

TCGACTCTGGGCTCGGC  
GGACTCGACACAGTT  
GCAAGGAGGC **NEXT** GC  
CCTA **GENERATION** CG  
TCAT **SEQUENCING** CA  
GGCTCGACACTGTGG  
CTCGACACAGATGTGT  
CACACTGTGC  
CAGTGTGCTA  
TGGGTGC  
GCTA

Whole Genome

Whole Exome

Targeted

Transcriptome

Single Cell

Epigenome

Metagenome



GACGCTGACTGTGCCTGCTTCAGCTCGAGCTGCTGACTCGTGTCCAGCGT  
 ATG**WEGBROADENCLIFETSCIENCEAKNOWLEDGECANDGACCELERAT**  
 ACGTT**SCALECBYGPROVIDINGGTAILOREDAANDGRELIABLECGENETI**  
 AAGCGGC**INNOVATIVECTECHNOLOGYCANDGDELIVERINGCDATAGO**  
 AAAGCAGCGTGCTCGACACGTGTGCTCGACACGAGTGTGTGTGTGCTGA

SERVICE	LIBRARY PREPARATION	SEQUENCING
WHOLE GENOME	<div> <span>ILLUMINA</span> <span>PACBIO</span> <span>OTHERS</span> </div>	<div> <span>ILLUMINA</span> <span>PACBIO</span> <span>OXFORD NANOPORE</span> </div>
WHOLE EXOME	<div> <span>ILLUMINA</span> <span>AGILENT</span> <span>TWIST</span> </div>	<div> <span>ILLUMINA</span> </div>
TARGETED	<div> <span>ILLUMINA</span> <span>AGILENT</span> <span>TWIST</span> </div>	<div> <span>ILLUMINA</span> </div>
TRANSCRIPTOME	<div> <span>ILLUMINA</span> <span>PACBIO</span> <span>OTHERS</span> </div>	<div> <span>ILLUMINA</span> <span>PACBIO</span> </div>
SINGLE CELL	<div> <span>10x GENOMICS</span> <span>SINGLERON</span> </div>	<div> <span>ILLUMINA</span> <span>PACBIO</span> </div>
EPIGENOMICS	<div> <span>ILLUMINA</span> <span>AGILENT</span> <span>OTHERS</span> </div>	<div> <span>ILLUMINA</span> <span>PACBIO</span> </div>
METAGENOMICS	<div> <span>ILLUMINA</span> <span>PACBIO</span> <span>OTHERS</span> </div>	<div> <span>ILLUMINA</span> <span>PACBIO</span> <span>OXFORD NANOPORE</span> </div>

## WHOLE GENOME

It the **most comprehensive genetic tool for detecting variants** such as single nucleotide polymorphisms (SNPs), indels, copy number variation (CNV) and structural variants (SVs). We provide Illumina and PacBio long reads workflows, or a combination of both. Get the maximum of it with our standard and customized bioinformatics data analysis available for de novo and resequencing projects.

## WHOLE EXOME

Choose efficient, cost-effective sequencing of protein-coding regions with MacroGen Europe's whole exome sequencing (WES) service using leading **hybridization-based library capture kits**. MacroGen Europe's WES service includes a range of bioinformatic analyses –for example SNP, indel and CNV discovery, annotating discovered genes using various databases, tumor–wild type paired analysis, family/trio analysis and many others.

GGGTGCTCTGCTGACTCGTGTCCAGCTAGCAGGGCGT  
 AAAG**COMMITTEDCTO**AGCACCTGACACGTGAGCTCGACTCGACAC  
 GAGT**SEQUENCINGGEXCELLENCE**GCTCGACACGATCGCGTGTGCTCGA  
 GAGCCGGTTTCGCGACACGTTTCGCGCACAGGGTGTGCTCGCGCTAGCTAT  
 ACACCCCTGCTCCACACACACACACCTCTCTCTCTCCACACACACCAT

GTGCTGACAGCTGCT  
TCGCAGTGAGCGGAGCTAGTCGC  
ET GENOMICS T DISCOVERIES GATGANY  
CG SEQUENCING C USING C THE G MOST CAA  
FG THE T UTTER MOST T QUALITY C AND G TRUST CA  
CTCTGCTGAAGACTACACGTGTGCTCGACACGTCGA

## TARGETED

It combines **cost-effective sequencing with ultrahigh coverage** of specific genes of interest. Macrogen Europe supports both hybridization- and PCR-based target enrichment to create specific libraries with genes of interest for applications such as cancer research. Macrogen supports custom targeted panel and experimental design, and we can handle all type of sample (fresh tissue, FFPE, blood, FNA...)

## TRANSCRIPTOME

A reliable, detailed picture of cell function and behavior by looking at diverse ranges and forms of RNA: **whole transcriptome, mRNA, small RNA, extracellular/exosome RNA full-length transcripts**. With standard and customized bioinformatic analysis services, Macrogen Europe provides clear data, **from short to long reads**, from de novo to resequencing, and from whole transcriptome to targeted RNAs.

## SINGLE CELL

Single cell RNA sequencing **reveals detailed transcriptome information at the single cell level**. It gives clear insights into, for example, **immune profiles and the existence of clusters and subpopulations of cells within a single sample**. Macrogen Europe supports a range of single cell libraries from 10x Genomics, Sinlgeron and many others, combined with Illumina sequencing and bioinformatics analysis.

## EPIGENOME

Elucidate the complex **association between external environmental factors and gene expression** for studying DNA: **methylation and DNA-protein interactions**, whole genome bisulfite sequencing (**WGBS**), **methyl-capture sequencing of CpG islands**, differentially methylated regions (**DMRs**), chromatin immunoprecipitation (**ChIP**) and assay for transposase-accessible chromatin (**ATAC**).

## METAGENOME

It is an effective way to analyze **similarities and differences in microbial communities across samples** to understand these communities and their environments. Our services includes **shotgun sequencing** for looking at functional genes of all microorganisms present in a sample, as well as **amplicon sequencing** for efficient identification of microorganism diversity in a sample through analyzing operational taxonomic units (OTUs)

ACACGTCGA  
TGAACCAGAGGTGCTCGCA  
TCCCTCCACACCTCTCCCACTTCCA

TCGACTCTGGGCTCGC  
GGACTCGACACAGTT  
CAGGGTCACTGTGGCT  
GGCTCG  
GGCTC  
GGA



Humanizing Genomics

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AMSTERDAM

PARIS

MILAN



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