Ampli 1™
OncoSeek Panel
for Illumina®

Targeted detection of SNVs, indels and CNAs

The *Ampli*1™ OncoSeek Panel enables the preparation of high quality targeted NGS libraries from DNA amplified with *Ampli*1™ WGA Kit.
It allows the simultaneous detection of single nucleotide variants (SNVs), insertions/deletions (indels) and focal copy-number amplifications (CNAs) in a panel of 60 clinically relevant oncology-related genes.

Main Features:

- First and only panel designed for single cell analysis
- Coverage of more than 2500 mutation hotspots in 60 oncology-relevant genes
- Detection of focal CNAs for a subset of 19 genes
- Very low Allelic Dropout Rate (ADO=12.7% ± 4.2%)
- Automated bioinformatic analysis available on the MSBiosuite platform

Product Specification:

- Input DNA: 10 ng of Whole Genome Amplified DNA obtained with *Ampli*1™ WGA Kit
- Time required: 4 hours
- Hands on time: 2 hours
- Up to 96 barcoded libraries compatible with Illumina® platforms
- Single tube procedure

Genes represented in *Ampli*1™ Oncoseek Panel

ABL1	CDK6	FBXW7	HRAS	MLH1	PTPN11
AKT1	CDKN2A	FGFR1	IDH1	MPL	RB1
ALK	CSF1R	FGFR2	IDH2	MSH6	RET
APC	CTNNB1	FGFR3	JAK2	MYC	SMAD4
AR	DDR2	FGFR4	JAK3	MYCN	SMARCB1
ATM	DNMT3A	FLT3	KDR	NOTCH1	SMO
BRAF	EGFR	GNA11	KIT	NRAS	SRC
CCND1	ERBB2	GNAQ	KRAS	PDGFRA	TP53
CDH1	ERBB4	GNAS	MAP2K1	PIK3CA	TSC1
CDK4	EZH2	HNF1A	MET	PTEN	VHL

SNV, indel
SNV, indel, CNA
CNA

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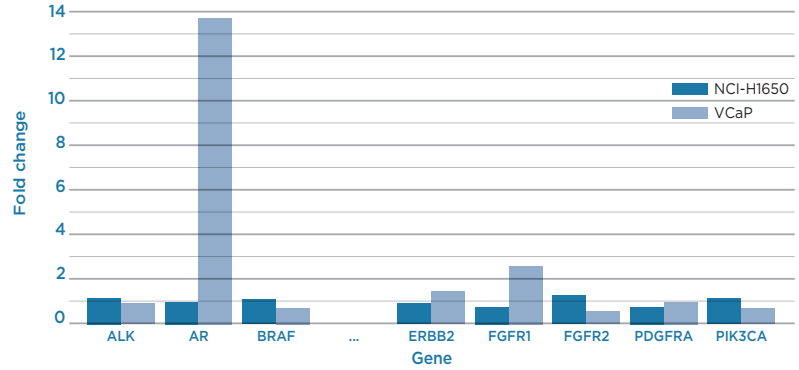
Accurate detection of somatic variants and focal CNAs

Gene	Chrom	Position	Ref	Alt	NCI-H1650	VCaP	Variant Class	Mutation	Effect
TP53	chr17	7,577,539	G	A	0	99,97	Somatic HOM	p.R248W	missense
APC	chr5	112,175,363	G	A	35,10	0,00	Somatic HET	p.A1358T	missense
TP53	chr17	7,577,610	T	C	67,18	0,00	Somatic HET	-	splicing



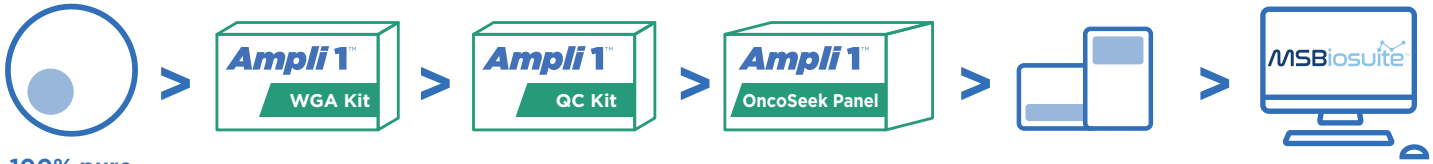
Detection of somatic variants in single cells from aberrant cell lines.

For each mutation, the alternative allele frequency is displayed and graphically represented with a colored filling bar.

Detection of focal copy-number amplifications in target genes.

Copy-number amplification analysis in VCaP single cells detected a focal high-level amplification of AR gene and a focal copy-number gain (>2 fold change) in FGFR1 gene.

Complete workflow for single cell analysis



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 CMD_MKT_007 Rev. 1 - 2019 May