

TP53 panel Long

Hereditary and somatic profiling in TP53-related cancers

4bases TP53 panel Long is an **amplicon-based** kit for rapid and cost-effective identification of germline and somatic mutations (SNVs, indels, CNVs) of TP53 gene in a single workflow.

It allows the identification of mutations in TP53 gene through **Next Generation Sequencing (NGS)**.

Thanks to its long-read capability, the kit allows for accurate analysis of complex and highly homologous genomic regions, and enables precise identification of coding regions.

The kit is validated for the analysis of **DNA extracted from blood and tissue (fresh, frozen) samples**.

4bases TP53 panel Long allows for **precise, reliable, and effective results, speeding up** genomic data analysis workflows.

From DNA to sequencing in less than 1.5 days with less than 2 hours hands-on time.



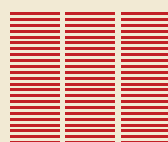
From gDNA



Enrichment PCR



Indexing PCR



Final library



Sequencing



Final Data

Straightforward protocol

Tailor-made protocol for operator's time schedule, presence of many stopping points, reduced hands-on time

Long read sequencing

Enables for accurate analysis of complex and highly homologous genomic regions and enables precise identification of coding regions.

Platform 4eVAR

Safe and secure data analysis via 4bases proprietary solution, with continuous experienced customer support

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Specifications

Sample type	DNA extracted from body tissues (blood or other)
Input	Minimum of 20 ng DNA per sample
Panel size	7.2 Kb
Gene content	TP53 (intronic regions and all coding regions)
Variant called	SNPS, indels, CNVs
Compatible Instrument	Oxford Nanopore Technologies
Data Analysis	4eVAR

Cod. kit

Product	Cod.	Tests number
TP53 panel Long	RH1040L	16
TP53 panel Long	RH1040L	96

4eVAR: Comprehensive output files for analysis and reporting



- Quality metrics
- Alignment
- CNVs status
- Full variant table
- Genotype
- Coverage
- Customizable report

Data Analysis

Product	Cod.	Tests number
4eVAR	A6060-RH1040L-16	16
4eVAR	A6060-RH1040L-96	96

If you wish to learn more:



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