

JAX: mutation - CTP,

Molecular Methods Description:

The variant data (point mutations and indels) has been analyzed from next-generation sequencing using CTP panel. CTP is a targeted panel of 358 cancer related genes known to be associated with various cancers. The gene targets are selected for their known association with cancer types in over 20 different cancer primary sites, enabling detection of mutations present in as few as 10% of the cells in the tumor specimen.

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](#)