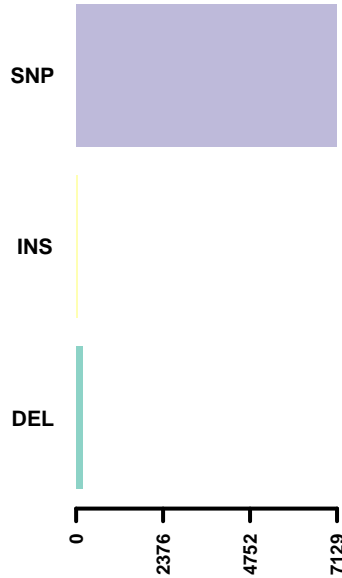


MAF summary

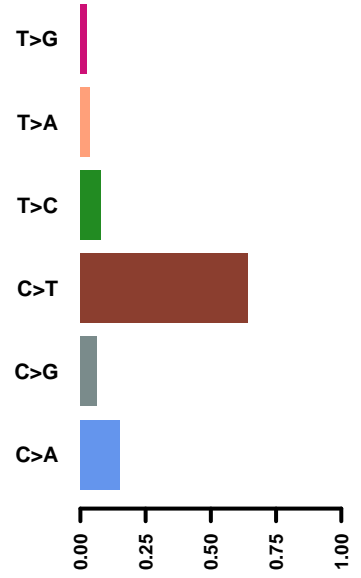
Variant Classification



Variant Type

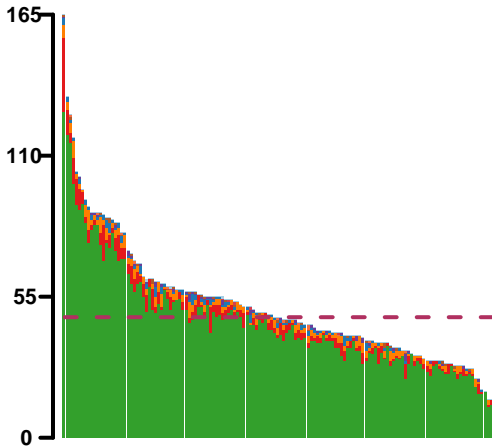


SNV Class

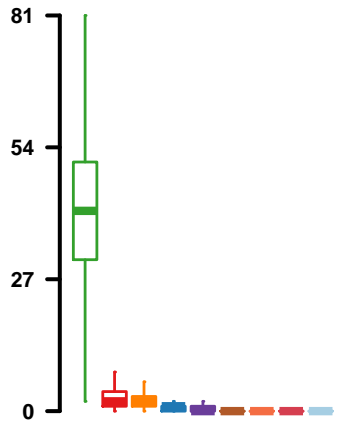


Variants per sample

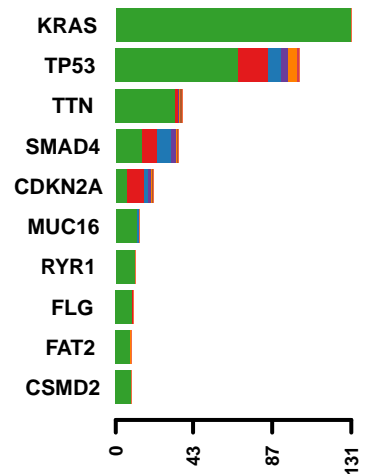
Median: 47



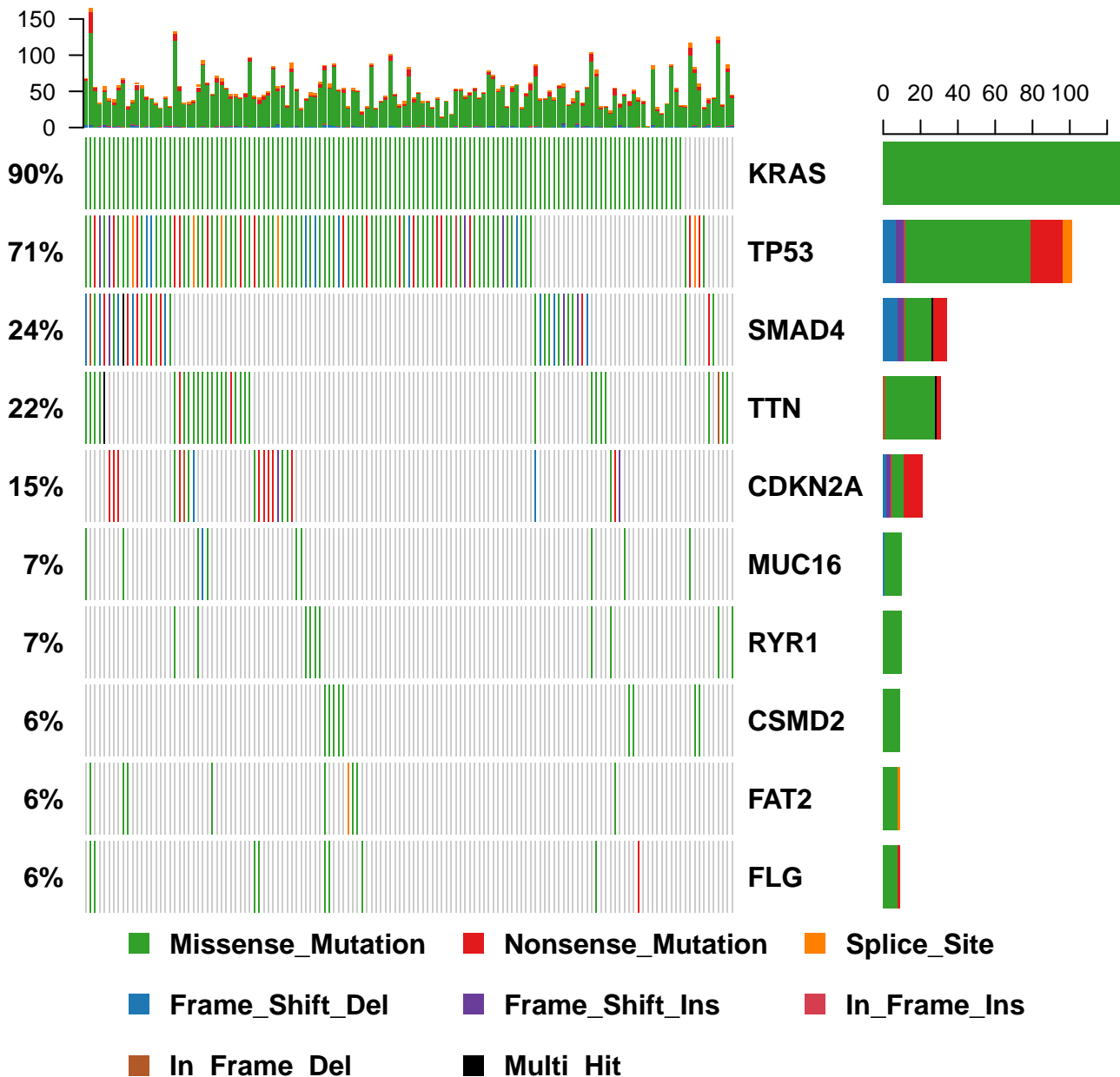
Variant Classification summary



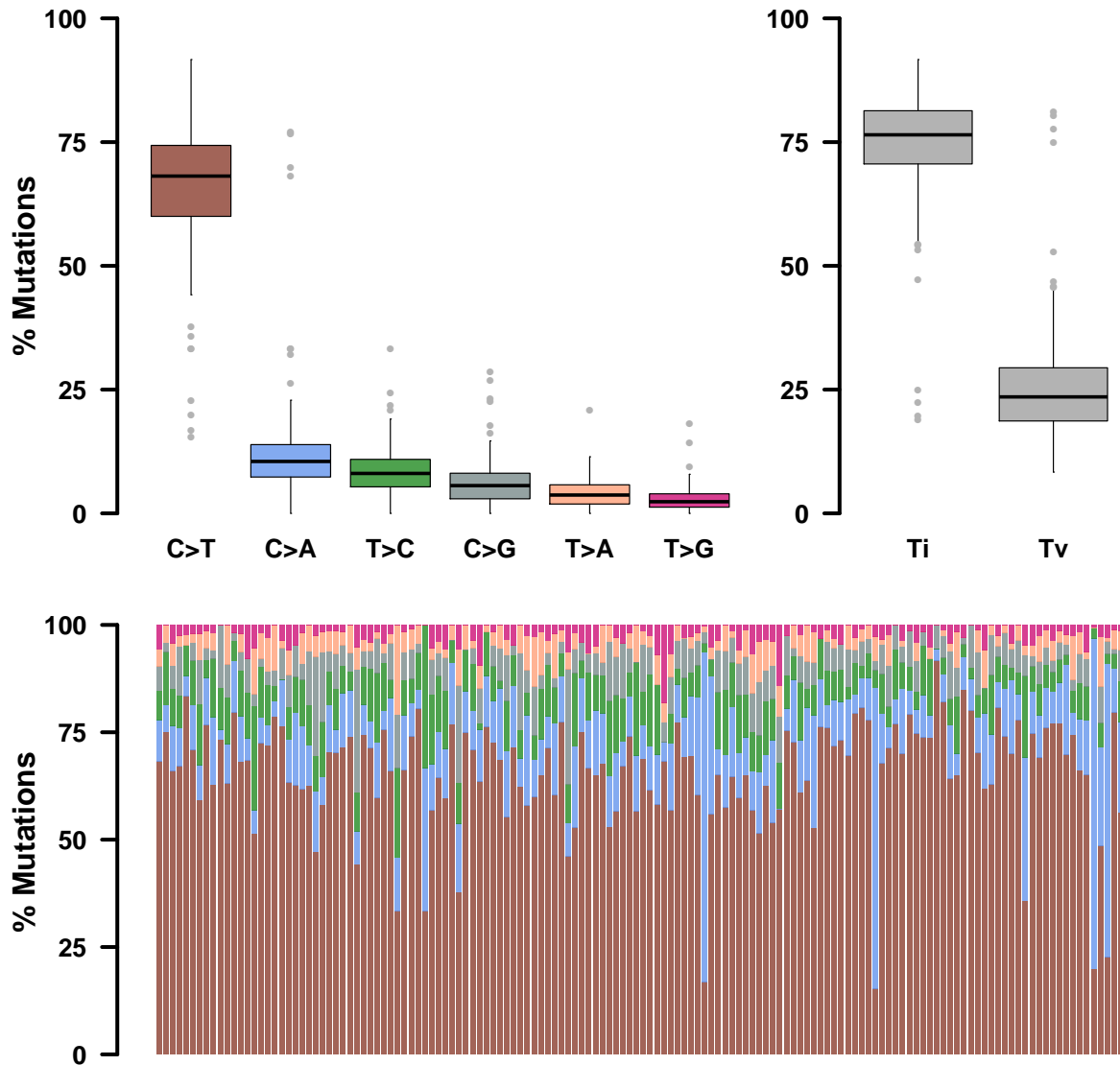
Top 10 mutated genes



Altered in 139 (97.89%) of 142 samples.



Transition and transversions distribution



Mutation load in TCGA cohorts

