biofidal

NEXT-GENERATION SEQUENCING SERVICES

Biofidal supports your research and diagnostics applications in diverse fields using molecular biology tools. We focus on custom DNA sequencing techniques, either Sanger capillary DNA sequencing and Next-Generation DNA sequencing.

Biofidal supports all your needs on Sanger DNA sequencing services, with a certifed complete process. This quality certification validates our laboratory skills, practices and methods and certifies the high quality and reproducibility of our process in Sanger DNA sequencing, on all types of templates.

Biofidal can also propose SNP genotyping by fragment analysis like microsatellite, MLVA, RFLP, MIRU, STR and ARISA.

Last but not least, our lab distributes a complete line of PCR, qPCR and post-PCR analysis reagents. Those high quality, robust products are used everyday in our own lab for our sequencing and genotyping services.

Quality is our value, reactivity our goal, adaptability our DNA, we are at work for the satisfaction of our customers.

NEXT-GENERATION SEQUENCING NGS

Based on our Illumina MiSeq system, Biofidal provides a complete solution to sequence your project by NGS sequencing in a very short time. The MiSeq system can produce up to 25 millions of reads with 15 Gb of output datas per run with paired-end 2x300 reads length.

Our dedicated team of scientists offers a custom support for each of your project with its expertise and reactivity, from the design according to your needs and requests, to the sample preparation, the NGS high-throughput sequencing and the bioinformatics analysis.

Our porfolio includes a broad range of applications (small whole genomes, massive amplicons, metagenomics, RNA-seq, etc.). Custom protocols can be developed by our team. Thanks to this, a large panel of indexes has been developed to multiplex up to 864 samples per sequencing run.

With our competitive prices that includes discount for volume and a rapid turn-around treatment, you can easily trust our experts and try our NGS services.

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MiSeq sequencer

Kit version	V2 Nano		V2 micro	V2			V3		
# Paired or Single reads	1 million		4 millions	15 millions			25 millions		
Run type	PE 2x150	PE 2x250	PE 2x150	SR 50	PE 2x150	PE 2x250	SR 150	PE 2x75	PE 2x300
Output	0,3 Gb	0,5 Gb	1,2 Gb	0,8 Gb	4,8 Gb	8 Gb	3,5 Gb	3,5 Gb	15 Gb
>Q30 Illumina threshold	> 80%	> 80%	> 80%	> 90%	> 80%	> 75%	> 85%	> 85%	> 70%

From the sample prep to the high-throughput sequencing and the bioinformatics analysis

SAMPLES RECEIPT → NUCLEIC ACID EXTRACTION → LIBRARY PREPARATION → SEQUENCING → DATA ANALYSIS → REPORT

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Applications

SMALL GENOME

Whole genome sequencing (WGS) is the best way to analyse your genomic DNA. WGS generates read datas to map to a reference sequence, a *de novo* assembly or both, in order to characterize genetic variations (SNP, InDel), reconstruction of unkonwn plasmid structure, to track disease outbreaks, etc. MiSeq can support small genomes sequencing (bacterial, viral and plasmids).

- Resequencing with reference genome
- *de novo* sequencing without reference for assembly

MASSIVE AMPLICONS

Amplicon ultra-deep sequencing is a highly targeted approache to analyze large number of PCR products with a very attractive cost, that enables phylogenetic studies, genotyping, genetic variations, rare variant detection, cancer genes sequencing, etc.

- Amplicon deep sequencing
- CRISPR-Cas9 screening
- SNP variant analysis
- Up to 864-plex with the possibility to develop more

METABARCODING

Metabarcoding studies genome diversity of a microbial flora (including non-culturable bacteria), qualitatively and quantitatively, on conserved phylogenetic marker genes. Samples can be from different origins and analyzed for various applications: environment (rivers, soils, etc.), medical (sputum, tissues, feces) or food (cheese, milk, meat).

- Bacterial 16S
- Eukaryote 18S
- Fungal ITS
- Animal COI
- Plant rbcL
- Others specific genes

GENE PANEL

Targeted gene sequencing is an effective solution to analyze a large-scale genes variations of interest from cancer, HLA typing, autism, cardiac conditions, and inherited disorders (metabolic, developmental, neuromuscular).

- Rare variant identification
- Gene associations with disease or phenotype

RNA-SEQ

RNA-seq is a highly sensitive and accurate method to sequence all RNA and measures their gene expression level for comparison between different samples and conditions. RNA-seq is also a powerful method to identify all the small RNA that are involved in the regulation of gene expression.

- Gene expression profiling
- Meta-transcriptomics
- Small RNA

READY-TO-LOAD

Biofidal can sequence NGS already constructed-libraries on MiSeq sequencer.

- Single Read 50, 150 bp
- Paired-End 75, 150, 250 or 300 bp
- 3 flow cells types : Nano, Micro and High Output
- Up to 25 millions of reads
- Time to results of 2 weeks

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Technical and general information

SAMPLE REQUIREMENTS

DNA and/or RNA should be suspended in water, low TE, or elution buffer and stored in low binding 1.5 ml tubes or 96-wells plates. If you have made some quality controls of your samples, please provide them at the sample submission.

Sample type	Minimal quantity	Minimal volume	Concentration	OD260/ 280	Other
gDNA	500 ng	30 µl	≥ 20 ng/µl	1.8 – 2.0	Intact gDNA
Amplicons	150 ng	20 µl	≥ 5 ng/µl		
ChIP	30 ng	15 µl	≥ 2 ng/µl	1.8 – 2.0	
Total RNA	2 µg	30 µl	≥ 60 ng/µl	1.8 – 2.0	RIN ≥ 7, DNAse I treated sample
rRNA depleted-RNA	Purified from mini 500 ng of total RNA	20 µl	N/A	1.8 – 2.0	No rRNA contamination
Poly(A) RNA	Purified from mini 500 ng of total RNA	20 µl	N/A	1.8 – 2.0	No rRNA contamination

SEQUENCING COVERAGE INFORMATIONS

Application	# Reads per sample (Illumina)	# Samples per run	Recommended run type	Other
Metagenomics	10 000 to 200 000	100 to 864	PE 2x300 bp V3 (PE 2x250 bp V2)	Mini 50 bp of overlap Longer insert size is the best for identification
DNA-seq whole small genome	30-1000× coverage	1 to 96	PE 2x300 bp V3	Coverage depends on application
DNA-seq long-range	0,6 to 0,9 M	17 to 25	PE 2x300 bp V3	
Chromatin immunoprecipitation (ChIP-seq)	15 M	1-2	SR 50 bp V2 (SR 150 bp V3)	15 M reads per sample for identification of transcription factor binding
Bacterial RNA-seq	20 M	1-2	SR 150 bp V3	Mini replicat size: 2
miRNA sequencing	5 M	1-8	SR 50 bp V2	Mini replicat size: 2

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