Altered in 26 (100%) of 26 samples.

Genes (top to bottom): KMT2C 35%, AHNAK2 27%, PDE4DIP 23%, ANKRD36C 19%, BAGE2 19%, MST1L 19%, ZIC2 19%, ADAMTSL4 15%, ALPP 15%, EGFR 15%, FLT3LG 15%, FRG1 15%, IRX5 15%, MUC4 15%, MYT1L 15%, NOTCH2NL 15%, PCMTD1 15%, PRAMEF4 15%, RHPN2 15%, RTP1 15%, SSPO 15%, ABCC5 12%, ACIN1 12%, AGXT 12%, AMMECR1 12%, ANAPC1 12%, ASH1L 12%, ATAD3B 12%, C11orf80 12%, CNTN5 12%, COL6A3 12%, CSPG4 12%, CTAGE6 12%, DMBT1 12%, EVL 12%, FBLN2 12%, GPR32 12%, GSAP 12%, HDAC2 12%, HNRNPCL2 12%, IGFN1 12%, LAMA5 12%, MLLT6 12%, MUC17 12%, MYH13 12%, NBPF12 12%, NF1 12%, PRB2 12%, WBP1 12%, ZDHHC11 12%

Samples: A_T1, A_T2, B_T1, B_T2, C_T1, C_T2, E_T1, E_T2, F_T1, F_T2, G_T1, G_T2, H_T1, H_T2, I_T1, I_T2, J_T1, J_T2, K_T1, K_T2, L_T1, L_T2, M_T1, M_T2, O_T1, O_T2

Mutation types legend:
- C>T
- C>G
- C>A
- T>A
- T>C
- T>G

- Missense_Mutation
- Frame_Shift_Del
- Nonsense_Mutation
- In_Frame_Del
- Frame_Shift_Ins
- In_Frame_Ins
- Splice_Site
- Multi_Hit