Next-Generation Sequencing

The application of gene expression profiling methods in deciphering cellular states associated with disease, tumor and exposure to environmental agents has been demonstrated over the past decade. Traditionally, gene expression microarrays (traditional and tiling) have been the technologies of choice. However, the advent of Next-Generation sequencing (NGS) approaches offers revolutionary tools going beyond the present state-of-the-art available for studying transcriptome complexity.

Acobiom offers a comprehensive range of Next-Generation Sequencing services using appropriate platforms (Illumina, Roche Diagnostics, etc.) according to the project and the team of biologists and bioinformaticians to deliver reliable and high quality results (see Bioinformatics).

Next-Generation Sequencing Services

- RNA-Seq - RNA sequencing approach for the deep sequencing of mRNA for expression and variant analysis supporting multiple applications including transcript identification, splice variant analysis and differential expression.
- DGE - RNA-tag sequencing (a SAGE-like method) approach for a high quantitative expression study supporting multiple applications including transcript identification, sense and anti-sense transcript exploration, and differential expression.
- Exome Sequencing - A high throughput exome sequencing approach to support variant discovery, ideal for Mendelian diseases and cancer.
- Small RNA Sequencing - RNA sequencing approach for the analysis of expressed small RNA in a sample allowing for the detection of rare transcripts and transcript variants, the determination of expression levels of known miRNA and the discovery of novel miRNA.
- ChIP-Seq - Combination of chromatin immunoprecipitation (ChIP) and next generation sequencing for research into gene regulatory networks, genetic pathways and epigenetic mechanisms in living cells.
- Whole Genome Sequencing - De novo genome sequencing, whole genome resequencing and targeted resequencing capabilities, available across the full range of major Next-Generation Sequencing platforms, for detecting SNPs, InDels and structural variations.
- De novo Genome Sequencing - Sequencing of uncharacterized genomes, known genomes where significant structural variation is expected and genomes with high plasticity. Options available include sequence assembly and gap closure.
- Targeted Resequencing - Targeted resequencing approach for deep sequencing of genomic regions of interest across large numbers of samples ideal for population studies or disease related variant discovery.
- Metagenomic Sequencing - Investigate microbial communities by sequencing the 16S gene or sampled fragments of the whole genome or transcriptome.
- De novo Transcriptome Sequencing - RNA sequencing approach for transcriptomes without a reference sequence enabling the discovery of novel transcripts and the detection of alternate splicing.

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