



Sequencing instruments and specifications

ILLUMINA - MiSeq

- V3_600c (300bp, 44 M paired reads, 13 Gbp output)

ILLUMINA - NextSeq500

- High-output 300c (150bp, 700M paired reads, 100Gbp output)
- High-output 150c (75bp, 700M paired reads, 45Gbp output)
- High-output 150c (150bp, 350M single reads, 45Gbp output)
- High-output 75c (75bp, 350M single reads, 23Gbp output)

ILLUMINA - NovaSeq6000

Regular production queue setup (minimum yields reported):

- S1 300c (150bp, 2600M paired reads, 390Gbp, 2 distinct lanes using XP workflow)
- S2 300c (150bp, 6600M paired reads, 960Gbp, 2 distinct lanes using XP workflow)
- S4 300c (150bp, 16000M paired reads, 2.4Tbp, 4 distinct lanes using XP workflow)

Custom setup examples (minimum yields reported):

- SP 500c (250bp, 1300M paired reads, 325Gb, 2 distinct lanes using XP workflow)
- SP 100c (100bp, 650M single reads, 65Gb, 2 distinct lanes using XP workflow)
- S1 100c (50bp, 2600M paired reads, 130Gbp, 2 distinct lanes using XP workflow)
- S1 100c (100bp, 1300M single reads, 130Gbp, 2 distinct lanes using XP workflow)
- S1 200c (100bp, 2600M paired reads, 260Gbp, 2 distinct lanes using XP workflow)
- S2 200c (100bp, 6600M paired reads, 660Gbp, 2 distinct lanes using XP workflow)

10X Genomics - Chromium

- Single-cell RNA-Seq (including cell-hashing or antibody feature barcoding)
- Single-cell ATAC-Seq
- Single-cell DNA-Seq

We can accept frozen cells, methanol-fixed cells or accept customers to bring fresh cells/tissue and cooperate in the first phase of manipulation (tissue dissociation, cell viability assessment).

<https://igatechnology.com/genomics-research-services/?area=human#scRNAseq>



List of technologies by application

RNA-Seq

- mRNA-Seq
- total RNA-Seq (with rRNA depletion or custom depletion)
- low-input total RNA-Seq (100 pg RNA)
- smallRNA-Seq
- single-cell RNA-Seq (up to 10,000 cells/run)

Depending on the input RNA (FFPE, degraded, low quantity) and experimental needs (custom depletion, strand-specificity, UMI count), IGATech can offer a wide selection of protocols and approaches to optimize results.

Established pipelines are already available for downstream analysis and our staff can assist on statistical tools for meaningful results.

<https://igatechnology.com/genomics-research-services/plantanimal/rna-seq/>

DNA-Seq

- standard/PCR-free DNA-Seq
- low-input DNA-Seq (ChIP-Seq)
- single-cell CNV (10X Genomics)

Internal pipelines are already available for the analysis of:

- Chip-Seq enrichment
- SNPs/Indel analysis
- CNV analysis
- Structural variants

<https://igatechnology.com/genomics-research-services/whole-genomics-sequencing/>



Agrigenomics Solutions - Genotyping

- Targeted genotyping (single-primer enrichment)
- ddRAD (restriction-based complexity reduction)
- Sequence Capture (capture enrichment with custom and pre-designed probes)

IGATech has a wide experience in custom experimental designs for large-scale experiments. Our portfolio of technologies can provide flexible and scalable solutions from low-plex genotyping, up to hundreds of thousands of loci enrichment. Samples can be multiplexed up to 1,536 per lane. Our pipelines can deliver genotyping calls in large cohorts, ready to be used in genomic selection, linkage, association and diversity studies. Support for downstream analysis and interpretation is also offered on request.

<https://igatechnology.com/agrigenomics-solutions/>

Exome sequencing

IGATech can offer exome sequencing with a large set of panel solution

- Agilent SureSelect (V7)
- Roche MedExome
- Sophia Genetics
- Twist Bioscience

IGATech can deliver already annotated and prioritized variant calls. A custom variant analysis for CNV analysis can be performed on request for large cohorts.

<https://igatechnology.com/genomics-research-services/?area=human#exomeSequencing>

Epigenetics

- Whole-genome BS-Seq
- RRBS-Seq
- small RNA-Seq
- Single-cell ATAC-Seq

Internal pipelines are already available for the analysis of differentially methylated regions.

<https://igatechnology.com/genomics-research-services/bs-seq/>



De novo assembly services

- HMW DNA extraction
- Nanopore sequencing
- Hi-C *in situ* libraries
- Scaffolding integration with genetic maps
- Genome annotation
- Genome hosting (JBrowse)

<https://igatechnology.com/genomics-research-services/plantanimal/de-novo-assembly/>

Metagenomics/Metabarcoding

- 16S/ITS Amplicon-Seq
- Custom Amplicon-Seq
- Whole Genome DNA-Seq
- Total RNA-Seq (meta-transcriptomics)

Dedicated DNA extraction services are implemented for stool samples

<https://igatechnology.com/microbiome-analysis/>