

Next Generation Sequencing

DNA Vision group, is a leading European provider of genetic & genomic analysis services.

Knowing the strengths and limitations of high throughput sequencing, we collaborate with our customers from experimental design to data interpretation.

Due to the complexity of data generated and cost of the process which remains significant, DNA Vision has put in place a multidisciplinary team to set up competences synergy and gather in-depth knowledge of available analysis tools from design optimization, sample preparation to complete data set analysis.

Roche/454 GS FLX

Technology : Pyrosequencing

Read Length : Average 350-400 bp

Throughput : 400 Mbp/run

Single-read accuracy : > 99.5%



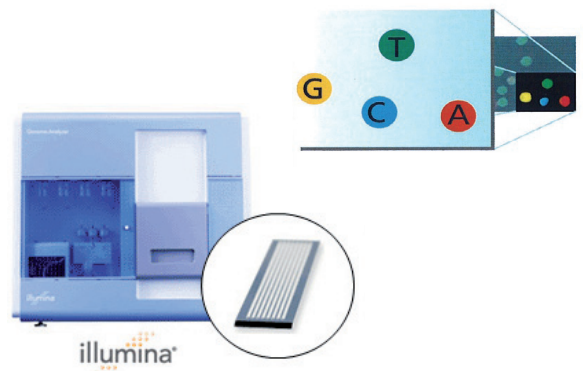
Illumina Genome Analyser

Technology : Reversible terminators and Clonal Single Molecule Array technology

Read Length : 36 bp, up to 75 bp (and growing)

Throughput : 1Gbp per single read,
> 3Gbp for paired-end libraries

Per base read accuracy : > 98.5%

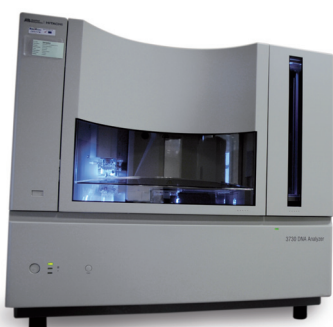


Applied Biosystems Sanger sequencing

Technology : Sanger dideoxy sequencing method

Read Length : up to 1,000bp

Throughput : About 1Mb/day and machine



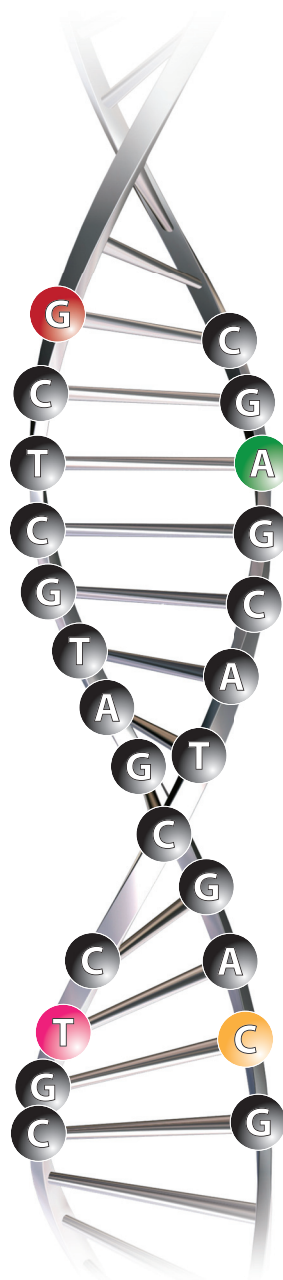
More than sequencing

Highly skilled Biostatisticians and Bioinformaticians to provide you with relevant data related to your project

Dedicated HPC (High Performance Computer) infrastructure to analyse your data

Special protocols :

- > cDNA normalization
- > Targeted sequencing (Sureselect or long-range PCR)
- > Paired end sequencing
- > Multiplex exon sequencing
- > Multiplexing by Tag identifier



Next Gen Sequencing



Genome Sequencing

- ▶ From prokaryotic, microbial to mammalian genomes
- ▶ For whole genome or targeted sequencing of large regions of interest
- ▶ De novo sequencing with hybrid strategy of next generation and Sanger sequencing
- ▶ Resequencing, when reference sequence is available

SNP analysis

- ▶ SNP discovery
- ▶ SNP confirmation
- ▶ Ultra deep mutation
- ▶ Detection of rare variants or somatic variation detection

Transcriptome analysis

- ▶ Whole transcriptome profiling
- ▶ Small RNAs (microRNAs, endogenous siRNAs and Piwi-interacting RNAs) analysis
- ▶ SAGE analysis
- ▶ Identification of novel transcripts
- ▶ Splice variant detection

ChIP-seq/Methylation/Epigenetics

- ▶ **ChIP-seq** : Combination of the chromatin immunoprecipitation (ChIP) with high-throughput sequencing
- ▶ **Methylation** : Applying a standard bisulfite-treatment procedure with high-throughput sequencing

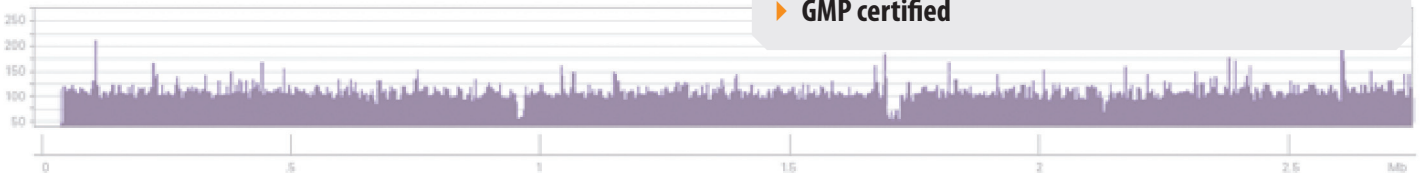
CNV & chromosomal rearrangements

- ▶ Analysis of deletions, insertions and/or translocation on a genome wide scale

Metagenomics & Microbial Diversity

Added value for your research

- ▶ **Expert assistance** : from design to results
- ▶ **Fast and flexible turnover** : from small to large studies
- ▶ **Studies according GLP and cGMP guidelines**
- ▶ **GLP certified for pharmacogenomic and toxicogenomic studies (IPH GLP D-01)**
- ▶ **ISO17025 accredited lab (Belac # 293-TEST)**
- ▶ **CLIA (99D1055506) & CAP accredited**
- ▶ **GMP certified**



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