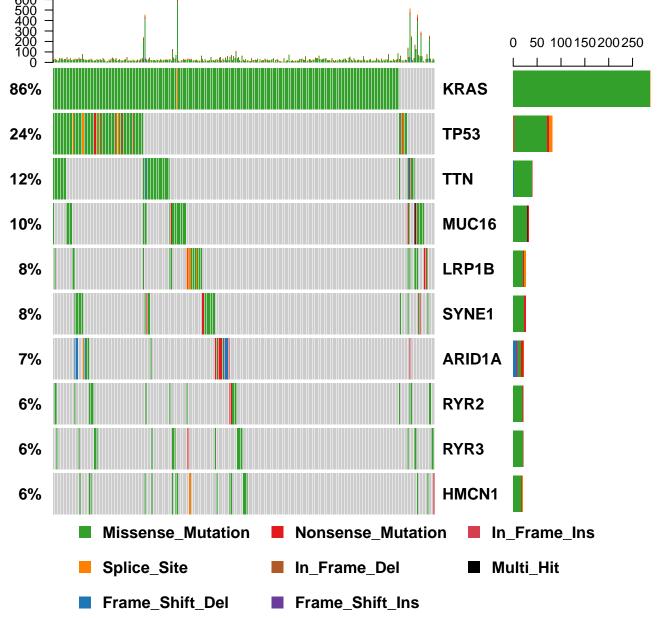
**MAF** summary **Variant Classification Variant Type SNV Class** Missense\_Mutation T>G **SNP** Nonsense\_Mutation T>A Splice\_Site Frame\_Shift\_Del T>C Frame\_Shift\_Ins INS C>T In\_Frame\_Del In\_Frame\_Ins Translation\_Start\_Site DEL C>A Nonstop\_Mutation 7128 10693 3933 7867 0.25 Variants per sample **Variant Classification Top 10** summary Median: 25 mutated genes 656-51 **KRAS TP53** TTN 437-34 **MUC16** LRP1B SYNE1 RYR2 17 218-ARID1A HMCN1 RYR3

Altered in 318 (94.64%) of 336 samples.



## Transition and transversions distribution

