

MainTumorSolution - GeneSGKit®

CE-IVD

Sistemas Genómicos has developed **MainTumorSolution-GeneSGKit®** to provide the reliable and efficient analysis of point mutations, Indels, large Indels, ALU insertions and CNVs, as well as analysis of fusions in the *ALK*, *RET* and *ROS1* genes associated with the diagnosis of somatic mutations in 38 genes related to sporadic cancer from paraffin-embedded solid tumor samples.

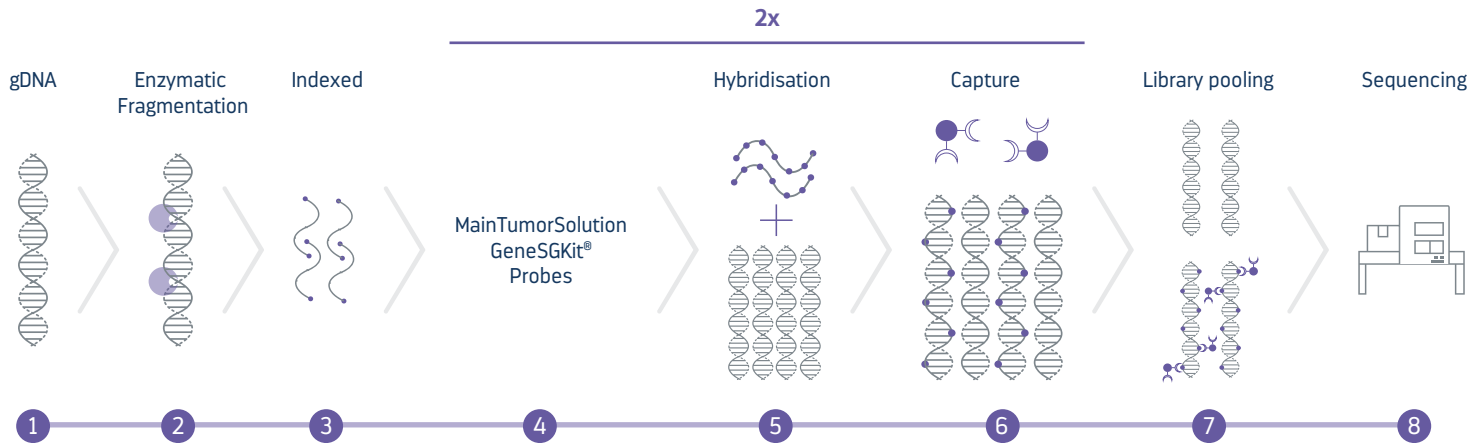
MainTumorSolution-GeneSGKit® has CE-IVD marking and contains reagents **to process 12 samples** with their corresponding bioinformatic analysis through the GeneSystems® platform.

The work process is streamlined to create libraries in a maximum of 2 working days. It also provides for the combination of different pools from other GeneSGKits® in a single run on Illumina® sequencing platforms, ensuring an equitable distribution of data between the different samples.

HIGHLIGHTS

- ✔ **Integrated solution unique in the market:**
Complete bioinformatics analysis and display of results: **MainTumorSolution-GeneSGKit®** contains reagents to process 12 samples with their corresponding bioinformatic analysis, visualization and prioritization of variants through the GeneSystems® platform. The kit, the bioinformatic computation and the visualization have CE-IVD marking.
- ✔ **Speed:**
The libraries are ready after just 2 days of work from 10-200 ng of DNA.
- ✔ **High sensitivity:**
Average coverage of 300x, ensuring the reliability of the data obtained without the need for alternative validations. Limit of detection up to 5% of the tumor percentage.
- ✔ **Complete bioinformatics analysis and display of results:**
The data is computed in less than 48 hrs and recorded against the main open and private databases reporting the prioritised variants according to different algorithms which are easily visualised, filtered and reported through GeneSystems®.
- ✔ **Complete Diagnostic Solution:**
Analysis of point mutations, Indels, large Indels, MNVs, CNVs and ALU insertions, as well as analysis of fusions in the *ALK*, *RET* and *ROS1* genes.

MainTumorSolution GeneSGKit® WORKFLOW



ABOUT US

Sistemas Genómicos is a pioneering company in the use of next-generation sequencing for genetic diagnosis. With more than 6,000 analyses per year, we are leaders in the sector, supported by years of experience and accredited and certified by the National Accreditation Body of Spain (ENAC) and the Spanish Association for Standardisation and Certification (AENOR).

OUR OBJECTIVE

To capitalise on all our experience in analysis and diagnosis by using NGS to develop a series of tools that enable genetic diagnosis in situ in hospitals and research centres. We have achieved this by developing a comprehensive solution, the only one of its kind on the market, based on more than 35 GeneSGKits® for various diseases, all with CE-IVD marking and the GeneSystems®.



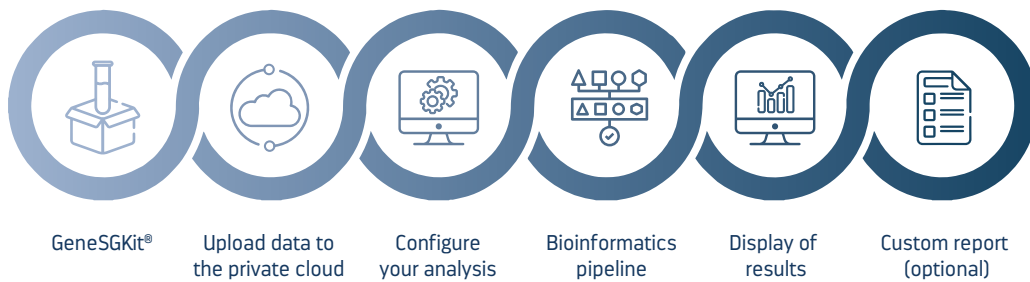
MainTumorSolution-GeneSGKit® provides high performance from only 10-200 ng of DNA. The design of the capture probes and bioinformatic **pipeline** guarantees high sensitivity and specificity for point mutation, Indels, large Indels, MNVs, ALUs and CNV screening detection with a recommended average coverage of 900x.



Sistemas Genómicos understands the vital importance of quality customer service and follow-up. This includes a personalised service that offers not only support over the telephone for all sorts of questions and concerns that may arise while using GeneSGKits® or the GeneSystems® analysis platforms, but also personalised training for the user who purchases the product. These training sessions will facilitate the set-up and roll-out of a genetic diagnostic service in situ at hospitals and laboratories using GeneSGKits®.

GeneSystems® is our bioinformatics tool for genetic diagnosis and research. It is a platform registered as a medical device with CE marking for diagnostic use *in vitro*, to process information from massive DNA sequencing, detect variants and help genetic diagnosis. Developed in a **Cloud Computing** environment, it can provide access your data from any computer device, at any time and place, without consuming the user's own resources.

GeneSystems® is designed to provide a solution to the different stages of the NGS data analysis step:

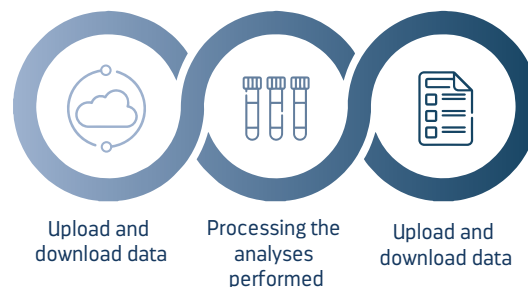


FEATURES OF GENESYSTEMS®

Integral infrastructure **bioinformatic analysis** for the data analysis from NGS platforms.

Automation of the entire data analysis process.

Cloud-Computing platform: access from any device with an internet connection.



It was developed by a multidisciplinary team of geneticists, bioinformaticians and engineers, and has been validated by over 200 companies, including hospitals, laboratories, research centres, universities and pharmaceutical companies. The platform has been independently audited and detects **SNPs, INDELS, large INDELS, MNVs, ALUs, CNVs and SVs**.

ANALYSIS OF SEQUENCING DATA WITH GENEBYTES

In the laboratory routine

- Cloud-based platform: no software installation required.
- Upload and download results quickly and easily.
- Bioinformatic analysis of results from raw data, BAM and VCF.
- Exhaustive report of the computation process.
- Resource optimisation: support for preparing pools of non-equimolar libraries prior to sequencing.
- View the results of computations in the corresponding application.

In research

- Gene, exome and genome panels: view and interact with the results obtained through NGS.
- Annotation of variants compared to the major public and private databases.
- Flexible filtering.
- Simultaneous analysis of samples.

In diagnosis

- Flexible viewing and prioritisation of the variants obtained.
- Identification of point variants, Indels, large Indels and structural variants (balanced and unbalanced).
- Simultaneous analysis of samples: optimised diagnostic analysis time.
- Full annotation for variant classification:
 - DBNLVar (Sistemas Genómicos' own database).
 - Public and private reference databases.
 - In silico predictors.
- Integrated IGV for a graphic analysis of the genomic environment.
- Customisable reports of genetic results.
- Generation of virtual panels to prioritise variants according to HPO terminology.
- Automatic classification of variants based on ACMG guidelines.
- Handles the major databases in the sector (DBNLVar, Ensembl, 1000Genomes, HGMD-Pro, ClinVar, etc.)
 - Pathogenicity indicators with links to scientific articles.

CATALOGUE - MainTumorSolution-GeneSGKit®

Technical data

GeneSGKit®

Size (MB)

MainTumorSolution-GeneSGKit®

0,28

References

MainTumorSolution-GeneSGKit® 12 reactions Ref.: LV4582 (CE-IVD)

MainTumorSolution-GeneSGKit®

38 genes

- ✓ Coding regions of all included genes.
- ✓ CNVs screening for all genes.
- ✓ SVs (fusions) for the most common genes *ALK*, *ROS1* and *RET*.
- ✓ TERT promoter included.

<i>AKT1</i>	<i>DDR2</i>	<i>KRAS</i>	<i>PTEN</i>
<i>ALK*</i>	<i>EGFR</i>	<i>MAP2K1</i>	<i>RET*</i>
<i>AR</i>	<i>ERBB2</i>	<i>MET</i>	<i>ROS1*</i>
<i>ARAF</i>	<i>ERBB3</i>	<i>MTOR</i>	<i>SMARCB1</i>
<i>ARIAD1A</i>	<i>ESR1</i>	<i>NF1</i>	<i>TERT Prom</i>
<i>ATM</i>	<i>FGFR3</i>	<i>NRAS</i>	<i>TP53</i>
<i>BRAF</i>	<i>HRAS</i>	<i>PDGFRA</i>	<i>TSC1</i>
<i>BRCA1</i>	<i>IDH1</i>	<i>PIK3CA</i>	<i>TSC2</i>
<i>BRCA2</i>	<i>IDH2</i>	<i>POLE</i>	
<i>CDKN2A</i>	<i>KIT</i>	<i>PTCH1</i>	

MILESTONES

