variants by chromosome

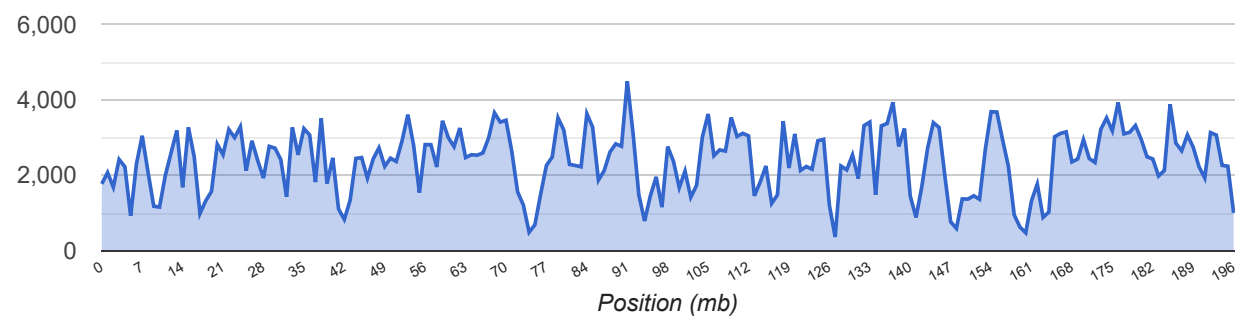


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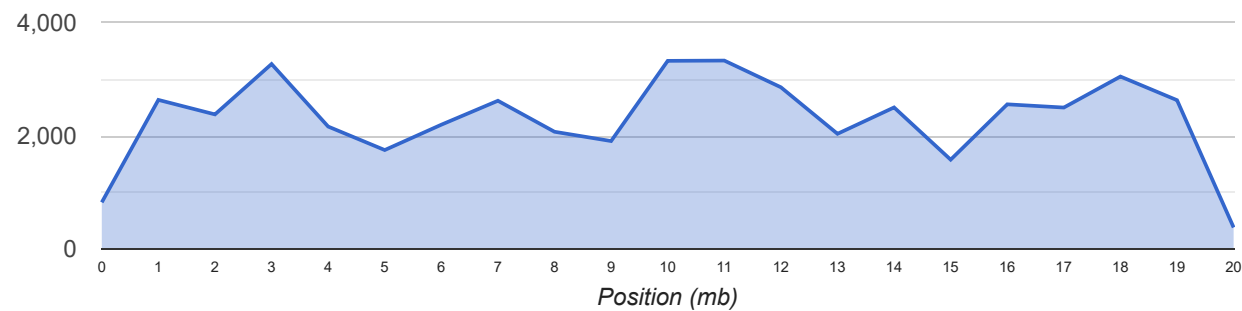
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Chromosome	Count
1	468,059
2	360,273
3	273,550
4	219,039
5	150,926
6	92,678
7	93,831
8	68,063
9	62,409

Distribution of variants on chromosome 1

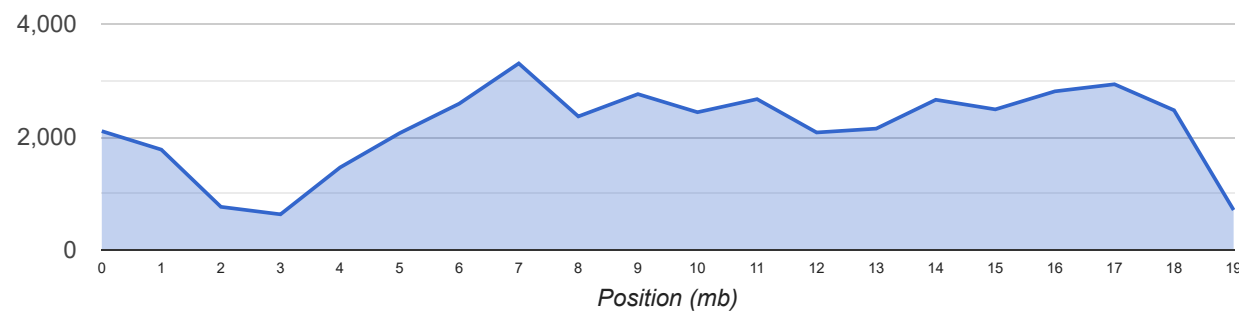
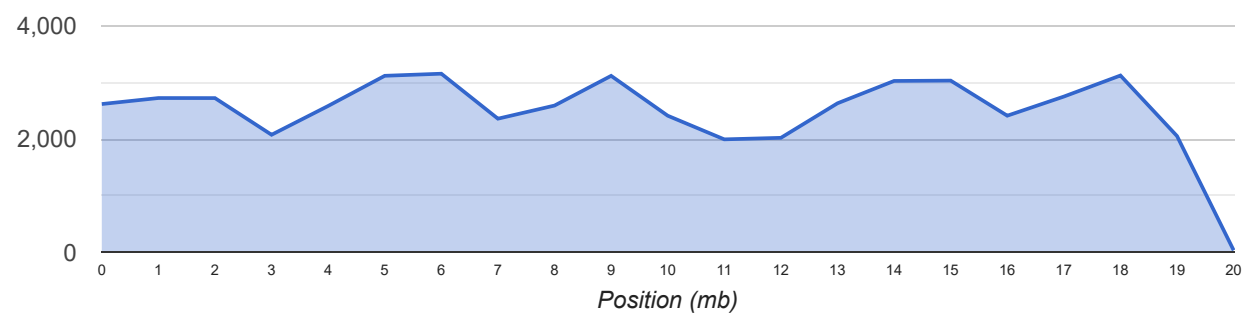
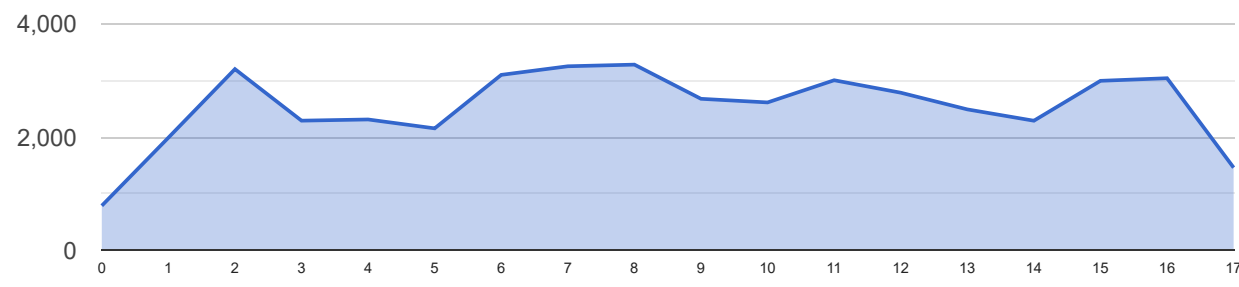


Distribution of variants on chromosome 10



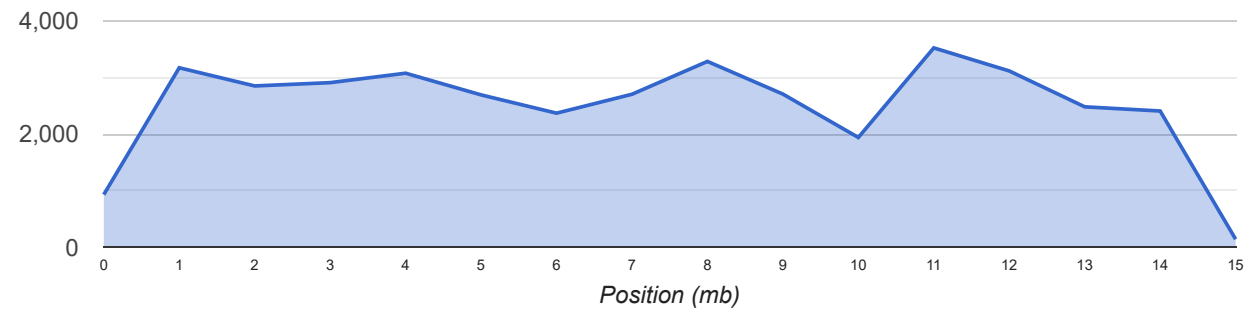
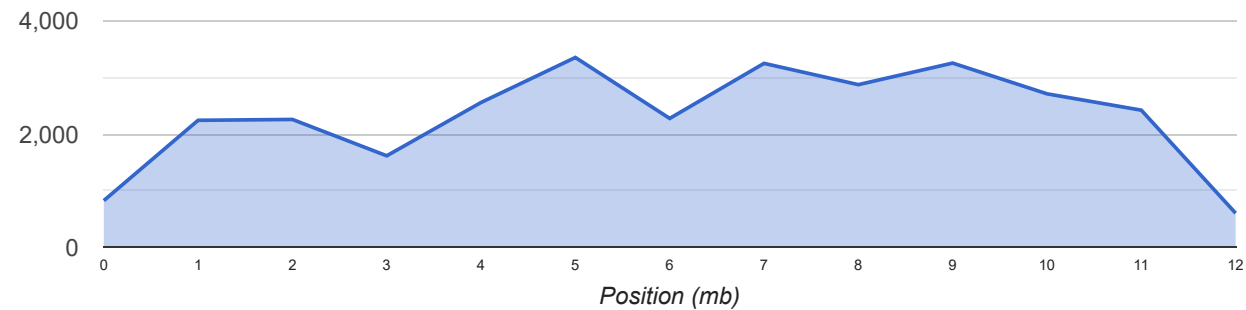
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Distribution of variants on chromosome 11**Distribution of variants on chromosome 12****Distribution of variants on chromosome 13**

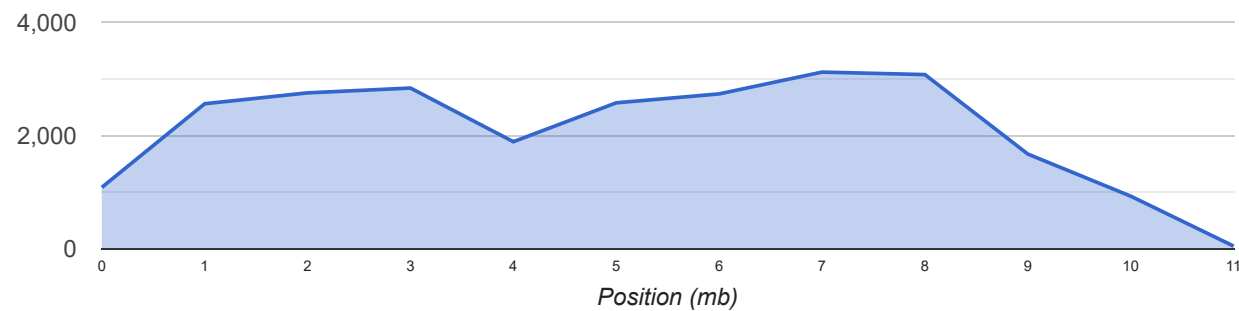
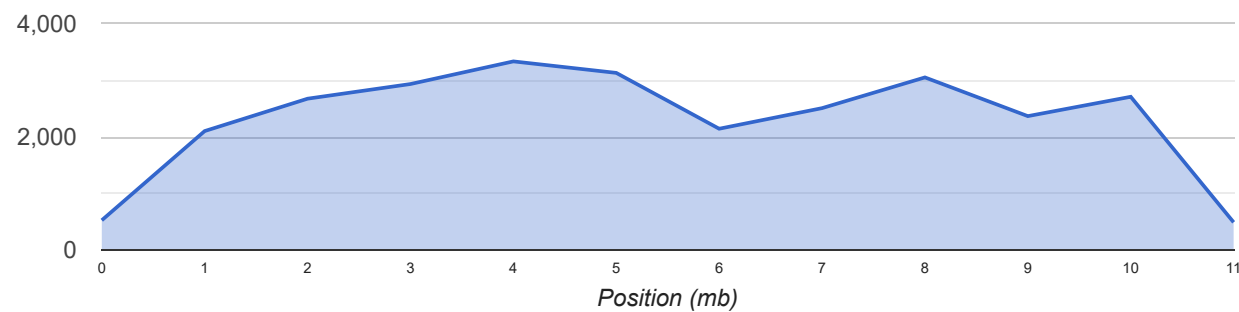
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*Position (mb)***Distribution of variants on chromosome 14****Distribution of variants on chromosome 15****Distribution of variants on chromosome 16**

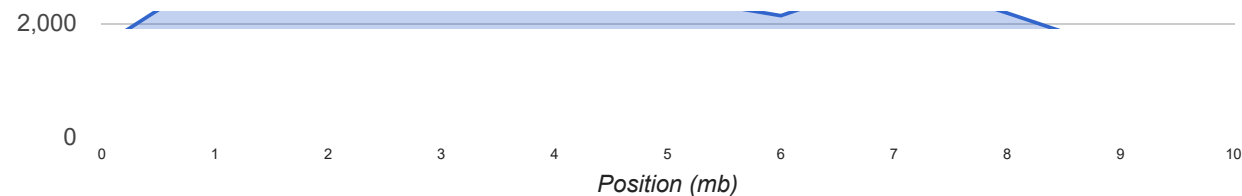
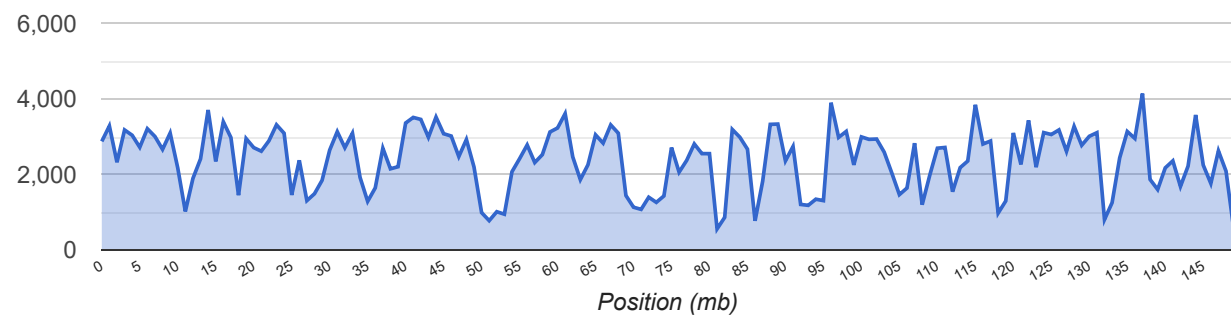
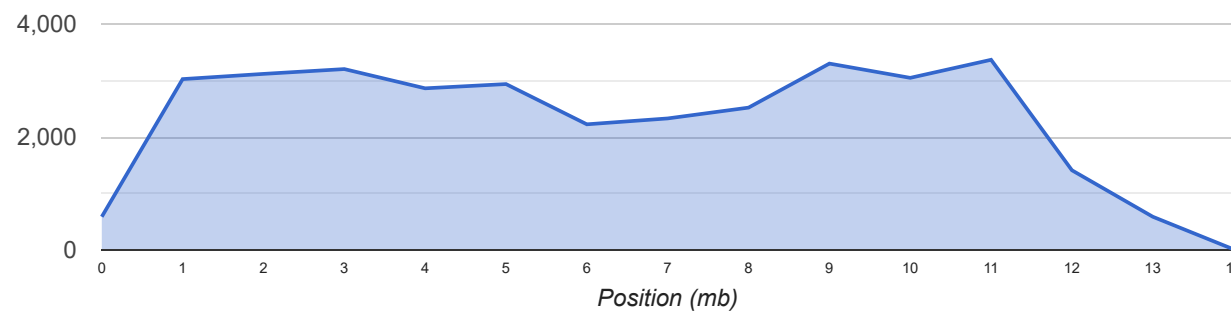
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**Distribution of variants on chromosome 17****Distribution of variants on chromosome 18****Distribution of variants on chromosome 19**

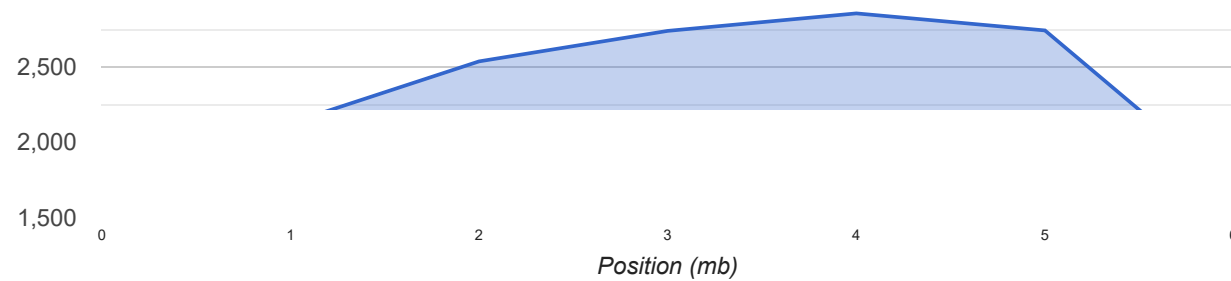
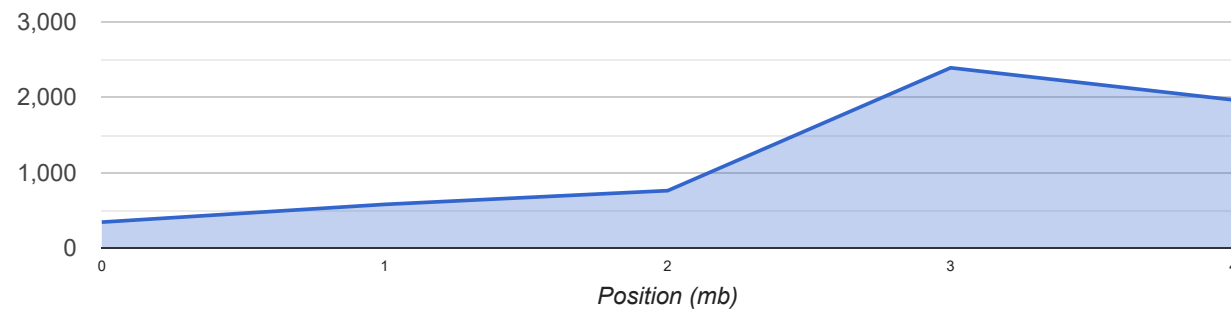
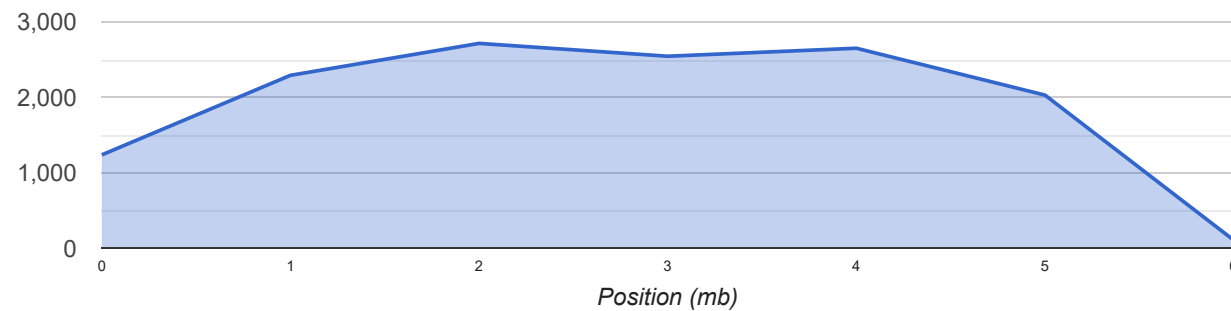
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**Distribution of variants on chromosome 2****Distribution of variants on chromosome 20****Distribution of variants on chromosome 21**

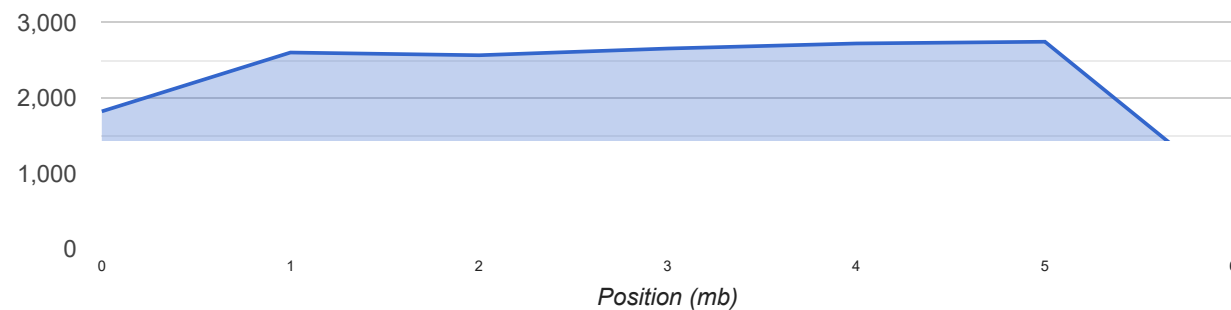
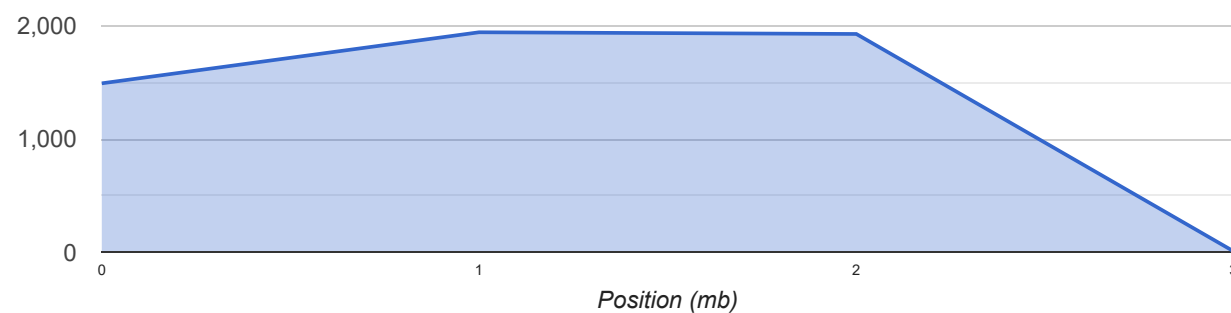
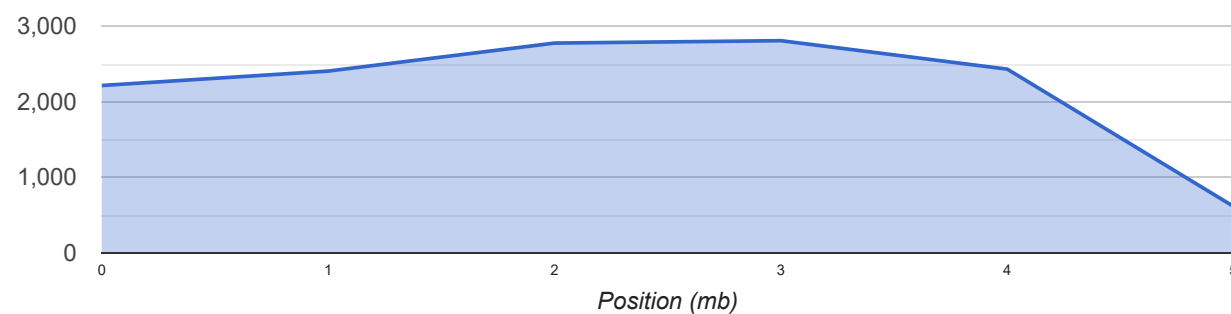
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**Distribution of variants on chromosome 22****Distribution of variants on chromosome 23****Distribution of variants on chromosome 24**

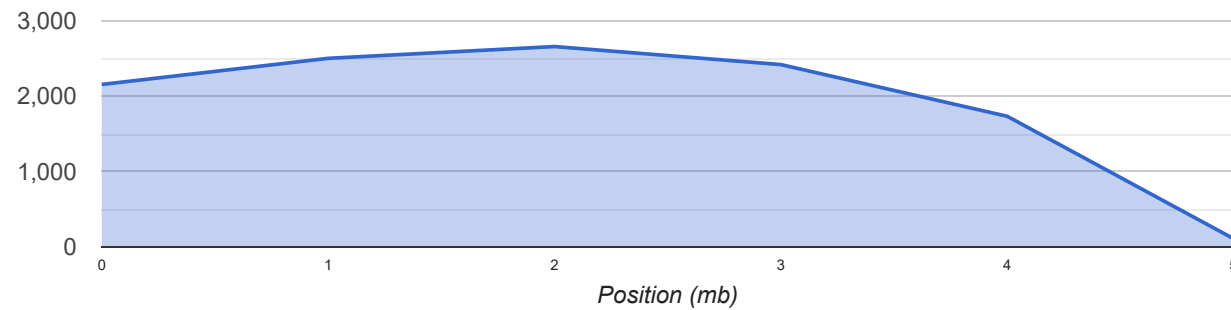
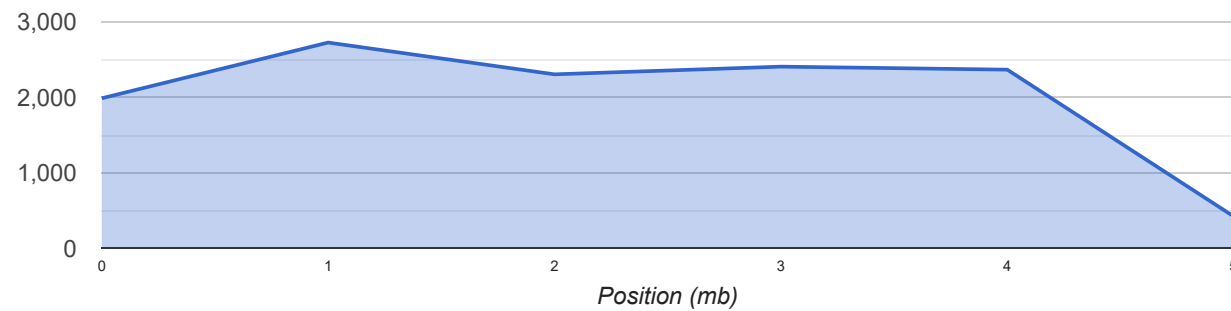
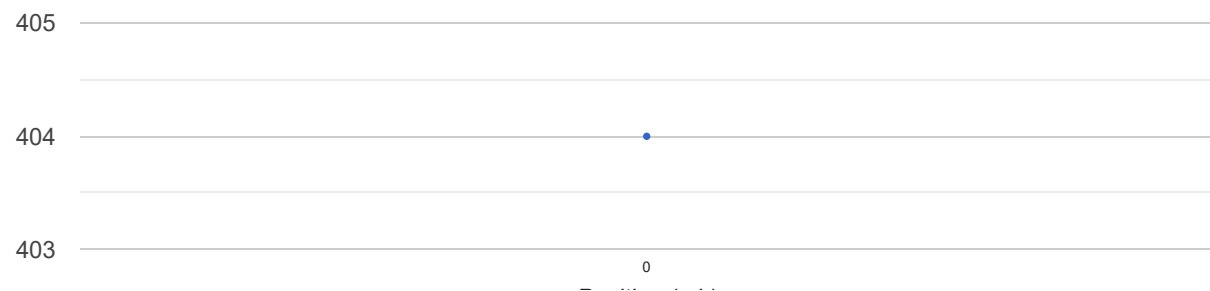
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**Distribution of variants on chromosome 25****Distribution of variants on chromosome 26**

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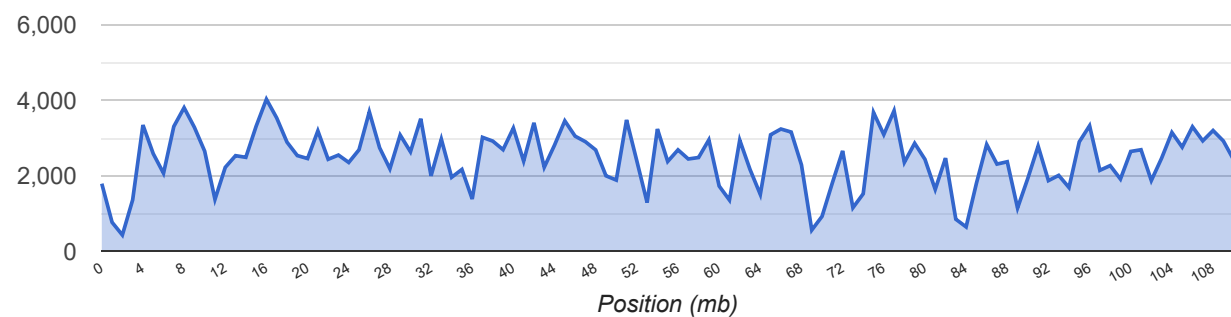
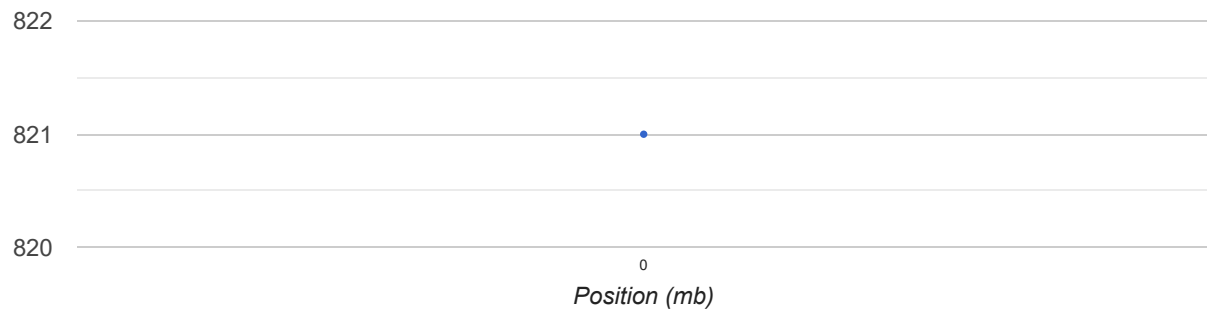
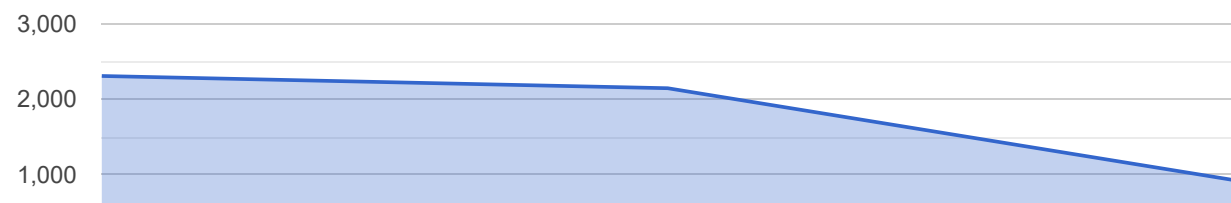
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Distribution of variants on chromosome 27**Distribution of variants on chromosome 28****Distribution of variants on chromosome 29**

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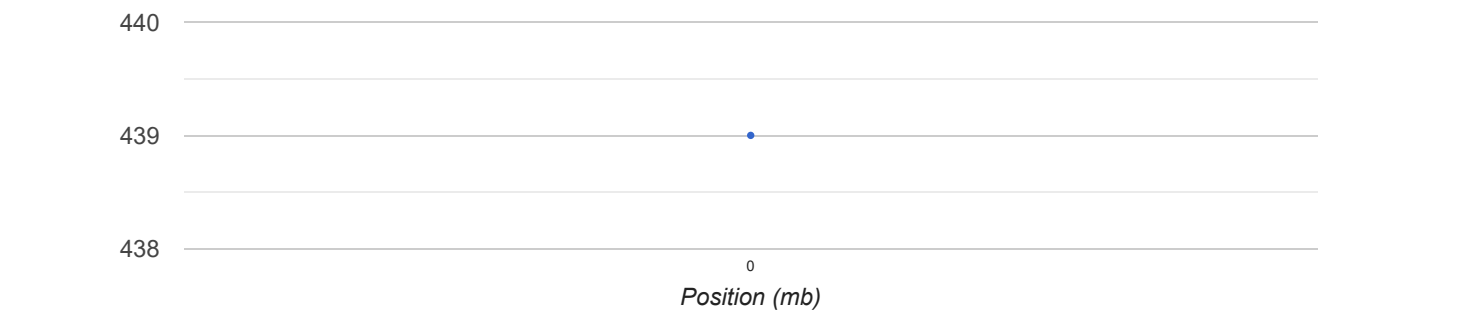
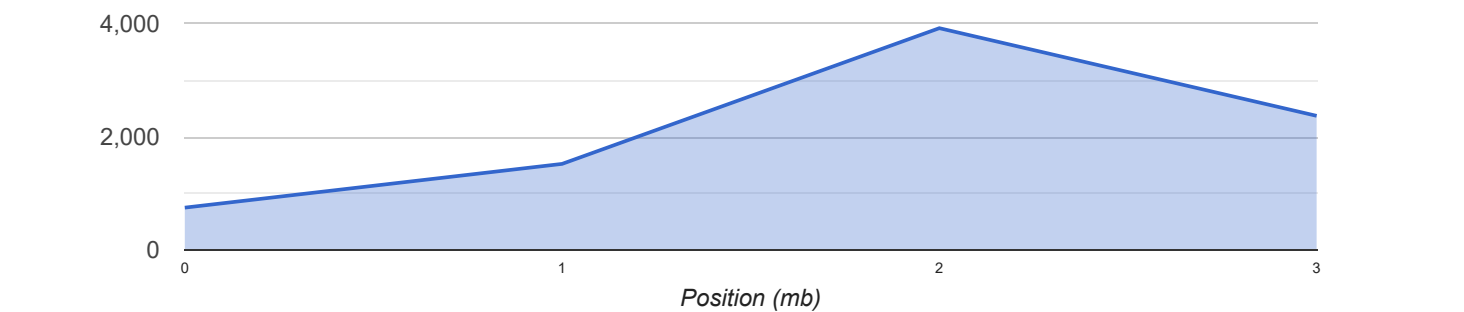
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Distribution of variants on chromosome 3**Distribution of variants on chromosome 30****Distribution of variants on chromosome 31**

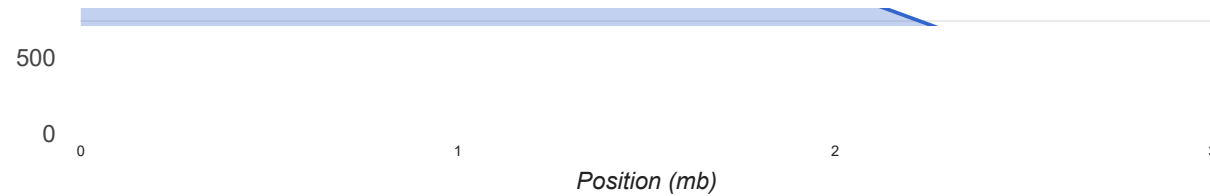
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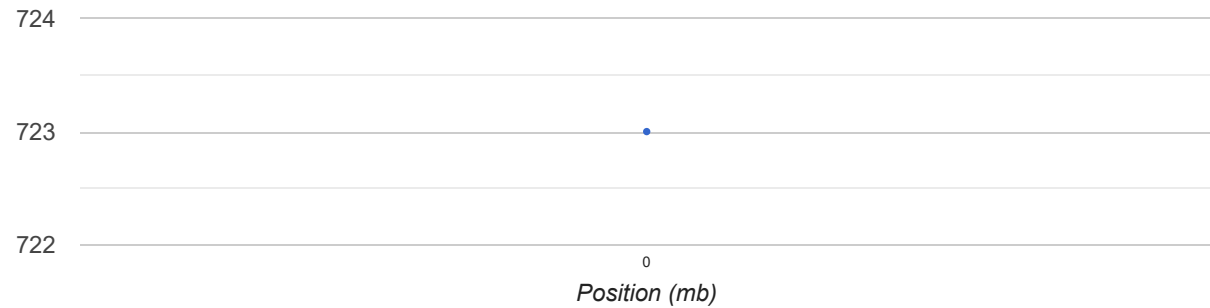
**Distribution of variants on chromosome 32****Distribution of variants on chromosome 33****Distribution of variants on chromosome 34**

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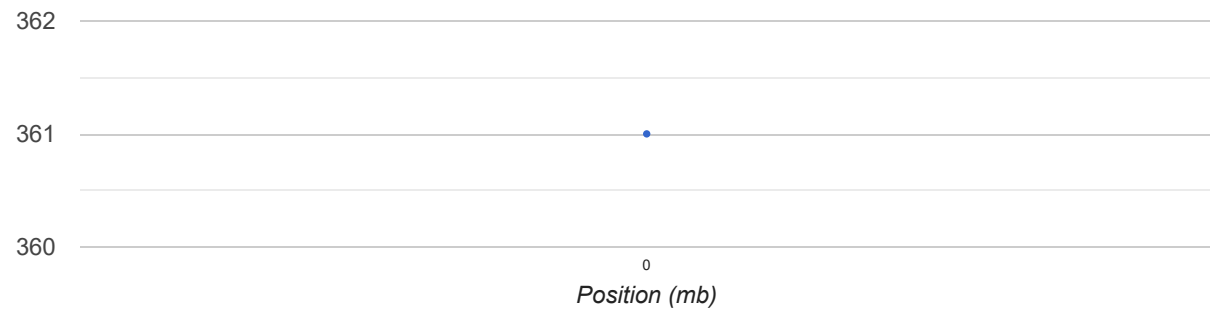
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Distribution of variants on chromosome 35



Distribution of variants on chromosome 36

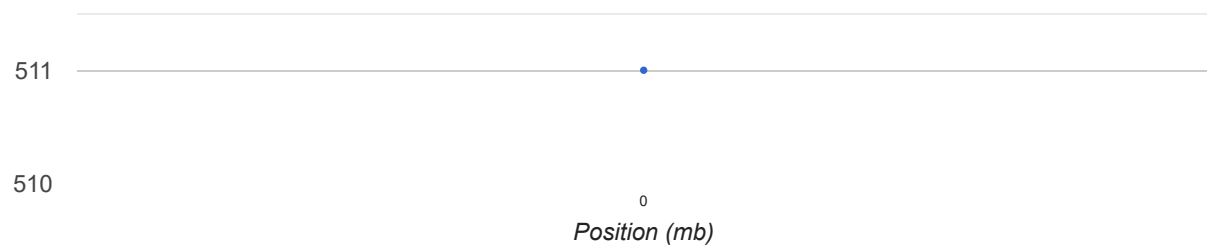
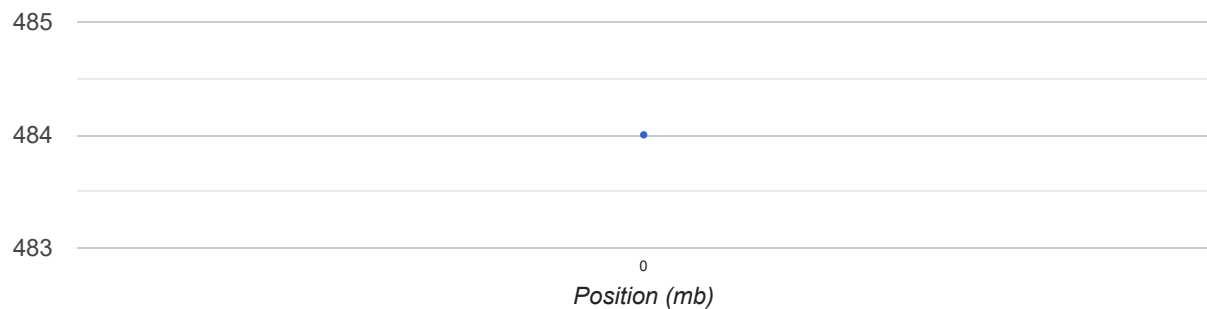
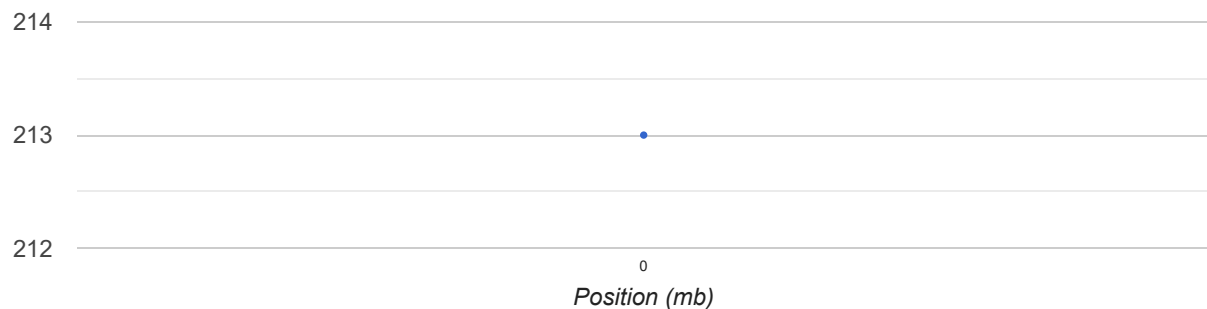


Distribution of variants on chromosome 37



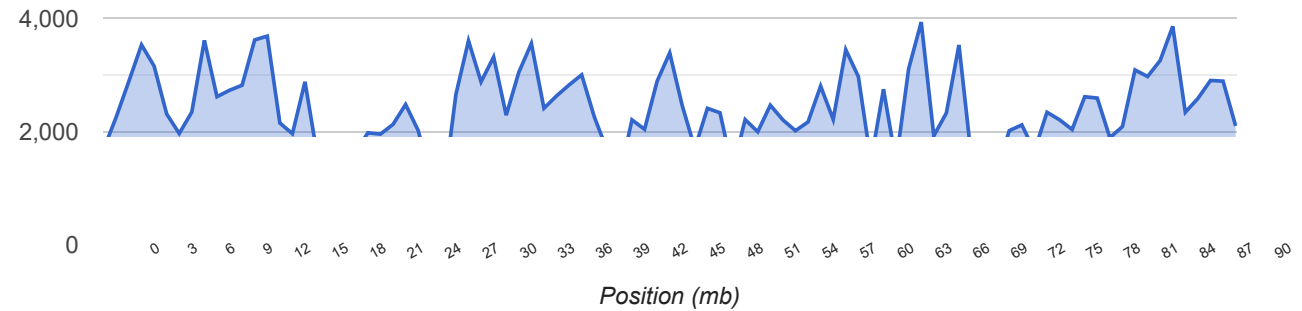
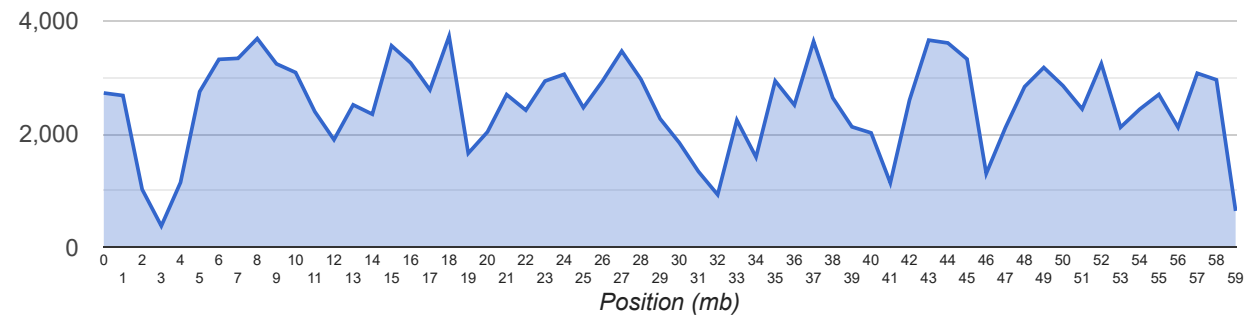
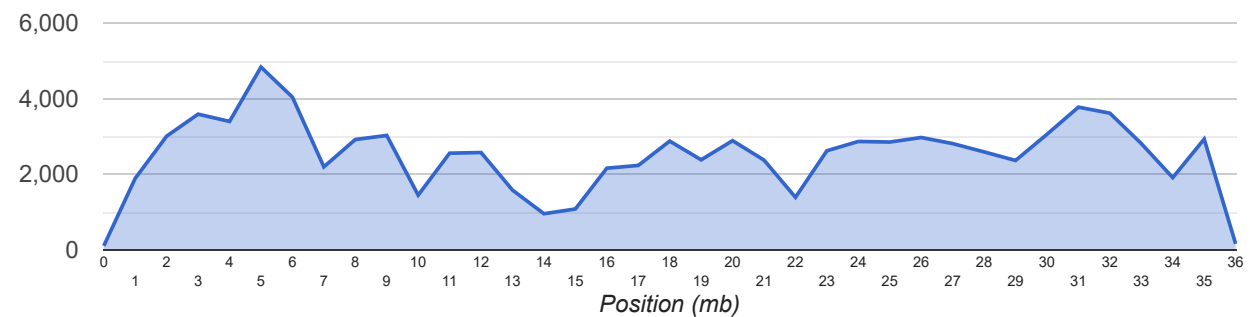
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**Distribution of variants on chromosome 38****Distribution of variants on chromosome 39****Distribution of variants on chromosome 4**

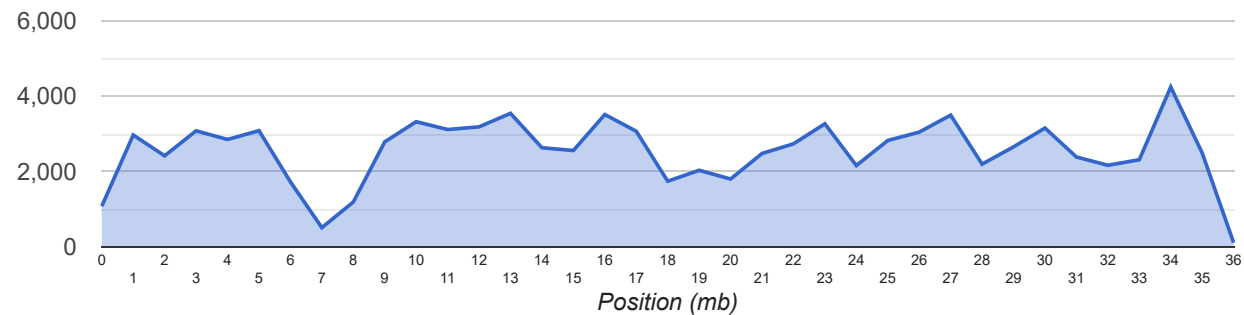
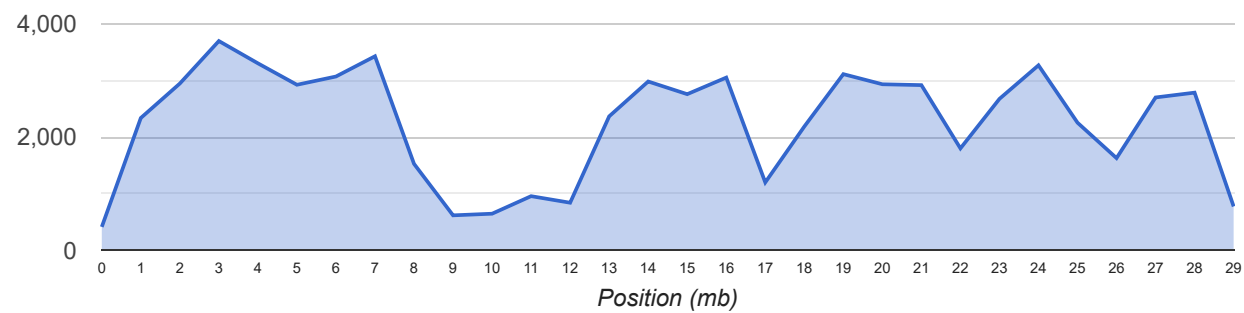
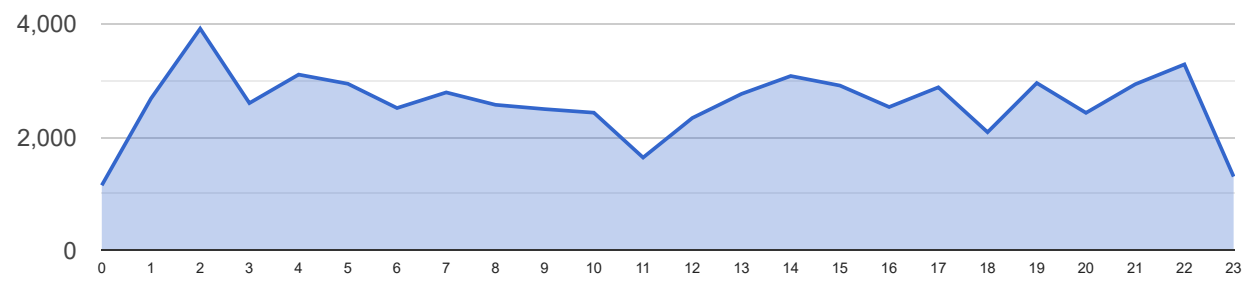
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**Distribution of variants on chromosome 5****Distribution of variants on chromosome 6**

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