

PMLB: copy number alteration - Illumina HumanOmni1-Quad or Infinium Omni2.5-8 BeadChip, microarray

Molecular Methods Description:

DNA was extracted from flash frozen tissue fragments from each PDX or germline sample (their matched patient normal) and was hybridized to Illumina HumanOmni1-Quad or Infinium Omni2.5-8 BeadChips. DNA samples were amplified, fragmented, and precipitated according to the manufacturer's protocol. The precipitated DNA were hybridized BeadChips, incubated at 48°C for 18 hours. The BeadChips were washed and the hybridized oligos were subjected to single-base extension as per the Illumina protocol and scanned on the iScan (Illumina).

Analysis Description:

The data files were quantified in GenomeStudio (Illumina), normalized against controls, background subtracted, and GC wave corrected. The signal intensity as Log2 R ratio (LRR) and B allele frequency (BAF) values were used to derive copy number, purity and ploidy of PDX with matched normal using ASCAT(v2.5, allele-specific copy number analysis of tumors).