

NOTICE INVITING TENDER



ALL INDIA INSTITUTE OF MEDICAL SCIENCES

ANSARI NAGAR, NEW DELHI-110 029

TENDER ENQUIRY DOCUMENTS (TED)

Advertised Tender Enquiry No : **XX-63/SO(DO)/EOI/Pediatrics/2026-27**

On behalf of Director, AIIMS, Ansari Nagar, New Delhi-110 029, online bids are invited in two bid system (Techno-Commercial Bid and Financial Bid) from reputed, eligible and qualified firms/manufacturer for supply of following Goods:

S. No.	Brief Description of Goods
1.	Expression of Interest for Diagnostic Genomic Testing services for OPD Patients.

CRITICAL DATE SHEET

Published Date & Time	12-08-2026 at 06.00 pm
Bid Document Download/Sale Start Date	12-08-2026 at 06.00 pm
Seek Clarification Start Date	NA
Seek Clarification End Date	NA
Pre Bid Meeting	20-08-2026 at 10.00 AM
Pre Bid Meeting Place & Address	Room No 840, 8 th Floor, Department of Pediatrics, Mother and Child Block, AIIMS New Delhi
Bid Submission Start Date & Time	29-08-2026 at 01.00 pm
Bid Submission End Date & Time	14-09-2026 (Monday) at 03.00 pm
Bid Opening Date & Time	15-09-2026 (Tuesday) at 03.00 pm

Technical Specifications for diagnostic genomic tests

EXOME AND GENOME SEQUENCING

Background:

Whole Exome Sequencing (WES), is a comprehensive genomic diagnostic test that interrogates the protein-coding regions of the genome to identify disease-causing variants. It is recommended for individuals with suspected monogenic disorders, heterogeneous phenotypes, and unsolved cases after first-tier testing. Whole Genome Sequencing (WGS) is a comprehensive genomic diagnostic test that interrogates the entire nuclear genome, enabling detection of single nucleotide variants, small insertions/deletions, copy number variants, structural variants, and selected non-coding and regulatory region variants. WGS is increasingly recommended for complex, unsolved, or critically ill cases where prior testing (CMA, exome sequencing) is inconclusive.

This tender seeks to empanel/select qualified laboratories or service providers capable of delivering high-quality, clinically validated exome and genome sequencing services with robust interpretation and reporting. These may include either proband-only sequencing or trio-sequencing (including proband and both parents).

Specification for sequencing data

The selected bidder shall provide end-to-end WES services, including:

- Sample collection guidelines and logistics
- DNA extraction (if applicable)
- Library preparation, sequencing, and bioinformatics analysis
- Clinical variant interpretation and reporting
- Turnaround time (TAT) assurance
- Reanalysis and post-test support

Sample Types and Requirements

Recd
4/14/20

Spec

GP

JP

2/

Recd

- Peripheral blood (EDTA): 2-3 mL per individual
- Saliva / buccal swab/ Dried blood spots (if offered, with validation data)
- Prenatal samples (if offered):
 - Amniotic fluid: 10-15 mL
 - Chorionic villus sample (CVS): as per standard guidelines
- DNA quality and quantity requirements to be specified

Test Configuration

The bidder must specify available configurations:

- Proband-only WES or WGS
- Duo WES or WGS (proband + one parent)
- Trio WES or WGS (proband + both parents)
- Rapid/STAT WES or WGS

See
4/4/20

Free

See

See

See

See

Test specifications

Test Name	Whole Exome Sequencing		Whole Genome Sequencing	
	(solo)	(trio)	(solo)	(trio)
Genes Covered	>20000 genes	>20000 genes	Complete genome	Complete genome
Sequencing Platform	Illumina	Illumina	Illumina	Illumina
Kit Specification	Twist exome 2.0 or equivalent or better version		Twist exome 2.0 or equivalent or better version	
	Name of the kit used		Name of the kit used	
Vertical coverage (Depth)	>80X		>80X	
	Horizontal coverage		Horizontal coverage	
Raw data requirements	>97% coverage		>97% coverage	
	Fastq files		Fastq files	
	BAM file		BAM file	
	Raw vcf file		Raw vcf file	
	Annotated vcf file		Annotated vcf file	
Coverage		Coverage	Coverage	Coverage

1

4/4/26

4/4/26

4/4/26

4/4/26

4/4/26

Capture and Coverage

- Clinical-grade exome capture kit to be specified
- $\geq 95\%$ of targeted exonic regions covered at $\geq 20\times$ depth
- Mean target coverage: $280-100\times$ (to be specified)
- Coverage metrics to be included in the report

Sequencing Technology

- Massively Parallel Sequencing (NGS) using Illumina or equivalent platforms.
- Paired-end sequencing (minimum 100 bp reads) in WES and Paired-end sequencing (≥ 150 bp reads preferred) for WGS

Detectable Variant Types

The assay must reliably detect:

- Single nucleotide variants (SNVs)
- Small insertions and deletions (indels)
- Copy number variants (exome-based CNV calling – if offered, specify limits)
- Homozygosity/ROH (if SNP data available)
- For WGS,
 - Structural variants (deletions, duplications, inversions, translocations) with stated limits
 - Repeat expansions (if bioinformatically supported, specify loci)
 - Regions of homozygosity (ROH) and uniparental disomy (UPD)
 - Mitochondrial genome variants (preferred, specify depth)

Limitations must be clearly stated, including:

10/1/14

10/1/14

10/1/14

10/1/14

10/1/14

- Low-level mosaicism detection limits
- Structural variants and repeat expansions (WGS)

Analytical Performance and Validation

Bidders must provide:

- Platform and pipeline validation data
- Sensitivity and specificity for SNVs, indels, CNVs, and SVs
- Minimum variant allele fraction detectable
- Reproducibility and QC performance metrics

Bioinformatics Pipeline

- Validated alignment, variant calling, and annotation pipeline
- Use of up-to-date reference genome (GRCh38 preferred; specify if GRCh37)
- Annotation using multiple databases (ClinVar, gnomAD, OMIM, HGMD or equivalent)
- Phenotype-driven analysis using HPO terms (preferred)

Variant Interpretation and Classification

- Variant classification according to ACMG/AMP guidelines (latest version)
- Structural variant interpretation using ACMG/ClinGen recommendations
- Clear categorization: Pathogenic, Likely Pathogenic, VUS, Likely Benign, Benign
- Gene-disease validity based on ClinGen or equivalent resources

Reporting Requirements

The WES/WGS report must include:

yes

yes

yes

yes

yes

- Patient identifiers and detailed clinical phenotype
- Test configuration (proband/duo/tri/rapid)
- Sequencing metrics and coverage summary
- Identified clinically relevant variants with:
 - Gene name and transcript
 - Genomic coordinates and HGVS nomenclature
 - Zygosity and inheritance pattern
 - Clinical interpretation and phenotype correlation
- Secondary/incidental findings policy (ACMG SF list – opt-in/opt-out)
- Recommendations for confirmatory testing (e.g., Sanger validation) and family studies
- Clear limitations of the test
- Authorized signatory (Medical Geneticist / MD / PhD Genetics)

Turnaround Time (TAT)

- Proband-only exome: 3-4 weeks
- Proband-only Genome: 6-8 weeks
- Trio exome: 3-4 weeks
- Trio Genome: 6-8 weeks
- Prenatal/Expedited/STAT exome (for time bound situations) - 10-14 days
- Rapid exome/genome (critically sick patients) - 5-7 days

Quality and Accreditation

4/11/24

[Signature]

[Signature]

[Signature]

[Signature]

The laboratory must:

- Be accredited by NABL (India) / CAP / ISO 15189 for NGS testing.
- Participate in External Quality Assurance Schemes (EQAS) for NGS
- Maintain documented SOPs, IQC, and audit trails

Ethical, Legal, and Regulatory Compliance

- Written informed consent covering scope, limitations, and secondary findings
- Compliance with national biomedical ethics guidelines
- Compliance with data protection and privacy laws
- For prenatal testing, compliance with PCPNDT Act

Data Management, Storage, and Reanalysis

- Secure data storage for FASTQ/BAM/VCF files
- Data sharing only with authorized stakeholders
- Defined data retention period
- Complimentary reanalysis within 12-24 months
- Policy for data sharing and patient access

Logistics and Sample Handling

- Defined sample acceptance/rejection criteria
- Cold-chain and transport requirements (if applicable)
- Mechanism for repeat analysis in case of QC failure or some other technical reason

Neer
04/12

Shruti

Shruti

Shruti

Rashmi

Evaluation criteria

Bids will be evaluated based on:

- Technical capability and coverage quality
- Interpretation depth and clinical reporting quality
- Accreditation and quality systems
- Turnaround time
- Cost effectiveness and experience

Expected numbers of NGS samples per month

Exome- 250-300

Genome- 50-100

OK

Rec'd
4/4/22

h

h

MR

Rec'd

Specification for Chromosomal Microarray

Chromosomal Microarray Analysis (CMA) is a first-tier diagnostic test for the detection of copy number variations (CNVs), including microdeletions and microduplications, across the genome. It is widely recommended for individuals with developmental delay, intellectual disability, autism spectrum disorder, multiple congenital anomalies, and selected prenatal indications. This tender aims to identify and empower qualified laboratories/service providers capable of delivering high-quality, reliable, and clinically interpretable CMA services in compliance with national and international standards.

The selected bidder shall provide end-to-end CMA services, including:

- Sample collection requirements and guidelines
- Laboratory processing and analysis
- Bioinformatics analysis and CNV interpretation
- Clinical reporting
- Turnaround time (TAT) assurance
- Post-test clarification and quality assurance support

Sample Types and Requirements

- Peripheral blood (EDTA): 2-3 mL (postnatal)
- Prenatal samples (if offered):
 - Amniotic fluid: 10-15 mL
 - Chorionic villus sample (CVS): as per standard guidelines
- Products of conception: fresh tissue or DNA (with clear acceptance criteria)

See
spec

See

See
spec

Test Name	Microarray
Total Probes	>7,00,000
CNV Probes	> 5,00,000
SNP Probes	>2,00,000
Detection Limit	
a) Gain	Till 200Kb
b) Loss	Till 100 Kb
c) Mosaicism	Till >15%
d) LOH analysis	-
Raw data requirements	Cell files/raw files Library QC Report
Turn around time	7-10 days

The assay must be capable of detecting:

- Copy number gains and losses
- Microdeletion and microduplication syndromes
- Aneuploidies and large chromosomal imbalances
- Mosaicism (with stated detection limits)
- Regions of homozygosity / consanguinity (for SNP-based arrays)

Balanced rearrangements (e.g., inversions, translocations) shall be clearly stated as limitations.

Logistics and Sample Handling

- Clear sample acceptance and rejection criteria
- Defined transport and storage conditions
- Mechanism for repeat analysis in case of QC failure

Wes 1/1/24

Wes

Wes

Wes

Wes

Data Management, Data Provision and Confidentiality

Secure Laboratory Information Management System (LIMS)

The final data should be made available on a hard disc drive as well as accessible on cloud for a period of two years after completion of sequencing. Files should be compatible with third-party software.

Data sharing only with authorized stakeholders

Expected numbers of samples per month

CMA-30-50

11/1/24

11/1/24

11/1/24

11/1/24

11/1/24

11/1/24

Non-invasive prenatal screening for aneuploidies

Non-invasive Prenatal Screening (NIPS), also referred to as cell-free fetal DNA (cfDNA) testing, is a screening test for common fetal aneuploidies using maternal blood.

The purpose of this tender is to empanel/select qualified laboratories or service providers capable of delivering high-quality, reliable, ethical, and clinically validated NIPS services in accordance with national and international standards

The selected bidder shall provide end-to-end NIPS services, including:

- Pre-analytical logistics (sample collection kits, transport)
- Laboratory testing and bioinformatics analysis
- Clinical interpretation and reporting
- Turnaround time (TAT) assurance
- Post-test support and quality assurance

Technical specifications

Sample Requirements

- Maternal peripheral blood: 8–10 ml
- Blood collection tubes validated for cfDNA stabilization (e.g., Streck or equivalent)
- Minimum fetal fraction threshold to be specified (e.g., $\geq 4\%$)

Conditions to be Screened (Minimum Requirements):

The assay must, at a minimum, screen for:

- Trisomy 21 (Down syndrome)

Lee
4/4/24

2

gate

2

2

Rashid

- Trisomy 18 (Edwards syndrome)
- Trisomy 13 (Patau syndrome)

Optional (clearly specified if offered):

- Sex chromosome aneuploidies (45,X; 47,XXY; 47,XXX; 47,XYY)

Laboratory Methodology

- Massively Parallel Sequencing (MPS) or validated equivalent technology
- Whole-genome or targeted sequencing approach (to be specified)
- Robust bioinformatics pipeline with validated algorithms

Performance Characteristics

Bidders must provide peer-reviewed or validation data demonstrating:

- Sensitivity ≥99% for Trisomy 21
- Specificity ≥99% for Trisomy 21
- Clearly stated sensitivity/specificity for Trisomy 18 and 13
- Reported no-call rate and redraw policy

Reporting Requirements

Reports must include:

- Patient and sample identifiers
- Gestational age at sampling
- Fetal fraction (mandatory)
- Risk classification (High risk / Low risk / No-call)

Wish
4/4/16

✓

Wish

Wish

Wish

Wish

- Clear statement that NIPS is a screening, not diagnostic, test
- Recommendation for confirmatory invasive testing for high-risk results
- Authorized signatory (MD/PhD in Genetics or equivalent)

Turnaround Time (TAT)

- Maximum TAT: 7-10 working days from sample receipt
- Faster TAT (if available) should be specified separately

The laboratory must:

- Be accredited by NABL (India) / CAP / ISO 15189 or equivalent
- Participate in external quality assurance programs (EQAS) for cfDNA/NIPS
- Maintain internal quality controls and documented SOPs

Ethical, Legal, and Regulatory Compliance

- Strict compliance with the PCPNDT Act (India), including:
 - No disclosure of fetal sex
 - Appropriate documentation and declarations
- Compliance with data protection and patient confidentiality norms
- Informed consent templates to be provided

Expected Numbers: 40-50 per month

Clear 4/4/24

[Signature]

[Signature]

[Signature]

[Signature]

Evaluation Metrics for Bidders

The following criteria of the bidders be assessed:

- Technical compliance and validation data
- Clinical reporting quality
- Turnaround time
- Cost-effectiveness
- Accreditation and quality systems - Lab should be NABL accredited/ISO certified
- Reporting as per standard guidelines (ACMG/AMP)
- Experience and track record

The laboratory performing DNA capture and sequencing should have data from their own wet lab and not from third party

20/11/20

20/11/20

20/11/20

20/11/20

20/11/20

20/11/20

Stemcare Solutions for BMT unit services

Graft engineering using CliniMACS® Technology in stem cell transplantation

Advancing clinical applications

1. TCR a/b and CD19 depletion

- a. Haploidentical Transplants for Malignant and Non-Malignant Diseases - This approach maintains the stem cells and immune effector cells, such as NK cells and TCR g/d in the cellular product. The CliniMACSTCra/b product line can also be used in combination with the CliniMACS CD19 Reagent to additionally remove the CD19+ B cells from the graft. NK cells and TCR g/d T cells are reported to induce GvL/T (graft-versus leukaemia/tumor) effects, while the potential risk of inducing GvHD may be reduced.

2. CliniMACS CD45RA

- a. CD45RA is expressed on naive CD4+ and CD8+ T cells as well as on cos+effector T cells. CD45RA is also present on parts of B cells and NK cells, as well as on plasmacytoid dendritic cells and parts of CD34+ hematopoietic stem cells.
- b. Maintenance of memory T cells in the graft or DLI product. Part of CD34 hematopoietic stem cells are also CD45RA+. This should be considered if memory cell infusion is planned to be combined with the initial transplant.

3. CD 34 (Hematopoietic stem cells) Enrichment

- a. The CliniMACS®CD34 Reagent System is an FDA-approved method for selecting hematopoietic stem cells from donor apheresis, while passively depleting T cells that can cause graft-versus-host disease (GVHD).
- b. Ex vivo T cell depletion can be a viable option to reduce GVHD incidences in patients with AML undergoing allogeneic stem cell transplantation
- c. In the autologous setting, CD34+ cell enrichment has been used for the depletion of tumor cells from the graft and in allogeneic settings to prevent GvHD (Booster stem cell dose&TRx)

Price List:

S. No	Description	Price	GST %
1	CD34 Enrichment consumables (Normal Scale)	Rs 6,25,000	12%
2	CD34 Enrichment Consumables (Large scale)	Rs 10,00,000	12%
3	CD56 (NK) Enrichment Consumables	Rs 6,25,000	12%
4	TCR a/b & CD19 Depletion consumables	Rs 12,50,000	12%
5	TCR a/b & CD45RA Depletion consumables	Rs 12,50,000	12%
9	Cold chain courier charges	Rs 5000	18%
a	GMP lab Processing Charges (Apheresis graft)	Included	
b	Flow analysis charges (Apheresis graft)	Included	
c	Logistics	Included	

High resolution HLA Typing technical specs.

- (i) High resolution HLA typing using Next Generation Sequencing platform e.g. Illumina Novaseq X Plus
- (ii) Coverage : High coverage of all the major HLA Gene regions. Should offer a flexibility of full Gene /Partial coverage for above locus HLA Type 1 & Type 2 (HLA A, HLA B, HLA C, HLA DRB1, HLA DPB1, HLA DQB1) upto 4 fields.
- (iii) Facility for isolation of genomic DNA from peripheral blood samples
- (iv) NGS with 2x150 bp reads. Library preparation should be done using GenDx Kit.
- (v) Should offer a flexibility of Multiplex or Singleplex based amplification strategy (06 or 11 loci)
- (vi) Complete bioinformatics data analysis. Should include the latest IMGT Database.
- (vii) No extra cost should be charged from the PI for re-run the HLA typing if generated data doesn't match the desired quality.
- (viii) The complete scope of work should be done by the vendor within India
- (ix) The vendor should provide a facility certificate to testify the possession of an in-house Illumina Novaseq X Plus explicitly in the name of the Company.
- (x) The vendor should have demonstrated scientific capability for the successful completion of undertaken genomics projects, as documented by the vendor having research publications in peer reviewed journals for at least 5 genomics study projects. An appropriate web link to support this claim should accompany the proposal.
- (xi) The vendor should have a CAP Accredited laboratory in India.
- (xii) Bidder must be providing regular HLA typing service for human disease diagnosis and must submit documentary proof for the same.

Handwritten signature

Handwritten signature

Handwritten signature

Handwritten signature

Handwritten signature

Handwritten signature

