आईआईटीआई दृष्टि सीपीएस फाउंडेशन, भारतीय प्रौद्योगिकी संस्थान इन्दौर
खंडवा रोड, सिमरोल, इन्दौर – 453 552, मध्य प्रदेश, भारत
IITI DRISHTI CPS Foundation, Indian Institute of Technology Indore
Khandwa Road, Simrol, Indore - 453 552, Madhya Pradesh, India

CIN: U73100MP2020NPL054322

Tender no.: IITI DRISHTI -CPS/EQP/15/AG/2025-26 (GeM Bid No: GEM/2025/B/6962820)
Date: 24/12/2025

PRE-BID REPORT

The meeting for pre-bid discussion was held at IITI DRISHTI CPS Foundation via Google Meet on 15/12/2025 from 11.00 AM onwards for Supply, Installation, Training and Commissioning of Next-Generation Sequencing System.

Different prospective bidder representatives joined the call as per below mentioned details-

- **M/s VK Traders**
- **M/s Premas Life Sciences**
- **M/s. Thermo Fisher Life Sciences**

The report of the meeting is as mentioned below along with queries and responses thereof:

Sl. No.	Reference of the Clause No. of the Tender Document	Query/Clarification/Deviation sought	Clarification/Response from IITI DRISHTI CPS Foundation
M/s VK Traders			
01	System should be the most successful and widely adopted sequencing chemistry worldwide. System should use nucleotides with reversible terminators and should mimic natural biological chemistry with simultaneous addition of all four bases in the sequencing reaction for competitive addition to the DNA template.	System should use a globally established, widely adopted NGS chemistry capable of high-accuracy base incorporation (e.g., reversible terminator SBS or semiconductor chemistry) without restricting to a specific manufacturer's chemistry.	Partially Accepted Systems employing reversible terminator–based sequencing by synthesis (SBS) or other globally accepted NGS chemistries, including semiconductor-based sequencing, shall be considered acceptable, provided they: • Are widely adopted and commercially proven worldwide, • Demonstrate high base-calling accuracy and data quality, and • Are supported by adequate peer-reviewed publications, installed base, and long-term vendor support.
02	Sequencing chemistry should be robust and globally proven,	Sequencing chemistry should be robust and globally proven,	Partially Accepted

	as demonstrated with greater than 6000 peer reviewed publications.	supported by substantial peer-reviewed publications	Systems supported by a large body of peer-reviewed publications demonstrating reliability, accuracy, and reproducibility across diverse applications shall be considered compliant. Vendors are requested to provide appropriate documentary evidence (such as representative publications, reviews, or bibliometric summaries) to substantiate the global acceptance and proven performance of the proposed sequencing chemistry.
03	System should offer flexible scalability from 10–240 Gb or more & 100-400 million cluster or more in a single run to support a broad range of applications, including sequencing of human whole exome sequencing, targeted onco panels, HLA typing, Single-cell RNA-Seq/ATACseq (4K cells, 50 K reads per cell) in a single run, metagenomic sequencing, human WGS, ChIP sequencing, transcriptome sequencing etc.	System should offer scalable throughput suitable for targeted panels, exomes and small genomes (up to 25 of Gb and >100 million reads per run), adequate for applications such as human exome sequencing, targeted oncology panels, HLA typing, metagenomics, ChIP-seq and transcriptome sequencing.	Partially accepted While mid-throughput systems suitable for exomes, targeted panels, and transcriptomic applications are acceptable, preference shall be given to platforms that offer scalable or upgradeable throughput to support advanced applications such as whole genome and single-cell sequencing, in alignment with the long-term research and skilling objectives of the facility.
04	The system should have onboard cluster generation in 8–42 hours, to perform integrated massively parallel sequencing of DNA/RNA libraries loaded directly on the system, through integrated cluster generation (emulsion free) and x-leap sequencing by synthesis and offers both single end and paired end sequencing (100, 200, 300, 600 cycles).	The system should support integrated massively parallel sequencing of DNA/RNA libraries loaded directly onto the consumable (chip or flowcell) with automated run setup. Both short and long read lengths suitable for targeted and exome sequencing should be supported, as per manufacturer's specifications	Partially accepted The system should have onboard cluster generation in 8–42 hours, to perform integrated massively parallel sequencing of DNA/RNA libraries loaded directly on the system, through integrated cluster generation (emulsion free) and x-leap sequencing by synthesis or ABC sequencing and offers both single end and paired end sequencing (100, 200, 300, 600 cycles).
05	The sequencing technology should offer accurate sequencing of homopolymers and highest read quality score	Sequencing technology should provide high base-calling accuracy (≥99% for the	Partially Accepted Sequencing platforms demonstrating ≥99.9% base-

	of Q30 or more for more than 85% of the base calls having greater than or equal to 99.9% accuracy ensuring quality control steps.	recommended read lengths) and robust performance on homopolymer regions, as per manufacturer's published specifications, with appropriate built-in quality control metrics.	calling accuracy (Q30 or equivalent) for a substantial proportion of reads, with validated performance in homopolymeric regions and built-in quality control metrics, shall be considered compliant. Vendors using alternative accuracy reporting metrics must provide clear equivalence to Q30-based performance benchmarks
06	System must have inbuilt hardware for ultra-rapid secondary analysis for a wide variety of genomic analysis solutions, including BCL conversion, mapping, alignment, sorting, duplicate marking, and variant calling to allow faster data analysis without the requirement of copying/transferring the data from NGS instrument to other device.	System must have inbuilt hardware and software for rapid secondary analysis, including base calling, mapping,alignment, and variant calling for supported applications, minimizing the need for extensive data transfer	Partially Accepted NGS systems offering integrated onboard hardware and software for rapid secondary analysis-covering base calling, mapping/alignment, and variant calling-are acceptable, provided that the core analysis can be performed on the instrument without mandatory transfer of raw data to external computing infrastructure.
07	The inbuilt bioinformatics platform should cater read alignment and variant calling and other steps of secondary analysis and lossless compression of FASTQ files up to 5 times.	The inbuilt bioinformatics platform should support read alignment, variant calling, and efficient data storage/archiving of sequence files, with options for compression or space optimization as per manufacturer's specifications.	Partially Accepted Systems that provide lossless compression or equivalent space-efficient data management mechanisms, demonstrably reducing storage footprint while preserving full data integrity, shall be considered compliant. Vendors must clearly specify: • The type of compression or optimization employed, • Whether the compression is lossless, • The typical or maximum achievable compression ratio, and • Any limitations associated with file formats or downstream compatibility.

08	The sequencing system should offer a secure and remote instrument performance support service for detection of risk failure preemptively, troubleshoot runs more efficiently, and prevent in-run failures to minimize unplanned downtime and avoid unnecessary sample loss by anticipating repairs and creating alert to field personnel to schedule maintenance visits.	The sequencing system should offer secure remote support and remote diagnostics for instrument performance, helping to troubleshoot runs efficiently and reduce unplanned downtime.	Partially accepted NGS systems that provide secure remote connectivity, real-time or near real-time diagnostics, and remote support tools that demonstrably improve run reliability and reduce downtime shall be considered compliant. Vendors must clearly outline: ● The scope of remote diagnostics and monitoring supported, ● Security measures employed for remote access, and ● The mechanisms used to alert service teams and schedule preventive maintenance.
09	The system should be compatible with more than 10 manufacturer panels other than the quoted parent company, and digital MLPA application.	The system should be compatible with multiple third-party target panels and should support integration without restriction to a single manufacturer's panels.	Partially Accepted NGS systems that demonstrate validated compatibility with a wide range of third-party panels, without proprietary lock-in, shall be considered compliant. Vendors must clearly specify: ● The number and names (or categories) of third-party panels validated on the system, ● The level of vendor support and documentation available for such panels, and ● Support for digital MLPA workflows or equivalent copy-number analysis methodologies, where applicable.
M/s. Imperial Life Sciences (P) Ltd,			
10.	The system should be compact benchtop occupy a minimal lab footprint and	The system should be compact benchtop occupy a minimal lab	Partially Accepted

	should be offered as a complete system with automated template DNA amplification, sequencing, and data analysis (base calling, alignment, variant calling, and reporting) onboard on machine.	footprint and should be offered as a complete system with automated template DNA amplification, sequencing, and data analysis (base calling, alignment, variant calling, and reporting) Onboard/extended with machine.	NGS systems offering an integrated end-to-end workflow-covering automated template amplification, sequencing, and data analysis-are acceptable, provided that analysis is performed onboard or through vendor-supplied, tightly integrated compute resources supplied as part of the complete system.
11.	System should be the most successful and widely adopted sequencing chemistry worldwide. System should use nucleotides with reversible terminators and should mimic natural biological chemistry with simultaneous addition of all four bases in the sequencing reaction for competitive addition to the DNA template.	System should use most successful and widely adopted sequencing chemistry worldwide. System should use nucleotides with reversible terminators and should mimic natural biological chemistry with simultaneous addition of all four bases or ABC sequencing chemistry in the sequencing reaction for competitive addition to the DNA template.	Partially Accepted Systems employing reversible terminator–based sequencing by synthesis (SBS) or other globally accepted NGS chemistries, including semiconductor-based sequencing, shall be considered acceptable, provided they: ● Are widely adopted and commercially proven worldwide, ● Demonstrate high base-calling accuracy and data quality, and ● Are supported by adequate peer-reviewed publications, installed base, and long-term vendor support.
12.	Sequencing chemistry should be robust and globally proven, as demonstrated with greater than 6000 peer reviewed publications.	Sequencing chemistry should be robust and globally proven, as demonstrated with greater than 100 peer reviewed publications.	Partially accepted Systems supported by a large body of peer-reviewed publications demonstrating reliability, accuracy, and reproducibility across diverse applications shall be considered compliant. Vendors are requested to provide appropriate documentary evidence (such as representative publications, reviews, or bibliometric summaries) to substantiate the global acceptance and proven

			performance of the proposed sequencing chemistry.
13.	The manufacturer should have reagents for library preparation of wide range of applications.	The manufacturer/vendor should have reagents/ for library preparation of wide range of applications.	Partially accepted NGS systems supported by a wide range of library preparation reagents are acceptable, provided that such reagents are supplied by the manufacturer or are manufacturer-validated third-party offerings with documented compatibility, application support, and assured supply.
14.	System should offer flexible scalability from 10–240 Gb or more & 100-400 million cluster or more in a single run to support a broad range of applications, including sequencing of human whole exome sequencing, targeted onco panels, HLA typing, Single-cell RNA-Seq/ATACseq (4K cells, 50 K reads per cell) in a single run, metagenomic sequencing, human WGS, ChIP sequencing, transcriptome sequencing etc.	System should offer flexible scalability from 10–500 Gb or more & 100- 2000 million cluster or more in a single run to support a broad range of applications, including sequencing of human whole exome sequencing, targeted onco panels, HLA typing, Single-cell RNA-Seq/ATACseq (4K cells, 50 K reads per cell) in a single run, metagenomic sequencing, human WGS, ChIP sequencing, transcriptome sequencing etc	Partially Accepted While mid-throughput systems suitable for exomes, targeted panels, and transcriptomic applications are acceptable, preference shall be given to platforms that offer scalable or upgradeable throughput to support advanced applications such as whole genome and single-cell sequencing, in alignment with the long-term research and skilling objectives of the facility.
15.	The system should have onboard cluster generation in 8–42 hours, to perform integrated massively parallel sequencing of DNA/RNA libraries loaded directly on the system, through integrated cluster generation (emulsion free) and x-leap sequencing by synthesis and offers both single end and paired end sequencing (100,200, 300, 600 cycles).	The system should have onboard cluster generation in 8–42 hours, to perform integrated massively parallel sequencing of DNA/RNA libraries loaded directly on the system, through integrated cluster generation (emulsion free) and x-leap sequencing by synthesis or ABC sequencing and offers both single end and paired end sequencing (100, 200, 300, 600 cycles).	Partially Accepted The system should have onboard cluster generation in 8–42 hours, to perform integrated massively parallel sequencing of DNA/RNA libraries loaded directly on the system, through integrated cluster generation (emulsion free) and x-leap sequencing by synthesis or ABC sequencing and offers both single end and paired end sequencing (100, 200, 300, 600 cycles).
16.	The sequencing technology should offer accurate sequencing of homopolymers and highest read quality score of Q30 or more for more than 85% of the base calls having	The sequencing technology should offer accurate sequencing of homopolymers and highest read quality score of Q30 and Q40 or more for more than 90% of the base calls having	Partially Accepted Sequencing platforms demonstrating ≥99.9% base-calling accuracy (Q30 or equivalent) for a substantial

	greater than or equal to 99.9% accuracy ensuring quality control steps.	greater than or equal to 99.9% accuracy ensuring quality control steps	proportion of reads, with validated performance in homopolymeric regions and built-in quality control metrics, shall be considered compliant. Vendors using alternative accuracy reporting metrics must provide clear equivalence to Q30-based performance benchmarks
17.	System must have inbuilt hardware for ultra-rapid secondary analysis for a wide variety of genomic analysis solutions, including BCL conversion, mapping, alignment, sorting, duplicate marking, and variant calling to allow faster data analysis without the requirement of copying/transferring the data from NGS instrument to other device.	System should have inbuilt/extended hardware for ultra-rapid secondary analysis for a wide variety of genomic analysis solutions, including BCL conversion, mapping, alignment, sorting, duplicate marking, and variant calling to allow faster data analysis without the requirement of copying/transferring the data from NGS instrument to other device.	Partially accepted NGS systems offering integrated onboard hardware and software for rapid secondary analysis-covering base calling, mapping/alignment, and variant calling-are acceptable, provided that the core analysis can be performed on the instrument without mandatory transfer of raw data to external computing infrastructure.
18.	The inbuilt bioinformatics platform should cater read alignment and variant calling and other steps of secondary analysis and lossless compression of FASTQ files up to 5 times.	The inbuilt/extended bioinformatics platform should cater read alignment and variant calling and other steps of secondary analysis and lossless compression of FASTQ files .	Partially Accepted Systems that provide lossless compression or equivalent space-efficient data management mechanisms, demonstrably reducing storage footprint while preserving full data integrity, shall be considered compliant. Vendors must clearly specify: • The type of compression or optimization employed, • Whether the compression is lossless, • The typical or maximum achievable compression ratio, and • Any limitations associated with file formats or downstream compatibility.

- Submission of OEM authorization in the prescribed format is optional; however, a valid authorization certificate for an authorized dealer or distributor issued by the OEM shall also be acceptable

- All correspondence concerning the tender must be directed to IITI DRISHTI CPS Foundation through the official channels specified in the tender notice.
- All prospective/willing bidders are requested to take note of this report as part of the tender document. All other terms and conditions of the tender remain unchanged.

Adity

Chief Executive Officer
IITI DRISHTI CPS Foundation, Indore