
Your partner in genomics

Tailored solutions to your requirements



NIMGenetics, founded in 2008, is a Spanish biotechnology multinational specialized in the design and commercialization of genetic diagnostic products and services. We expand the value of our high-performance genomic products and services in the international market, becoming a specialized benchmark in genomic analysis and human genetic diagnosis.

In addition to Spain, NIMGenetics is currently present in Portugal, Mexico and Brazil.



NIMGenetics has a wide infrastructure with state-of-the-art technology that, together with highly qualified staff and highly specialised bioinformatics, allows the company to offer research support services with high-quality standards and certifications.

The main R&D services offered by NIMGenetics are:



Next Generation Sequencing (NGS)



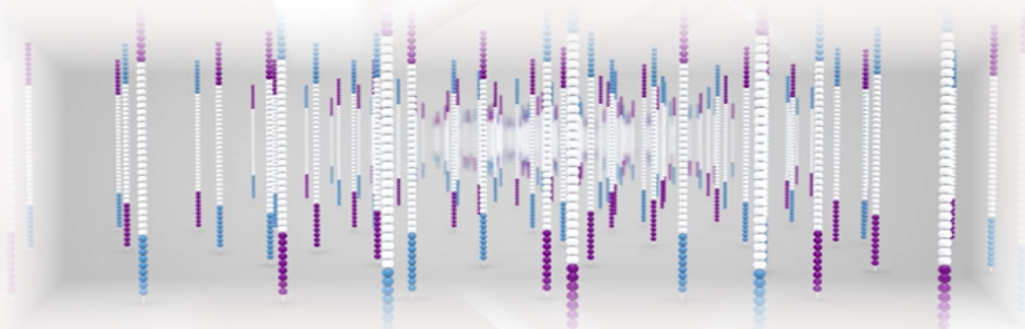
Bioinformatics



Genomic services for Therapy and Cell Biology



Consultancy projects

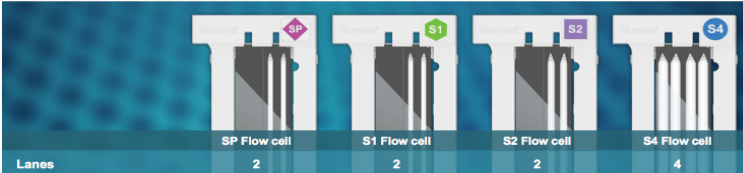


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Next Generation Sequencing Services (NGS)

NIMGenetics offers next-generation sequencing services using platforms with different abilities, with the aim of covering all types of projects, both those that require a high sequencing capacity (**NovaSeq 6000**) and a moderate one (**MiniSeq**).

Sequencing platforms like **NovaSeq 6000** provide users with the performance, speed and flexibility to complete projects more efficiently. Availability of multiple types of flow cells, possibility of loading libraries in individual lanes and diverse combinations of read length, allowing adaptation to almost any study need.



	SP Flow cell	S1 Flow cell	S2 Flow cell	S4 Flow cell
Lanes	2	2	2	4
Output (based on read length)	80 – 400 Gb	167 – 500 Gb	417 – 1250 Gb	2000 – 3000 Gb
Single Reads (clusters passing filter)	0.8 B	1.6 B	4.1 B	10 B
Run Time	13 – 38 hours	13 – 25 hours	16 – 36 hours	36 – 44 hours
Maximum Read Length	2x251		2x151	

NovaSeq system configurations

The main NGS sequencing services that NIMGenetics offers are:

🔍 Whole-Genome Sequencing (WGS)

Whole genome sequencing (WGS) is the most comprehensive tool available to researchers that allows them to tackle highly complex projects, identifying a wide range of biomarkers in DNA, such as:

- Single nucleotide polymorphisms (SNPs)
- insertions and deletions (Indels)
- structural variants (SV)
- copy number variants (CNVs)

While this method is commonly associated with sequencing human genomes, the scalable, flexible nature of NGS makes it equally useful for sequencing any species, such as livestock, plants, or disease-related microbes.

🔍 Whole-Exome Sequencing (WES)

Human Whole Exome Sequencing (WES) is a powerful and affordable tool that enables researchers to identify variants contained in the coding region that answer to their hypotheses, without being limited to a specific gene capture. Likewise, the study of WES applied to populations allows to carry out association studies in the investigation of diseases of complex inheritance. More commonly, it is used to identify variants that originate diverse pathologies with genetic origin.

🔍 Transcriptome Sequencing (RNA-Seq, WTS)

RNA-Seq is the first tool available for detecting the presence of RNA and its expression level by means of NGS. Additionally, it enables the detection of new genes structures, alternative splicing isoforms, gene fusions, SNPs, Indels and the specific expression of alleles.

Tailored solutions

RNA-Seq provides a better coverage and resolution of the dynamic nature of the transcriptome than microarrays, enabling the identification of new and unexpected transcripts. This is because, unlike microarrays, RNA-Seq does not require an *a priori* knowledge of the sequence and it does not suffer the problems inherent to microarrays (cross-hybridisation and quantification of low expressivity genes).

DNA-encoded chemical libraries (DEL) sequencing

DNA-encoded chemical libraries (DEL) is a technology for the synthesis and screening on unprecedented scale of collections of small molecule compounds. The aim of DEL technology is to accelerate the drug discovery process. NIMGenetics offers a library preparation service that is compatible with Illumina index and sequencing adapters, sequencing by NovaSeq 6000 System, and data analysis.

Confirm CRISPR edits and off-target analysis with NGS

NGS is the only assay that provides both qualitative and quantitative information at high resolution across the full range of modifications, meets the needs of any throughput, and can be used to monitor off-target effects. NGS-based targeted sequencing provides a cost-effective solution for confirming CRISPR-induced edits and analyze off-target sites previously predicted in silico.

Bioinformatics service

NIMGenetics analyses NGS data using cutting edge technology platform DRAGEN™ for primary and secondary phases. Furthermore, bioinformatics department is available to customize every required step, from cohort analysis or somatic calling to biostatistical validation.

Genomic services for Therapy and Cell Biology

NIMGenetics integrates the best and most adapted technologies for the control of cellular stability and cross contamination in cell cultures, factors that are specially critical for biosafety in the handling of therapeutic cells.

- **KaryoNIM Stem Cell:** CGH array designed by NIMGenetics to control the stability of cultured cells that detects CNVs and aneuploidies in the whole genome. It analyzes 407 genes associated with genomic instability with high resolution, increasing the detection capacity of the conventional karyotype up to 20 times. In addition, not metaphase cells are required, as it works with DNA.
- **KaryoNIM STR:** qf-PCR platform to characterise the identity of therapeutic cells by STR analysis (Short Tandem Repeats).

Consultancy projects

We understand research, development and innovation (R+D+i) as one of our strategic points, which allows us to continuously improve, generating new services and products, thereby minimising the risk of technological standstill.

Our multidisciplinary consultants team is at your disposal to collaborate in the personalized development of your project, looking for the best solutions at all times.

NIMGenetics has an extensive equipment infrastructure that covers all fields of genomics, both at the level of sequencing and searching for CNVs, among which we highlight the NGS sequencing systems.

The technology used by our platforms is based on sequencing by synthesis (SBS), which gives them the following advantages:

- Allow a massive and parallel sequencing in millions of fragments (reads) of DNA.
- Offer the highest performance of error-free reads, resulting in robust and accurate data for each sequenced base.
- Solve homopolymers in an efficiently way.
- Facilitate a great diversity of applications, being able to sequence from panels of genes and small genomes, to exomes, transcriptomes and genomes of both humans and other species in a single experiment.

NovaSeq 6000

NovaSeq 6000 system incorporates flow cell patterned technology (*Image 1*), with billions of nanowells in fixed locations that provides uniform spacing of sequencing clusters, providing significant increases in the number of sequencing reads and in system performance.

Data-intensive applications, such as human WGS, high-depth exome, and full transcriptome can now be performed more cost-effectively.

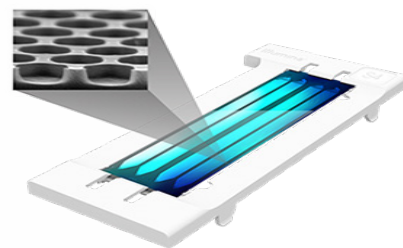


Imagen 1. Flow cell patterned



MiniSeq

MiniSeq system (*Image 2*) offers the quality and confidence of NGS in a powerful and affordable benchtop sequencer with a small footprint. Availability of two types of flow cells, and various combinations of read length, without needing to wait to pool the samples to sequence them on a high-performance instrument.



Imagen 2. MiniSeq system

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