



Next generation sequencing



Next generation sequencing

- **De novo sequencing including gap closure**
(of prokaryotic and eukaryotic genomes using Roche / 454, Illumina HiSeq 2000 and Sanger sequencing as well as other state-of-the-art techniques)
- **Re-sequencing of genomes**
- **Transcriptome sequencing and analysis**
(of eukaryotic and prokaryotic organisms)
- **Metagenome sequencing and analysis**
- **Analysis of:**
 - methylation patterns
 - amplicons (e.g. 16S rDNA)
 - pools of tagged fosmids / BACs
- **ChIP and small RNA sequencing**

Special customised applications:

- **Targeted re-sequencing**
(re-sequencing of enriched individual genomic regions of interest e.g. exomes, chromosomal intervals etc.)
- **Sample multiplexing**
- **Sequence enrichment**

Roche / 454 GS FLX + Titanium

- ▶ Deep sequencing
 - up to 1000 bp read length
- ① *De novo* sequencing by whole shotgun approach and closure of gaps using paired-end applications and Sanger sequencing
- ② Re-sequencing and comparative genomics including sequence assembly and mapping to a reference genome
- ③ Transcriptome analysis by generating standard or normalised full-length optimised cDNA libraries
- ④ Metagenome analysis by sequencing the whole genomic content or 16S rDNA in a complex sample (high specificity due to long read length; sorting and clustering of reads)
- ⑤ Amplicon sequencing and analysis of variants (SNPs) using state-of-the-art analysis tools (e.g. Roche GS Amplicon Variant Analyzer)
- ⑥ Sequencing of tagged fosmids / BACs
- ⑦ ChIP-sequencing
- ⑧ DNA methylation analysis

Illumina HiSeq 2000

- ▶ Ultra high-throughput sequencing
 - up to 3 billion reads per flow cell
 - up to 300 Gb per flow cell
- ① Genome sequencing and re-sequencing to discover SNPs and chromosomal rearrangements
- ② Transcriptome analysis, generation of expression profiles, detection of splice variants *etc.*
- ③ Small RNA / microRNA discovery and analysis
- ④ ChIP-seq application resulting in the identification and quantification of protein-DNA interactions
- ⑤ DNA methylation analysis to discover methylation variable positions across the whole genome



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Next generation sequencing services by LGC Genomics feature:

Extensive consultation and experiment design assistance by our experienced scientific staff.

Bioinformatic services

- *De novo* assembly of genomes
- Mapping to reference genomes
- Sorting of tagged sequences
- Metagenomics data analysis
- SNP analysis of amplicons
- Clustering of transcripts
- Various sequence alignment procedures
- Clipping of adaptors, linkers *etc.*

Expertise

- Publication quality sequencing of several **bacterial and fungal genomes**
- Development of a novel method to sequence **complete transcriptomes** starting from normalised full-length optimised cDNA libraries. Our method yields balanced transcriptome sequences without the usual 3' or 5' biases.
- Vast experience in sequencing **metagenomes** from various habitats

A reference list can be provided upon request.

To order a
Next generation sequencing
run or project,
please contact us
to discuss your specific project.

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