

PMLB: copy number alteration - Illumina HiSeq 2000, WES

Molecular Methods Description:

Paired-end sequencing was performed on the Illumina Hi-Seq 2000 using Illumina TruSeq Exome Enrichment kit library.

Analysis Description:

- Sequencing regions were aligned with hg19
- variants were identified using gatk version 3.6 for hyplotypcaller and mutect2, mutect version 1.1.5, and varscan version 2.4.2.