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Ref. No.: IGIMS/ 2019/ 913 **/ Store** **Date:** 29**/11/ 2019**

CORRIGENDUM

Amendment Notice to the Tender Document bearing E-Tender Notice No.-04/2019-20/Biomedical Eqpt../IGIMS/Store for the Supply, installation and commissioning of Biomedical Equipment to the various dept. of IGIMS, Patna.

Amendments mentioned hereunder are notified:

Description	Specifications mentioned in the Bidding Document	Should be read as follows:
Group B – Advance Molecular Microbiology and Molecular Genomics		
1. Next Generation Sequencing Platform		
S.No.1. Point No.1.	• The NGS platform workflow should be Fast, simple, scalable bench top type next generation sequencing platform that should enable highly accurate variant detection, extremely uniform coverage, and sensitivity to detect low-frequency variants.	• The NGS platform workflow should be Fast, simple, scalable bench top type next generation sequencing platform that should enable highly accurate variant detection, extremely uniform coverage, and sensitivity to detect low-frequency variants **without use of any steps involving emulsion PCR.**
S.No.1. Point No.2.	• The system should be a single instrument capable of performing all range of low to high throughput applications like targeted resequencing of small to large gene panels, de novo assembly/whole genome sequencing of microbes, metagenomics, aneuploidy detection (PGS), high res HLA Typing in the small to mid-range data throughput segment as well as mouse/ human whole exome/ whole transcriptome, small/microRNA sequencing or NIPT in the high data throughput segment etc.	• The system should be a single instrument capable of performing all range of low to high throughput applications like targeted resequencing of small to large gene panels, de novo assembly/whole genome sequencing of microbes, metagenomics, **preimplantation gene diagnosis**, high res HLA Typing in the small to mid-range data throughput segment as well as mouse/ human whole exome/ whole transcriptome, small/microRNA sequencing or NIPT in the high data throughput segment **along with capability to run cytogenetic methylation micro arrays on the same instruments.** **The cost per sample for whole exome sequencing at 100x coverage for approximately 40 MB exome on the system should be less than USD 420 including sequencing and Library preparation Cost.**
S.No.1. Point No.3.	• The system should be able to do automated clonal amplification (templating/ clustering) to sequencing step should be on board or by attaching additional instrument to reduce manual intervention.	• Automated clonal amplification (templating/ clustering) to sequencing step should be on board **along with additional capability to scan cytogenetic and methylation arrays on the same instrument.**
S.No.1. Point No.5.	• Sequencing should support sequencing	• Sequencing should support sequencing read

	read length in the range of 200-600 bp in single or paired end direction.	length in the range of **150-300 bp** in single or paired end direction.
S.No.1. Point No.6.	• The System should generated 15 GB or 80 million single/ paired end tags or more which should enable multiplexing of at least 2 whole exome/ whole transcriptome samples per sequencing run with 30-40 million reads/tags per sample	• The System should generate **120 Giga bases output or 400 million single or 800 million paired** end reads or more which should enable multiplexing of at least **12** whole exome/ whole transcriptome samples per sequencing run with 30-40 million reads/tags per sample
S.No.1. Point No.7.	• The NGS system should be provided with user friendly software and should not require bioinformatician for secondary data analysis and interpretation	• The NGS system should be provided with user friendly software and **also a** bioinformatician for secondary data analysis and interpretation
S.No.1. Point No.8.	• The system have option for providing complete automation of library preparation to ensure complete walk-away type workflow and increase productivity and reproducibility as and when required in future	• The system **should have capabilities for microarray scanning for cytogenetic/methylation applications and should be provided with ancillary instruments for the same.**

The document also can be downloaded from www.eproc.bihar.govt.in and the IGIMS website www.igims.org.

28/11/19

Director
I.G.I.M.S, Patna

Copy to- Supt. Engineer (Biomedical Engineer): For Uploading on website/ Notice Board.

28/11/19

Director
I.G.I.M.S, Patna