Altered in 73 (69.52%) of 105 samples. 6185 TMB 73 No. of samples **NRAS** 32% PLCB4 15% PLCB1 13% ADCY8 12% GNAS 10% ITPR1 10% **EGF** 9% ITPR2 9% MAP2K1 9% GUCY1A3 8% ADCY1 7% GRM1 7% **PDGFRA** 7% ADCY5 6% HTR2A 6% TJP1 6% ADCY4 5% ADCY7 5% DRD1 5% PRKG2 5% 70% p junction sample_group Missense_Mutation Translation_Start_Site sample_group Nonsense_Mutation ■ Multi_Hit high_risk Splice_Site pathway low_risk