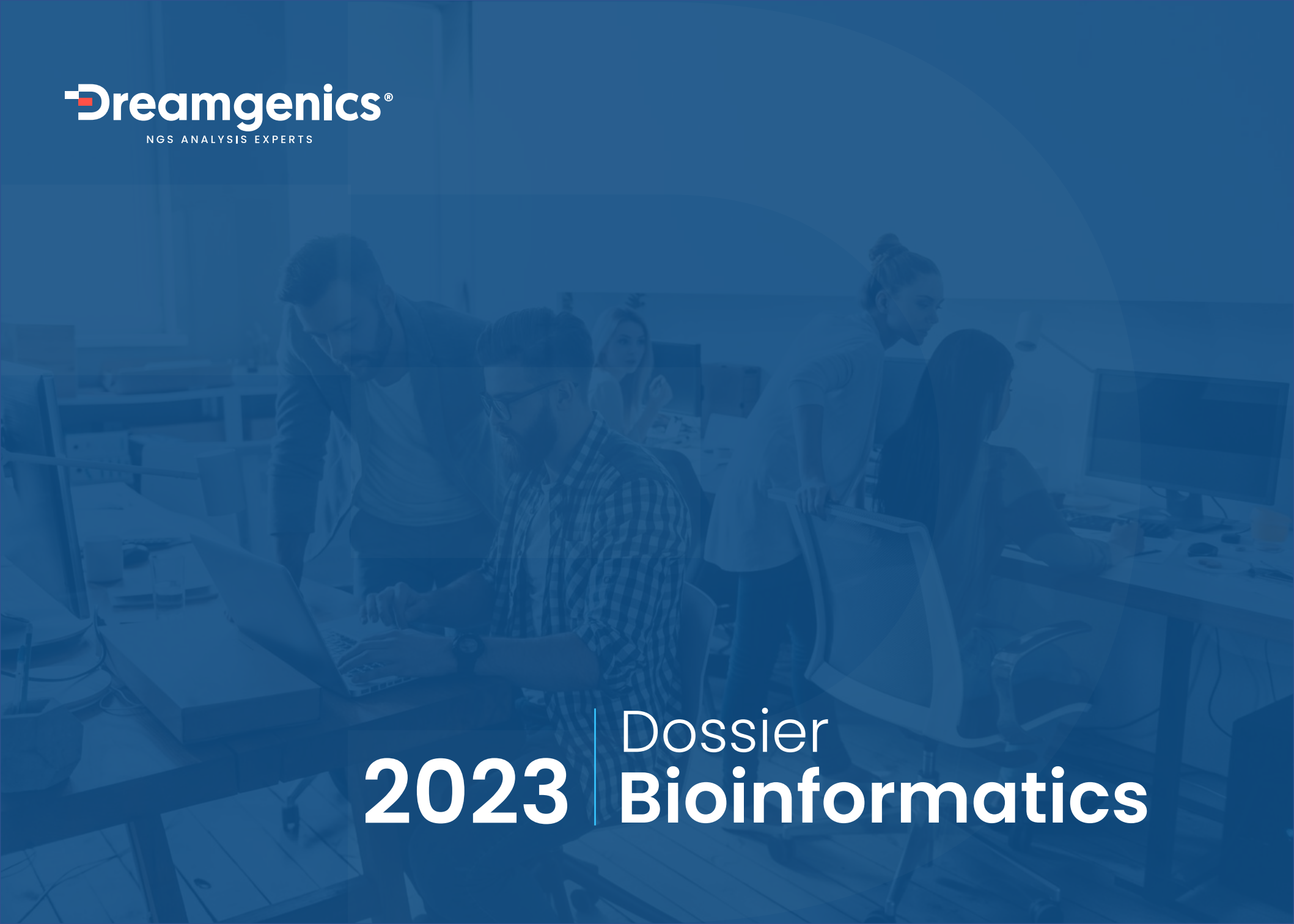
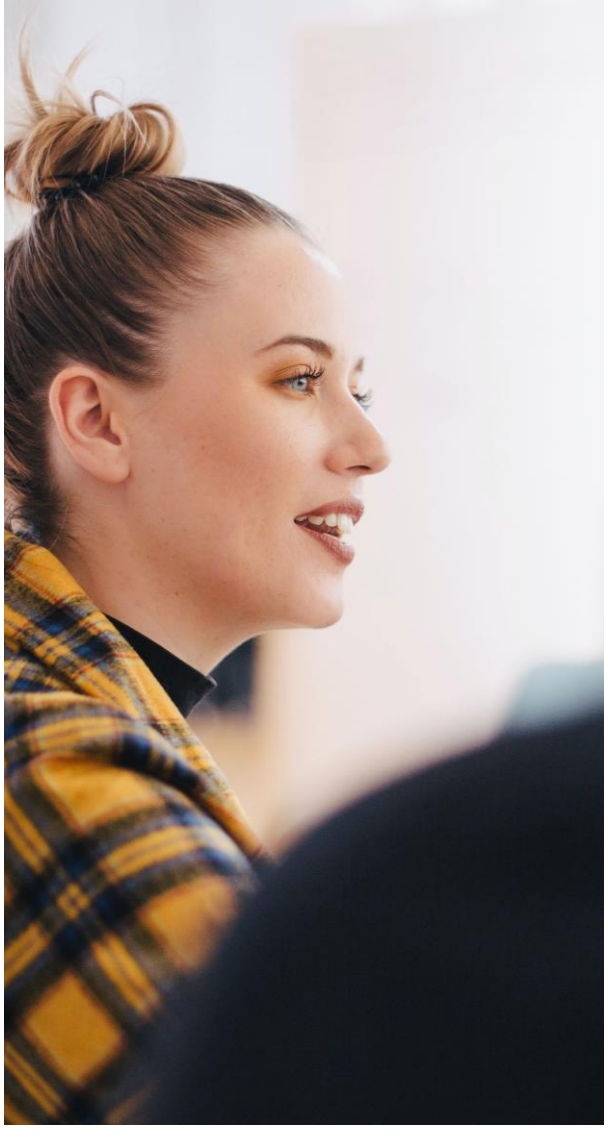
Dreamgenics®

NGS ANALYSIS EXPERTS



2023 | Dossier Bioinformatics



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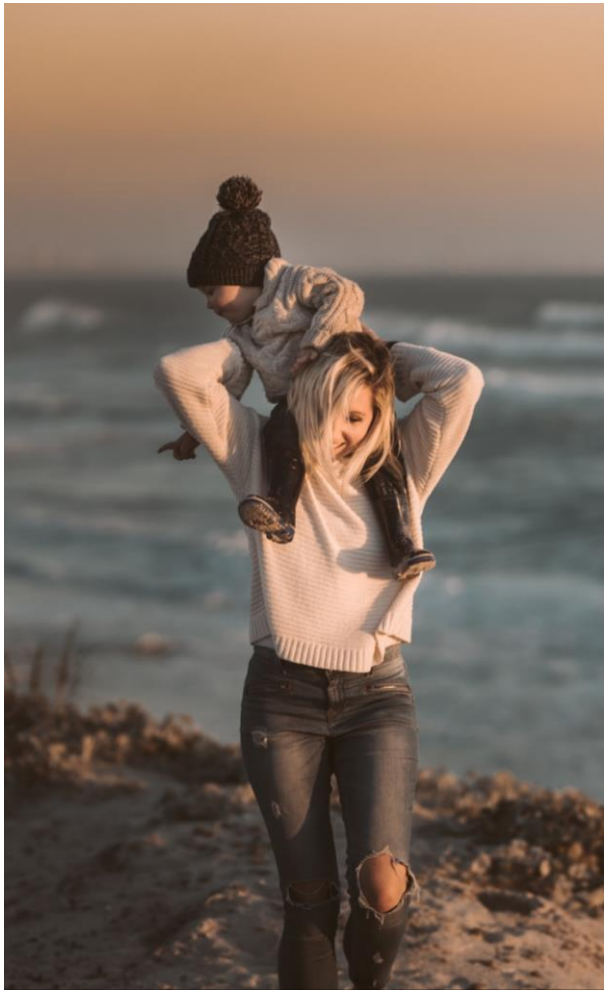
1. Mission, Vision and Values

Dreamgenics is formed by a **group of people passionate about our work**. We are aware about the impact that our performance can have on the health and quality of life of the people and therefore we make an effort to improve every day, revising all the processes that we do, looking for improvements to offer our clients a wider catalogue of services and more advanced products. In the same way, **we feel committed to take advantage of our technology and great knowledge of our team** to contribute to the development of Personalized Medicine, which enables the individual characterization of the disease of each patient and therefore receive the treatment according to its necessities.



Mission

Provide **clinicians and researchers** with genomic and bioinformatic solutions that help to understand the molecular basis of the diseases.

Vision

Each person working in Dreamgenics is proud of being able to contribute to **Precision Medicine** and we hope to continue improving every day to keep helping people.

Values

We try our best to perform our activities **respecting the environment,** following the established standards in the corresponding norm, minimizing our impact by reducing the residues produced and decreasing energy consumption.

2. Quality

The ISO certifications are documents that prove that a specific company is following the ISO norm. In this way, it is demonstrated that the stardards required by this legislation have been implemented and prove that the company is reliable in relation to the products and services that it offers. In Dreamgenics, **the Quality is the base of what we develop in our daily work.** We are certified since 2018 by the Asociación Española de Normalización y Certificación (AENOR) in the ISO 9001:2015, UNE-EN ISO 13485:2018 and UNE-ISO/IEC 27001:2017 norms, which allow us to offer to our clients products and services that fulfill the most demanding quality standards.

ISO Certifications and CE-IVD marking

ISO 9001:2015

International standard of certifiable character that regulates the **Quality Management Systems.**

UNE-EN ISO 13485:2018

Quality management norm that has been especially designed for manufacturers of **sanitary devices and products.**

UNE-ISO/IEC 27001:2017

International norm that allows the **assurance, confidentiality and integrity** of the data and of the information.

CE-IVD marking

Our software **Genome One has CE-IVD marking** (License number: 7157-PS).

Sanitary registry

Dreamgenics is registered as a diagnostic center in the Registry of Centers, Services and Sanitary establishments of the Principado de Asturias with the **number C.2.5.6./6466.**

EIBT certification

Dreamgenics has been recognized by the National Association of Spanish CEEIs (ANCES) as an Innovative Company of Tehnological Base (EIBT).

This recognition is awarded to companies whose practical knowledge and skills are based on the **application of new technologies,** through the development of basic research.

3. Genome One Easy

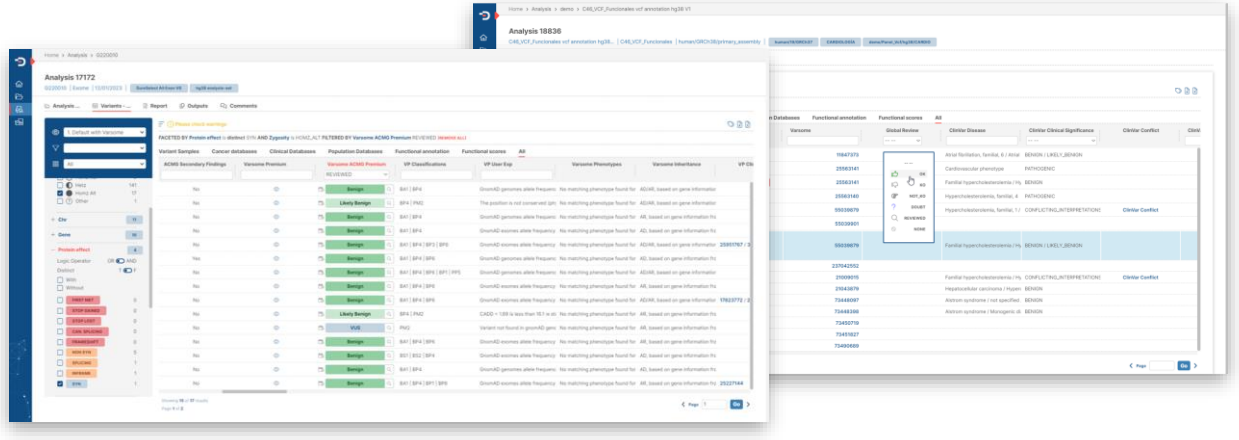
Genome One Easy is a simplified version of our Genome One software which works with **VCF files obtained by Illumina®, MGI and Ion Torrent sequencing platforms.** Genome One Easy has been designed to facilitate the daily work to its users through the automatization of multiple processes, thus **it is very easy and intuitive to use and does not require previous experience in bioinformatics**. Moreover, all the analyses performed with Genome One Easy follow the necessary requirements of the CE-IVD marking and the UNE-EN ISO 13485:2016 norm.

Simplify your daily work with Genome One Easy

1. **Annotate the variants using different databases**
2. **Filter and revise the variants**
3. **Create a database with the revised variants**

Main advantages

- It has an intuitive interface.
- It offers an analysis and samples repository.
- It allows the automatization of processes.
- Tracking the analyses is possible.
- Compative analysis of previous analyses is possible.
- It is compatible with any sequencing platform and library kit.
- It allows the generation of own databases by variant revision.
- It allows the configuration of views and filters.



3.1. Genome One Reports

Visualization is essential for **a correct interpretation of the results** after the bioinformatic analysis. However, the quantity and complexity of the data obtained is a challenge for many users. Therefore, we hand in our bioinformatic results with our **Genome One Reports platform,** an intuitive web interface capable of managing a lot of data allowing the revision and visualization of the results in a simple way.

Easy to use

Genome One Reports is a web platform which is very easy to use, since it does not require bioinformatic experience by the user.

Revision of variants

It allows the interactive and collaborative revision of variants by different team members.

Own databases

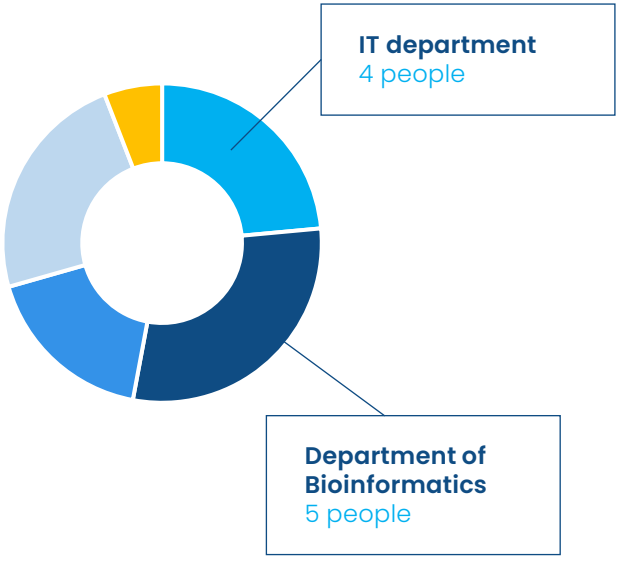
Generation of databases of variants previously revised.

Multiple options

- ✓ Filters and custom views
- ✓ Exportable tables and figures
- ✓ Automatic generation of reports

Support

The IT and Bioinformatics departments are available for our clients to help them out and give them **counseling and support,** before the Project to select the best characteristics and after the delivery of the results.



+50 **Scientific publications**

Our work has appeared in the last years in **more than 50 scientific papers** published by our clients in journals of high impact factor

4. Genomics

The NGS data analysis is a complex process that requires a lot of bioinformatic knowledge and great processing and storage resources. In Dreamgenics, we have **our own software and pipelines** for the analysis of NGS data obtained from the sequencing of **genomes, exomes, exome trios and gene panels.** Moreover, our service of personalized counseling allows us to offer the best option according to the necessities of each person.

The input files can be FASTQ, BAM and VCF from Illumina® or MGI and VCF files in case of Ion Torrent

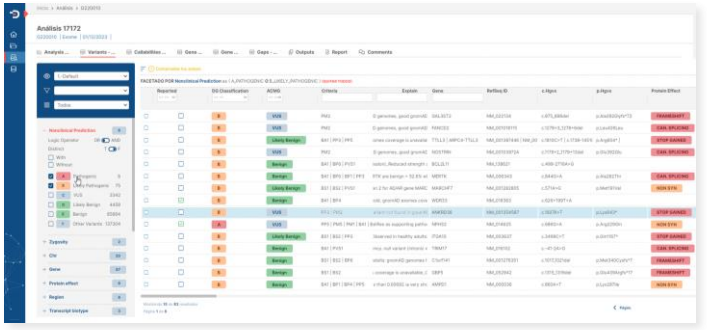
Our analysis includes

- Quality control of the sequences.
- Alignment of reads against the reference genome.
- Detection of high-quality variants (SNVs, translocations and CNVs).
- Filtering of variants that are common in the population.
- Annotation of the variants obtained with multiple databases and prediction algorithms.
- Comparison between samples and identification of recurrent variants.

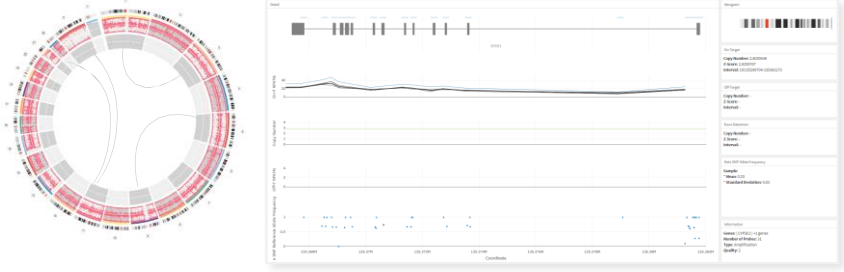
Results

The results are handed in using our web platform called **Genome One Reports** for the advanced visualization and interactive revision. Moreover, Genome One Reports allows the automatic generation of custom reports.

Variant list



Visualization of CNVs



4.1. Sequencing + Bioinformatic analysis

We work with the **sequencing leader Macrogen** to provide our clients with a complete service that includes the sequencing of the DNA samples and the posterior bioinformatic analysis. Depending on the sample and the analysis, different libraries can be used, therefore we **assess our clients to choose the best conditions for their project.**

Contact
985 088 180 / 634 524 714
info@dreamgenics.com

We offer an integral service

- **Initial assessment for your project**
- **Support in the delivery of samples to Macrogen**
- **Direct reception of the FASTQ files**
- **Support after the handing in of the results in Genome One Reports**

Genome

Sequencing + Bioinformatic analysis

- ✓ Illumina® NovaSeq 6000 platform
- ✓ Illumina® TruSeq Nano DNA Library
- ✓ Mean coverage >30x
- ✓ >1 µg of genomic DNA or >100 ng of FFPE
- ✓ 75-180 Gb/sample
- ✓ SNVs, indels and CNVs analysis*
- ✓ Results in Genome One Reports

Exome

Sequencing + Bioinformatic analysis

- ✓ Illumina® NovaSeq 6000 platform
- ✓ SureSelect Human All Exon V6/V8 Library
- ✓ Mean coverage >100x
- ✓ >1 µg of genomic DNA or >200ng de FFPE
- ✓ 9-36 Gb/sample
- ✓ SNVs, indels and CNVs analysis*
- ✓ Results in Genome One Reports

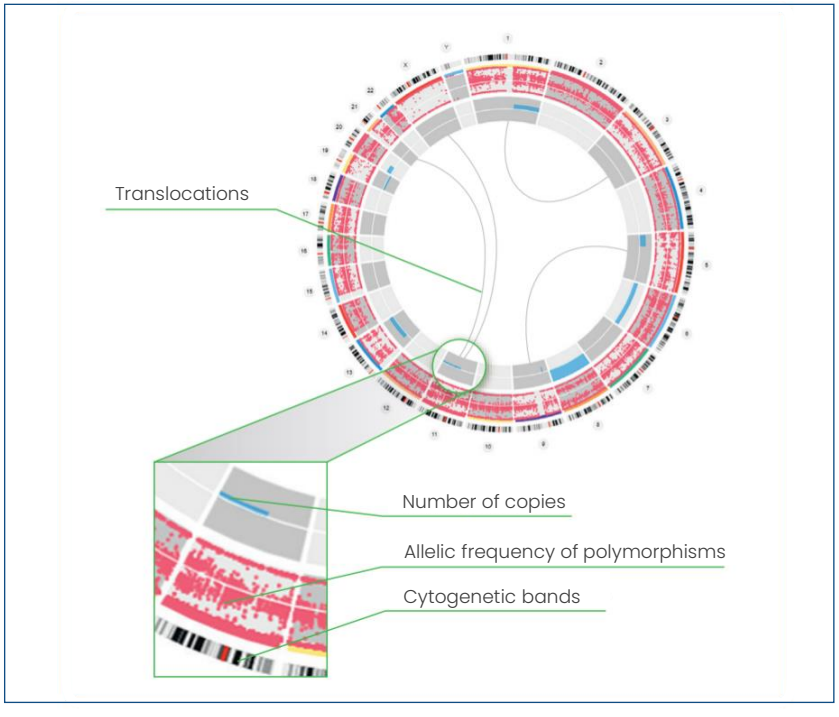
*CNVs whenever the experimental design allows it.

4.2. CNVs analysis

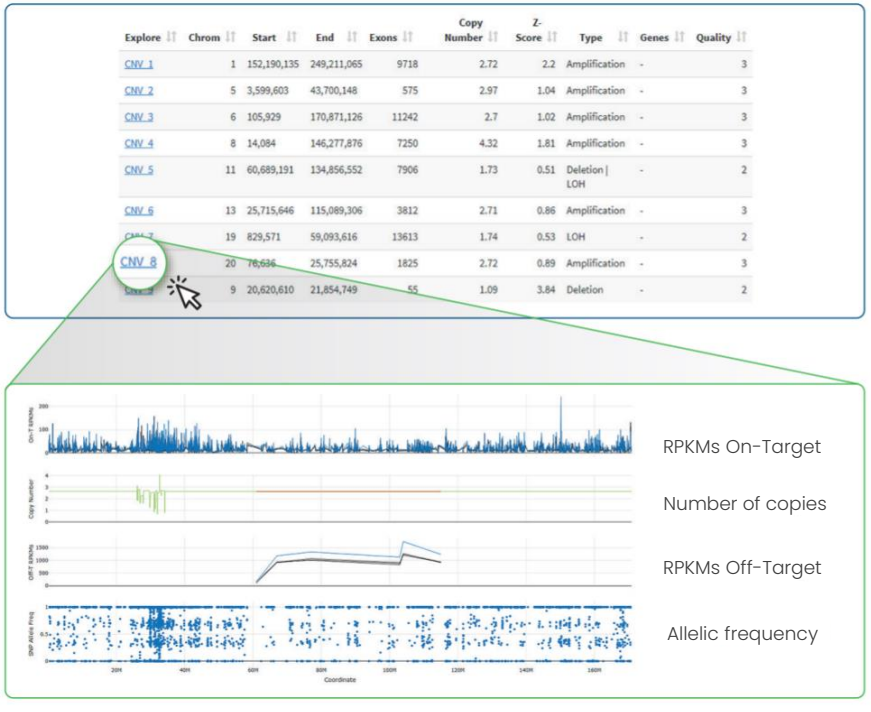
Structural variants in the genoma include **Copy Number Variations (CNVs),** mobile genetic elements, inversions and translocations. The correct identification and characterization of structural variants is essential for the diagnosis of many genetic diseases and to establish prognostic, preventive and treatment strategies. In Dreamgenics, we do CNVs analysis with our Genome One software and **using an algorithm designed by us[1].**

The results of the analysis are handed in using our web platform Genome One Reports.

Circos plot representing the identified CNVs



Interactive table summarizing the detected CNVs



[1]Valdés-Mas R, et al. PLoS One. 2012;7(12):e51422.

5. Transcriptomics

The transcriptomic analysis allows the **quantification of gene expression** using NGS platforms. The interpretation of data obtained from RNA sequencing (RNA-Seq) has become a very demanding service due to its high sensitivity and precision. In Dreamgenics, we have a **wide experience in the bioinformatic analysis of RNA-seq** and we offer our clients a personalized assessment during the experimental design and in the interpretation of results.

We perform transcriptomic analysis from Illumina® FASTQ files.

Our analysis includes

- Quality control of the sequences.
- Alignment of reads against reference sequences.
- Quantification of gene expresión in the sample.
- Differential gene expresión analysis between different samples.
- Study of gene ontology enrichment and pathways.
- Study of isoforms formed by alternative splicing*.
- Identification of other RNAs (smallRNAs and ncRNA)*.

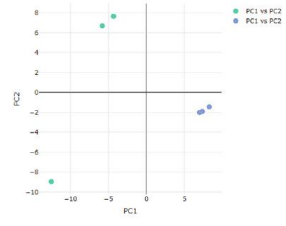
*When the experimental design and the coverage allows so..

Results

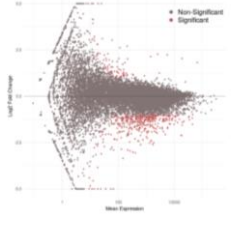
The report with the results is handed in through our web plastform **Genome One Reports**, which allows the advanced visualization and interactive revision.

Data is represented in tables and graphs easy to interpret. Moreover, all the information is exported in different formats for its use in scientific papers.

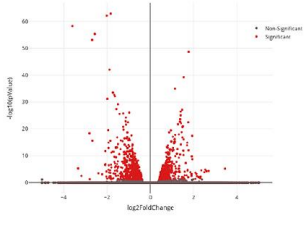
PCA plot



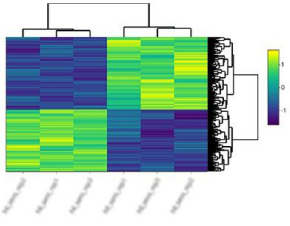
MA plot



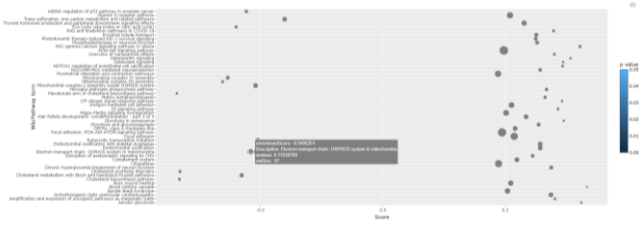
Volcano plot



Heatmap



GSEA plot



5.1. Sequencing + Bioinformatic analysis

The libraries used in an experiment of RNA-Seq depend on the sample and type of RNAs that will be studied. We work with the **sequencing leader Macrogen** to offer our clients a wide variety of sequencing options, therefore we assess them to always choose the **best conditions for their project.**

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mRNA-Seq

Sequencing + Bioinformatic analysis

- ✓ Illumina® NovaSeq 6000 platform
- ✓ Illumina® TruSeq stranded mRNA Library
- ✓ mRNA analysis
- ✓ >1ug of RNA with RIN>7
- ✓ 30-40 M/sample
- ✓ At least 3 samples per condition
- ✓ Differential expression, ontologies and pathways
- ✓ Results in Genome One Reports

Total RNA-Seq

Sequencing + Bioinformatic analysis

- ✓ Illumina® NovaSeq 6000 platform
- ✓ Illumina® TruSeq stranded Total RNA Library
- ✓ mRNA and lncRNA analysis
- ✓ >1ug of RNA with RIN>7
- ✓ 40-60 M/sample
- ✓ Ribo-Zero Globin treatment*
- ✓ At least 3 samples per condition
- ✓ Differential expression, ontologies and pathways
- ✓ Results in Genome One Reports

*Removes ribosomal RNA and globin mRNA in blood samples.

6. Research

Our mission as a biotech company is to provide **clinicians and researchers** with genomic and bioinformatic solutions that will decipher the molecular basis of the diseases. To achieve so, **we carry out different I+D+i projects** with the objective of developing new projects and services to offer our clients. In the same way, we participate with hospitals and research centers in **projects associated with human health** to which we contribute by providing the researchers with our expertise in NGS data analysis..

9 Research projects

2 European I+D+i projects

+1 M€ of investment in I+D+i in the last years

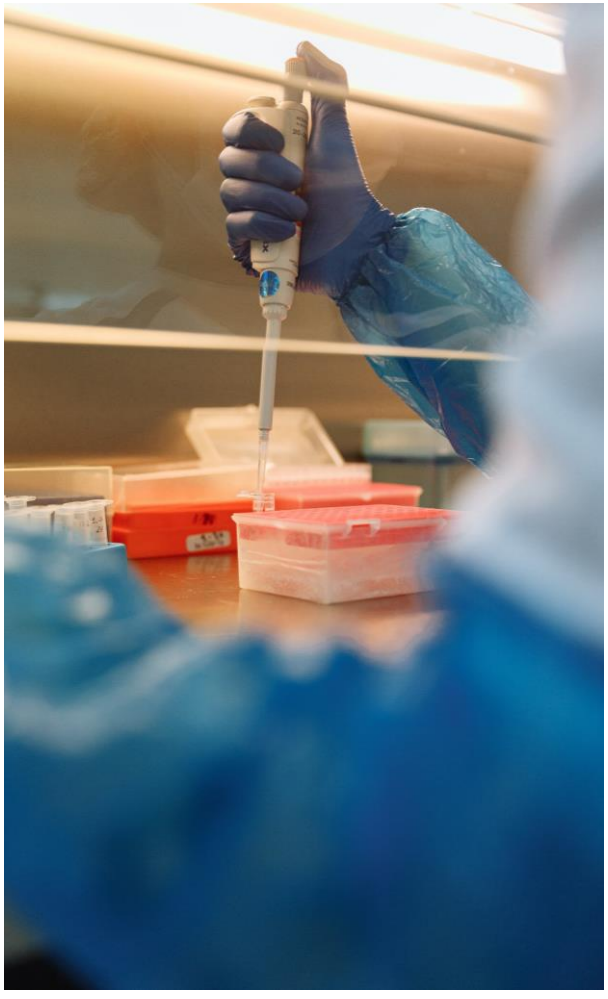
Highlighted Projects

MOLECULAR PROFILE STUDY IN PERIPHERAL BLOOD TO PREDICT THE RESPONSE TO ICIS IN PATIENTS WITH ADVANCED NSCLC

Project done in collaboration with the Instituto de Investigación Sanitaria de Santiago de Compostela (IDIS) and the Service of Medical Oncology of the Hospital Universitario de Santiago.

INSPIRING THE INNOVATION IN THE EARLY DETECTION OF INFANT HEARING LOSS IN THE SUDOE SPACE: TOWARDS A PERSONALIZED MEDICINE BASED ON GENOMIC DIAGNOSTIC TOOLS

European Project done in collaboration with the Clínica Universidad de Navarra and other hospitals of France and Portugal.



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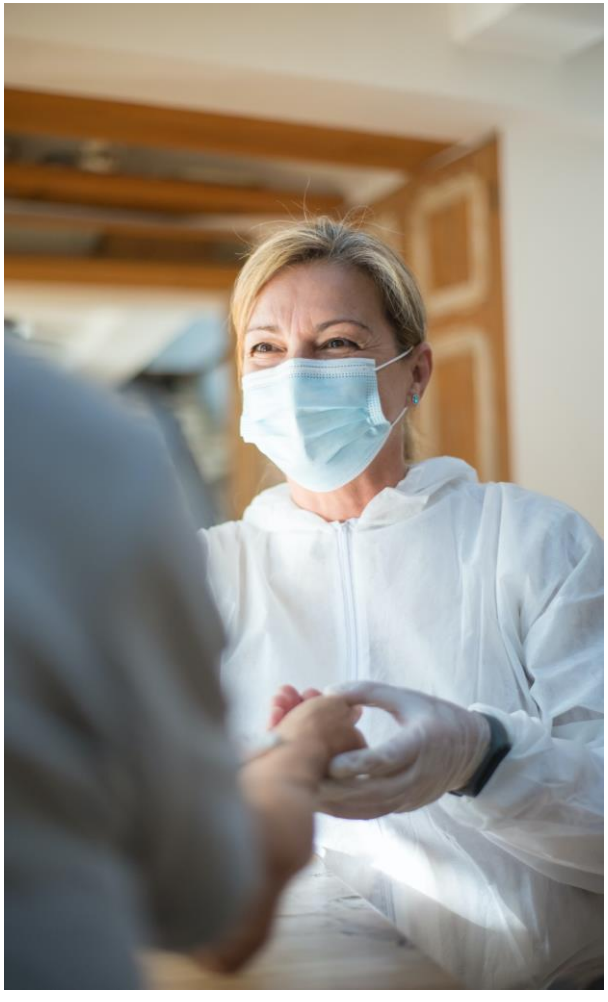

Contact details

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Friday from 8:00 to 15:00

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