

NGS kits for analyses of KRAS, NRAS, BRAF, EGFR and IDH 1/2 genes

We developed user-friendly diagnostic kits with excellent analytical parameters and extremely fast processing.

Strengths of our fastGEN technology

- Simple, ultra-sensitive, specific and effective technology
- Unique system for one step NGS library preparation on Illumina platform
- It provides an examination of the mutation status of oncomarkers in samples (DNA isolated from tumor or circulating DNA) by ultra-deep sequencing
- Excellent speed (<30 min hands on time)
- Significantly lower probability of mistakes, uniform coverage for different amplicons and different samples
- Robustness achieved by using short amplicons obtained by a single polymerase chain reaction with special tagged hybrid primers

Catalog number	Product	Gene	Detail	Utilization
RDNGS0001	fastGEN Solid Cancer kit	NRAS KRAS BRAF	for rapid preparation of the sequencing library for genotyping the KRAS, NRAS (codons 12, 13, 59, 61, 117, 146) and BRAF (codon 600) genes	to indicate proper therapy for metastatic colorectal tumors or for melanoma patients
RDNGS0002	fastGEN Lung Cancer kit	EGFR	for rapid preparation of the sequencing library for genotyping the EGFR gene (exons 18, 19, 20, 21).	to indicate proper therapy for metastatic lung tumors
RDNGS0003	fastGEN Brain Cancer kit	IDH 1/2	for rapid preparation of the sequencing library for genotyping the IDH1 and IDH2 genes (codons 132 and 172).	for the prognosis and stratification of brain tumors

Kit contains ready-to-use Master Mixes with 16 sample indices, read1, read2 seq primers and index seq primers.

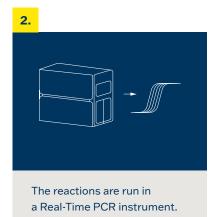
Workflow

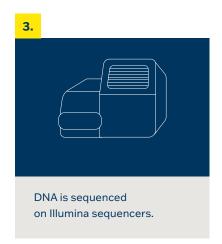
The simplicity of the fastGEN method is into mix one particular Master Mix with a DNA sample and insert it into a Real-Time thermocycler. The procedure is

designed to allow parallel processing of samples for RAS genes, EGFR and IDH 1/2 genes. The genes are then sequenced in one sequencing run on Illumina, Inc.

The scheme of genotyping procedure







GENOVESA software fastGEN module

It is a cloud all-in-one solution for the analysis of raw data (FASTQ files) with technical and application support.

Data evaluation:

- Advanced quality control of sequencing data
- Automatic notification of low-coverage regions for simple filtering of relevant variants
- Monthly update of annotation databases
- Customization
- Store patient data and variants in an internal database
- One-click report

PRODUCER:

DISTRIBUTOR:



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