



GenomeScopeNICU

for sick NICU/PICU Babies

- A Breakthrough that is Need of the Hour

Name of Salesperson: Contact:

 support@mfine.co

 www.mfine.co



Genetic Diseases are common and leading cause of Mortality in NICU and PICU settings.¹ The disease progression can be rapid in infants, performing genetic testing at the first clinical indication can shorten the time to a diagnosis, guide immediate changes in medical management, and direct towards optimal care.

When The Clock Is Ticking...

Currently, comprehensive exome sequencing requires weeks or months to obtain actionable test results as conventional high throughput sequencing platforms run cases by batch, reducing flexibility for individual prioritized cases!

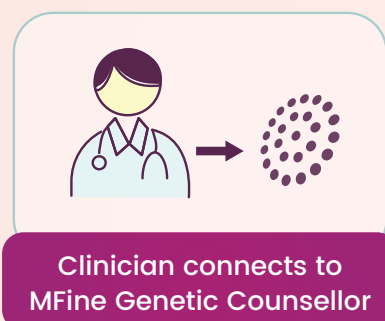
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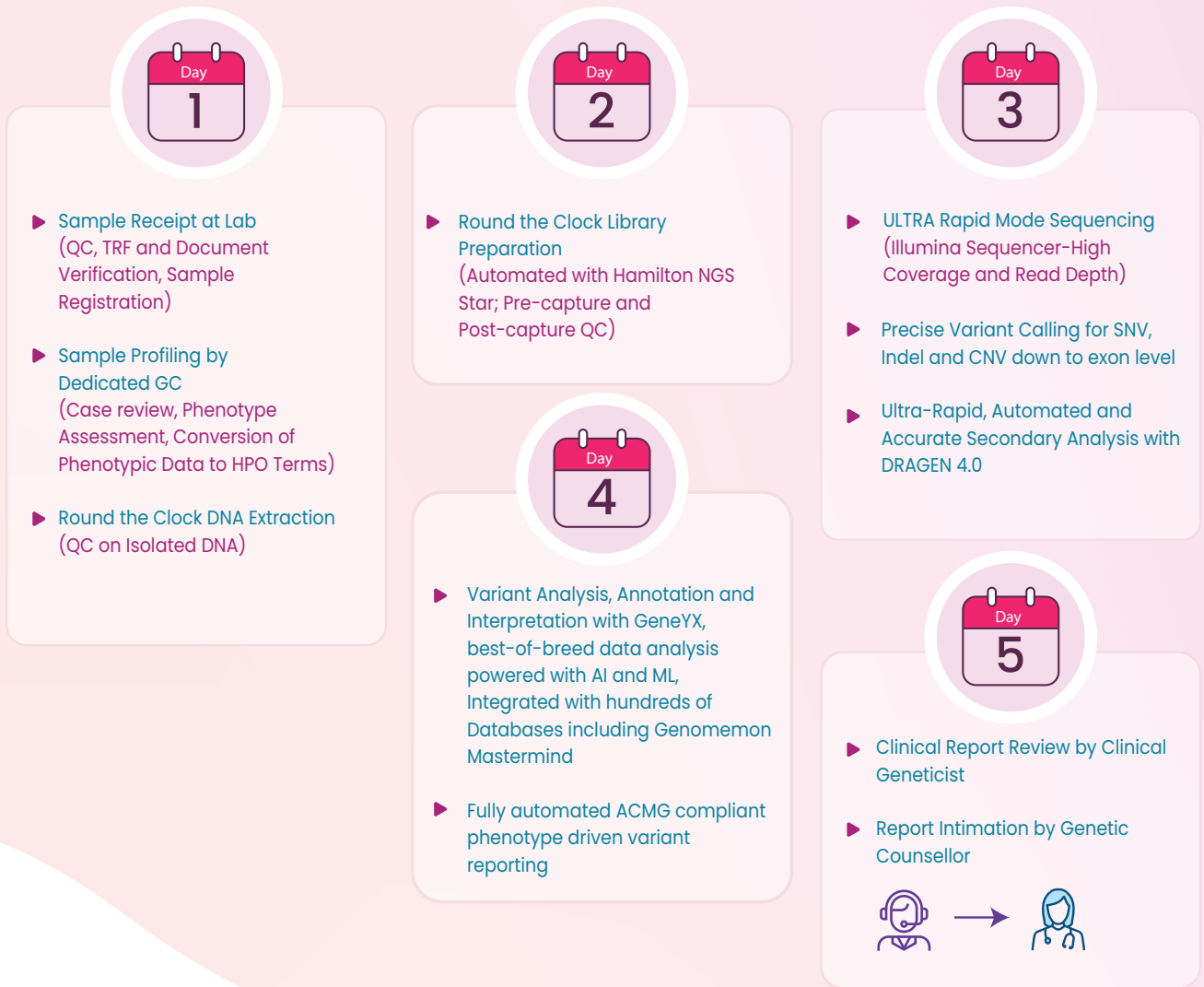
India's First Lightning Speed Gene Sequencing for
Sick NICU/ PICU Babies

GenomeScopeNICU

MFine presents, for the first time in India, GenomeScopeNICU, Advanced Next Generation Sequencing based test panels that breaks the time barriers to give you results in JUST 5 DAYS - helping to improve outcomes in critically ill newborns by expediting an accurate diagnosis and effective treatment.

Referral Process and Patient Selection





Pathogenicity Score:



Rare:

Given the severity of the Phenotype, the allele has <1% frequency in population



Protein Altering:

Most likely to have a biological consequence like Loss of Function



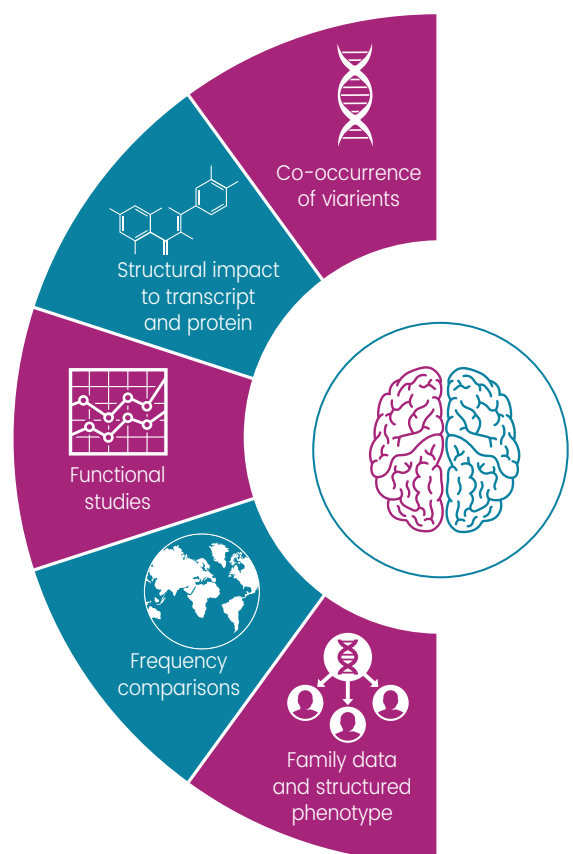
Know Disease Gene:

Variant present in a Gene and locus known to be associated with Mendelian Disease



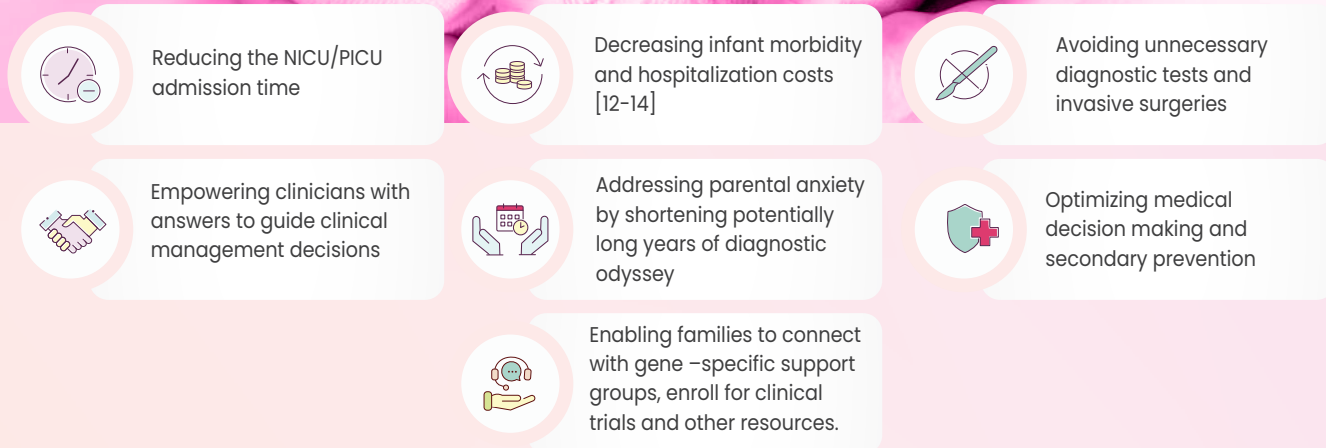
Literature Evidence:

HGMD, ClinVar, Mastermind and many more

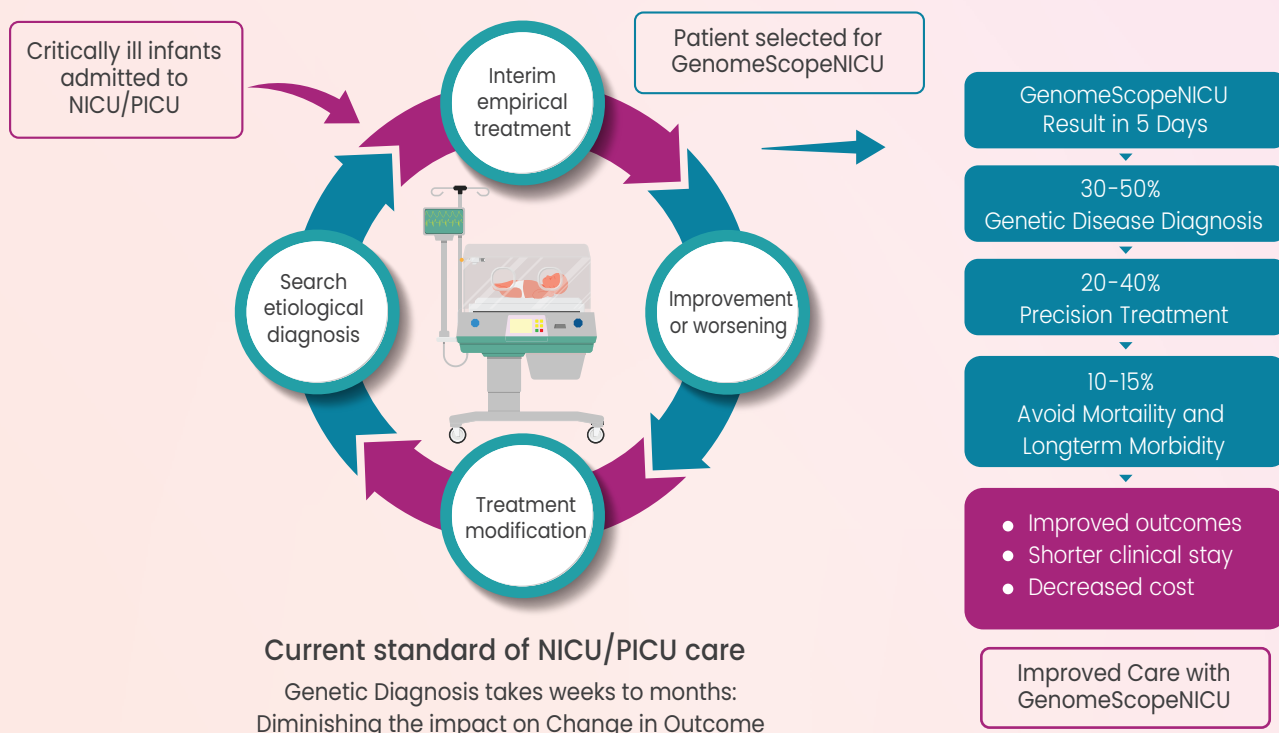


Why Choose GenomeScopeNICU?

Genetic disorders and congenital anomalies affect ~6-7% of live births, and are the leading reason for hospitalization and mortality in infants.² Most genetic conditions do not present noticeably distinct symptomatology at early stages, especially in the neonatal stage. Choosing right genetic test can have a huge impact in:



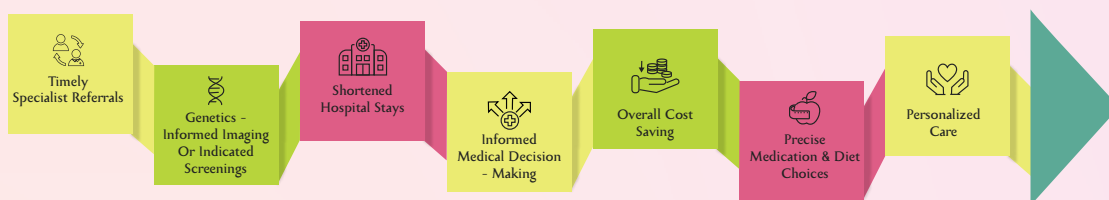
Paradigm Shift in NICU/PICU Standard of Care with GenomeScopeNICU



Proven Statistical Benefits Of Rapid Genetic Testing

- 31%** diagnostic yield in the Intensive Care Settings, more effective when ordered early for critically ill newborns along with parent samples.³
- 32%** of babies who received a diagnosis from rapid genome testing had a change in clinical management.⁴
- 33%** of babies who received positive results from rapid genome testing were not previously suspected of having a genetic condition.⁵
- 50%** Clinical Sensitivity reported in identifying the cause of the infant's condition ^{1,6}

Achieve more with GenomeScopeNICU Panels



Reveal more with GenomeScopeNICU Panels

The exome is estimated to encompass approximately 1% of the genome, yet contains approximately 85% of disease-causing mutations. GenomeScopeNICU is an application of Next Generation Sequencing designed to include all clinically relevant Coding (Exonic) regions as well as known pathogenic deep non-coding (Intronic) regions and nucleotide sequences flanking exon-Intron boundaries (~10bp).

- ▶ GenomeScopeNICU enables the simultaneous identification of single nucleotide variants (SNVs), gene level copy number variations (CNVs) up to aneuploidies, and small insertions or deletions (indels), as well as rare de novo mutations that may help gain comprehensive insights into Mendelian and complex disorders. This makes it possible to offer Dual Diagnosis in some cases.
- ▶ Mean depth is 80-100x with >95% of targeted regions covered at 20x; > 85% of bases have a Q30 sequencing quality score
- ▶ Detects SNVs and Indels with sensitivity >99%
- ▶ Offers superior coverage of major genetic databases like RefSeq, CCDS, GenCode, Clinvar, ACMG73 etc and of clinically relevant non-coding pathogenic and likely pathogenic variants

GenomeScopeNICU-CES provides coverage of 6800+ genes, with focused in-depth coverage of genes selected from various databases like ClinVar, OMIM, Decipher, DisGenNET, HPO, ACMG with strong to moderate support on its association with disease phenotype. Specificity is >99% for all reported variants

GenomeScopeNICU-WES provides Coverage of ~22000 genes and spiked coverage for Human Core Exome and Mitochondrial genome over noncoding regions that are known to carry pathogenic or likely pathogenic variants. This panel's high uniformity and low off-target rate deliver best-in-class sequencing efficiency. Specificity >95% for all reported variants

GenomeScopeNICU panels may also uncover pathogenic variants in genes unrelated to the patient's primary concern, but are medically actionable, known as secondary findings. The American College of Medical Genetics and Genomics (ACMG) recommends disease-causing variants in certain cancer, cardiovascular and other genes be reported, even if they are not related to the patient's condition because monitoring or early treatment may be available. Other medically actionable incidental variants in non-ACMG genes may be reported at laboratory's discretion.



Expert Recommended

The American College of Medical Genetics and Genomics (ACMG) recommends exome and genome testing as a first-tier test when an infant presents with congenital anomalies.⁸

Establishing an etiologic diagnosis in children will ensure timely implementation of precision medicine and optimal outcomes, particularly to guide weighty clinical decisions such as surgeries, extracorporeal membrane oxygenation, therapeutic selection, and palliative care.⁹

Indications for GenomeScopeNICU Testing

The diagnostic yield of whole exome sequencing has surpassed that of historically recommended tests in a clinically heterogeneous cohort.⁸

- ▶ Rapidly deteriorating clinical status
- ▶ Under the age of 1 year and presenting with congenital anomalies
- ▶ NICU/ PICU patients with no history of trauma, infection, or prematurity
- ▶ Unclear or atypical presentation of a genetic disorder
- ▶ Long list of differential diagnosis
- ▶ Child's medical history and physical exam findings strongly suggest that there is an underlying genetic aetiology

Presenting with unclear symptoms which can be part of a genetic condition like Bleeding diathesis, Blood abnormalities (anaemia), Bone fragility, Failure to thrive, Heart abnormality/arrhythmia, Hepatosplenomegaly, Hypotonia, Ichthyosis/epidermolysis bullosa, Metabolic abnormalities, Microcephaly, Neutropenia, Abnormal newborn screening results, Respiratory failure, Skeletal abnormalities/craniosynostosis, Skin fragility, Unclear seizures

- ▶ Family History of unexplained neonatal deaths
- ▶ Parental Consanguinity in the background

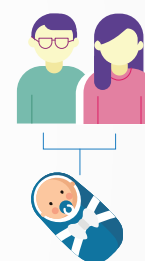
What Makes GenomeScopeNICU TRIO-Exome Sequencing The Better Choice?

Inheritance is the process by which genetic information is passed on from parent to child. The child gets one copy of the genetic material from each of the parents.

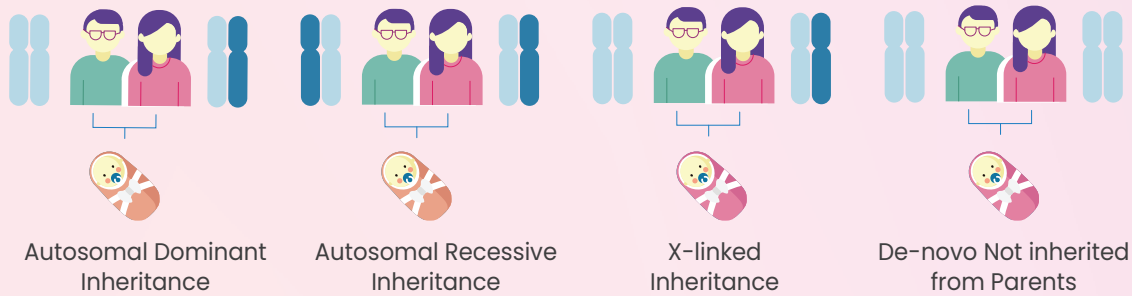
If there is a variation in the parent's genetic material, this can also be passed on from parent to child.

Sometimes these disease-causing variations occur during Embryo development (de-novo) and are not present in the parents.

GenomeScopeNICU-TRIOExome panels offer an advanced approach for detecting inherited variations that may become a cause of illness in babies.



Modes of Inheritance of a Genetic Disease



Because this test targets millions of genes, thousands of DNA changes (Variants) are detected which may be harmless, disease causing or have an unknown effect. Compared to GenomeScope NICU-Proband, where only the baby's DNA is analysed, GenomeScopeNICU-TRIO analyses the genetic data of the biological parents (mother and father) simultaneously along with the baby. This model offers commendable advancements including:

Clear demarcation of the mode of inheritance (Dominant, Homozygous or Compound Heterozygous Recessive, X linked) or identification of de novo mutations in a child and aids in classification of causal variants.

Huge reduction in the chance of finding a Variant of Unknown Significance (VOUS) where the interpretation is not always straightforward and need for follow-up testing may arise.

Combined variant calling increases the accuracy of variant calling and ability to make variant calls in low coverage regions

10-15%¹⁰ additional increase in the diagnostic yield.

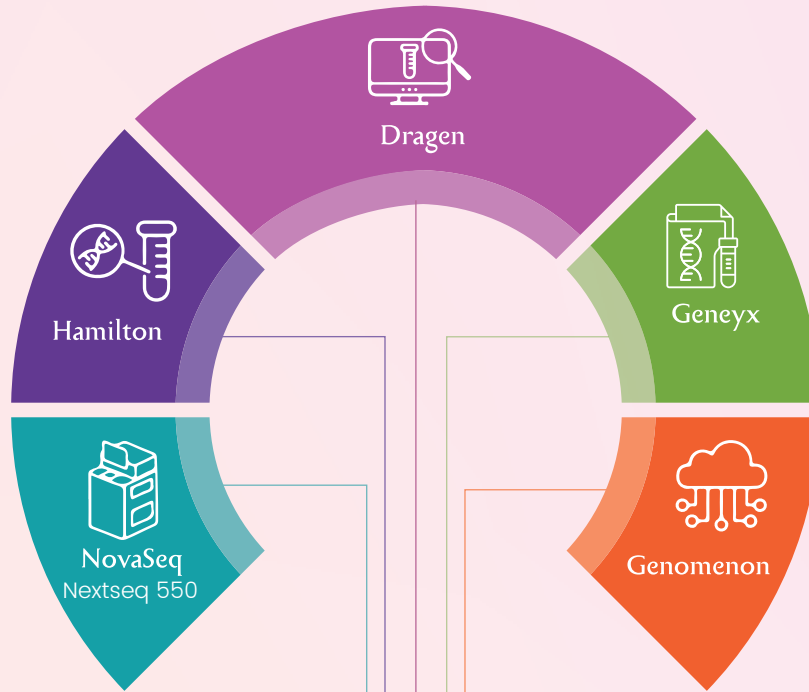
Allows the laboratory to ascertain significance of clinically relevant variants and exclude the ones which do not conform to Mendelian transmission, thereby reducing the false positive calls and narrowing down the potential candidate variants.

As far as the cost is concerned, on the surface, it may seem like a slightly expensive option. However, considering its enormous benefits in medically actionable and timely diagnosis, the TRIO model is preferred worldwide.



MFine's Next Generation Sequencing Solutions

Use Of Best-in-class Tools To Deliver Robust Content And Performance.




Illumina Systems provides high scalability and flexibility to accommodate diverse applications with deeper and broader coverage for a comprehensive view of the genome at a rapid turnaround time.

Hamilton NGS Star is pioneer in high-precision automated library preparation that increases workflow efficiencies, sample throughput, and quality in results.

Dragen is used for accurate, ultra-rapid secondary analysis of sequencing data. It offers increased genome coverage with Illumina Machine Learning and DRAGEN Graph genome mapping for an unprecedented accuracy across all read technologies for difficult-to-map regions, all benchmark regions and Major Histocompatibility Complex (MHC) regions. This enables the detection of challenging and medically relevant variants.

Mastemind by **Genomenon** uses artificial intelligence to connect the genetic mutations buried in 30 million medical research publications > with patient data and 4.1 million genomic variants obtained from genetic sequencing.

Geneyx A clinical genetics data management platform with best-of-breed AI-based data analysis and interpretation tools. Integrated with >150 knowledgebase, it doubles the diagnostic yield 25-30% to ~60%. Increases phenotype driven interpretation from 2 to 20%. Analyses a greater percentage of the genome while significantly reducing (~ 959%) the analysis time. Offers Cloud Data storage. protection and privacy and Compliance with ACMG & ClinGen.

 Phenotype-Driven Results

 Actionable Next Steps

 Expert Clinical Support



Extensive, Unparalleled Support

Our Clinical Geneticists, Genetic Counsellors, MD/PhD scientists, clinical and molecular genomics specialists enable us to provide clear, accurate, and meaningful test reports. Their deep knowledge helps in assisting you with any questions that you may have at various stages of the genetic testing process.



Express Genetic Counselling Services

We offer pre- and post-test genetic counselling with Board Certified Genetic Counsellor at no additional charge for patients when testing is ordered through LifeCell.



Innovation Pioneers

We have been at the forefront of genetic innovation, pioneering incorporation of new technologies and gene inclusions. Our unmatched experience enables us to offer greater diagnostic accuracy, fewer VUS (variants of uncertain significance), and data-backed answers for your patients.



PAN India Presence

Apart from the central Lab at Chennai, we have 8 regional labs and 62 collection centers across India and are expanding further every day.



Proven Track Record with Assured Quality

We are a CAP, NABL and ISO 9001: 2015 laboratory associated with more than 2000 clinics. Our experience of offering Prenatal screening to more than 7,00,000 ; Newborn screening to more than 4,60,000 and Exome sequencing to more than 15,000 patients remains unparalleled!

Test Code	Test Name	Sample Requirement	Documentation Requirement	Turnaround Time
GEN0721	GenomescopeNICU WES-TRIO (*Preferred Globally)	<ul style="list-style-type: none"> Dried blood spot (DBS) -for Proband Whole Blood in lavender-top (EDTA) tubes 	<ol style="list-style-type: none"> Duly Filled TRF Parent's and ordering Clinician's Consent Mobile Number and Email of ordering Clinician. 	10 Days
GEN0725	GenomescopeNICU WES -DUO	<p>Note:</p> <p>Frozen Samples are unacceptable</p>	<ol style="list-style-type: none"> Child's age , gender and detailed Clinical History, Three generation Pedigree Chart 	10 Days
GEN0726	GenomescopeNICU WES- Proband		<ol style="list-style-type: none"> Family History and Consanguinity related information must be shared 	10 Days
GEN0727	GenomescopeNICU CES-TRIO		<ol style="list-style-type: none"> Clinician's notes/ OPD cards/ Dr's prescription/ Discharge Summary 	10 Days
GEN0728	GenomescopeNICU CES-DUO		<ol style="list-style-type: none"> Reports of any investigation carried out like abnormal MRI/Echo/Ultrasound/X-Ray or metabolic test results 	10 Days
GEN0729	GenomescopeNICU CES -Proband		<ol style="list-style-type: none"> Any past genetic test results of family members detailing diagnosis/symptoms and age of onset in each relative 	10 Days
GEN0729	GenomescopeNICU CES -Proband			

References:

- PMID: 25937001; PMCID: PMC4479194
Title: Whole-Genome Sequencing For Identification Of Mendelian Disorders In Critically Ill Infants: A Retrospective Analysis Of Diagnostic And Clinical Findings
- <https://www.nhp.gov.in/disease/gynaecology-and-obstetrics/congenital-anomalies-birth-defects>
Title: Congenital Anomalies (Birth Defects)
- JAMA Pediatr. 2021;175(12):1218-1226. doi: 10.1001/jamapediatrics.2021.3496.
Title: Effect Of Whole-Genome Sequencing On The Clinical Management Of Acutely Ill Infants With Suspected Genetic Disease: A Randomised Clinical Trial
- Am J Hum Genet. 2021;108(7):1231-1238. doi: 10.1016/j.ajhg.2021.05.008.
Title: Project Baby Bear: Rapid Precision Care Incorporating RwgS In 5 California Children's Hospitals Demonstrates Improved Clinical Outcomes And Reduced Costs Of Care
- <https://www.sciencedirect.com/science/article/pii/S1098360022003331>
Improving Access Equity For A Precise Genetic Diagnosis In The NICU
- CMAJ . 2016;188(11):E254-E260.
Title: Next-Generation Sequencing For Diagnosis Of Rare Diseases In The Neonatal Intensive Care Unit
- Genome Biol 12(9):R84.
Title: The Functional Spectrum Of Low-Frequency Coding Variation
- Genet Med. 2021;23(11):2029-2037. doi: 10.1038/s41436-021-01242-6
Title: Exome And Genome Sequencing For Paediatric Patients With Congenital Anomalies Or Intellectual Disability: An Evidence-Based Clinical Guideline Of The American College Of Medical Genetics And Genomics (ACMG)
- Semin Perinatol. 39, 623-631 (2015)
Title: Rapid Whole Genome Sequencing And Precision Neonatology
- JAMA Pediatr. 2017:e173438.
Title: Use of Exome Sequencing for Infants in Intensive Care Units: Ascertainment of Severe Single-Gene Disorders and Effect on Medical Management
- Genet Med . 2017;19(2):249-255.
Title: Recommendations For Reporting Of Secondary Findings In Clinical Exome And Genome Sequencing, 2016 Update (Acmg Sf V2.0): A Policy Statement Of The American College Of Medical Genetics And Genomics
- npj Genom. Med. 3, 10 (2018)
Title: Rapid Whole-Genome Sequencing Decreases Infant Morbidity And Cost Of Hospitalisation
Sci. Transl. Med. 11, 489 (2019).
- Title: Diagnosis Of Genetic Diseases In Seriously Ill Children By Rapid Whole-Genome Sequencing And Automated Phenotyping And Interpretation
- J. Med. Genet. 55(11), 721-728 (2018)
Title: Rapid Paediatric Sequencing (Raps): Comprehensive Real-Life Workflow For Rapid Diagnosis Of Critically Ill Children



support@mfine.co



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