Sequencing services

For Research Use Only.
Not for use in diagnostic procedures.

BIOSEARCH™ TECHNOLOGIES
GENOMIC ANALYSIS BY LGC

Trust your project to our experience

Flexibility and expertise are the key features of our sequencing service

Running projects that take advantage of the latest sequencing technology can be complicated, costly, and time-consuming. Outsourcing can be a simpler solution for many laboratories, ensuring the latest technology is used and projects benefit from years of sequencing experience. So why not try our convenient laboratory service solutions? Do you know the best approach for your next generation sequencing (NGS) project? Perhaps you just need a quick and professional way to generate NGS data? For those situations and many more, we have a range of convenient laboratory services.

At LGC Biosearch Technologies we are constantly finding new ways to address the challenges faced by researchers so you don't have to. Our experts will help you achieve better sequencing results.

We have more than 25 years of experience in delivering large and small-scale sequencing projects, providing both traditional Sanger and NGS services to a global customer base. With our optional DNA purification, PCR and bioinformatics services, we are able to carry out projects from start to finish. As part of our services, we can offer full technical support, assist with project design, and provide advice on difficult targets and genomes

We will generate a service proposal that drives maximum benefit and cost-effectiveness to match your needs.

NGS and applications

Consultation and the delivery of optimised solutions that meet the specific needs of a particular project are the foundation of our NGS service offerings. We have a number of different NGS applications available, including:

1. Genotyping by sequencing (GBS)

***De novo* SNP and indel identification**

The method of choice for *de novo* SNP detection in genomics selection, marker assisted breeding and population genetics. Biosearch Technologies is the only company in Europe with a full commercial license from KeyGene[1], including all species. It allows cost-effective sequence-based SNP discovery after reduction of genome complexity by use of restriction enzyme(s). We have developed a modified GBS method to enhance complexity reduction of the genome. This enables the enrichment of gene islands, resulting in a higher rate of discovery of informative SNP markers.

[1] Keygene N.V. owns patents and patent applications protecting its sequence based genotyping technologies, as described by Truong *et al.*, PLoS ONE 7: e37565, 2012. Biosearch Technologies has a licence from KeyGene N.V. to offer the GBS service for any organisms provided that use and application in human and animal shall be limited to research use only.

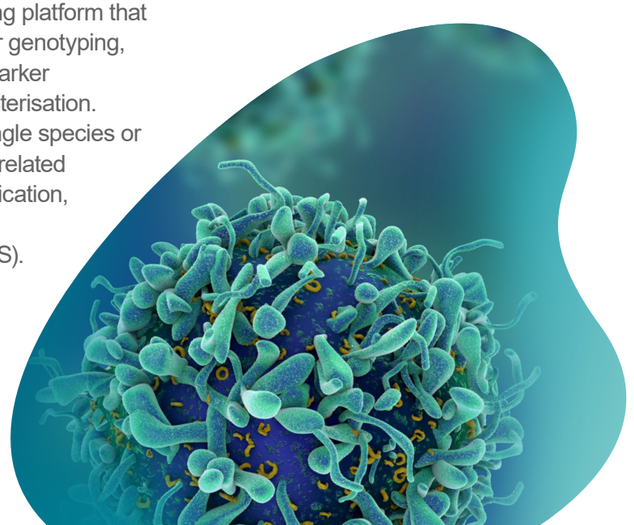
2. Targeted GBS

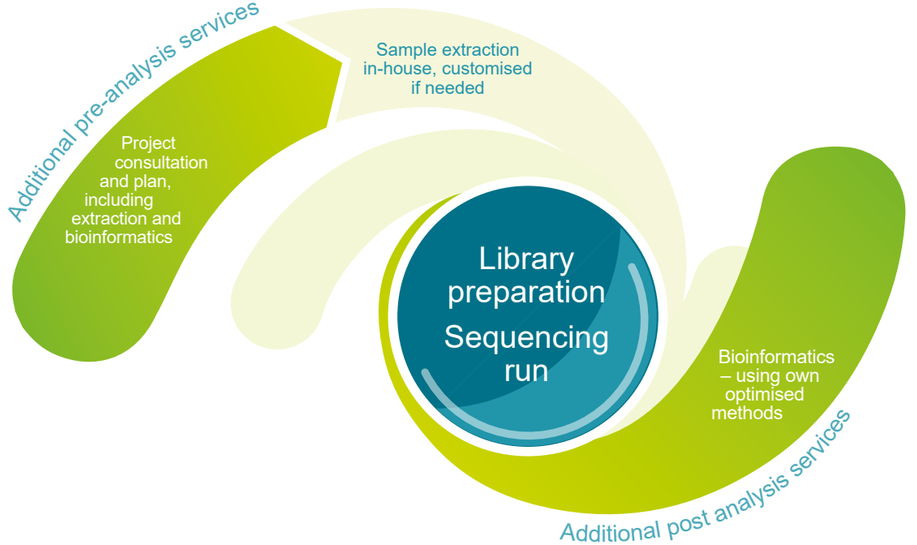
Flex-Seq™ service

If your project requires screening 1000's of samples against 1000's of variants cost-effectively, Flex-Seq is the service for you. It is optimised for targeting 100s to 10,000+ variants. It also enables identification of *de novo* variants in the target SNP region. Markers sets are flexible and markers are easily converted for high throughput assays.

Capture-Seq service

Does your project require you to be able to characterise 1,000 to 450,000+ genomic targets, including complex polyploids? Capture-Seq is a targeted next generation sequencing platform that is optimised for this. It is suitable for genotyping, haplotyping, genomic prediction, marker discovery, insertion and site characterisation. Samples can be comprised of a single species or a mix of closely related or distantly related taxa. It is flexible in scope and application, yielding less missing data than restriction enzyme genotyping (GBS).





3. Human targeted re-sequencing

Discover or interrogate SNPs, indels or structural variation

Common applications for targeted re-sequencing include (human) exome sequencing and sequencing of gene panels, for example:

- Oncology
- Pathology
- Forensics.

The large amounts of data generated can be challenging to analyse. Our bioinformatics experts can help. Please enquire.

4. mRNA expression profiling

Identify key changes in expression patterns

We combine our expertise in library preparation and sequencing with our in-house expertise in preparing RNA from critical samples. We have been doing purifications on-site for more than 20 years, using our own methods. Services include:

- Establishment of tailored RNA sampling pufication methods
- In-house RNA purification including sample storage
- Depletion of ribosomal RNA if appropriate
- Expression profiling and/or analysis of splice variants.

We also offer 3-prime sequencing when only gene counts are required.

For more information, please check our website.

5. Targeted re-sequencing

Interrogate known genetic alterations or investigate microbial communities in metagenomic samples

With the highly targeted sequencing of PCR amplicons, you're able to identify and characterise variants efficiently.
Flexible service modules guarantee a cost-effective and customer orientated strategy depending on the issue in question and the data needed. Starting materials can be challenging when analysing microbial communities or metagenomics samples, so our service is available for a broad range of starting materials, e.g. air filters, soil, water samples. We prepare high-quality shotgun libraries for low quantity samples at high multiplexing levels, optionally with whole genome amplification to process difficult and highly degraded samples. Our sequencing team offers an extensive support through the whole process including bioinformatics. Amplicon sequencing enables researchers to analyse specific genomic regions with targeted analysis of genetic variation. Correct primer selection is critical. We have great expertise in selecting primers with our own primer set database. For any new sample types or species/species populations, we test primer sets in-house following a literature review to be sure you get the best possible result.

Amplicon sequencing can be used for several applications including:

- 16S
- 18S
- ITS
- Amplicon pools in frame of metagenomics projects
- Genotyping in Thousands by sequencing (GT-seq).

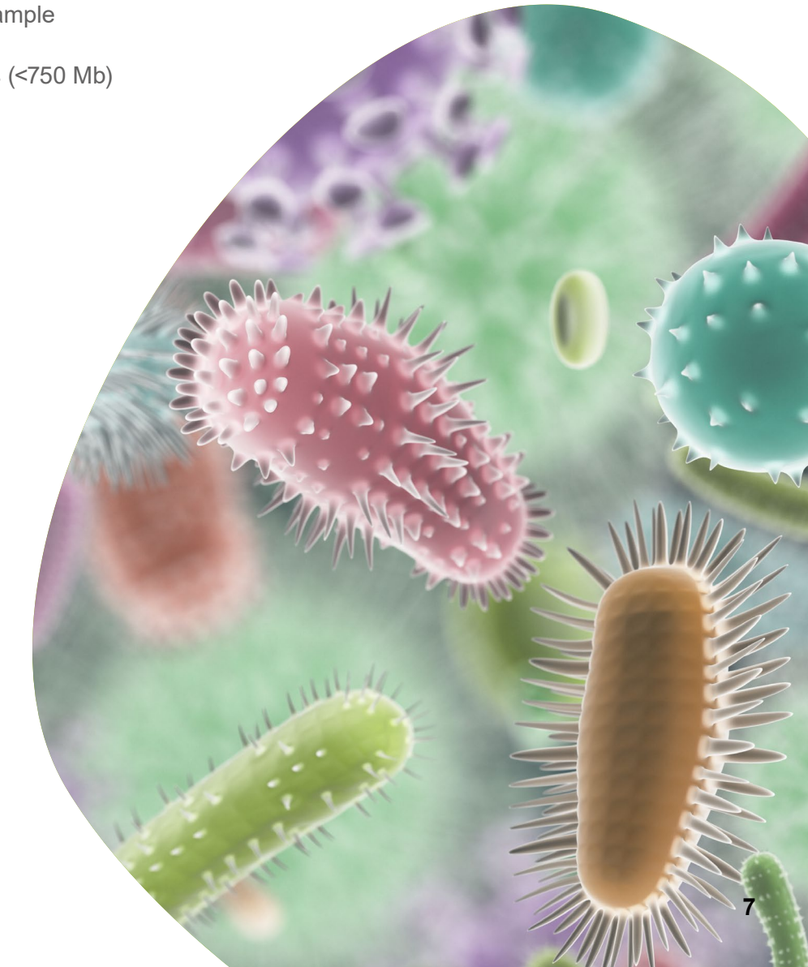
Using an in-house tagging strategy (inline barcodes and indexes) it is possible to get up to 1000 samples per instrument run depending on the sample origin, saving both time and money. Amplicon read lengths of up 500 bp can be achieved. Even with very low microorganism loads we can still successfully carry out microbiome analysis. This enables the enrichment of gene islands, resulting in a higher rate of discovery of informative SNP markers.

For more information, please check our website.

6. *De novo* whole genome sequencing of new organisms

Whole genome shotgun sequencing is a standard technique, frequently used for de novo genome sequencing and for example microbiome analysis. It is available for the following sample types:

- Genomes of up to 50 Mb, for example bacteria, yeast and fungi
- Small plant and animal genomes (<750 Mb)



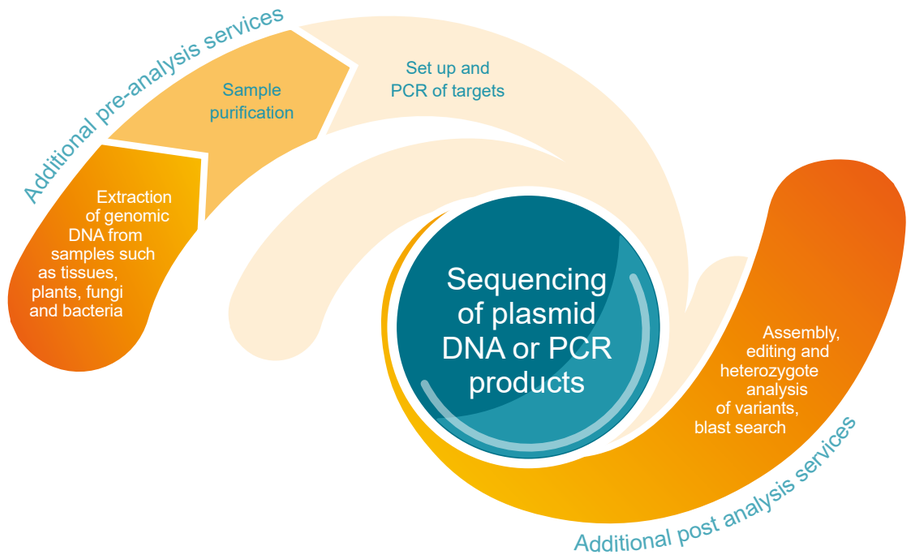
[2] Guichoux *et al.* Current trends in microsatellite genotyping. *Molecular Ecology Resources* (2011) 11, 591-61. Based on 24 SSRs analysed in 500 samples vs. Biosearch Technologies all-inclusive pricing (incl. DNA extraction and design).

Sanger sequencing services

Sanger sequencing is still the method of choice for a wide range of research applications. It is ideal for sequencing single gene targets of 1-96 amplicons (or multiples of 96) amplicons or plasmids.

With our extensive experience, we can provide you with high quality sequence data, as proven by consistently coming in the top three of the Reference Institute for Bioanalytics (RfB) bi-annual proficiency test since the start of our participation in 2007[3]. We have dedicated customer support with project managers acting as the interface between our customers and our laboratory, so we are always available to speak about your project.

To provide flexibility, our services have three different levels so you can pick the service that suits you best. We can provide high-throughput sequencing of up to 96 samples (96-well plate format) at a time with read lengths up to 1,100 bases each, or lower throughput with a single tube format. We are also able to store both your samples and primers for up to three months if needed.



[3] Information accurate on 22 Dec 2016. The RfB is one of two German proficiency testing organisations officially tasked by the German Medical Association with providing proficiency tests for external quality control. The coordinating RfB provides each of the voluntary participants with two PCR-products and sequencing primers. Technical objectives are editing the raw data, and providing the longest unambiguous and clear DNA sequence read. DNA sequencing was performed in Biosearch Technologies' sequencing laboratories in Berlin, Germany.

Applications

- De novo sequencing of certain gene regions in a particular organism
- Targeted re-sequencing and identification of indels and heterozygous positions in a particular gene region
- Species identification of a single organism using particular gene regions
- Validation of variants detected on other sequencing platforms

Standard service packages[4]

Ready2 Run	Flexi Run	Premium Run
Sequencing of purified PCR products or plasmid DNA	Sequencing of purified PCR products or plasmid DNA	Quality check and DNA quantification via agarose gel
Pre-pipetted primer by customers	Submitted primer in separate tube	Complex/difficult templates/ large constructs (e.g Cosmid, BACs)
Fixed volume and adjusted DNA concentration[5]	>100 universal primers available or shipment of customer primers	Technical support by our experienced scientific team
Volume: 10 µL DNA + 4 µL primer[5].	Up to 15 runs per sample	>100 universal primers available
	Volume: min.15 µL (1 run) + 4 µL for each additional run of template DNA	• Storage of templates and primers for three months
	Adjusted DNA concentration[5]	Repetition of failed runs
	Storage of templates and primers for three months	Additional services: Primer design and synthesis PCR clean-up/plasmid preparation
	Repetition of failed runs	
	Additional service: Primer synthesis	

[4] Service packages including purification through to assembly are also available.
[5] Sample specifications can be found on our website at www.lgcgroup.com/services/dna-sequencing/sanger/

Bioinformatics and analysis services

We understand that getting the maximum information from the sequencing data is critical to project success. Our bioinformatics experts have gathered extensive experience (a minimum of nine years each) with sequence data analysis for standard and custom sequencing projects. We provide complete bioinformatics support for any species, including but not limited to sequence pre-processing, clustering, alignment and variant analysis.

Our standard analysis packages include:

- Genome re-sequencing: detection of SNPs, indels, structural variants and copy number variations
- De novo assembly for genomes, transcriptomes, metagenomes and metatranscriptomes
- Human exome analysis
- Expression profiling on RNA-Seq data
- Microbial diversity analysis on 16S, 18S or ITS amplicons or whole genome shotgun libraries.

For more information, please check our website.

We also offer customised solutions to accommodate your specific needs.

Services

Sequencing services

Sample management and project support services
Flex-Seq targeted GBS
Capture-Seq targeted GBS
Sanger sequencing
Next generation sequencing services (Illumina NextSeq and MiSeq)
Genotyping by sequencing (GBS) services

For Research Use Only.
Not for use in diagnostic procedures.

Related services

All-inclusive genotyping services
DNA purification services
KASP SNP and indel genotyping
Whole genome amplification (WGA)
Oligo/probe/primer manufacturing

For further information about our complete products and services portfolio, please visit **biosearchtech.com**

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