We have developed NGS expertise in areas such as:

- **ChIP-Seq Analysis**
- ***de novo* Sequencing and Assembly**
- **Genome Re-Sequencing (targeted or whole genome)**
- **RNA Sequencing**
- **Metagenomics / Bacterial or Fungal Diversity**

Next-Generation Sequencing Workflow

Generic workflow for NGS

Library Construction

DNA fragmentation and tagging of respective adaptors based on platform requirements

Sequencing

Libraries undergo template amplification before the sequencing proceeds, producing reads by the millions

Basic Data Analysis

Each platform comes installed with their own proprietary software to convert the raw data to give a read-out of the DNA sequences

1st BASE NGS Concierge Workflow

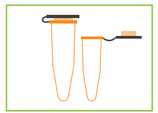
How Does It Work?

Initial Meeting & Consultation

We set up a meeting to fully understand your NGS project requirements.

Project Proposal

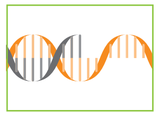
We work with your requirements to develop our proposal. This includes the project scope from library construction, NGS sequencing and basic data analysis, and even any extras that you may require.



Sample Preparation

We can provide further upstream preparation services before samples undergo Library Construction.

Libraries are prepared based on the requirements demanded by the selected NGS platform.



NGS Sequencing

Libraries undergo sequencing.

Bioinformatics and Delivery

Data generated will be processed by en-suite software. Analysis of data by our team of Bioinformaticians is available.

Results and reports are delivered to you.

If you are new to NGS, or thinking about using NGS, our website has information on the technology and links to the platforms that we utilise. Feel free to call or email our technical experts to find out more.

Data Analysis and Information Management

In addition to our standard analysis using CLC Genomics Workbench, a 30-day evaluation copy of this software will be provided to our clients.

If you wish to explore additional bioinformatics services, we have our in-house bioinformatics consultants with experience in ChIP-Seq and genome assembly. Customers may work with us to match and engage consultants with specific areas of expertise suited to the nature of your project and the objective of your study.

Confidentiality

All information pertaining to your project will be kept in full confidence.

Pricing and Timeline

Pricing and the timeline of a sequencing project depends on each individual project and the requirements that come with it. Contact us for a consultation.

Valued Solutions come from Dedication and Experience

Definitive success doesn't lie merely in the NGS platform or software tools. It's about getting the best advice, the best design, sample prep and sequencing done by a provider with years of experience, and of course, multiple data analysis options. We'd like to think we have what it takes to ensure the success of your project. Arrange for an appointment with us to move on to the next generation.

Information to the questions below forms the basis of your NGS project. Call us for a NGS consultation today.

- What is the nature of the samples you are interested in?
- Is there a reference genome?
- What are the objectives of this sequencing project?
- How do you plan to use the sequencing data?
- Do you prefer to utilise any specific Next Generation Sequencing Platform?
- Do you require any upstream / downstream processes?
  These include application-specific sample preparation, additional bioinformatics analyses.

1st BASE
YOUR RESEARCH, OUR BUSINESS
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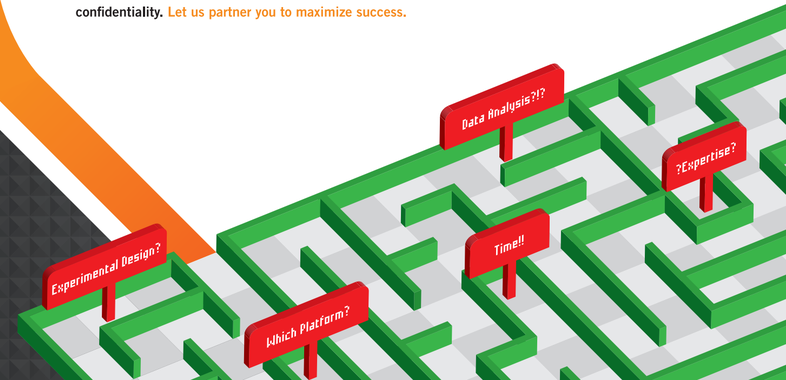
LEVEL UP
to the Next Generation with 1st BASE

Next-Generation Sequencing (NGS) is driving **growth and possibilities** in the fast developing field of genomics, and revolutionising the way scientists and clinicians think about their projects. A myriad of sequencing options are available today, **but don't get lost in the maze.** We understand that the diversity of scientific research means that personalised support and a flexible, robust suite of sequencing services plays a big part in the successful integration of NGS into your projects.

1st BASE proudly introduces our NGS Concierge Services to partner scientists in their NGS pursuits. We offer the latest in NGS technologies, together with cross-platform expertise in choosing the best technology to meet your sequencing needs. Our technical experts will meet with you to discuss your research aims and design, and recommend the most suitable NGS platform for your project.

Find out how our team can help you get the quality results you need, with speed and customer confidentiality. Let us partner you to maximize success.



1st BASE NGS Concierge Services | The complete solution to your sequencing project

We Personalise each Project
Every request that comes in as unique as you, that is why at 1st BASE, listening to you comes first. Meet with our team of technical experts, and let us understand your project aims and scope, experimental design and strategy.

Flexibility of Platforms
In 1st BASE, we have access to all 3 platforms as well as up-to-date technologies, ensuring that the most suitable platform or a combination of platforms is selected for your project.

Clear Documentation
All processes, approaches and deliverables are clearly specified and documented in the project agreements before your sample needs to be submitted, so you'll have peace of mind, knowing exactly what you'll get and when you'll get it.

Expertise and Experience Counts...
Our team is headed by Ph.D. consultants with several years of experience in genomic technologies.

Customised Bioinformatics and Data Analysis
At 1st BASE, we understand that delivering quality data is only part of the solution. We have a team of experienced bioinformatics consultants who can help you analyse your data.

Project Support
Technical support is just a call or email away should you face any difficulties. Our team is available throughout the duration of the project to lend a helping hand.

Multiple Sequencing (NGS) Platforms at Our Fingertips

Leverage on the unique strengths of each platform to address specific requirements in your NGS applications.

Our Sanger and Next-Generation Sequencing Technologies give us capabilities that include:

- **Long Read Lengths or numerous short-reads**
- ***de novo* or re-sequencing applications**
- **Full genome sequencing by primer walking or shotgun assembly via Sanger sequencing**

1st BASE gives access to three major players in Next-Generation Sequencing Technologies

Applied Biosystems™ SOLiD™ Sequencing Technology

What is SOLiD™ sequencing about?

SOLiD™ Sequencing involves the generation of clonal bead populations via emulsion PCR. The major difference between SOLiD™ sequencing and other high-throughput sequencing platforms is its unique "sequencing by ligation" instead of "sequencing by synthesis" chemistry. Sequential ligations of fluorescently labeled probes detect every combination of two adjacent bases.

What are the steps in SOLiD™ sequencing?

1. **Library Preparation**
   A fragment or mate-paired library is prepared, depending on your choice of application.
2. **Emulsion PCR and Bead Deposition**
   Emulsion PCR is performed; beads carrying extended templates are selected and covalently attached onto a glass slide. A key advantage is the ability to accommodate high bead density per slide, resulting in a higher level of throughput.
3. **Sequencing by Ligation**
   Fluorescently-labeled dibase primers compete for ligation to the sequencing primer. In each ligation reaction, every 1st and 2nd base is interrogated, thus achieving specificity of the dibase probe. Multiple rounds of ligation, detection and cleavage are performed.
4. **Primer Reset**
   After a series of ligation cycles, the template is reset with a complementary primer at the n-1 position for a second round of ligation cycles. Multiple rounds of primer reset, followed by ligation cycles, ensure that virtually every base is interrogated at least twice in independent ligation reactions. This provides the SOLiD™ system with its unparalleled accuracy.

Specifications

Read Lengths	Up to 50bp
Reads per Run / Throughput	Fragment library: ~500M
System Accuracy	Greater than 99.94% accuracy due to 2 base encoding
Quality Score	>80% of bases at >QV30
Data Format	SOLiD native, SAM

Information taken from
https://products.appliedbiosystems.com/ab/en/US/adirect/ab?cmd=catNavigate2&catID=604416&tab=TechSpec
Accurate as of June 2010

What are some of the recommended applications of SOLiD™ Sequencing?

SOLiD™ Sequencing can be used for *de novo* sequencing, whole genome or targeted resequencing, ChIP-sequencing, methylation analysis and whole transcriptome analysis.

For more about SOLiD™ sequencing technology, please visit:
http://www.appliedbiosystems.com/absite/us/en/home/applications-technologies/solid-next-generation-sequencing.html

Illumina Sequencing Technology

What is Illumina sequencing about?

The Illumina sequencing platform relies on parallel sequencing of millions of fragments using their proprietary reversible terminator-based sequencing chemistry. This novel approach ensures high accuracy and true base-by-base sequencing, eliminating sequence-context specific errors and enabling sequencing through homopolymers and repetitive sequences.

What are the steps in Illumina sequencing?

1. Prepare gDNA Library
Duration: 3 hrs hands-on (6 hrs total)

- Fragment genomic DNA
- Repair ends
- Phosphorylate & add A-overhang
- Ligate adapters
- Purify library

2. Generate Clusters
Duration: <10 mins hands-on (4 hrs total)

- Place pre-packaged reagents into cBot
- Attach single manifold to flowcell
- Press Start

3. Sequencing by Synthesis
Duration: <1 hr hands-on

- Place reagents into the Genome Analyzer
- Place Flow cell into Genome Analyzer
- Start run
- Image processing, real-time analysis, base calling

4. Post-Run Data Analysis
Duration: ~1 day

- Alignment
- Variant analysis
- Summary reporting

1. **Preparation of gDNA Library**
   An adaptor-ligated gDNA library is prepared and purified.
2. **Generation of DNA Clusters**
   The DNA fragments are attached to a planar, optically transparent surface. Attached DNA fragments are extended and bridge amplified to create an ultra-high density sequencing flow cell with hundreds of millions of clusters, each containing ~1,000 copies of the same template.
3. **Sequencing by Synthesis and Analysis**
   These templates are sequenced using a robust four-color DNA sequencing-by-synthesis technology that employs reversible terminators with removable fluorescent dyes.

Specifications

Read Lengths	Up to 100bp
Reads per Run / Throughput	180-200M per flowcell
System Accuracy	Greater raw read accuracy of 99% and above
Quality Score	70-90% of base calls at >QV30
Data Format	Illumina Native, SRF

Information taken from
http://www.illumina.com/technology/sequencing_technology.ilmn
Accurate as of June 2010

What are some of the recommended applications of Illumina sequencing technology?

The combination of up to 100nt read lengths and large numbers of reads per run makes Illumina a highly flexible system well suited for multiple applications, including DNA sequencing, SNP genotyping, gene expression analysis, transciptome analysis among others.

For more about illumina sequencing technology, please visit: http://www.illumina.com

Roche 454 Sequencing Technology

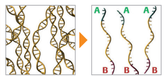
What is 454 sequencing?

One Fragment = One Bead = One Read

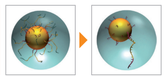
454 sequencing is based on sequencing by synthesis, involving parallel pyrosequencing of bead-bound DNA templates.

What are the steps in 454 Sequencing?

1. **Sample Prep and Library Generation**
   A wide variety of staring materials (genomic DNA, cDNA, PCR products, BACs) can be used. Ligation with standard adaptors follows, and the sample library is used for subsequent sample preparation steps.



2. **Immobilization and Emulsion PCR (emPCR) Amplification**
   The DNA library is immobilized onto DNA capture beads, and amplified in an emulsion, resulting in each microreactor containing amplified products of just one specific library fragment.



3. **Loading and Sequencing**
   The DNA-carrying capture beads are loaded onto a PicoTiterPlate device for sequencing. Only one bead is contained within each PicoTiterPlate well, and nucleotides are added in a fixed order across the wells. Sequencing –by-synthesis is detected via a chemiluminiscent signal, and is recorded.

4. **Data Analysis**
   The combination of signal intensity and positional information generated allows the software to determine the sequence of more than 1,000,000 individual reads per 10 hour instrument run simultaneously. 454 sequencing is characterised by having the longest read length of the 3 currently available NGS platforms, which makes it uniquely suited to many applications.

Specifications

Read Lengths	Modal length = 500 bases Average length = 400 bases
Reads per Run / Throughput	>1 million high-quality reads
System Accuracy	99% at 400 bases (and higher for prior bases)
Quality Score	QV20
Data Format	SFF

Information taken from
http://454.com/products-solutions/system-features.asp
Accurate as of June 2010

What are some of the recommended applications for 454 sequencing?

The long read, high accuracy and high throughput allows 454 sequencing to be used for *de novo* sequencing, resequencing of whole genomes and target regions, metagenomics and RNA analysis.

For more about 454 sequencing technology, please visit: http://454.com