

JAX: mutation - Whole_Exome_BAYLOR,

Analysis Description:

Data were processed through quality control steps prior to using Xenome to extract human sequences. Sequence reads that passed all pre-processing steps were mapped to the reference human genome (build GRCh38.p5 with 262 alternate loci) using the BWA-MEM alignment tool with ALT-Aware mapping. SAM/BAM files were sorted and duplicates removed using Picard, then the base quality scores were recalibrated using the GATK toolkit. Variants were called using Mutect2 and Pindel, then filtered and annotated.