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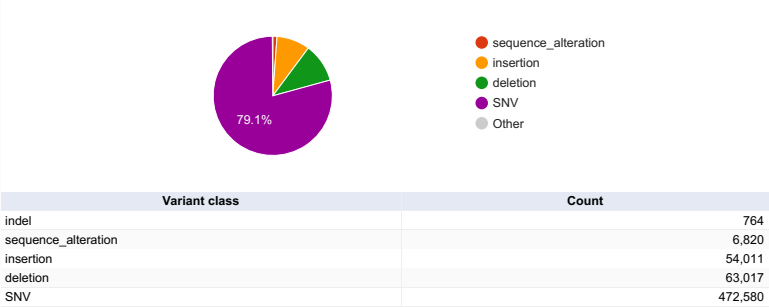
VEP run statistics

VEP version (API)	111 (111)
Annotation sources	Cache: /opt/vep/.vep/homo_sapiens/111_GRCh38; Custom: clinvar.vcf.gz (exact)
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, C
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

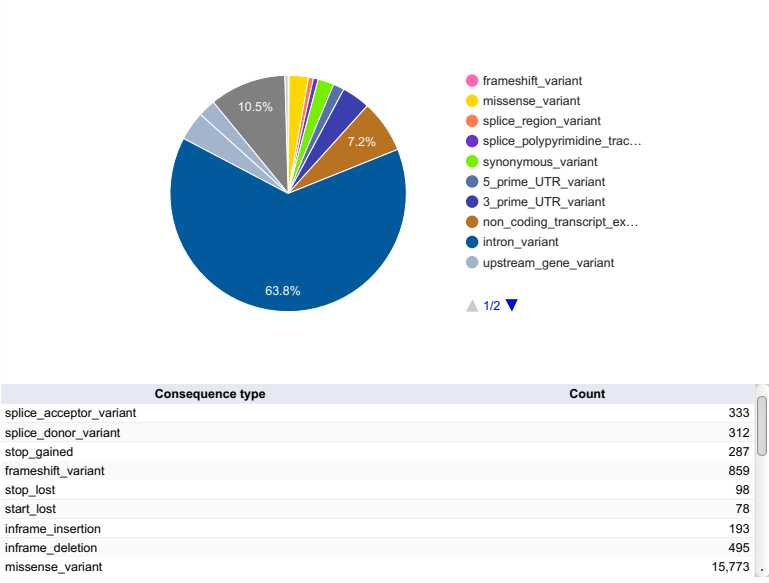
General statistics

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

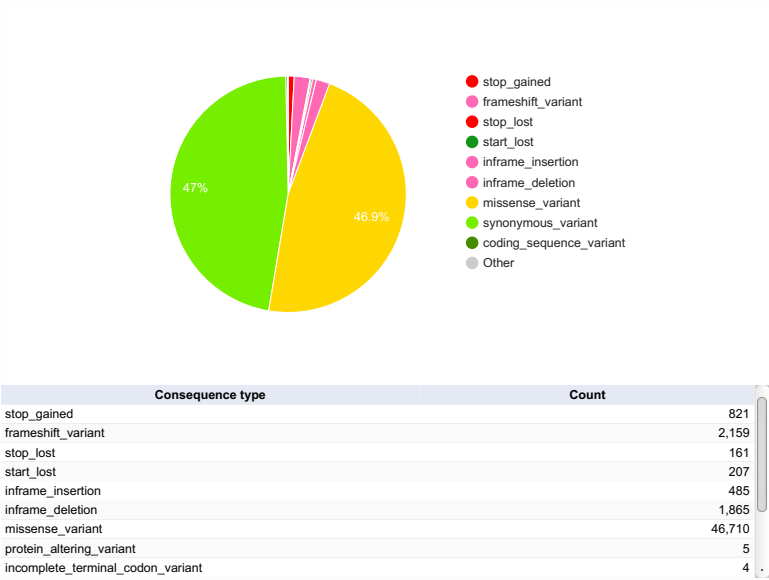
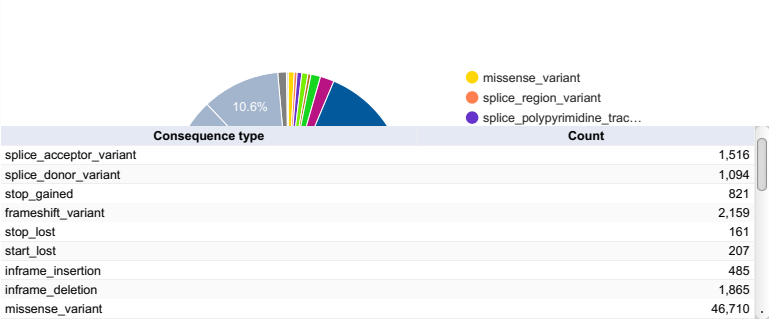
Variant classes



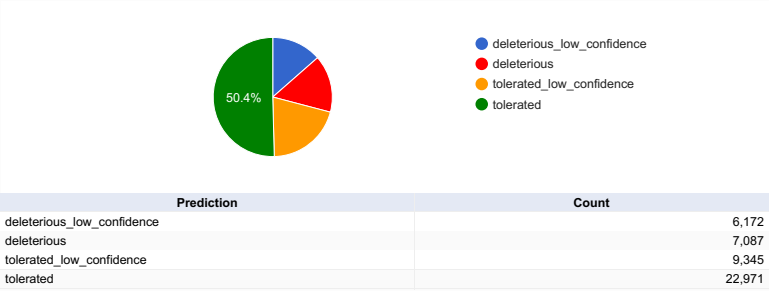
Consequences (most severe)



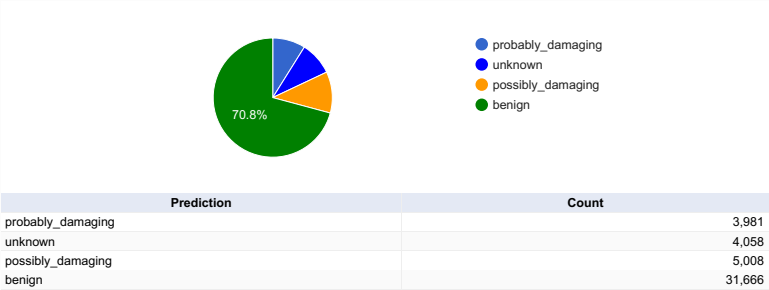
Consequences (all)



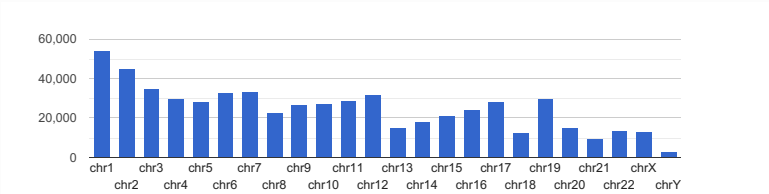
SIFT summary



PolyPhen summary



Variants by chromosome



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

