1. Next Generation Sequencing Platform

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 without use of any steps involving emulsion PCR.
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, 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 witch capability to run cytogenetic methylation micro arrays on the same instrument . 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
3. 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.
4. Sequencing should be based upon robust and globally proven with numbers of peer-reviewed publications.
5. Sequencing should support sequencing read length in the range of 150-300 bp in single or paired end direction
6. 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
7. The NGS system should be provided with user friendly software and also a bioinformatician for secondary data analysis and interpretation
8. The system should have capabilities for microarray scanning for cytogenetic/methylation applications, and should be provided with ancillary instruments for the same.
9. The secondary data analysis should be followed of industry standard like FASTQ, SFF, BAM and VCF
10. Analysis should capable to automated SNV calling and provide option to itsverification
11. Variants can be verified manually using alignment and other qualityparameters
12. Analysis should also be capable enough to call CNV and Gene Fusion events as perinstruction
13. Analysis pipeline should also be able to process UMI Based sequencing reads for bias free CNV detection and good quality and improved sensitivity and specifically for variantcalls
14. Analysis pipeline parameters can be customized uniquely for each panel as per user requirement
15. The software should provide the options to export alignment and variant results in PDF or excel format.
16. Specification variants of interest should be recognized automatically
17. Support for Clinical interpretation of identified variants and actionability
18. Should have at least 12TB of data storage option on board or by attaching additional hardware/server to the quoted instrument
19. Vendor should supply the ancillary instrument, if required for preparing libraries using kits along with thesystem
20. The vendor should have a fully functional NGS support lab in India for providing back up support if required for performing any troubleshooting activities
21. Vendor should have strong base/resources available locally for providing quick onsite support with respect to instrument maintenance, application and bioinformatics training/troubleshooting exercises

****