

JAX: mutation - TEX_DFCI,

Molecular Methods Description:

- mRNA was extracted from mouse-depleted PDX leukemia and lymphoma cells using magnetic microbeads (uMACS mRNA Isolation Kit, Miltenyi Biotec). * Non-stranded RNA-seq libraries were generated using the TruSeq RNA Sample Prep Kit (Illumina) on a Sciclone NGS platform (Perkin Elmer). mRNA underwent fragmentation, cDNA synthesis, and next-generation library synthesis via end repair, polyadenylation, adapter ligation, and PCR amplification. * Libraries were sequenced on a NextSeq instrument (Illumina) using a paired-end 75 protocol.

Analysis Description:

RNAseq data were processed with Xenome to extract human sequences. The human sequences were aligned to the hg38 genome with Bowtie2, with expression levels estimated by RSEM. RSEM estimated counts were upper quantile normalized.