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VEP run statistics

VEP	
version	111 (111)
(API)	

 $\begin{array}{ll} \text{Annotation} & \text{Cache: /opt/vep/.vep/homo_sapiens/111_GRCh38; Custom: clinvar.vcf.gz (exact)} \end{array}$

Species homo_sapiens

Command

line options --cache --custom file=clinvar.vcf.gz,short_name=ClinVar,format=vcf,type=exact,coords=0,fields=CLNSIG%CLNREVSTAT%CLNDN --everything --fields Location, @

Start time 2024-03-21 22:18:35 End time 2024-03-21 23:39:26 Run time 4851 seconds

Input file normal_sample.deepvariant.vcf

Output file output/clin_var_output2.tsv

General statistics

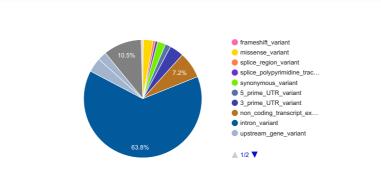
Lines of input read	597192
Variants processed	597192
Variants filtered out	0
Novel / existing variants	104868 (17.6) / 492324 (82.4)
Overlapped genes	48365
Overlapped transcripts	225159
Overlapped regulatory features	0

Variant classes



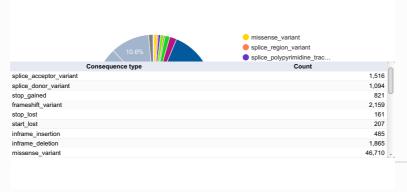
Variant class	Count
indel	764
sequence_alteration	6,820
insertion	54,011
deletion	63,017
SNV	472,580

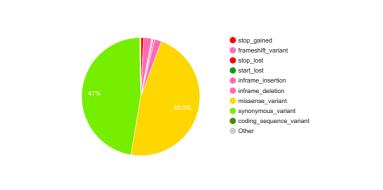
Consequences (most severe)



	Consequence type	Count
splice_acceptor_variant		333
splice_donor_variant		312
stop_gained		287
frameshift_variant		859
stop_lost		98
start_lost		78
inframe_insertion		193
inframe_deletion		495
missense_variant		15,773

Consequences (all)





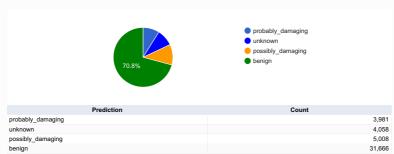
Consequence type	Count
stop_gained	821
frameshift_variant	2,159
stop_lost	161
start_lost	207
inframe_insertion	485
inframe_deletion	1,865
missense_variant	46,710
protein_altering_variant	5
incomplete_terminal_codon_variant	4

SIFT summary



Prediction	Count
deleterious_low_confidence	6,172
deleterious	7,087
tolerated_low_confidence	9,345
tolerated	22,971

PolyPhen summary



31,666

Variants by chromosome	Variants	by	chromosome
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Chromosome	Count
chr1	54,314
chr2	44,989
chr3	34,873
chr4	29,877
chr5	28,114
chr6	32,691
chr7	33,021
chr8	22,489
chr9	26,734

Position in protein

