GENOMICS AND BIOINFORMATICS

We provide a variety of sequencing services, from whole viral, bacterial and eukaryote genome sequencing, the processing of thousands of metagenomic environmental samples, up to the massive transcriptomic studies and human genome sequencing projects.

16S METAGENOMICS

Metagenomics could be defined as the study of DNA samples directly recovered from the environment, usually composed of multiple genomes. The specific sequencing of the gene encoding the ribosomal 16S RNA, enables the researcher to find the natural bacterial diversity profile of each sample. This gene is approximate 1,500 bp long and contains nine variable regions (V1-V9) interleaved between conserved regions. These variable regions are commonly used to classify organisms phylogenetically.

In INDEAR we offer the sequencing of the V3-V4 regions, allowing to identify the diversity within and between each sample (Alpha- and beta-diversity, respectively).

Sequencer: MiSeq
Run configuration: PE 2 x 300 pb
Maximum plex/run: 180 samples

Primers:
16S Amplicon PCR Forward Primer =
5' TCGTCGGCAGCGTCAGATGTGTATAAGAGA CAGCCTACGGGNGGCWGCAG 3'
16S Amplicon PCR Reverse Primer =
5' GTCTCGTGGGCTCGGAGATGTGTATAAGAG ACAGGACTACHVGGGTATCTAATCC 3'

Bioinformatic Analysis
Quality control
Stitch pair ends
Filter stitched reads by score
Chimeras filter
Pick OTU's
Remove low confidence OTU's
Rarefaction
Alpha diversity
Beta diversity

HIGH PERFORMANCE TRANSCRIPTOMICS – RNASEQ

RNA sequencing is a revolutionary, accurate and sensitive technique that could be used to study the transcriptome of almost all biological organisms. It provides a temporary visualization of the transcriptional state of the organism, allowing the comparison of several transcriptomes associated to different conditions. RNA-Seq allows the detection of new and known features in a single assay, allowing the discovery of transcripts isoforms, gene fusions, SNVs, specific allele expression, and even the coding strand of the transcript (RNA-seq stranded).

At INDEAR we offer the power of our NextSeq 500 to cover the experimental conditions you need.

Sequencer: NextSeq 500
Run configuration: PE 2 x 75 pb

Bioinformatic analysis - Differential gene expression

Quality control
Tophat alignment
Cufflinks assembly
Differential expression analysis

Bioinformatic analysis – *De novo* transcriptome

Quality control
De novo assemblies
Estimate abundances
Differential expression
Transcriptome annotation

Bioinformatic analysis – Transcriptome with reference

Quality control
Tophat alignment
Cufflinks assembly
Differential expression
Sequencer: NextSeq 500
Run configuration: PE 2 x 75 pb

HIGH RESOLUTION GENOTYPING – GENOTYPING BY SEQUENCING (GBS)

The genotyping process allows the identification of differences at the genetic level of different individuals. This study can take advantage of the power of NGS technologies to detect a huge number of variants.

INDEAR offers a screening method for the discovery of SNP markers that was validated in different organisms. This technique is based on a genomic reduction by means of a digestion with restriction enzymes, and the sequencing of samples from a population under study. Our platform has applied this technology to various species such as *Oryza sativa, Zea mays* and *Glycine Max* using the ApeKI enzyme. This system is offered by default, so the digestion of the genome of other species must be properly evaluated by the user.

Bioinformatic analysis:
Quality control
Quality trimming
Stacks

Sequencer: NextSeq 500
Run configuration: SR 1 x 75 pb

Advantages:
Informative SNPs discovery for each population under study
Low cost
Reduces the "verification bias" compared to arrays
Identification of additional variants besides SNPs (indels and microsatellites)
Reference genome not required

WHOLE SMALL GENOME SEQUENCING (WGS)

Small genomes (<5 Mb) from bacteria, viruses and other organisms can be isolated and sequenced using NGS techniques. This could be used to specie identification, gene annotation, low frequency variant or genomic rearrangements detection. INDEAR offers this application based on the Nextera® technology of Illumina® using a DNA mass starting from 1 ng.

Bioinformatic analysis
Quality control
Quality trimming
De novo assemblies
rRNA prediction
RAST annotation

Sequencer: MiSeq
Run configuration: PE 2 x 300 pb