JAX: mutation - Truseq_JAX,

Molecular Methods Description:

The variant data (point mutations and indels) has been analyzed from next-generation sequencing using The Illumina TruSeq Amplicon Cancer Panel covering 48 cancer-related genes.

Analysis Description:

• The analysis of the sequencing output uses the Xenome tool to remove contaminating mouse sequences before alignment and variant calling. * BWA, GATK, and SnpEff are utilized for alignment (GRCh38 human reference), variant calling and annotation. * The high quality variants are further filtered to remove likely false positives, variants with low and modifier impact based on SnpEff annotations, and putative germline variants. * More details on the analysis can be found here