PMLB: copy number alteration - Illumina HiSeq 2000/2500, WES

Molecular Methods Description:

Paired-end sequencing was performed on the Illumina Hi-Seq 2000/2500 on PDX models and their matched patient normal. Whole exome sequencing was performed using samples prepared with the Agilent SureSelect Human All Exon V4 capture kit. Illumina's CASAVA software (version 1.8.2) converted the sequencing base calls to fastq format reads.

Analysis Description:

Xenome was used to remove any mouse contamination reads. Reads were aligned to the human reference genome (hg19_random). Somatic single nucleotide mutations were called using both Strelka (version 1.0.7) and MuTect (version 1.1.4), while indels were called using only Strelka. ANNOVAR was used to annotate all the final mutation calls. Somatic copy number variation was assessed using CELLULOID.