

Feature name	Source	Description
silent fraction	Calculated from mutations	Fraction of mutations that are silent mutations
nonsense fraction	Calculated from mutations	Fraction of mutations that are nonsense mutations
splice site fraction	Calculated from mutations	Fraction of mutations that are 2bp consensus splice site mutations
missense fraction	Calculated from mutations	Fraction of mutations that are missense mutations
recurrent missense fraction	Calculated from mutations	Fraction of mutations that are recurrent missense
frameshift indel fraction	Calculated from mutations	Fraction of mutations that are frameshift indel mutations
inframe indel fraction	Calculated from mutations	Fraction of mutations that are inframe indel mutations
lost start and stop fraction	Calculated from mutations	Fraction of mutations that are either lost start or lost stop mutations
normalized missense position entropy	Calculated from mutations	See above
missense to silent	Calculated from mutations	Ratio of missense to silent mutations. A pseudo count is added to silent mutations to avoid divide by zero.
non-silent to silent	Calculated from mutations	Ratio of non-silent to silent mutations. A pseudo count is added to silent mutations to avoid divide by zero.
normalized mutation entropy	Calculated from mutations	Normalized entropy score (see above). Missense mutations are binned together based on codon position. Each silent mutation is regarded in its own bin. Potentially inactivating mutations (nonsense, splice site, lost stop, and lost start) mutations are grouped into a single bin.
mean missense MGAEntropy	Calculated from mutations. MGAEntropy scores obtained from SNVBox (30).	Mean MGAEntropy score for missense mutations (30). MGAEntropy for a missense mutation is the entropy of the column for a protein-translated version of UCSC's 46-way vertebrate alignment
mean VEST score	Calculated from mutations	Mean score. Score for missense mutations are taken as the VEST score, silent mutations receive a score of 0, and other mutations receive a score of 1.
inactivating SNV p-value	Calculated from mutations	Statistical significance of proportion of inactivating mutations. SNV=single nucleotide variant.
missense entropy p-value	Calculated from mutations	Statistical significance of normalize missense position entropy
missense VEST p-value	Calculated from mutations	One-tailed tatistical significance of proportion of having higher mean VEST score for missense mutations
missense combined p-value	Calculated from mutations	Combined p-value composed of missense entropy and missense VEST p-value using Fisher's method
gene degree	BioGrid	Number of other genes that are connected in the BioGrid interaction network
gene betweenness centrality	BioGrid	Fraction of shortest paths that pass through a gene's node in the BioGrid interaction network
gene length	Longest SNVBox transcript	CDS length of reference transcript
expression CCLE	MutsigCV (4)	Average expression of a gene in the Cancer Cell Line Encyclopedia
replication time	MutsigCV (4)	DNA replication time during cell cycle
HiC compartment	MutsigCV (4)	HiC measures open vs closed chromatin