IRCCS-CRC: copy number alteration - Illumina HiSeq 2000, Targeted capture

Molecular Methods Description:

• Baits corresponding to a cancer gene panel were designed using SureSelect DNA platform (Agilent genomics).
• 75 pb paired-end Sequencing was done using a HISEQ 2000 v4 system (Illumina).

Analysis Description:

Data analysis has been performed by Dr Aikaterini Chatzipli in Ultan McDermott group at the Wellcome Trust Sanger Intitute, UK.

• The algorithms used for the analysis are the following Xenome ** was used to separate human from mouse reads interrogating the bam files Calling for mutations (substitutions, insertions and deletions) was done using Caveman and Pindel algorithms (versions 1.5.3 and 4.2, respectively) Calling for Copy Number analysis was done using CNVkit (0.9.7.b1)
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Table:

IRCC GENE PANEL
ACVR1B
ACVR2A
APC
ARFGEF1
ARID1A
ARID2
ARID4A
ASXL1
ATM
ATR
ATRX
AXIN2
BAI3
BCL9L

BCLAF1
BCOR
BRAF
BRCA2
CARD11
CBL
CDC27
CDC73
CDH1
CDK12
CDK8
CDKN2A
CLSPN
CREBBP
CSPP1
CTNNB1
DKK2
DUSP16
EGFR
ELF3
EP300
EP400
ERBB2
ERBB3
ERBB4
EZH2
FAM123B
FBXW7
FGFR1
FGFR2
FLT1
GATA3
GNAS
H3F3A
H3F3B
HNF4A
IGF2
IKBKB

IRS2
JAK2
KAT6A
KDM3B
KDM6A
KDR
KIT
KLF5
KRAS
LIG1
MAP2K4
MAP3K4
MARK1
MET
MGA
MLH1
MLH3
MLL2
MLL3
MSH2
MSH3
MSH6
MTOR
MYC
NF1
NF2
NRAS
PCBP1
PDGFRA
PIK3CA
PIK3R1
PMS2
POLE
PPP1R3A
PTCH1
PTEN
PTPN11
RB1

RET
RNF43
RSPO2
RSPO3
SETD2
SMAD2
SMAD3
SMAD4
SOX9
STAG2
STK11
TBX3
TCF7L2
TGFBR2
TOP2B
TP53
TP53BP1
TPTE
TRIM23
TRRAP