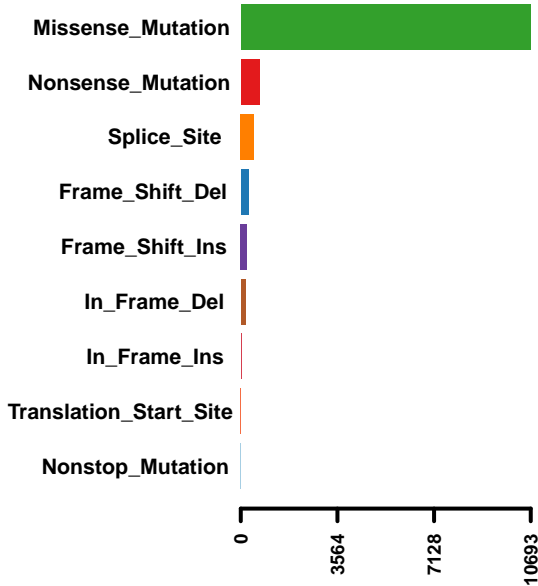
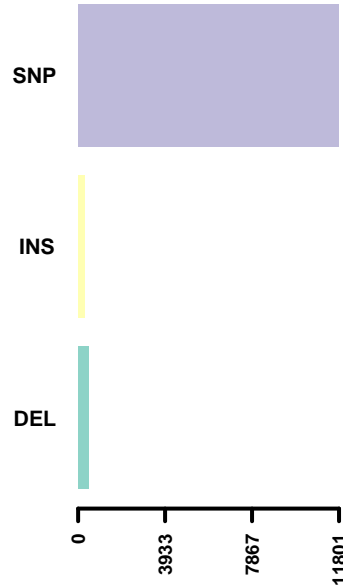


# MAF summary

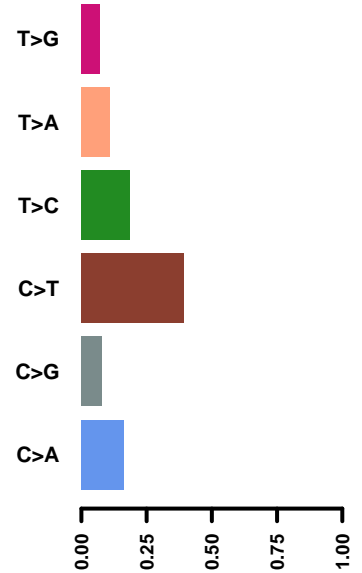
Variant Classification



Variant Type

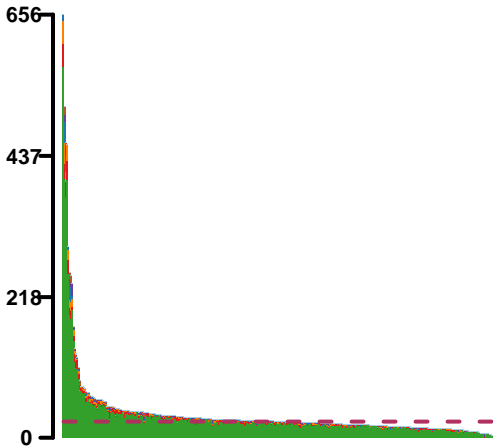


SNV Class

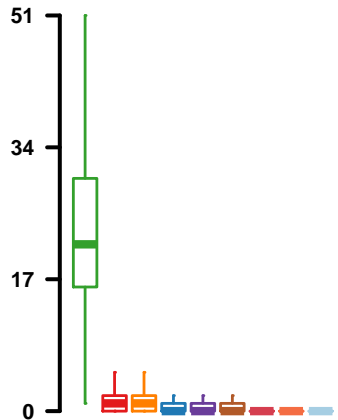


Variants per sample

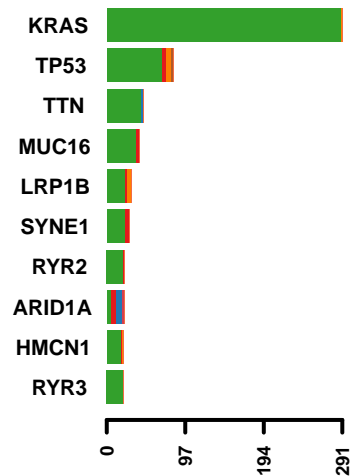
Median: 25



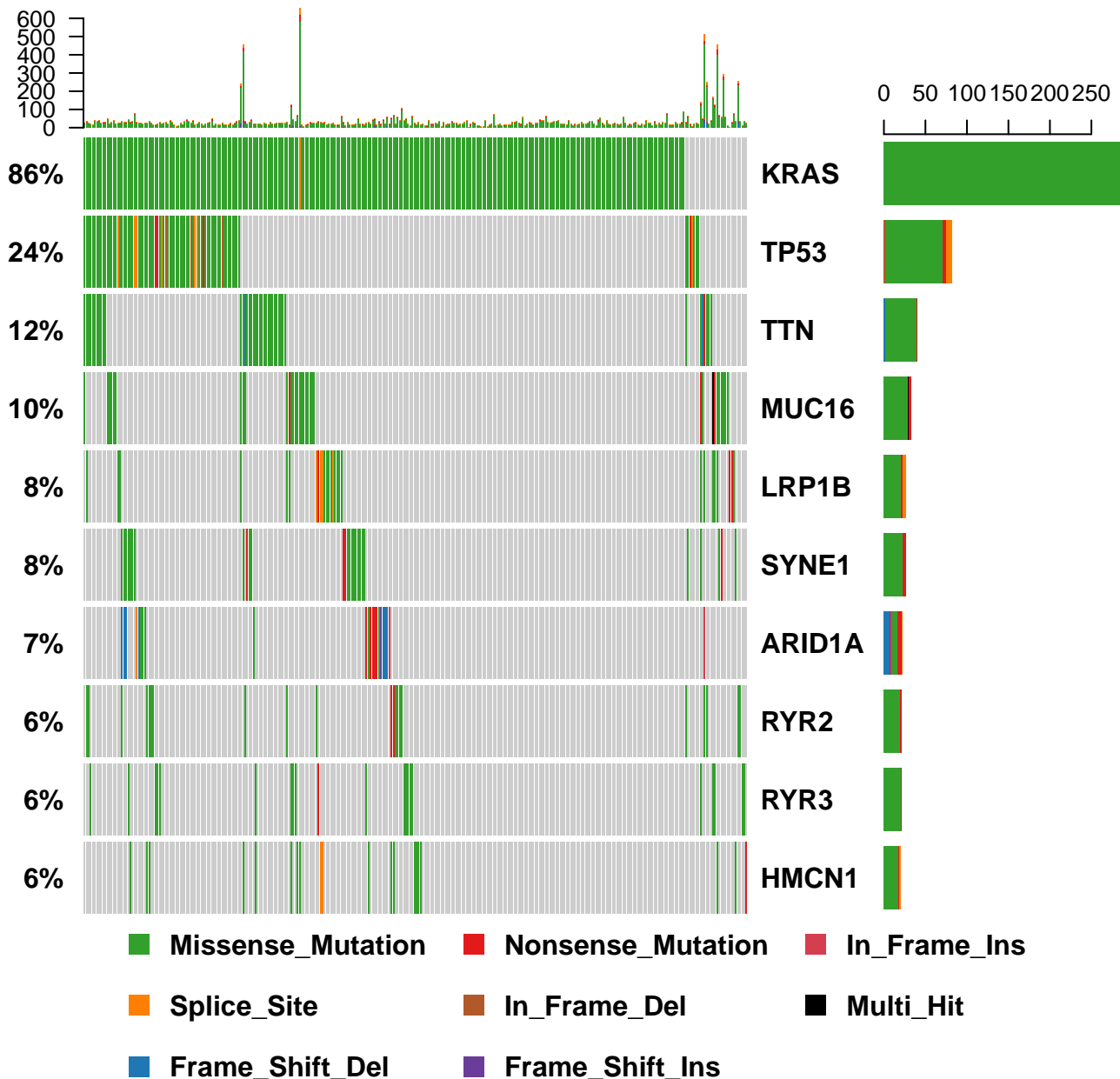
Variant Classification summary



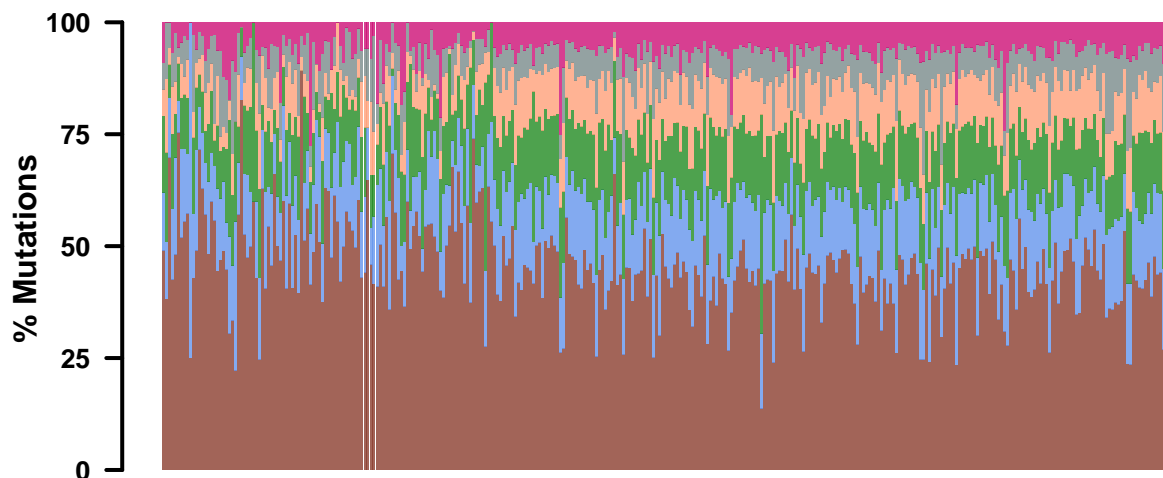
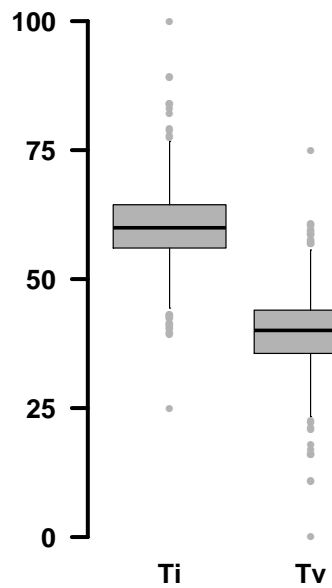
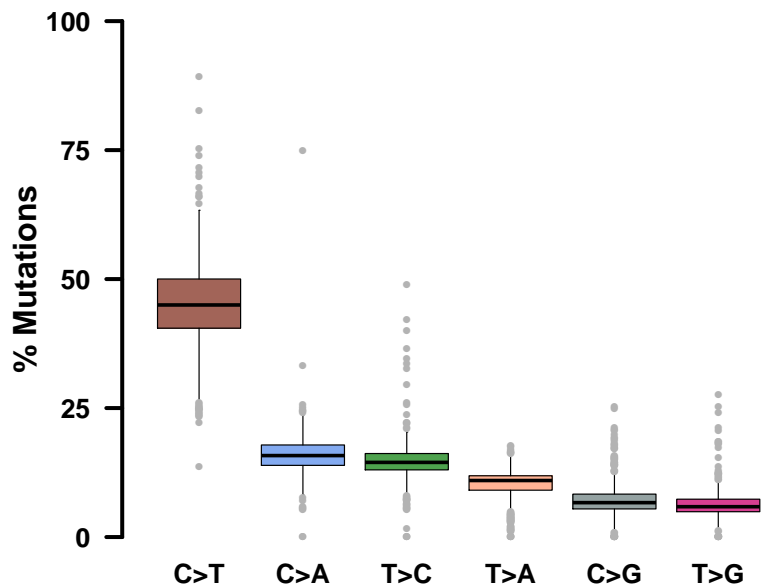
Top 10 mutated genes



Altered in 318 (94.64%) of 336 samples.



## Transition and transversions distribution



**Mutation load in TCGA cohorts**

