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| **Common P/LP Somatic Variants (n=126), n (%)** | **Fusions (n=125),** **Identified on (DNA) vs. (RNA) \* denotes novel fusion in OS** | **Incidental P/LP Germline****Variants from T/N-matched Sequencing (n=71), n (%)**  | **Prevalence of Immune Markers (n=125 for TMB-H, 113 for MSI-H, 55 for PD-L1), n (%)** |
| *TP53*: 4 (35%) *RB1*: 22 (17%) *CDKN2A*: 21 (17%) *CDKN2B*: 19 (15%) *UGT1A1*: 19 (15%)*CDK4*: 18 (14%)*MAP*: 16 (13%)*ATRX*: 14 (11%)*FLCN*: 14 (11%)*NCOR1:* 14 (11%)*PTEN:* 11 (8.7%), *SLC47A2:* 11 (8.7%)*YEATS4*: 11 (8.7%) | *EWSR1-PATZ1* (DNA)*EWSR1-CREB3L1*(DNA)*TP53-DAH2* (DNA)*FGFR3-TACC3* (DNA)\**KAT6A-TRIM35*(RNA)\**DSCR4-ERG* (DNA)\**TP53-TBC1D22B* (DNA)\**HMGA2-ARNTL2*(RNA)\**EWSR1-PLA2G6*(DNA)\*FUS-NFATC2(RNA) | *MUTYH*: 2 (2.8%)*PMS2*: 2 (2.8%)*RB1*: 1 (1.4%)  | TMB-H: 2 (1.8%)MSI-H: 1 (0.8%)PD-L1+: 6 (11%) |

P/LP=pathogenic/likely pathogenic; T/N=tumor/normal; TMB-H=tumor mutational burden-high, defined as ≥10 mutations/megabase; MSI-H=microsatellite instability-high