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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