

IRCCS-CRC: copy number alteration - Illumina HiSeq 2500, WES

Analysis Description:

Amplification analyses were performed using the digital karyotyping approach Leary 2007 by comparing the number of reads mapping to a particular gene with the average number of reads mapping to each gene in the panel, along with a minor allele fraction analysis of heterozygous single nucleotide polymorphisms contained within each gene. The Bioconductor package was used to add gene annotations starting from the gene symbol which was available in the starting calls. For the coordinates Liftover was used to convert them from hg18 (original coords) to hg38.