SEQUENCING | GENOTYPING | BIOINFORMATICS

SPECIES IDENTIFICATION | TRACING AND DIAGNOSTIC KITS

FIND **YOUR** GENOMIC SOLUTION

GenoScreen

EDITO

Our company was created with one ambition: contributing to the exploration of DNA and the exploitation of its properties. In the process, our development has been driven by abundant and successful research in molecular biology. This research continues to lead to important scientific discoveries, as well as innovative applications and solutions that meet the needs of many sectors, including healthcare, environment and agrifood.

Our history is an exciting adventure, made by shared values with those who use our services, or who choose us as a research partner. These values that guide us are excellence, responsibility, honesty and respect. Such a policy has enabled us to earn trust and respect from our customers and partners.

This catalog presents a broad range of services, all carried out under ISO 9001 quality standards. To be able to offer you appropriate and adapted solutions, please contact us to let us know your needs and expectations.

Listening, understanding and considering your issues is our main commitment.

I would also like to mention our teams of experienced researchers. Rich from their academic relationships, they ensure effective and competitive intelligence, making it possible for us to innovate in genomics, metagenomics and bioinformatics. This distinctive asset is a great help, improving our analytical protocols, as well as developing accurate and robust solutions through molecular biology. For these reasons, GenoScreen stands by your side as the ideal partner in your genomic research projects.

André Tordeux
President and founder of GenoScreen

At GenoScreen, we know that our *raison d'être* and why we strive for progress is you, our customers. This is why I invite you to talk to our specialists and experts, who are available at your service.

Best regards,

André Tordeux

CONTENTS

ABOUT GENOSCREEN

GenoScreen is an independent Innovative Services Company, specialising in genomics and bioinformatics. With more than 20 years of experience, GenoScreen enjoys international recognition, particularly in molecular microbiology.

Through ongoing investments in R&D, the company has become competitive in the field of scientific services and has designed and marketed highly effective kits for typing and diagnosing bacterial pathogens.

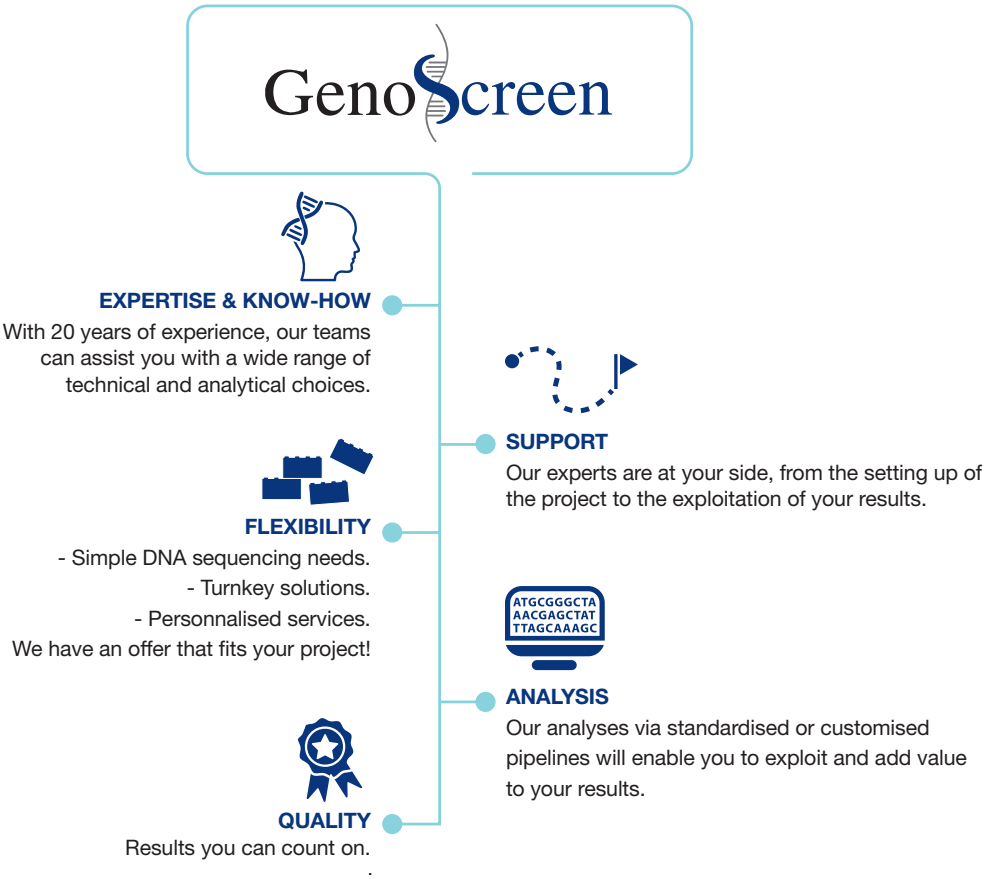
Thanks to its size (< 50 people), GenoScreen can flexibly respond to analysis requests which focus on quality and value the prior needs assessment and discussions.

Beyond the services listed in this catalog, the company provides tailored solutions to meet specific requests.

Analytical engineering consulting and training to assist those who are involved in genomic research projects are also part of the offer.

GenoScreen clients benefit from:

- Services ranging from sequence generation, on Sanger, NGS Short and Long-Read platforms, to in-depth bioinformatics analysis of the results,
- Quality assurance, with ISO 9001 certified services, carried out by our ISO 13485 certified company,
- A confidentiality guarantee and backup of their data,
- The ability to communicate directly with R&D operators and managers before, during and after the completion of their projects.

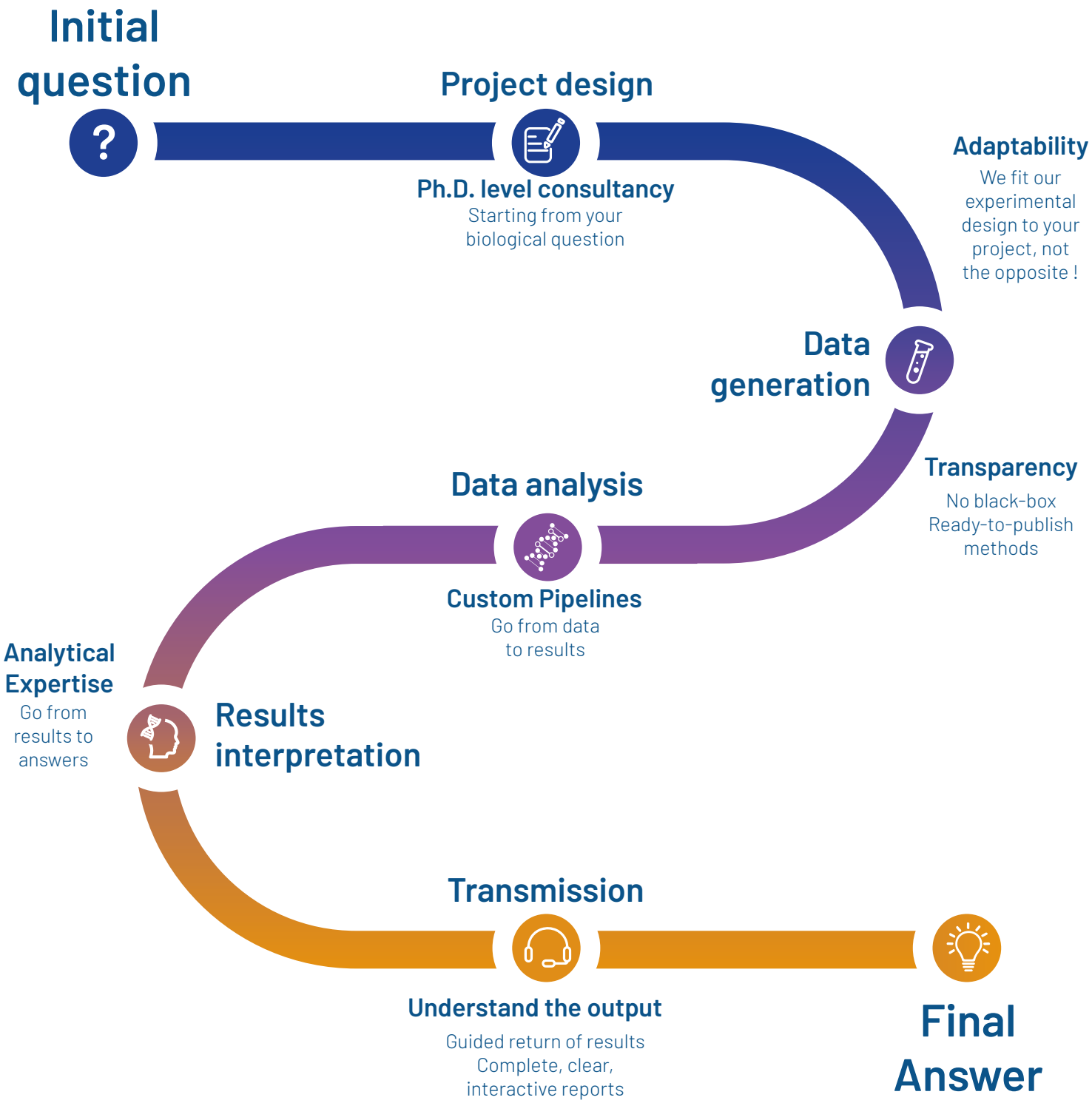


REDEFINE SERVICE

A NEW DIMENSION IN GENOMICS SERVICES

Our team provides transparent support, from project design to data interpretation.

The customer experience is at the core of our concerns. That is why we offer personalized service, ongoing dialogue and comprehensive support.



MAKING GENOMICS ACCESSIBLE TO ALL

Whether you need full support through to results delivery, or a trusted partner to generate your data, GenoScreen will meet your expectations.

OUR HUMAN AND TECHNICAL RESOURCES

OUR TEAM

GenoScreen is first and foremost a team of passionate scientists at your service.

You can count on our technicians, engineers and doctors to provide know-how, advice and expertise in genomics.

OUR SEQUENCING PLATFORMS

For 20 years, the technical means developed on our platforms have never ceased to evolve, remaining at the cutting edge of the latest technologies, whether for nucleic acid extraction, quality control, sequencing or analysis, in order to provide you with the best results in the shortest time.

SANGER SEQUENCING

- Responsiveness and flexibility in processing your samples.
- A processing capacity of several thousand sequences per day.

NGS SEQUENCING

Whatever the size and nature of your sequencing project, we have the technical solutions to make it happen:

Long read solutions:

Pacific Biosciences
Sequel II

Oxford Nanopore Technologies
GridION

Short read solutions:

Illumina	**MiSeq**
	NextSeq
	HiSeq
	NovaSeq

BIOINFORMATICS

- Significant computing power with over 500 CPU cores (+ GPU computing capacity).
- Secure long-term storage of data on magnetic tapes.
- Secure access to your analysis and sequencing data.

SEQUENCING

As a sequencing pioneer since 2001, GenoScreen operates sequencing platforms covering all your genomic needs, regardless your project size and nature.

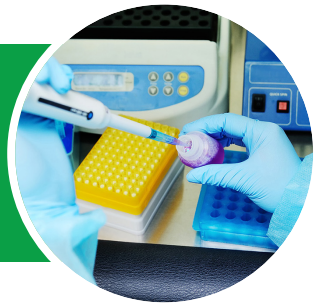
Our platforms have evolved over the technological revolutions to offer you a wide range of solutions.

SANGER SEQUENCING

With over 20 years of experience in Sanger sequencing, GenoScreen provides you a scalable service adaptable to any kind of project.

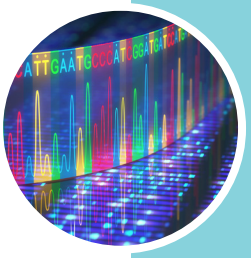
APPLICATIONS

- Identification and checking of the absence / presence of mutations
- Confirmation of NGS data
- Validation of plasmid constructs or clonings



Discover the GenoScreen offer:

	One-Shot	One-Shot Plus	Optimized
Results in 24-48h after reception	✓	✓	✓
Technical support by e-mail or phone	✓	✓	✓
Accepted sample formats : - Tubes - Plates (complete or not)	✓	✓	✓
Free sample purification (on demand)	✓	✓	✓
Reading up to 1200 pb	✓	✓	✓
Validation of sequences and corrections with IUPAC annotation		Semi-automated	Manual by operator
Deliverables	.seq/.ab1	.seq/.ab1	.seq/.ab1 QC (Quality Control) report with playback commentary for each sequence
Reprocessing with optimised protocol (on request)			✓
Monthly activity report (including remaining credits)	✓	✓	✓



COMPLEMENTARY ANALYSES

To go further, GenoScreen offers additional services to complement sequencing:

- Primer walking for longer fragments,
- Purification of PCR products by gel cutting,
- Primer design and synthesis,
- Analysis of results according to IUPAC coding.

- Flexible sequencing offer adaptated to your needs
- Personalized follow-up for your projects
- Simple ordering system
- Monthly billing or prepaid account
- Free shipment of your samples by a GenoScreen approved operator (under conditions)
- Optimised protection of samples in Genobox

WHOLE GENOME SEQUENCING

We offer both short- and long-read services, covering all your sequencing needs, from viral to eukaryotic genomes.

APPLICATIONS

- Genome comparison
- Variant detection (SNV, Indels, Structural variants)
- Genome exploration, gene of interest identification, metabolic pathways
- Regulatory dossiers (EFSA, FDA, ANSES, etc.)

Discover the GenoScreen offer:

	Short Short-Read sequencing	**Long** Long-Read Sequencing	**Hybrid** Long-Read Sequencing
	Suitable for large **resequencing** projects	Obtain **contiguous** and **complete** genomes	For the **most accurate** overview of your genomes of interest
Assembly	3/10 Highly fragmented assemblies	10/10 Contiguous assemblies	10/10 Contiguous assemblies
Variant detection	7/10	9/10	10/10

GENOREF

Characterise your industrial strains, therapeutic or pathogenic interest!

Obtaining a complete, assembled and annotated genome is the ideal, unbiased solution for characterising, studying and comparing samples. GenoScreen offers a turnkey solution that can be adapted to your needs to generate genomes of a quality equal to a reference genome. Through the combination of different sequencing technologies and an optimised and standardised bioinformatics pipeline where your data is systematically reviewed and manually reprocessed by our bioinformaticians. Our Genoref offer maximises your chances of obtaining complete chromosomes and plasmids (circularised if necessary) and the most accurate sequence possible.

DNA Extraction
Integrity and purity of the DNA preserved

Sequencing
Multiple technologies used

Assembly
Data manually expertised

Sequence repository
NCBI databases

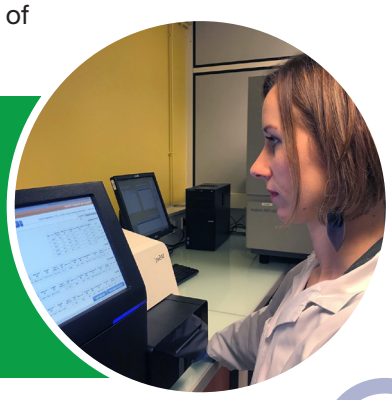
Our offer can be adapted to your needs, from DNA extraction to the deposit of sequences on NCBI databases.

TARGETED SEQUENCING

Sequencing the entire genome is not always necessary to answer a given problem. Targeted sequencing interrogates only a fraction of the genome and can therefore efficiently identify variants (SNPs, insertions, deletions) in a wide range of targets and individuals.

AMPLICON SEQUENCING

Get high sequencing depth for your amplicons to have a high power of detection of rare mutations.



APPLICATIONS

- Identification of somatic mutations in specific cancers
- Use in breeding for reproduction and maximisation of certain traits of interest
- Metabarcoding for taxonomic profiling of complex samples

DEEPLEX

The all-in-one solution for the characterisation of *Mycobacterium tuberculosis*

The Deeplex® Myc-TB kit is a complete and innovative solution to diagnose antibiotic resistance of a strain to 15 anti-TB molecules, all without a cell culture step and in less than two days. The test is based on deep amplicon sequencing and automated analysis via a dedicated and secure web application.

Deeplex® Myc-TB detects TB heteroresistance down to 3%. It also allows the identification of non-tuberculous *Mycobacteria* as well as TB lineages and their spoligotype.

This innovative approach allows to efficiently guide the management of TB patients, by giving a rapid prediction of the antibiotic resistance profile.

Deeplex® Myc-TB is available in CE-IVD and RUO kits. GenoScreen also offers this test as a service.

SEQUENCE CAPTURE/ENRICHMENT

The use of labelled DNA probes, specific to your regions of interest, will allow the sequencing of the fraction of interest only. It is therefore possible to create custom panels composed of thousands of probes that can target, in total, several dozens of megabases of genomic regions.

APPLICATIONS

- Whole Exome Sequencing
- Capture of viral sequences in a sample
- Depletion of the host genome to enrich it with sequences of interest
- Genotyping of a large number of targets

TRANSCRIPTOME SEQUENCING (RNA-Seq)

Transcriptome sequencing allows a complete and objective analysis of RNA. Depending on the application chosen, it is possible to sequence total RNAs (coding and non-coding) or to select only messenger RNAs.
GenoScreen will assist you in developing the most appropriate experimental protocol for your project.

APPLICATIONS

- Differential expression analysis between several conditions
- Confirmation of genome annotation by checking gene expression
- Search for biomarkers
- Identification of isoforms from alternative splicing of a pre-messenger RNA

DIFFERENTIAL EXPRESSION ANALYSIS

DIFFSEQ

Explore genes and functions differentially expressed according to your experimental conditions

Highlight differentially expressed genes under known and controlled variables (different culture conditions, different tissues, etc.)

This complete and customisable offer allows you to obtain direct exploitable results with differentially expressed genes, as well as a functional analysis to determine the metabolic functions impacted.

Experimental design	RNA Extraction	Sequencing	Differential expression analysis
Design assistance	Protocols optimized		Precise and synthetic report

Would you like to carry out the extractions yourself? Don't worry, our offer is adapting to your needs.

MEASURING THE EXPRESSION LEVEL OF GENES

You only want to know the expression level of a few targets? We offer gene expression measurement by RT-qPCR.

APPLICATIONS

- Verification of the expression of exogenous products
- Confirmation of the expression level of identified targets by differential analysis
- Measurement of the expression level of a restricted panel of genes on several samples

LONG READ RNA-SEQ

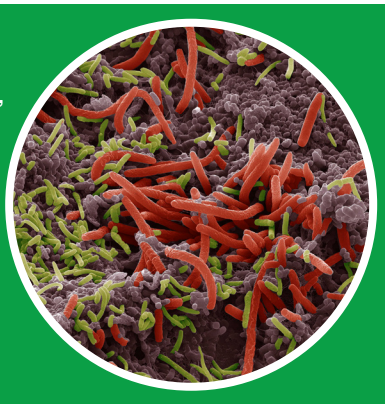
Want to test Long read sequencing for transcriptomics?
To go further in the detection of isoforms? Discuss it with our specialists.

METAGENOMICS

GenoScreen has been particularly well known for its expertise in metagenomics for almost 10 years. Metabiote® allows the characterisation of microbiota, both at the level of taxonomy and active functions, by measuring changes in population abundance and diversity.

APPLICATIONS

- Evolution studies in a microbiota after treatment (drugs, antibiotics, food supplements, cosmetics, etc.)
- Investigation of microbial population dynamics in pathologies
- Studies of microbial flora in fermentation processes (cheese, wine, beer, kombucha, kefir, etc.)
- Monitoring of natural ecosystems (water, soil, sediment)
- Detection of new biomarkers (medicine, nutrition, agriculture, soil remediation)



GENOBIOME® POWERED BY GENOSCREEN

GenoBiome® : The integrative solution for studying microbial communities.

GenoBiome offers a complete range of support services for microbial community analysis.

- Ph.D. level consultancy in microbial ecology or genomics
- Methods adaptable to the project and the matrix
- Specific analyses according to initial matrix: Cutaneous, Intestinal, Environmental
- Experimental results repeatability and reproducibility
- Interactive reports
- Data delivery support

The reports supplied with GenoBiome can be adapted to suit the purpose of your project:
Research - High level of scientific detail and support from genomics experts
Marketing - Simple results suitable for allegations, with guidance on how to use them
Regulatory - Transparency and support for file preparation

Our years of experience in metagenomics allow us to work on a wide variety of matrices (human, animal, environmental (eDNA) or plant).

GenoBiome®
Powered by GenoScreen

GENOMIC SOLUTIONS FOR MICROBIOME STUDIES

Customized solution for taxonomic and functional exploration of microbial communities for:

Impact studies | Clinical studies | Exploratory R&D

EXPERIMENTAL DESIGN

SAMPLING STRATEGY

PROPRIETARY ANALYSIS PIPELINES

CUSTOMIZED SAMPLES ANALYSIS

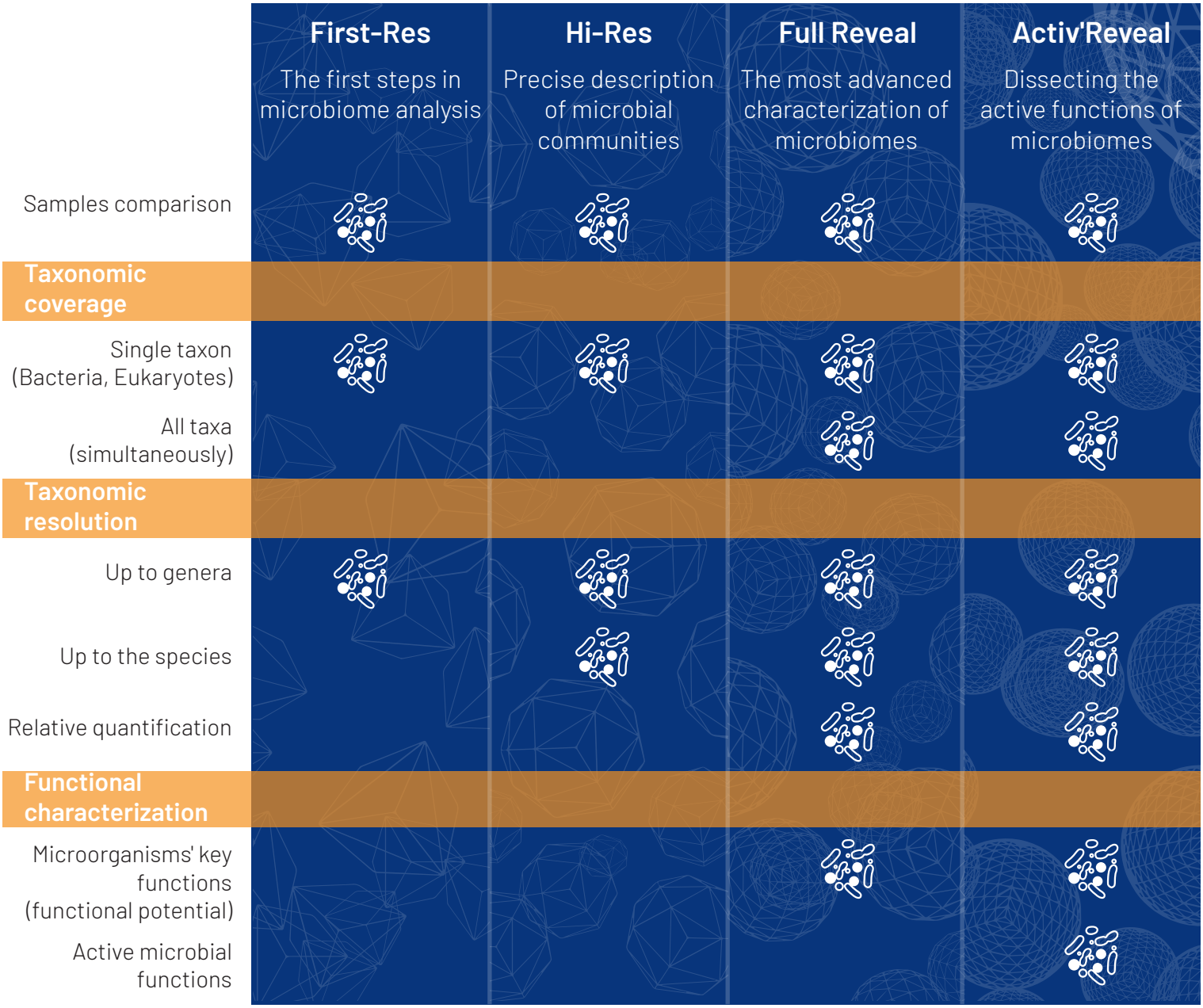
RESULTS INTERPRETATION

EXPERT SUPPORT

Let our experts support you every step of the way

OUR METAGENOMIC PORTFOLIO

A complete range of technical solutions for your microbial community analysis projects



First-Res and Hi-Res: "Metabarcoding" targeted metagenomics

A gateway to the description of microbial communities, targeted metagenomics makes it possible to describe and compare the taxonomy of different samples. With **First-Res**, explore the taxonomic diversity of your samples down to genus level, or go even further with our **Hi-Res** offer based on the latest "Long-read" sequencing technologies, with resolution down to species or even strain level.

Full Reveal: shotgun metagenomics

By sequencing all the DNA present in a complex sample, our **Full Reveal** offer enables you to describe the taxonomic composition and diversity of a community of organisms, and its functional capacities. These analyses can complement metabarcoding studies, for example on a representative subgroup of samples.

Activ'Reveal: Multi-omics approach

The latest innovation from GenoScreen, and the result of our extensive expertise in community analysis, our **Activ'Reveal** offer combines the power of metagenomics and metatranscriptomics in a single sample. An analysis that compares the genes present in the genomes of the microorganisms present in your samples with those actually expressed, in order to highlight functional effects.

BIOINFORMATICS

Our bioinformatics services are constantly evolving to ensure the highest quality results. Numerous algorithms and specific analysis pipelines are developed and updated to speed up the interpretation of results and to provide more readable and richer scientific information.

PRIVACY
Your data is analysed and stored on our servers.

SECURITY
We ensure data storage and archiving for several years with on-site and off-site copies.

QUALITY
Get results you can trust, with detailed step-by-step reports.

STANDARDISED ANALYSIS

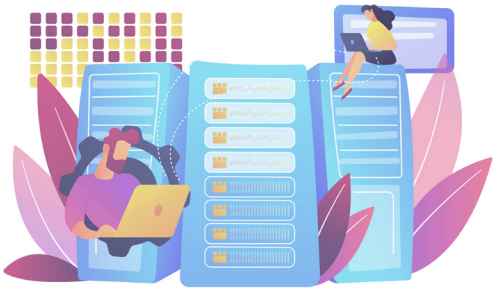
Our analysis pipelines are built, tested and validated on large datasets in order to provide you with the highest quality. The methodology and the main results of these analyses are reported in a clear and detailed manner.

STANDARDISED ANALYSES WITH OUR PIPELINES:

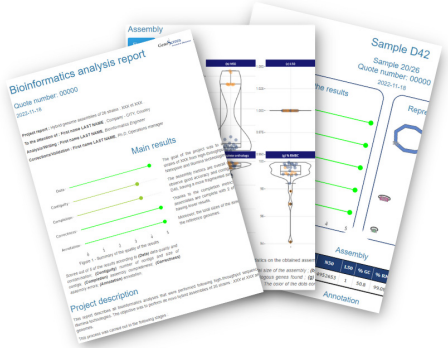
Optimised results thanks to our regularly upgraded analysis pipelines.

Reproducibility is ensured thanks to our transparency on the methods and tools used.

Quality assurance through our pre- and post-analytical quality controls.



	Snap Quick and easy results	Precision Comprehensive analysis, expert review	Clarity Comprehension and support
Analytical pipeline	• Pipeline owner	• Pipeline owner	• Pipeline owner
Report	• Summary report • File description • "Ready to publish" methodology	• Full report • Interactive report • In-depth QC • "ready to publish" methodology	• Full report • Interactive report • QC in-depth • Sample report • Ready to publish methodology
Expertise		• Commented results • Manual data control	• Commented results • Manual data control • Restitution and interpretation of results live by visio • Unlimited support
Data storage and access	• 6 months	• 2 years	• 3 years



INTERACTIVE RESULTS:

More than a simple analysis report, it is an exploratory tool for your data.

Dynamic and interactive figures and tables.

Discover, explore, understand your data.

ANALYSIS OF YOUR DATA:

Do you have data but cannot analyse it yourself?

Would you like to have your data analysed by another service provider?

Send us your data:

- Preliminary quality control to ensure that your data meets our quality standards.

BIOINFORMATICS ANALYSIS PIPELINES

Solutions for analyzing the genomes of isolated organisms

de novo assembly

- Genome and plasmid assembly
- Structural and functional annotation
- Search for genes of interest (e.g. antibiotic resistance genes)

Differential expression analysis

- Transcript abundance in impact studies (test/control)
- Functional enrichment

Phylogenetic analysis

- Whole-genome strain identification
- Genetic proximity of strains

Variant calling

- Identification of genomic differences between strains
- SNV, Indel, Structural variants

Specific sequence identification

- Highlighting specific strain regions
- Strain-specific PCR/qPCR design

CUSTOMIZED ANALYSIS

Our bioinformatics development skills extend far beyond our standardized pipelines. We put our know-how at your disposal to meet all your analytical needs.

EXPERTISE AND ADVICE :

Let us guide you to implement original, robust and customized solutions for all your analytical questions. Discuss your projects now with our bioinformaticians.

TAILOR-MADE DEVELOPMENT:

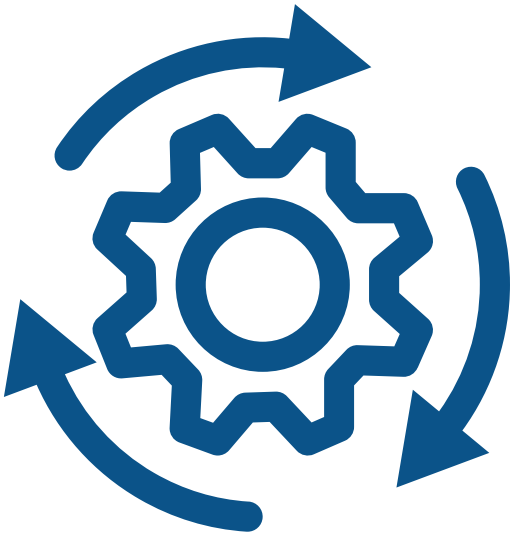
A distinctive analysis that is out of the ordinary? A recurring need for quality control? Our bioinformaticians can provide you with tailor-made solutions, based on specifications you have already drawn up, or jointly developed around your specific needs.

PROCESS AUTOMATION:

For routine analyses, we put our expertise in process automation at your disposal to provide "one-click" solutions with a graphical interface. Applications can be deployed on site or via a dedicated server.

CUSTOMIZE RENDERING:

The reports we provide are adaptable in both form and content. Whether you need a special format to match your internal standards, or a "lighter" version to focus on specific points, we are here to help.



SPECIES IDENTIFICATION

The ability to identify organisms is a priority for understanding the world around us. GenoScreen is therefore in line with this objective by offering you a precise and rapid characterisation of any organism thanks to a molecular determination, based on universal databases.

ISOLATED MICROORGANISMS

Use of the principle of molecular barcoding: amplification and sequencing of universal reference genes according to the type of studied organism (bacteria, yeast, fungal strain, microalgae).

USUAL TARGETS: **RIBOSOMAL DNA (16S, 18S, 28S, ITS)**

APPLICATIONS

- Identification of contaminating strains in a production line or any controlled environment
- Quality control/traceability of microorganisms
- Confirmation of a phenotypic/spectrometric identification

In addition, optional typing is possible for the referenced species, targeting other genomic regions (rpoB, gyrB...) to specify obtained identification and adapt it to your request (for example: discrimination within a group of sub-species sharing the same ribosomal DNA sequence).

Finally, to remove any doubt and obtain the most accurate characterisation of your microorganisms, a whole genome sequencing (WGS) is recommended.

MÉTABARCODING

Historiquement axé sur l'identification d'espèces isolées, l'avènement des techniques de séquençage haut-débit nous permet désormais d'identifier les différentes espèces présentes dans une communauté complexe (microbiote). Consultez notre offre Metabiote® pour plus d'informations sur le profilage de communautés microbiennes.

OTHER ORGANISMS

By the same principle of molecular barcoding, other organisms, such as plants, fishes, insects, etc. can be identified by amplification and sequencing of universal reference genes.

USUAL TARGETS:
MITOCHONDRIAL AND/OR CHLOROPLAST MARKERS (COI, CYTB, MATK, RBCL)

APPLICATIONS

- Identification of species present in an environment
- Confirmation of presumed visual identifications
- Phylogenetic study of samples of the same species

QPCR

GenoScreen assists you in developing and optimising your custom qPCR tests. Our team designs specific assays adapted to your needs, whether it is detecting genetically modified strains, differentiating between species at the desired taxonomic level or analysing genes of interest.

QPCR

IQUANT

Development and optimisation of your custom qPCR tests. Our team designs specific assays adapted to your needs for the detection of genetically modified strains, the differentiation of species at the desired taxonomic level or the analysis of genes of interest.

Primer design / verification in silico → **Development & optimisation** of the qPCR test → **Analysis of results** Quantification or detection → **Interpretation & reporting** → **Transfer** method / **Supplied as a kit**

APPLICATIONS

- Quantification of specific strains
- Regulatory dossiers for genetically modified strains

TARGETED ANALYSIS OF THE SKIN MICROBIOME BY QPCR

Specific quantification of *C. acnes, S. epidermidis* and *S. aureus* in skin samples.

APPLICATION

- Impact study of a product on the main microbial biomarkers of the skin

RESIDUAL DNA ASSAY

In accordance with quality requirements, we measure residual DNA in products based on recombinant strains (LBP, vaccines, vectors, etc.). Our offer includes a standard targeting method *KanR* or custom development tailored to your target sequence.

APPLICATION

- Gene therapies / vaccines

MICROBIAL BIOMASS ANALYSIS

Based on the 18S/16S ratio, it enables the estimation of the fungal-bacterial balance in a rapid and actionable manner, without the need for bioinformatic processing.

APPLICATION

- Evaluation of digestive or environmental microbiota

PMA-QPCR

With the Propidium Monoazide qPCR, access a targeted analysis of viable cells only. A powerful solution to refine your quality controls.

Chemical treatment with PMA → **Optimisation** depending on the sample type → **Internal controls** to verify treatment efficacy → **Comparative results** with vs without PMA

APPLICATIONS

- Evaluation of microbial viability in food or pharmaceutical products
- Monitoring the effectiveness of antimicrobial treatments

GENOTYPING

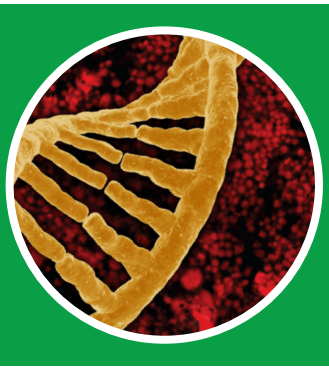
The use of genetic markers such as microsatellites (short genomic repeats) and point mutations (substitutions, insertions, deletions) makes possible to differentiate and/or gather individuals belonging to the same population.

MICROSATELLITE SERVICES

Microsatellites are characterised by a variable number of short sequence repeats. Their analysis is based on a size measurement (in bp) of fragments obtained by PCR.

APPLICATIONS

- Measurement, monitoring and/or control of the genetic diversity of a population (natural/domesticated)
- Determination of the degree of relatedness between individuals
- Phylogeny
- Genetic mapping
- Selection of individuals for breeding



DEVELOPMENT OF *DE NOVO* MARKERS

GENOSAT

The microsatellite genotyping solution for microsatellite markers

Geno Sat® is a standardised and flexible solution for:

- Microsatellite libraries production using next-generation sequencing,
- Development of relevant polymorphic markers,
- Population genotyping.

GENO SAT®
Microsatellite discovery using next-generation sequencing
+
Bioinformatics analysis
+
Primer pairs design on microsatellites flanking regions

GENO SAT® PACK
Geno Sat®
+
Biological validation of primer pairs, followed by polymorphism study of validated primer pairs

GENO SAT® PACK+
Geno Sat® Pack
+
Optimisation of multiplexed PCR and/or genotyping of large populations using polymorphic markers of interest

USE OF EXISTING DATA OR MARKERS

We can also work with previously published microsatellite markers, even for closely related species (cross-amplification).

FRAGMENT ANALYSIS - STR/CLA/MSI

- STR (Short Tandem Repeat) print: Cell line authentification (CLA).
- Microsatellite instability (MSI).

We perform PCR, migration and analysis of all types of microsatellite-based polymorphisms (VNTR, STR, SSR).

Migration of your labelled PCR products on capillary sequencer, with raw data sent within 1 to 2 working days (up to 16 plates of 96 wells).

SNP SERVICES

SNPs (Single Nucleotide Polymorphisms) represent the main source of genetic variation in a natural population. GenoScreen offers analyses that can be carried out over the entire genome, in order to identify unknown genotype-phenotype associations or already known genetic variations. Depending on the number of SNPs studied and the number of samples, GenoScreen develops complementary approaches adapted to each purpose.

DETECTION/VERIFICATION OF MUTATIONS (SANGER)

Detecting or confirming the presence of mutations on one or more loci, on a population or on an individual.

APPLICATIONS

- Detection of a low number of mutations in a population
- Verification/validation of a mutation detected by NGS sequencing

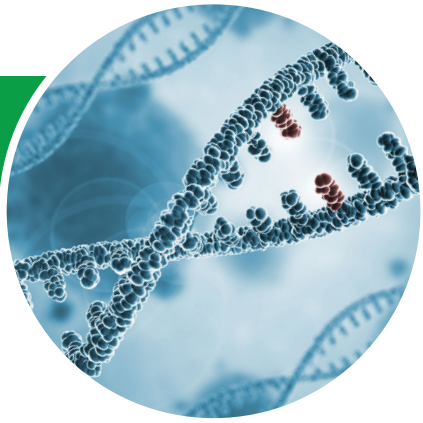
KASPAR / TAQMAN GENOTYPING

Genotyping without the need to sequence and obtaining a bi-allelic resolution to characterise heterozygous sites. Access to a wide range of referenced trials to target, in particular, predisposing mutations for certain diseases, in the frame of clinical studies.

We can also create a custom project with probe design from provided sequences and targets.

APPLICATIONS

- Detection of heterozygous mutations (SNPs and indels)



GENOTYPING BY SEQUENCING (GBS)

Several approaches can be employed : by amplicons, by capture (hybridization of probes) or by digestion using restriction enzymes.

APPLICATIONS

- Study of genotype/phenotype relationships by linkage or association analysis (GWAS) on a large population
- Tracking of selection markers for agriculture, agronomy
- Phylogenetic studies

RADSEQ / DDRADSEQ

For de novo detection of SNP, for example for a species without a reference genome, GenoScreen proposes RAD-Seq (Restriction-site Associated DNA sequencing) approaches. This technology reduces the complexity of analyses and makes it possible to examine a fraction (0.1 to 10%) of a selected genome to discover new genetic markers and/or genotype them. This represents a more cost-effective alternative to WGS for large sample panels or genomes of significant size (>10Mb).

TYPING / MICROBIAL TRACING

GenoScreen offers to characterise your microorganisms more precisely (subspecies or strain characterisation) using standardised and validated molecular biology methods such as MLST (MultiLocus Sequencing Typing) or MLVA (Multiple Loci VNTR Analysis) for the referenced species.

APPLICATIONS

- Specify a bacterial identification made by classical barcoding on 16S
- Ensure the bacterial subspecies/strain used in a process
- Epidemiological monitoring of pathogenic strains

GENOTYP Mycobacterium

Ensuring rapid and accurate tracking of *Mycobacterium tuberculosis* strains

GenoScreen is the world leader in genotyping and tracing strains of *Mycobacterium tuberculosis* complex, agent responsible for tuberculosis.

Our solutions, in the form of kits or services, can be adapted to any problems:

- Research: population structure of strains, evolution, comparison of virulence properties,
- Public health: tuberculosis control and epidemiological surveillance,
- Clinical trials: distinction between relapse and exogenous infection in case of treatment failure,
- Clinical management: detection of cross-contamination, discrimination of close strains (clonal complexity).

Discover also GENOTYP Brucella for epidemiological monitoring of brucellosis.

CUSTOMIZED SERVICES

Do you have a specific need? Did you not find a suitable solution in our catalog? Do the different DNA sequencing technologies seem rather unclear to you and you don't know what to choose?

Tell us about your project or your biological question as part of our customised services, then let GenoScreen take care of the next steps. Depending on your needs, we provide you with a multidisciplinary team that will guide your project to success:

- **Definition and characterisation of your need:** Our technical and scientific specialists show you how to transform your questions into a project and to study its feasibility.
- **Identification and selection of the technology:** Each sequencing platform has its own specificities. To best address your problem while limiting costs, our teams determine with you the technologies and parameters (sequencing depth...) to use.
- **Definition of the protocol:** How do we collect and process samples? How many samples and quality controls are needed to ensure the reliability of the analysis? Our engineers will assist you in defining the optimal protocol.
- **Performance of sequencing:** Our technical teams carry out the sequencing and its analysis, as defined in the project you have accepted.
- **Explanation of conclusions:** Our teams help you to understand the analytical data obtained.
- **Valorisation of results:** Co-development, research collaboration and white label studies.

With our customised services, you benefit from the same advantages as our other solutions:

- **An experienced company:** GenoScreen carries out many customised services every year;
- **A trusted company:** Respect for confidentiality, cost reduction… GenoScreen focuses on meeting your needs;
- **An adaptable company:** Splitting othe project over time, retention of sequencing or bioinformatics data. GenoScreen meets your expectations.

Through our customised services, we bring all our expertise and technical means at your disposal as we work together to find the solution that best meets your needs.

REGULATORY SERVICES

Discover our regulatory expertise and gain access to analyses that meet the requirements set by regulatory bodies

GenoScreen offers turnkey solutions for all requests related to genomic strain characterisation and efficacy, particularly through impact studies for products that act on the microbiome.

REGULATORY SERVICES

Leveraging our expertise in international standards and cutting-edge genomic tools, we streamline your path to market access in line with current regulations.

APPLICATIONS

- EFSA (European Food Safety Authority) dossier
- ANSES (French National Agency for Food, Environment and Occupational Health & Safety) evaluation
- FDA (Food and Drug Administration) validation

HUMAN HEALTH & NUTRITION

ANIMAL HEALTH & NUTRITION

NOVEL FOOD

BIOINPUTS & BIOCONTROL

"IDENTIFICATION AND CHARACTERISATION OF THE STRAIN"

Improve your chances of success, save time and reduce your regulatory workload! GenoScreen offers turnkey solutions for all requests related to **genomic characterisation and strain safety**.

Characterisation of the production strain → **Search for genes of interest / genes of concern** → **DNA search of the strain in the matrix** → **GMO strain** Stability check / **Kinetic study** in the ground → **Preparing the dossier**

HOW TO MAXIMISE THE IMPACT OF YOUR REGULATORY DOSSIER?

Some results obtained may complicate or delay obtaining regulatory validation. To anticipate possible requests for additional analyses, we suggest you carry them out before the submission of your dossier, either directly in our laboratories or via our network of specialised partners.

We provide you with methods that comply with regulatory requirements, ready-to-use reports and an expert advisor to assist you.

TRAINING

As a training organisation, GenoScreen also offers training sessions on bioinformatics tools and sequencing technologies.

These sessions are offered in-company or inter-company.

TRAINING

GENOSCREEN'S TRAINING COURSES ARE ABOVE ALL:

- Exclusive educational content,
- Programs tailored to your objectives,
- An active and participative teaching method led by specialists, for a quick and efficient implementation,
- Individual or group training (12 people maximum).

TRAINING IN BIOINFORMATICS

Discover our new training offer with Galaxy

Do you want to become more autonomous in your NGS data analysis but you are a novice and don't know where to start?

GenoScreen's complete range of bioinformatics training courses will help you learn the theoretical and practical aspects of many analyses.

- User interface that makes it easy to learn the tools.
- No need to use the command line.
- No computing infrastructure required.

Quality control of NGS data

Assess the quality of NGS datasets and learn how to extract the best from them.

Genome assembly

Assemble genomes, regardless of size or sequencing technology. Ensure quality of assemblies by controlling multiple parameters.

Annotation and BLAST

Practical experience in structural and functional annotation of prokaryotic and eukaryotic genomes. Discover the potential of BLAST to make the most of nucleic acid or protein queries.

Search for variants

Detect nucleotide variants, small insertions and deletions from NGS data to highlight differences between multiple nucleotide sequences.

TRAINING IN TARGETED METAGENOMICS

Become autonomous in the processing of targeted metagenomic data. Discover and use the tools for analysing the taxonomic diversity of microbiota of interest. Perform statistical analyses to estimate the richness of biodiversity in your samples.

We also offer in-company training courses

whose content and duration can be adapted to your objectives.

Ask for our detailed training catalogue.

Registered training organisation (n°31 59 06657 59 DRTEFP Lille)

TRACING AND DIAGNOSTIC KITS

Innovative and optimised solutions to detect, identify, characterise and trace microorganisms.

We offer researchers and health professionals a range of tools and solutions for diagnosis, epidemiological monitoring and detection of epidemic episodes.

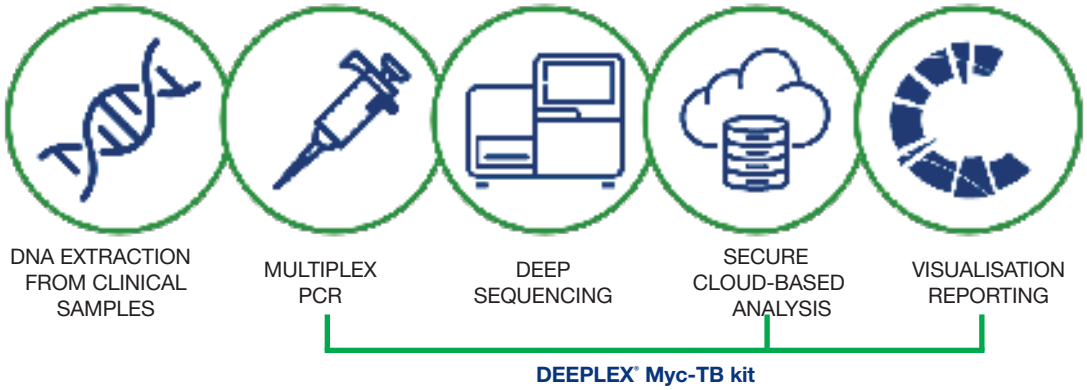
DEEPLEX® Myc-TB (recommended by the WHO)

Deeplex® Myc-TB is an all-in-one test for species identification, genotyping and antibiotic resistance prediction of *Mycobacterium tuberculosis* complex strains.

Based on next-generation sequencing (NGS), Deeplex® Myc-TB consists of a targeted molecular amplification kit for direct use on clinical samples. It also provides typing information for the incriminating strains and allows the identification of other mycobacteria. Deeplex® Myc-TB incorporates an easy-to-use web-based application, hosted on a secure cloud solution for rapid analysis and interpretation of results.

Our solution is used in over 50 countries worldwide and by more than 15 national and supranational reference centers.

DEEPLEX® MYC-TB WORKFLOW:



- No culture step required, applicable on clinical samples
- Simultaneous prediction of antibiotic resistance to 15* anti-tuberculosis drugs
- Detection of MTBC heteroresistance up to 3%**
- Spoligotyping and genotyping of MTBC
- Identification of over 140 mycobacterial species (NTM)
- Speed of analysis (less than 48h)
- Access to the Deeplex® Myc-TB web application included

The World Health Organization (WHO) has recently updated its "Consolidated Guidelines on Tuberculosis", recommending targeted next-generation sequencing (tNGS) as a preferred method for diagnosing drug-resistant tuberculosis (DR-TB).

	Number of responses	RUO	CE-IVD
Deeplex® Myc-TB	48	GNSRUOTB01-48	GNSDMTB01-48
	16	GNSRUOTB01-16	
	96	GNSRUOTB01-96	

Deeplex® Myc-TB predicts resistance to first-line antibiotics (rifampicin, isoniazid, pyrazinamide, ethambutol), as well as second-line drugs, including aminoglycosides (kanamycin, amikacin, capreomycin, streptomycin), fluoroquinolones (levofloxacin amikacin, capreomycin, streptomycin), fluoroquinolones (levofloxacin, moxifloxacin and ciprofloxacin), ethionamide, clofazimine, as well as bedaquiline and linezolid.

** Results of an in silico analysis against the culture-based WGS dataset of "Dr Timothy Walker, Whole-genome sequencing for prediction of *Mycobacterium tuberculosis* drug susceptibility and resistance: a retrospective cohort study, Lancet Infect. Dis. 15, 1193-1202 (2015)".

Learn more on www.deeplex.com

DEEPLEX® HelP

Deeplex® HelP is the cutting-edge solution for *Helicobacter pylori* infections diagnosis.

DEEPLEX HELP — RESEARCH USE ONLY

ABOUT *H.PYLORI* INFECTIONS

Helicobacter pylori infection is a global health issue, causing stomach diseases such as gastritis, peptic ulcers and even cancer in rare cases. This bacterium affects about **50% of the world's population**, with varying prevalence across geographical regions. The pathogenicity and treatability of *H. pylori* are dependent on a complex interplay between various factors, among which bacterial characteristics such as **strain identity, strain virulence and antibiotic resistance**.

Based on trageted next-generation sequencing (tNGS), Deeplex® HelP is a culture-free assay, for strain type identification, virulence and antibiotic resistance prediction of Helicobacter pylori. The test, developed by GenoScreen, is the only prognostic and diagnostic test designed to prevent diseases associated with *H. pylori* infection based on tNGS.

DEEPLEX® HELP WORKFLOW:

DNA EXTRACTION FROM CLINICAL SAMPLES | DEEPLEX MULTIPLEX PCR | SEQUENCING | AUTOMATED ANALYSIS PIPELINE

DEEPLEX® HelP kit

With **Deeplex® HelP,** clinicians can have access to *H. pylori* strain identity, virulence and antibiotic resistance without the need for culture and in a single assay, facilitating guided therapy thus **reducing the risk of treatment failure and preventing complications such as gastric cancer**.

AVAILABLE AS A KIT OR A SERVICE

- No culture step required, applicable on clinical samples (biopsies)
- 6 antibiotics screened for resistance prediction
- 7 targets for strain type identification
- 2 targets for virulence prediction
- Speed of analysis (48-72h)

	Number of responses	RUO
Deeplex ® HelP	12	GNSRUOHP01-12

Learn more on www.deeplex.com

DEEPLEX® Myc-Lep

Deeplex® Myc-Lep is the all-in-one solution for leprosy drug resistance detection and epidemiological control.

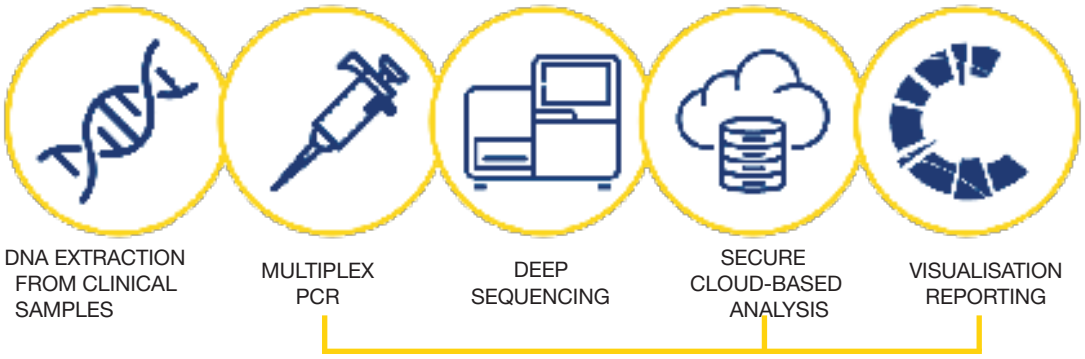
DEEPLEX MYC-LEP RESEARCH USE ONLY

ABOUT LEPROSY (OR HANSEN'S DISEASE)

Leprosy, is a chronic infectious disease caused by ***Mycobacterium leprae*** and more rarely, by *M. lepromatosis*. It predominantly affects the skin and peripheral nerves. Left untreated, the disease may cause **progressive** and **permanent disabilities**. Unlike commonly thought, **leprosy is still present**, with a significant impact in various regions of the world, including South-East Asia, Africa and South America.

Deeplex® Myc-Lep, is an innovative culture-free solution for detection of leprosy drug resistance. **Directly usable from skin biopsies** and **slit-skin smears**, it uses a tailored multi-target sequencing technology to simultaneously **predict (hetero-) resistance** of *Mycobacterium leprae* to four used anti-leprosy drugs (rifampicin, dapsone, fluoroquinolone and bedaquilin) and to **identify strain type** for epidemiological surveillance.

DEEPLEX® MYC-LEP WORKFLOW:



Deeplex® Myc-Lep represents a **comprehensive** solution to both **guide rapid clinical-making decision** for leprosy treatment and for **molecular tracing** of (drug resistant) leprosy strains.

AVAILABLE AS A KIT OR A SERVICE

- No culture step required, applicable on clinical samples (skin biopsies / slit-skin smears)
- Prediction of (hetero)resistance or suceptibility to 4 antibiotics
- Prediction of hypermutator strains
- High ressolution *M. leprae* strain typing
- Identification of over 100 mycobacterial species (incl. *M. lepromatosis*)
- Speed of analysis (48-72h)

	Number of responses	RUO
Deeplex ® Myc-Lep	12	GNSRUOLEP01-20

Learn more on www.deeplex.com

MIRU-VNTR

MIRU-VNTR (Mycobacterial Identification Repetitive Unit-VNTR) analysis is an MLVA (Multiple Loci VNTR Analysis) scheme specific to *Mycobacterium tuberculosis*. It allows the strain to be genotyped by counting the number of VNTR copies present in 24 identified loci.

GenoScreen's MIRU-VNTR solution has become the global standard for the MIRU-VNTR method. This complete solution is optimised to produce the best possible results with a standardised approach, while ensuring very high reproducibility.

MIRU-VNTR HYPERVARIABLE, A SCHEME ADAPTED TO STRAINS OF THE BEIJING LINEAGE

Mycobacterium tuberculosis strains identified as belonging to the so-called "Beijing lineage" cannot be discriminated using the 24 standard loci.

The sub-lineages making up this family are identified using MIRU analysis of a set of 4 additional hypervariable VNTR loci.

THE MIRU RANGE, A COMPLETE OFFER

We offer kits for the implementation and use of the MIRU-VNTR method on capillary sequencers.

MIRU-VNTR	Calibration kit	1 capillary sequencer calibration	785-60VQuad
	Validation kit	1 validation of the capillary sequencer settings	795-60VQuad
	24 marker typing kits	100 reactions (PCR + migration typing kit on capillary sequencer)	790-60VQuad
MIRU-VNTR hypervariable	Calibration kit	1 capillary sequencer calibration	885-60VHV
	Validation kit	1 validation of the capillary sequencer settings	895-60VHV
	Second line typing kit (4 markers) suitable for strains of the Beijing lineage	50 reactions (PCR + migration on capillary sequencer)	890-60VHV

QUALITY POLICY AND CSR

GenoScreen has been working for several years to respond to the challenges of sustainable development and to protect the environment.

Our CSR (Corporate Social Responsibility) commitments are translated into concrete actions that are in line with our values.

As such:
- We participate in the integration of young people,
- We ensure the comfort and protection of our employees,
- We seek to reduce our environmental print,
- And we fight against all forms of discrimination.

SOCIAL ENGAGEMENTS

FAIR RECRUITMENT

Our recruitment policy is based on the principle of fairness between candidates. It is based on various objective criteria, such as qualifications, skills and years of experience. All those involved in our recruitment process are aware of and apply our non-discrimination policy.

TRAINING

We pay particular attention to the development of our employees' skills to enable them to achieve their full potential through their work, while meeting the needs of our clients. Our training policy offers personalised and certifying training courses that aim to meet the wishes and needs of each individual.

PROMOTING THE INTEGRATION OF YOUNG PEOPLE

We place great importance on the training and employment of young people. In 2022, 18% of the company's employees was under the age of 25 and in many cases GenoScreen is their first job.

FIGHTING AGAINST PRECARIOUS EMPLOYMENT

We seek to work with our employees in a sustainable way to reduce (on our scale) job insecurity. We favour the use of permanent and full-time contracts, and reserve fixed-term contracts for specific situations (in 2022, more than 95% of our employees had permanent contracts).

THE PROTECTION OF OUR EMPLOYEES

HEALTH AND SAFETY AT WORK

In 2022, 5.4% of employees were certified as first aiders. This percentage demonstrates the importance we attach to the safety of our employees.

ENVIRONMENT

DIGITISATION OF PROCEDURES AND DOCUMENTS

In order to reduce internal printing, we are digitalising our procedures. In 2019-2020, we have dematerialised almost 100% of our purchasing procedures. In 2020-2021, our HR procedures (leave requests, time management, payslips, etc.) were largely dematerialised. In 2021, we succeeded in digitising a large part of our accounting procedures and we will continue this work in 2022.

RESPONSIBLE CONSUMPTION

We favour eco-responsible or reasoned suppliers and products. For example, our paper mills are FSC certified.

WASTE RECYCLING AND SORTING

Our employees take particular care to sort waste within the company. Almost all of our paper waste is collected and recycled by the ELISE network, and our partnership with Multisupplies Ecofrance allows us to recycle our pens, printer cartridges, telephones (...) on behalf of associations.

REDUCING THE IMPACT OF OUR PACKAGING

From the outset, we have sought to limit the amount of packaging of our products. Our customers receive a reusable and recyclable Genobox to send us their samples, thus limiting the use of non-returnable packaging and ensuring that the samples will not be damaged during transport. The packaging of our kits, which is not reusable, is made of natural products (cardboard from certified eco-responsible forests).

GenoScreen

1 rue de Professeur Calmette
59 000 Lille - FRANCE
Phone: +33(0) 362 263 777

https://www.genoscreen.fr/en/

SANGER TECHNICAL SUPPORT
seq1@genoscreen.fr / seq2@genoscreen.fr
Phone: +33 (0)3 62 26 37 86

SALES DEPARTMENT
commercial.dept@genoscreen.fr
Phone: +33 (0)3 62 26 37 76

MINISTÈRE DE L'ENSEIGNEMENT SUPÉRIEUR ET DE LA RECHERCHE
Liberté Égalité Fraternité
Crédit Impôt Recherche CIR

ISO 9001
ISO 13485
BUREAU VERITAS Certification

CE IVD