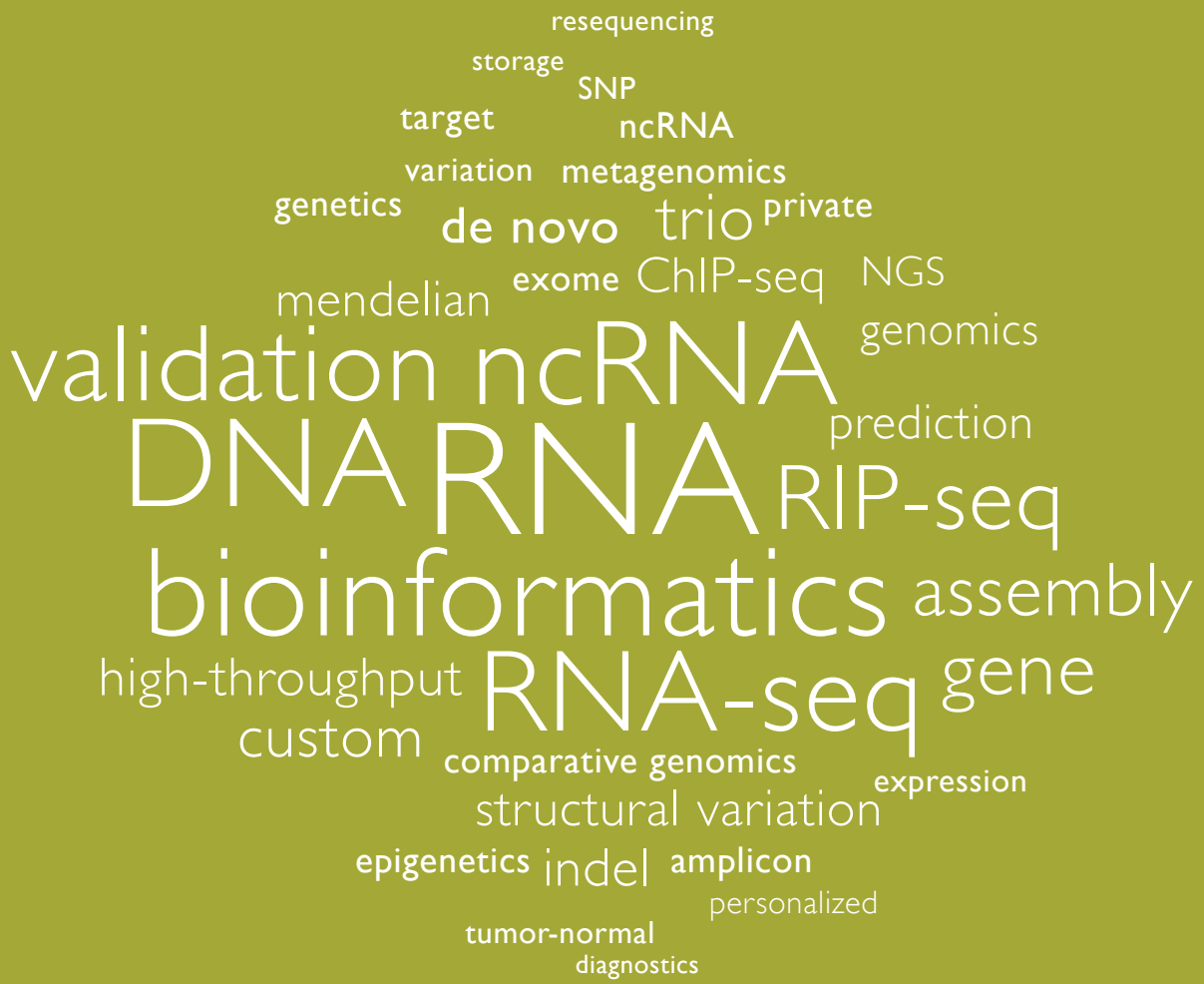
RNA Sequencing

IGATech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NGS Next Generation Services

IGATech

IGATech is the leading Italian provider of genomic research services using Illumina Next Generation Sequencing (NGS) technology.

We are the largest lab in Italy offering these services on a wide range of organisms: we have experience with humans, other animals, plants and microorganisms.

The company has direct access to the scientific and technological resources of its founder, the Institute of Applied Genomics (IGA), which has gained an outstanding reputation in genomic research through participation in genome sequencing projects both at a national and international level.

Among the genomic research services provided, the company also offers a wide variety of bioinformatic services such as conventional and custom analyses and customer-oriented software development.

Transcriptomics

ILLUMINA SEQUENCING TECHNOLOGY

The Illumina massively parallel sequencing technology makes multiple gigabases of data from several million templates economically available, enabling new approaches to genomic characterization. The Illumina technology allows tipically genome center-like studies to be accomplished at the individual laboratory level. A single technology workflow is capable of supporting genome-wide analyses as different as DNA sequencing (de novo and resequencing), gene expression, transcriptome characterization and expression control including small RNA discovery, protein-DNA interactions and CpG methlyation status. We are a certified service provider (CSPro) of Illumina genomic sequencing.

RNA SEQUENCING

Qualitative and quantitative transcriptome characterization

RNA-Seq is a powerful method for discovering, profiling, and quantifying RNA transcripts across the entire transcriptome. Constant technological improvements allow for robust analysis on a wide range of samples, including low-quality and FFPE. The amount of valuable information that can be obtained from RNA-Seq data is truly enormous. In addition to gene expression analysis, deep sequencing of RNA samples enables the detection of alternative splicing events, rare or novel transcripts, and gene fusions. It also allows discovery of SNPs, identification of non-coding RNAs and their targets, and measurement of allele-specific expression.

Highly customizable Targeted RNA-Seq expression assays generate data equivalent to individual RT-PCR assays and offer an accurate and powerful method for validating gene expression arrays and RNA-Seq studies.

De novo assembly of RNA-Seq data allows for transcriptome studies for non-model organisms lacking well-defined genomes or for cancer samples, permitting downstream RNA-Seq analyses.

RIP-Seq, i.e. sequencing of RNA-binding protein immunoprecipitation, maps RNA-protein associations in vivo by discovering genome-wide RNA molecules of any type that physically interact with a regulatory protein or protein complex.

Services list

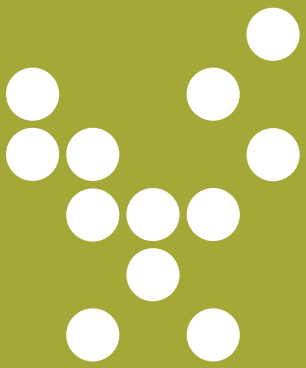
LIBRARY PREPARATION AND SEQUENCING

- mRNA-seq
- Strand oriented RNA-seq
- Small RNA-seq
- Targeted RNA Expression
- RIP-Seq
- Low-quality and FFPE

BIOINFORMATICS SERVICES

- Quality control and alignment to a reference
- Differential expression analysis
- Allele-specific expression analysis
- Cross-species comparison
- Detection of new exons, splice variants and gene fusions
- SNP detection
- Deriving strand information with high precision
- Non-coding RNA analysis
- De novo assembly
- Prediction of new microRNAs and lncRNAs and their targets
- RIP-Seq analysis

Our team is always available to consult with you on study design to ensure correct sequencing and bioinformatics strategies are used to meet your goals.



IGA TECHNOLOGY SERVICES SRL
c/o Parco Scientifico e Tecnologico L. Danieli
Via Linussio 51 – 33100, Udine (Italy)
Tel. +39 0432 629911

www.igatechnology.com