

Response to inputs received from vendors during pre-bid meeting held on 10<sup>th</sup> July 2019 for NGS  
Vendor: Premas Life Sciences:

Tender Specifications	Input / explanation from the vendor	Response from the Institute
SL 3: Quoted system should provide a walk-away, reproducible solution for completely automated library preparation, automated template preparation, automated template preparation and sequencing, thereby reducing the sources of variability & yielding consistent result for users at all experience levels	We have automated on- board cluster generation, template preparation and sequencing. Automated library preparation demands for costly robotic systems supplied by Hamilton, Tecan or Beckman. We provide training on manual library prep workflow at the time of installation.	Suggestions considered with modification: <b>Quoted system should provide reproducible solution for completely automated template preparation, and sequencing, thereby reducing the sources of variability &amp; yielding consistent result for users at all experience levels</b>
SL 4: System should be capable of generating up to 100M reads per run.	Miseq system can produce 25M reads (max 50M paired end). Majority of the applications are covered using 50M paired end reads. NextSeq can generate 400M reads (no other instrument can match this point)	Suggestions not accepted.
SL 5: Read length: single end reads of 200 & 400 bp	Read length- Miseq offers 300bp single end read. NextSeq Offers 150bp single end read.	Suggestions considered with modification: <b>single end reads or paired end reads of 150bp or more.</b>
SI 6: Throughput: up to 22-25 GB per run	Miseq offers max 15 Gb data output. Nextseq offers 120 Gb ( no other instrument can match this point)	Suggestions not considered.
SI 8: Library preparation should be completely automated and should also have an option of barcodes for large number of sample multiplexing.	PI defines sample multiplexing up to 384. Automated library prep demands for high end costly robotic systems supplied by Hamilton, Tecan or Beckman.	Suggestions not considered: Needs not to be defined, large number of samples itself making the same meaning.
SI 10: System vendor should include all necessary reagents and instruments for complete workflow starting from the raw genetic material till final data analysis, which include Instruments & reagents for DNA quantification, Size selection, & other equipment's & reagents as the workflow demands.	Kindly specify no of reactions to be included for DNA quantification, Size selection.	System vendor should include all necessary reagents (Quality control kits for library preparation, template preparation, sequencing, Barcode for 100 reactions, instruments and reagents for DNA quantification, inbuilt software/s for data analysis and quality check of genome data and any upgradation of software's should be free of cost during warranty period.

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		Deep freezers for storage of adapter, barcodes and library preparation reagents, DNA quantification accessories and reagents, fridge for storage of reagents at 4°C and other accessories like Spin win, vortex, cables etc.
<b>SI 11:</b> The instrument should have a complete end-to-end on-board solution with necessary software & server (internal or external) of >200 GB RAM & internal usable Storage of >20 TB for processing signals, calling bases, variants and alignment of sequence.	Miseq and NextSeq system has internal storage of 750Gb. This means, you can store data for 2 or 3 runs on the instrument. External server is already asked in tender and data can be stored on server. PI Specify external server requirements in the tender specs.	Suggestions are not considered.

**Vendor: ILS:**

Tender Specifications	Input / explanation from the vendor	Response from the Institute
SI 5: Read length: single end reads of 200 & 400 bp	Read length: single end reads of 100 bp	Suggestions are not considered.

**Vendor: Thermo Fisher**

Tender Specifications	Input / explanation from the vendor	Response from the Institute
<b>SL 7:</b> The sequencer should be able to read through at least 15 bases homo-polymer stretches in the genome accurately	We Request You to Kindly amend the same to "10 bases Homo Polymer stretches." As all the Models in our NGS Portfolio are capable of sequencing accurately up to 10 bases of Homo Polymer region.	<b>Suggestion Considered:</b> The sequencer should be able to read through at least 10 bases homo-polymer stretches in the genome accurately.
<b>SL 10:</b> The bidder' should have manufactured/ supplied at least five of equipment mentioned in the schedule of Requirement in at least one of the last three years ending on 31 <sup>st</sup> March 2019 and out of which at least three numbers of offered version/model of the quoted equipment should be in successful operation for at least two years on the date of bid opening.	If we participate through our authorized Distributor, can we submit the reference supply order copies & Performance Certificates addressed to the manufacturer/principal company Kindly clarify	The manufacturer should be the bidder.

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