

Supplementary table 5. The 68 genes involved in the panel used for this study.

Sequence analyses for 68 well-characterized cancer genes.

Rearrangement analyses (*) for selected regions of 4 well-characterized cancer genes.

Sequence and copy number analyses (red font) for the coding regions of 8 well-characterized cancer.

ACVR1	AKT1	ATRX	BCOR	*BRAF	BRCA1	BRCA2
CDK6	CDKN2A	CDKN2B	CHEK2	CIC	CTNNB1	DAXX
EGFR	FAT1	FGFR1	*FGFR3	FUBP1	GNAQ	GNAS
HIST1H3B	HIST1H3C	HRAS	IDH1	IDH2	KDR	KIT
KRAS	MDM4	MEN1	MET	MLH1	MSH2	MSH6
MYCN	NF1	NF2	NOTCH1	NRAS	PDGFRA	PIK3CA
PLCG1	PMS2	PPM1D	PTCH1	PTEN	PTPN11	RB1
RGPD3	SETD2	SMARCB1	SMARCE1	SMO	TERT	TP53
TSC1	TSC2	USP8	*YAP1			

CDK4

DDX3X

H3F3A

KLF4

MYC

PIK3R1

*RELA

TRAF7
