



SNP resequencing validation target exome de novo trio mendelian custom comparative genomics structural variation inde high-throughput



NGS Next Generation Services



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.

IGATECH

Genomics

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.

DNA SEQUENCING At the roots of diversity

WHOLE GENOME SEQUENCING

NextGen sequencing technologies have enabled rapid sequencing of entire genomes, expanding the number of available genomes while unlocking the potential for comprehensive identification of their underlying genetic variations. Sequenced reads can require de novo assembly or can be mapped against already published reference sequences to discover and confirm SNPs, to identify chromosomal rearrangements, to map break points and to detect rare variants.

TARGETED RESEQUENCING

From Amplicon-Seq to Whole Exome-Seq, this highly flexible and fully customizable application allows for systematic identification of common and rare variants in genomic regions of your particular interest across large numbers of samples, ideal for population studies or disease-related variant identification.

Focusing on regions most likely to yield relevant data enhances sensitivity through increasing depth of coverage, thereby increasing the likelihood of new discoveries as well as the detection of rare variants or variants present in highly heterogeneous samples, such as cancer.

METAGENOMICS

NextGen sequencing enables studies of microbial populations and their impact on the environment and human health without the need for culturing. By sequencing the marker gene of choice or sampled fragments of the whole genome, metagenomics offers a path to study community structures, phylogenetic composition, species diversity, metabolic capacity and functional diversity.

Services list

LIBRARY PREPARATION AND SEQUENCING

- DNA-seq
- Amplicon-Seq (custom and ready-to-use panels)
- Custom target solution hybridization enrichment and sequencing
- Human whole-exome sequencing

BIOINFORMATICS SERVICES

- Quality control
- De novo assembly
- Alignment to a reference
- Coverage statistics and metrics
- Variant calling (SNPs, small indels, CNVs and other structural variants)
- Variant functional annotation
- Comparative analysis (trio, matched tumor and normal pairs, etc.)
- Metagenomic 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.









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