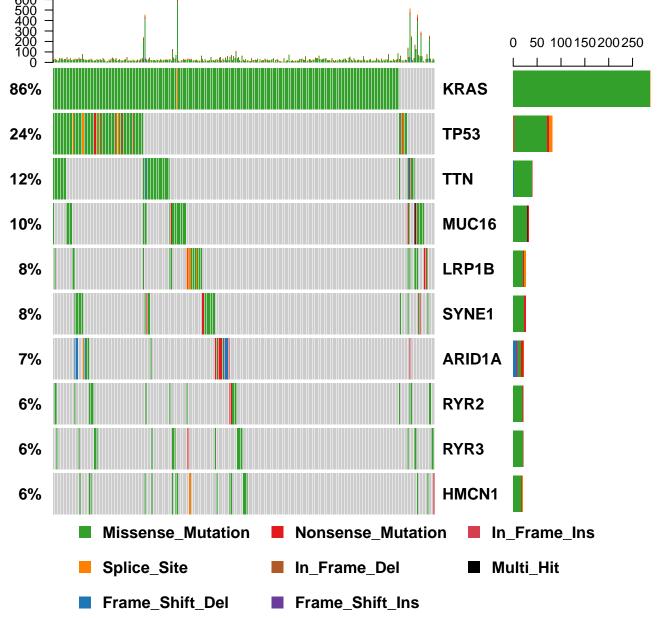
MAF summary **Variant Classification Variant Type SNV Class** Missense_Mutation T>G **SNP** Nonsense_Mutation T>A Splice_Site Frame_Shift_Del T>C Frame_Shift_Ins INS C>T In_Frame_Del In_Frame_Ins Translation_Start_Site DEL C>A Nonstop_Mutation 7128 10693 3933 7867 0.25 Variants per sample **Variant Classification 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

