Hex Color	*	SO term	SO description	SO accession	Old Ensembl term
#02599C		intron_variant	A transcript variant occurring within an intron	SO:0001627	Intronic
#32CD32		non_coding_exon_variant	A sequence variant that changes non-coding exon sequence	SO:0001792	Within non coding gene
#32CD32		nc_transcript_variant	A transcript variant of a non coding RNA	SO:0001619	Within non coding gene
#458B00		coding_sequence_variant	A sequence variant that changes the coding sequence	SO:0001580	Coding unknown
#458B00		mature_miRNA_variant	A transcript variant located with the sequence of the mature miRNA	SO:0001620	Within mature miRNA
#636363		intergenic_variant	A sequence variant located in the intergenic region, between genes	SO:0001628	Intergenic
#76EE00		stop_retained_variant	A sequence variant where at least one base in the terminator codon is changed, but the terminator remains	SO:0001567	Synonymous coding
#76EE00		synonymous_variant	A sequence variant where there is no resulting change to the encoded amino acid	SO:0001819	Synonymous coding
#7AC5CD		5_prime_UTR_variant	A UTR variant of the 5' UTR	SO:0001623	5prime UTR
#7AC5CD		3_prime_UTR_variant	A UTR variant of the 3' UTR	SO:0001624	3prime UTR
#7F7F7F		feature_elongation	A sequence variant that causes the extension of a genomic feature, with regard to the reference sequence	SO:0001907	Feature elongation
#7F7F7F		feature_truncation	A sequence variant that causes the reduction of a genomic feature, with regard to the reference sequence	SO:0001906	Feature truncation
#A2B5CD		upstream_gene_variant	A sequence variant located 5' of a gene	SO:0001631	Upstream
#A2B5CD		downstream_gene_variant	A sequence variant located 3' of a gene	SO:0001632	Downstream
#A52A2A		TFBS_ablation	A feature ablation whereby the deleted region includes a transcription factor binding site	SO:0001895	Tfbs ablation
#A52A2A		TFBS_amplification	A feature amplification of a region containing a transcription factor binding site	SO:0001892	Tfbs amplification
#A52A2A		TF_binding_site_variant	A sequence variant located within a transcription factor binding site	SO:0001782	Regulatory region
#A52A2A		regulatory_region_ablation	A feature ablation whereby the deleted region includes a regulatory region	SO:0001894	Regulatory region ablation
#A52A2A		regulatory_region_amplification	A feature amplification of a region containing a regulatory region	SO:0001891	Regulatory region amplification
#A52A2A		regulatory_region_variant	A sequence variant located within a regulatory region	SO:0001566	Regulatory region
#FF0000		transcript_ablation	A feature ablation whereby the deleted region includes a transcript feature	SO:0001893	Transcript ablation
#FF0000		stop_gained	A sequence variant whereby at least one base of a codon is changed, resulting in a premature stop codon, leading to a shortened transcript	SO:0001587	Stop gained
#FF0000		stop_lost	A sequence variant where at least one base of the terminator codon (stop) is changed, resulting in an elongated transcript	SO:0001578	Stop lost
#FF00FF		incomplete_terminal_codon_variant	A sequence variant where at least one base of the final codon of an incompletely annotated transcript is changed	SO:0001626	Partial codon
#FF4500		NMD_transcript_variant	A variant in a transcript that is the target of NMD	SO:0001621	NMD transcript
#FF69B4		frameshift_variant	A sequence variant which causes a disruption of the translational reading frame, because the number of nucleotides inserted or deleted is not a multiple of three	SO:0001589	Frameshift coding
#FF69B4		transcript_amplification	A feature amplification of a region containing a transcript	SO:0001889	Transcript amplification
#FF69B4		inframe_insertion	An inframe non synonymous variant that inserts bases into in the coding sequence	SO:0001821	Non synonymous coding
#FF69B4		inframe_deletion	An inframe non synonymous variant that deletes bases from the coding sequence	SO:0001822	Non synonymous coding
#FF7F50		splice_donor_variant	A splice variant that changes the 2 base region at the 5' end of an intron	SO:0001575	Essential splice site
#FF7F50		splice_acceptor_variant	A splice variant that changes the 2 base region at the 3' end of an intron	SO:0001574	Essential splice site
#FF7F50		splice_region_variant	A sequence variant in which a change has occurred within the region of the splice site, either within 1-3 bases of the exon or 3-8 bases of the intron	SO:0001630	Splice site
#FFD700		initiator_codon_variant	A codon variant that changes at least one base of the first codon of a transcript	SO:0001582	Non synonymous coding
#FFD700		missense_variant	A sequence variant, that changes one or more bases, resulting in a different amino acid sequence but where the length is preserved	SO:0001583	Non synonymous coding