DEPArray™ OncoSeek Panel

Targeted detection of SNPs, Indels and CNAs

The DEPArray™ OncoSeek Panel enables the preparation of high-quality targeted NGS libraries **from FFPE cell populations or from fresh tissue** isolated with the DEPArray™ technology. It allows the simultaneous detection of SNVs, indels and CNAs in a panel with oncology relevant genes starting from very low amount of input DNA.

The kit includes all the reagents for generating ready-to-sequence libraries, including primer pairs and indexed sequencing adapters compatible with Illumina® Platforms.

Main Features

- **Designed for small amounts of input DNA**
- **Detection of SNPs, indels and CNAs**
- **Coverage of 63 oncology relevant genes**
- **Single tube procedure**
- **Enables multiplexing of up to 96 unique libraries**
- **Leverages the high fidelity of the Illumina® Platforms**

Sample Types

- FFPE
- Fresh tissues
- Cell lines

Product Specification

- Input DNA: 400 pg for fresh cells
  660 pg for FFPE (100 cells)
- Time required 4 hours
- Hands-on time 2 hours
- Number of amplicons 440
- Amplicon size 71-184 bp (mean=116 bp)
- Total target size 38,4 kbp
- On target Percentage ≥80%

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DEPArray™ TECHNOLOGY

High resolution genetic analysis from low input DNA

Genes represented in DEPArray™ OncoSeek Panel

ABL1	5	*CDK4*	10	*ERBB4*	8	*GNA11*	2	*KDR*	9	*MYCN*	9	*RET*	6
AKT1	2	*CDK6*	10	*EZH2*	1	*GNAQ*	2	*KIT*	24	*NOTCH1*	3	*SMAD4*	10
ALK	12	*CDKN2A*	2	*FBXW7*	6	*GNAS*	2	*KRAS*	11	*NPM1*	1	*SMARCB1*	4
APC	9	*CSF1R*	2	*FGFR1*	12	*HNF1A*	4	*MAP2K1*	5	*NRAS*	3	*SMO*	5
AR	10	*CTNNB1*	1	*FGFR2*	13	*HRAS*	2	*MET*	16	*PDGFRA*	13	*SRC*	1
ATM	19	*DDR2*	1	*FGFR3*	14	*IDH1*	1	*MLH1*	1	*PIK3CA*	19	*STK11*	5
BRAF	12	*DNMT3A*	1	*FGFR4*	9	*IDH2*	2	*MPL*	1	*PTEN*	14	*TP53*	21
CCND1	8	*EGFR*	19	*FLT3*	4	*JAK2*	2	*MSH6*	4	*PTPN11*	2	*TSC1*	1
CDH1	3	*ERBB2*	14	*FOXL2*	1	*JAK3*	3	*MYC*	9	*RB1*	12	*VHL*	3

Fig. 1

Genes with contiguous, overlapping coverage

Genes with comprehensive coding exon coverage

Genes with amplicons for CNA calling and SNV calling

Genes with only amplicons for CNA calling

Fig. 1: The table depicts the genes represented, followed by the number of amplicons for each gene.

Detection of gene amplification

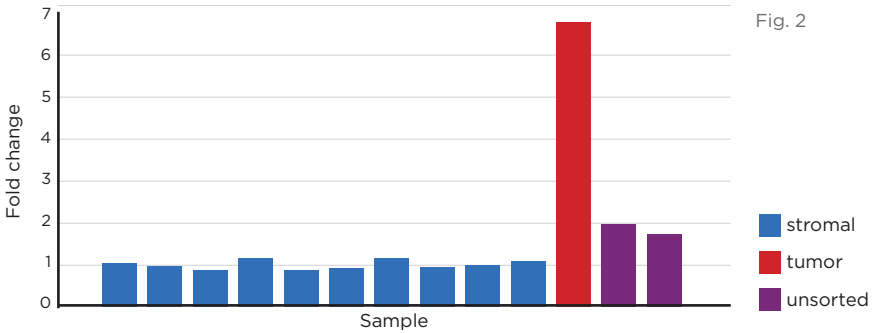

Fig. 2

Fig. 2: Detection of HER2 amplification by OncoSeek Panel on a breast cancer FFPE sample with low tumor cellularity. ~6.8-fold amplification is detected in the pure tumor sorted sample (75 cells); conversely, signal is dilutes to <2 times in the unsorted samples due to normal cells.

Detection of somatic variants

Fig. 3

chromosome	position	ref	alt	gene	effect	annotation	gmaf	mutation	unsorted	stromal	tumor	type
chr10	123346116	G	A	FGFR2	intron	rs2981575	G:0.4762	-	59,6	51,6	56,3	germline heterozygous
chr10	43613843	G	T	RET	synonymous	rs1800861	G:0.2875	-	100,0	100,0	99,9	germline homozygous
chr12	25398284	C	T	KRAS	missense	COSM521	-	p.Gly12Asp	7,5	0,0	51,4	somatic heterozygous
chr17	7577120	C	T	TP53	missense	COSM10660	T:0.0002	p.Arg273His	13,1	0,0	93,4	somatic homozygous
chr18	48586344	C	T	SMAD4	intron	rs948588	T:0.0387	-	32,2	52,1	0,0	loss of heterozygosity (LOH)

Fig. 3: Analysis of a pancreas ductal adenocarcinoma FFPE sample performed using OncoSeek panel. Unsorted cells were compared with pure stromal and tumor population sorted with DEPArray™ system. In the table the alternative allele frequency of polymorphisms and variants identified in at least one population is displayed. KRAS and TP53 somatic mutations are clearly detected in sorted samples, while in the unsorted fraction they are near or below the limit of detection (10%).

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