MAF summary **Variant Classification Variant Type SNV Class** Missense_Mutation T>G **SNP** Nonsense_Mutation T>A Splice_Site Frame_Shift_Del Frame_Shift_Ins INS C>T In_Frame_Del Translation_Start_Site In_Frame_Ins DEL C>A Nonstop_Mutation 0.25 **Variant Classification** Variants per sample Top 10 summary Median: 47 mutated genes 165-81 **KRAS TP53** TTN 110-54 SMAD4 CDKN2A **MUC16** RYR1 55. 27 **FLG** FAT2 CSMD2 ₽ 87

Altered in 139 (97.89%) of 142 samples. 150 100 50 20 40 60 80 100 90% **KRAS** 71% **TP53** 24% SMAD4 TTN 22% CDKN2A 15% 7% **MUC16** RYR1 7% 6% CSMD2 6% FAT2 6% **FLG** Missense_Mutation Nonsense_Mutation Splice_Site Frame Shift Del Frame Shift Ins In Frame Ins In_Frame_Del Multi_Hit

Transition and transversions distribution



