mfine /diagnostics

INDIA'S FIRST PRIVATE CELL BANK FOUNDED IN 2004

2004-2022

17

YEARS

From the last 17 years -

We have diversified from being the first and largest stem cell bank to providing INNOVATIVE & COMPREHENSIVE preconception, Prenatal & Newborn Diagnostic Services as well as COVID 19 detection & management testing.

Being the market leader in performing the Most Complex Diagnostics Test, utilising years of experience coupled with skilled team, MFine is now going to offer a complete

Comprehensive Diagnostic Solution for Oncology

About MFine

Everything that you need to know about MFine Limited

mfine /diagnostics

The Footprints | 17 Global Locations | 130 Cities

Now Serving | 2K Hospitals | 10K Doctors

#1 in the Prenatal Screening of Aneuploidies and in Noncancer Karyotyping

Market Leader

1.5Mn+ Newborns and Pregnancies Screened, makes us Market Leader

Experienced Team

Highly experienced team of Pathologists, Microbiologists, Biochemists, and Scientists

Lab Cities

Chennai (National Reference Lab), Pune, Mumbai, Hyderabad, Delhi NCR, Bangalore & Kolkata

State of the art Labs at Chennai

High-end Transplant Diagnostics

High-end Fetal Autopsies

Why choose us

06 REGIONAL REFERENCE LABS

Market Leader in Reproductive Markers & Genomics

Highly Skilled & Experienced Technical Team

State of the Art National Reference Laboratory at Chennai

Cutting Edge Technology

Wide Test Menu & NGS Solutions

- Library preparation with Hamilton NGS star for high precision automation
- Novaseq 6000 sequencing platform for deeper & broader coverage
- Ultra rapid secondary analysis with Dragen

Strong Logistics Across 130 Cities

Amplicon Sequencing Services

NGS-based amplicon sequencing allows the detection of low-frequency variants, quantitative analysis of mixed populations, and scalable analysis of a large number of samples. Whether you are looking to validate/discover variations in specific genomic regions or are interested in screening clones, Lifecell offers multiple options for ultra-deep sequencing of amplicons <500 bp size.

Library Preparation Kits	:	NEBNext Ultra II DNA Library Prep Kit for Illumina
TAT	:	3 weeks to generate the raw data
Sequencing Platform	:	Illumina Novaseq 6000 and Illumina MiSeq
Read Length	:	150 & 300
Data Requirement	:	1 Gb

Sample Requirements

PCR Amplicons : ≥ 100 ng Concentration : ≥5ng/µL

Volume : 20 µL

Amplicon Size : 200bp to 500bp

Whole Genome Re-sequencing

MFine's plant and animal whole genome sequencing involves sequencing the entire genome of a plant/animal/Microorganism and comparing the sequence to that of a known reference genome. Re-sequencing of the genome will identify genetic variations such as SNPs and In-Dels and is often applied for the identification of functional genes and markers of important traits to facilitate molecular breeding and to improve agricultural production and conservation.

WGS provides a more comprehensive, accurate and efficient tool for plant and animal genomics projects that traditionally have used legacy technology such as genotyping arrays or genotyping-by-sequencing. The WGS approach outperforms these methods by providing an order of magnitude more data, greater statistical power, and enhanced variant discovery capabilities, easier analysis – all at a lower cost. Our end-to-end workflow can support you with a broad range of species

Receive the comprehensive genome analysis you need for your research project. Whole genome sequencing (WGS) provides unprecedented access to genomic information — expediting breakthroughs in human healthcare, oncology, biomarker discovery, agriculture, and metagenomics.

MFine's expertise in the latest technologies and bioinformatics enables us to deliver high-quality data and analysis for the genomes of all organisms, including humans, animals, plants, bacteria, and viruses.

Library Preparation Kits	:	NEBNext Ultra II FS DNA Library Prep Kit for Illumina NEBNext® Ultra™ II DNA PCR-free Library Prep Kit for Illumina
TAT	:	3 weeks to generate the raw data
Sequencing Platform	:	Illumina Novaseq 6000
Read Length	:	150PE
Data Requirement	:	30 X

Sample Requirements

Regular Samples :

- With PCR

Mass : ≥1000

Concentration : ≥20ng/µL

- PCR-Free

Mass : ≥2µg

Concentration : ≥50ng/µL

Metagenomics Solutions

Metagenomics can leverage next-generation sequencing to rapidly analyse the diversity of microbial communities and elucidate the role of constituent species. We offer a suite of metagenomics solutions ranging from targeted assays (16S for prokaryotes and ITS2 for fungi) to whole genome analysis.

Our sequencing scale and proprietary technology ensures highly competitive pricing while our extensive experience across a vast range of metagenomics projects ensures our experts are able to provide custom bioinformatics solutions that can help elucidate the relationship between host-associated microbial communities and host phenotype

Library Preparation Kits	: NEBNext Ultra II FS DNA Library Prep Kit for Illumina
TAT	: 3 weeks to generate the raw data
Sequencing Platform	: Illumina Novaseq 6000 and MiSeq
Read Length	: 150 & 300
Data Requirement	: 5 Gb for WGMG and 0.1M reads for 16S and 18S

Sample Requirements

Regular Samples :

Intact genomic DNA : ≥ 500ng (Recommend ≥ 1000ng)
Concentration : ≥ 25ng/µL
Volume : ≥ 20µL

Low Input Samples :

Intact genomic DNA : ≥ 10ng
Concentration : ≥ 2.5 ng/µL
Volume : ≥ 15µl

Chip Sequencing

ChIP-Sequencing is widely used to analyze protein interaction with DNA. It combines chromatin immunoprecipitation (ChIP) with massively parallel DNA sequencing to identify binding sites of DNA-associated proteins and can be used to precisely map global binding sites for any protein of interest. ChIP sequencing offers higher resolution and more precise and abundant information in comparison to array-based ChIP-chip approaches.

Library Preparation Kits	: NEBNext Ultra II DNA Library Prep Kit for Illumina
TAT	: 3 weeks to generate the raw data
Sequencing Platform	: Illumina Novaseq 6000
Read Length	: 150PE
Data Requirement	: 30M Reads

Sample Requirements

ChIP DNA : ≥ 10ng (Recommend ≥ 50ng), with fragments in the range of 200 to 400 bp
Concentration : ≥ 1ng/µL
Volume : ≥ 20µL

Targeted Sequencing

Targeted Sequencing is an effective method for analyzing your selected gene(s) of interest by next-generation sequencing. Whether you are interested in a few genes, or a few hundred genes, targeted resequencing panels offer high sensitivity and specificity, providing in-depth coverage, and resulting in high-quality data.

With Custom Targeted Sequencing gene panels, you can discover point mutations, insertions/deletions (INDELs), copy number variations (CNVs), and gene rearrangements.

Library Preparation Kits	:	Illumina/Twist/Agilent
TAT	:	8 to 10 weeks to generate the raw data
Sequencing Platform	:	Illumina Novaseq 6000 and Miniseq
Read Length	:	150
Data Requirement	:	Depends on the panel size

Sample Requirements

Intact genomic DNA : 1000ng (Recommend ≥ 2000ng)
Concentration : ≥ 50ng/µL
Volume : ≥ 20µL

Small RNA Sequencing

Small RNAs are a type of non-coding RNA (ncRNA) molecule that are less than 200nt in length. They are often involved in gene silencing and post-transcriptional regulation of gene expression. Our sequencing scale and extensive experience ensure high-quality, fast small RNA services at unbeatable pricing. Small RNA sequencing is used to discover novel small RNAs, examine the differential expression of all small RNAs and to characterize variations with single-base resolution.

Library Preparation Kits	:	QIAseq miRNA Library Kit
TAT	:	3 weeks to generate the raw data
Sequencing Platform	:	NextSeq 550
Read Length	:	75
Data Requirement	:	20M Reads

Sample Requirements

Regular Samples :

Mass : ≥ 1µg
Concentration : ≥ 50ng/µl
Volume : 15 µl

General Quality Requirements :

RIN ≥ 6.5 (plant)
RIN ≥ 8.0 (human/animal)
(Note, we can process degraded samples at lower quality thresholds)

Whole Genome Bisulfite Sequencing (WGBS)

Whole Genome Bisulfite Sequencing (WGBS) provides a scalable solution for cell characterization and gene expression profiling of hundreds to millions of cells. Methylation of DNA at the fifth position in cytosine (5-mC) is a stable epigenetic modification and plays an important role in many biological processes, including gene silencing, suppression of transposable elements, genomic imprinting and X chromosome inactivation. Detection and quantification of methylation are critical to understand gene expression and other processes subjected to epigenetic regulation.

Whole genome bisulfite sequencing (WGBS) is used to detect methylated cytosines by treating the DNA with sodium bisulfite before sequencing. WGBS has become the gold standard for studying genome-wide methylation at single base resolution.

Library Preparation Kits	: Zymo-Seq WGBS Library Kit
TAT	: 3 weeks to generate the raw data
Sequencing Platform	: Novaseq 6000
Read Length	: 150PE
Data Requirement	: 30X

Sample Requirements

Mass : ≥ 1µg

Concentration : ≥ 50ng/µl

Volume : 20 µl

Genomic Platforms

Discovery

Illumina
NOVASeq 6000

Illumina
MiSeq

Validation

Illumina
iScan

Affymetrix
GeneChip
3000 7G

Fluidigm
EP1

Thermo Fisher Scientific
3730xl

Thermo Fisher Scientific
QuantStudio 5

Next-Generation Sequencing (NGS) Overview

Whether it is your first next-generation sequencing project or your hundredth, the MFine team is dedicated to helping you find the right NGS solution for your research projects. We have spent years optimizing our processes to deliver the highest quality results that meet your budget, deadline and outcome. MFine provides complete NGS solutions from our state-of-the-art laboratory in Chennai and we offer both standard and custom services starting from NA extraction, library preparation, sequencing, and bioinformatics on Illumina sequencing platforms like Novaseq 6000, Nextseq 550 and Miniseq.

RNA Sequencing

RNA sequencing (mRNA and mRNA+lncRNA) is a powerful method for studying the transcriptome at the whole genome level qualitatively and quantitatively. It can be used for research such as novel transcriptome, fusion gene, alternative splicing, and mutation information as well as inter-gene expression profiles

We at MFine provide unparalleled flexibility in the analysis of different RNA species (coding, non-coding, and small transcripts) from a wide range of starting materials using short-read (150PE) sequencing.

Library Preparation Kits	:	NEBNext Ultra™ II RNA Library Prep Kit for Illumina NEBNext Ultra™ II Directional RNA Library Prep Kit for Illumina
TAT	:	3 weeks to generate the raw data
Sequencing Platform	:	Illumina Novaseq 6000
Read Length	:	150PE
Data Requirement	:	30M for mRNA and 60M reads for mRNA+lncRNA
Q30	:	>90%

Sample Requirements

Total RNA : ≥ 1000ng, **Concentration :** ≥ 50ng/µl

General Quality Requirements:

RIN : ≥ 7.0 **28S/18S :** ≥ 1.0

(Note, we can process degraded samples at lower quality thresholds)

Whole Exome Sequencing

Whole exome sequencing (WES) is a powerful tool to investigate genetic variations underlying cancers, Mendelian diseases, and complex human disorders. Targeting only protein-coding regions, WES provides a more cost-effective approach than whole genome sequencing.

Library Preparation Kits	:	Twist Biosciences Human Comprehensive Exome Agilent SureSelect Human All Exon V6+UTR
TAT	:	3 weeks to generate the raw data
Sequencing Platform	:	Illumina Novaseq 6000
Read Length	:	150
Data Requirement	:	8 Gb

Sample Requirements

Intact genomic DNA : ≥ 1000 ng **Concentration :** ≥25ng/µL

Volume : 50 µL