Curie-LC: copy number alteration - Affymetrix Genome-Wide Human SNP Array 6.0, WGS

Molecular Methods Description:

PDX were profiled using Affymetrix genomics array with SNP 6.0 or with Cytoscan HD array. Genome-wide copy number analysis was conducted by means of Affymetrix SNP arrays, as previously described (Laurent et al.,2013 and Crepin et al. 2017).

500 and 250ng of gDNA was respectively used for SNP 6.0 and Cytoscan HD as starting material as recommended by the supplier.

Analysis Description:

Raw data were normalized with Genotyping console for SNP 6.0 and Chromosome Analysis Suite for Cytoscan HD.

Focal amplification of oncogenes was defined by log ratio>1.58 (6 copies per diploid genome) and maximum size <10 megabases. Biallelic inactivation of tumor suppressor genes was defined by homozygous deletion or truncating mutation associated with heterozygous deletion.

All PDX copy numbers were represented by the Circular Binary Segmentation algorithm as implemented in the DNAcopy package for R using a minimum width of 3, alpha less than 0.01 and up to 10,000 permutations.

The BRCAness signature was defined with large-scale state transitions, defined as chromosomal break between adjacent regions of at least 10Mb initially described by T. Popova **

Table:

Gene List								
AKT1		AKT2		AKT3		ALK		
APC		ARHGAP35		ARID1A		ARID2		ATM
BRAF		BRCA1		BRCA2		CDK12		CDKN1B
CDKN2A		CTNNB1		DDR2		EGFR		ESR1
FAT1		FBXO16		FBXW7		FGFR1		FGFR2
FGFR3		FRFR4		GENE LIST		H3F3A		HER2/Erbb2
HER3/Erbb3		HER4/Erbb4		HRAS		IDH1		IDH2
KDR		KEAP1		KIT		KRAS		MAP2K1
MAP2K2		MAP2K4		MAP3K1		MBD1		MEK1
MET		MLL3		MTOR		NBPF1		NF1
NFE2L2		NRAS		PALB2		PBLD		PDGFRA
PIK3CA		PIK3R1		POLE		PPP2R1A		PTEN
PTPN11		RAD51B		RAD51C		RB1		RBM10
RET		RIT1		ROS1		SLC39A6		SLC4A5

SMAD4		SMARCA4		STK11		STX2		TP53
TSC1		TSC2		U2AF1		VHL		ZNF774