AIT biotech
Advanced • Innovative • Trusted

Next-Generation Sequencing (NGS) Services

One-stop
solution for all your
NGS needs

ABOUT US

Established in 2009, AITbiotech provides a one-stop solution for all of your NGS needs. Leveraging on our dedicated and experienced NGS team based in Singapore, our goal is to provide you with the full spectrum of NGS services from library preparation to customized bioinformatics solutions.

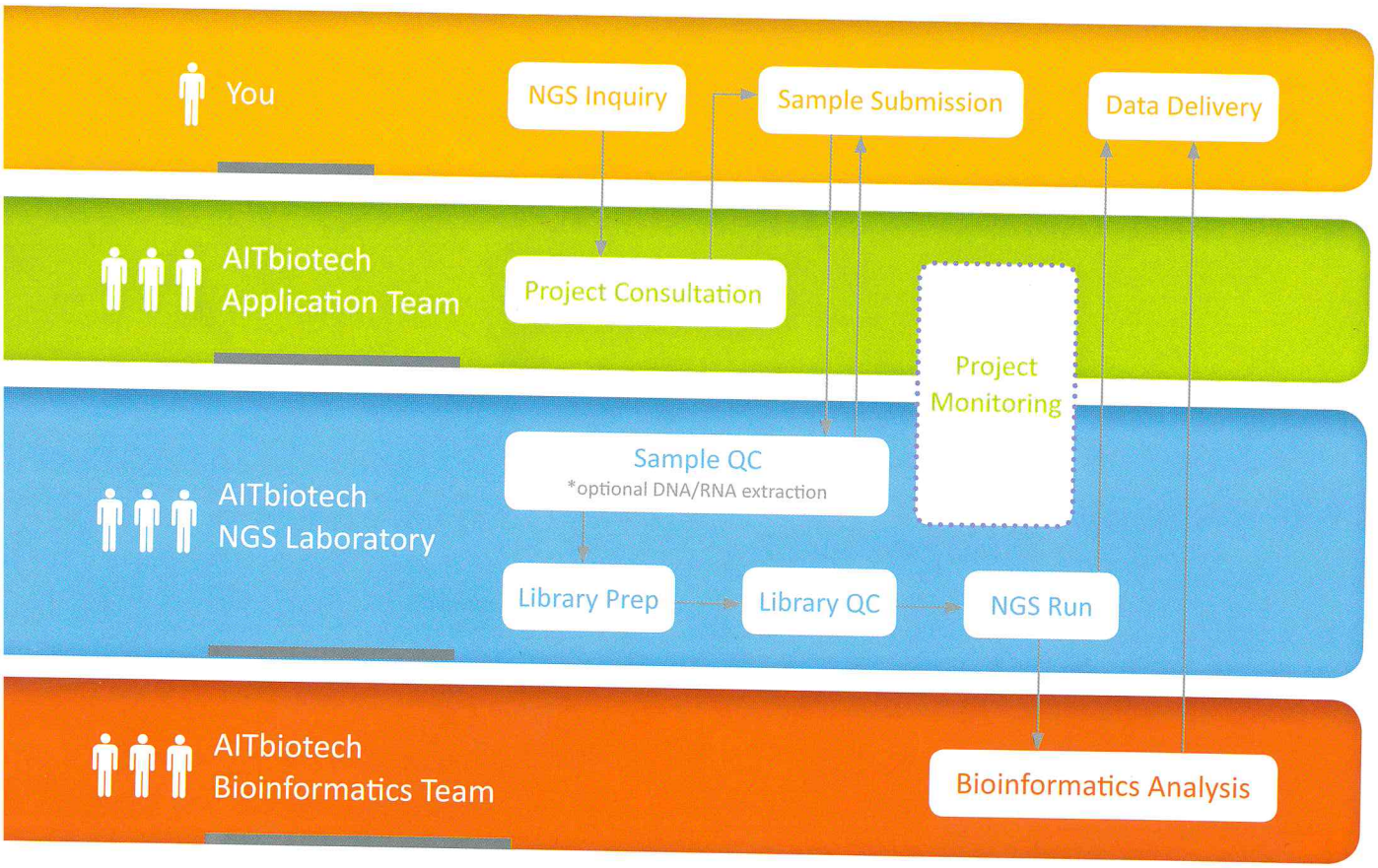
Key Features

- Comprehensive NGS solutions, from sample preparation to bioinformatics analysis
- Rigorous quality control at every step of the NGS workflow
- Fast turnaround time with Singapore based laboratory (only for Singapore customers)
- Experienced technical and scientific support to advise on NGS experiment plan and design
- Personalized NGS services based on project-specific needs

Available Platforms

- Illumina HiSeq 2000/2500/4000
- Illumina MiSeq
- Illumina NextSeq
- Life Technologies Ion Torrent PGM
- Life Technologies Ion Torrent Proton
- Pacific Biosciences RS II

Service Workflow



AITbiotech provides a comprehensive one-stop solution for your NGS needs: from sample preparation to bioinformatics analysis

AITbiotech offers the best solution for your application. Employing state-of-the-art technologies by Illumina, Ion Torrent and PacBio, AITbiotech offers expert advice and a full spectrum of services for the following applications:

SERVICES

1. Whole Genome Sequencing

Whole genome sequencing can be performed on a variety of organisms including small microbial genomes, mammalian genomes and plant genomes. With a wide scope of applications ranging from sample size of small to large genomes, obtaining the genome maps of species of interest, or re-sequencing genomic samples for variant detection whole genome sequencing captures all in a single assay.

De novo Whole Genome Sequencing

De novo whole genome sequencing is required for uncharacterized genomes with no reference genome available, or for known genomes where significant structural variation is to be expected. For a successful *de novo* genome assembly, a special library preparation approach is required which usually combines small fragment libraries and mate pair libraries.

Our *de novo* whole genome sequencing solution includes:

- Short fragment, mate pair and PacBio SMRTbell library preparation
- High-throughput sequencing on Ion Torrent, Illumina and PacBio platforms
- Data analysis, which includes
    - QC and data filtering
    - Assembly of reads (short-read/PacBio/hybrid)
    - Gene prediction and annotation
    - Other customized analysis

Whole Genome Resequencing

For genomes with available genome references, whole genome resequencing can be carried out to study genetic variation such as SNPs, Indels, or structural variations. Whole genome resequencing can be carried out on a wide range of samples such as microbial, animal, plant, human or microbial samples.

Our whole genome resequencing solution includes:

- Library preparation services
- High-throughput sequencing on Ion Torrent, Illumina and PacBio platforms
- Data analysis, which includes
    - QC and data filtering
    - Read alignment to reference genome
    - Variant calling
    - Variant annotation
    - Other customized analysis

2. Targeted Resequencing

An alternative to whole genome resequencing, targeted resequencing focuses on a subset of the genome and is ideal for studies that requires ultra-deep sequencing of targeted regions of interest to identify genetic variants such as SNPs, indels and gene rearrangements. This is achieved with the design of gene panels that enrich specific genes of interest with high sensitivity and specificity prior to sequencing on the NGS platform.

AITbiotech provides target enrichment solutions with pre-designed or custom commercial panels as well as AITbiotech custom gene panels which can be designed based on your specific genes of interest.

Our targeted resequencing solution includes:

- Pre-made or custom target enrichment library preparation services
- High-throughput sequencing on Ion Torrent and Illumina platforms
- Data analysis, which includes
    - QC and data filtering
    - Read alignment to reference genome
    - Variant calling & annotation
    - Other customized analysis

3. *De novo* Transcriptome Sequencing

Unlike traditional approaches which require a prior knowledge of transcript sequence, the *de novo* transcriptome sequencing approach enables the sequencing of transcriptomes for organisms without a reference sequence. The resulting sequencing reads are assembled to reconstruct full length transcripts, which can then be used as a reference for future studies.

Our *de novo* transcriptome solution includes:

- RNA library preparation services
- High-throughput sequencing on Illumina platform
- Data analysis, which includes
    - QC and data filtering
    - Transcriptome assembly
    - Mapping to reference transcriptome of choice
    - Other customized analysis

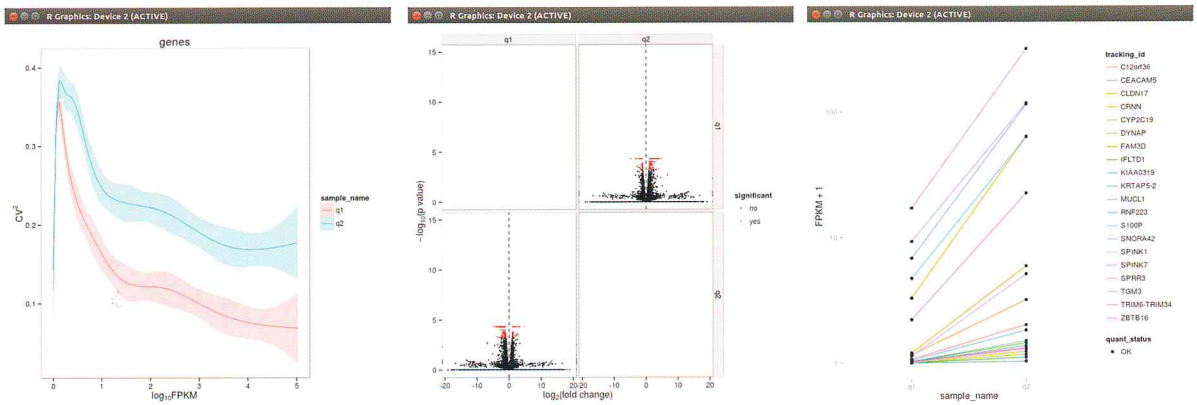
4. RNA-Seq (mRNA, Total RNA)

RNA-Seq analysis is used for gene expression profiling studies and enables the mapping and digital quantification of transcript expression as well as identification of novel isoforms and alternative splicing events.

Different library preparation options are available depending on the goals of the research project, this includes poly-A enrichment or ribosomal RNA depletion, as well as stranded library construction. Poly-A enrichment only allows the detection of poly-A coding RNA in the samples, whereas for the ribosomal RNA depletion method, only the ribosomal RNA is removed and both coding and non-coding RNA can be interrogated.

Our RNA-Seq solution includes:

- RNA library preparation services (mRNA, ribosomal RNA depleted total RNA, stranded)
- High-throughput sequencing on Illumina platform
- Data analysis, which includes
    - QC and data filtering
    - Alignment to reference genome/transcriptome
    - Transcript identification and quantification
    - Differential expression analysis between groups/treatments
    - Other customized analysis



RNA-Seq Differential Gene Expression Analysis. RNA-seq data processed through the TopHat-Cufflinks analysis system yields transcript expression level & annotation data. Using cummerbund, data can be visualised in different formats: SCV plot, density plot, scatter plot, volcano matrix plot, heatmap analysis, expression plots and more.

5. Small RNA Sequencing

Small RNAs play an important role in the post-transcriptional regulation of gene expression in many organisms. Ultra-deep sequencing of the small RNAs is made possible with the high-throughput capabilities of NGS, allowing for the discovery and profiling of these small transcripts. Two types of small RNA sequencing workflow services are available: microRNA sequencing and small RNA sequencing. While the former is only focused on the sequencing of microRNAs (15-30nt), small RNA sequencing is targeted for the analysis of other small RNA targets such as snRNA and tRNA (30-200nt).

Our Small RNA-Seq solution includes:

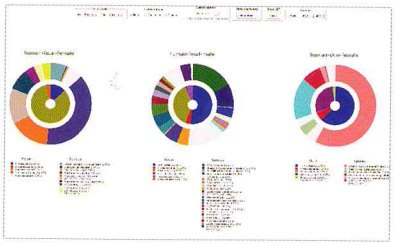
- Small RNA library preparation services (miRNA, small RNA)
- High-throughput sequencing on Illumina platform
- Data analysis, which includes
    - QC and data filtering
    - Alignment and quantification of small RNA
    - Novel small RNA
    - Differential expression analysis between groups/treatments
    - Other customized analysis

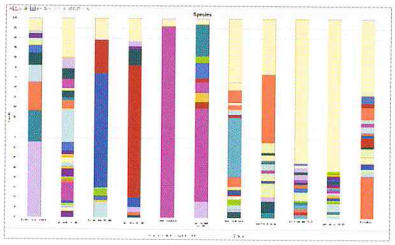
6. Metagenomic Sequencing (Shotgun, 16S rDNA, ITS)

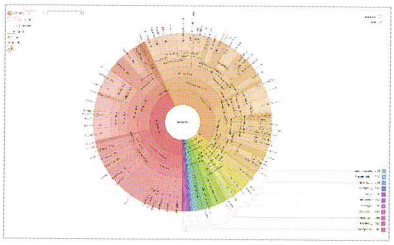
Metagenomic sequencing using NGS technologies provides researchers with a comprehensive view of the diversity of the microorganisms directly sampled from microbiome or environmental samples without the need for culturing. A comprehensive metagenomics sequencing solution is available using whole shotgun metagenomic sequencing, 16S or ITS sequencing for the study of complex microbial communities.

Our Metagenomic Sequencing solution includes:

- Whole Shotgun/16S/ITS library preparation services (customizable to your region of interest)
- High throughput sequencing on both Illumina and Ion Torrent platform
- Comprehensive metagenomics data analysis solution using ChunLab CLcommunity™ software which includes
    - Phylogenetic identification and taxonomic assignment down to species level
    - Free CLcommunity™ bioinformatics software and CLC format files
    - Other customized analysis







No more excels! The CLcommunity™ bioinformatics software allows analysis of alpha & beta diversity indices, rarefraction curves, rank abundance, environmental correlations, source tracking, clustering, UniFrac multivariate analysis, canonical correspondence analysis at the click of a button.

7. NGS Training Workshops

The **Introductory NGS Laboratory Course** aims to provide the beginner with the basic knowledge of the available NGS platforms, technologies, and applications. Participants will also have hands-on experience with the NGS workflow from sample preparation to data output on two popular NGS sequencers.

The **Practical Bioinformatics Course** is for the researcher who wants to develop their bioinformatics skills, from setting up a bioinformatics workstation to using common software tools to develop specialised workflows and pipelines for their own needs. Topics will include analysis of DNA-Seq, RNA-Seq, metagenomics and pathogen discovery.

Try out AITbiotech's
NGS Service Solutions Today!

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Employing state-of-the-art technologies by Illumina, Life Technologies and Pacific Biosciences, AITbiotech offers expert advice and a full spectrum of services for the following applications:

- Whole Genome Sequencing (*De novo*, resequencing)
- Targeted Resequencing
- *De novo* Transcriptome Sequencing
- RNA-Seq (mRNA, total RNA)
- Small RNA Sequencing
- Metagenomic Sequencing (Shotgun, 16S rRNA, ITS)
- NGS Training Workshops (Introduction to NGS Technologies Course, Bioinformatics Course)

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