CORRIGENDUM – 1

Tender Reference No: GTB9/MAHA/2023/06/CELLANALSYS

Tender Name: High Throughput Single Cell Analysis System

Corrigendum details: Amendment in Technical Specification

Amendment in Technical Specification

Bidder Eligibility Criteria-I

Sl. No.	**Bidder Eligibility Criteria-I**	**Complied /Not Complied**	**Reference Page No.**
1.	The bidder/OEM should have supplied at least 3 similar items to IITs, NITs, IISERs, CSIR Labs or other globally reputed R&D organizations in the last 5 years, PO copies or installation certificates along with contact details of end user need to be submitted as the proof of supply. IIT Madras reserves its right to verify the claims submitted by the bidder and the feedback from the previous customers will be part of technical evaluation.		
2.	The bidder should provide local service engineer details to attend service related issues		

Technical Specifications II

SL No	**SPECIFICATION**	**Complied / Not Complied**	**Reference, Page No**
1.	The system should perform automated in instrument workflow consisting of successive rounds of fluorescent probe hybridizatiom, imagining, and prove removal to generate optical signature for each transcript.		
2.	The system should perform automated on-instrument workflow consisting of successive rounds of fluorescent probe hybridization, imaging, and probe removal to generate optical signature for each transcript.		
3.	The automation should include integrating sample handling,liquid handling, and wide-field epifluorescence imaging.		
4.	The system should offer single cell and subcellular resolutionacross entire tissue sections (15 mm x 20 mm).		
5.	The platform should be compatible with both fresh frozen (FF) and formalin-fixed, paraffin-embedded (FFPE) tissues, organoids/spheroids, cell culture. System must be able to detect RNA in degraded FFPE samples with RIN scores of less than 3 to undetectable.		
6.	The system should allow detection of 400 to 1000 RNA transcriptsat sub cellular resolution with commercially available panels. System must also have commercially available panels to detect 64 plex protein. System should offer upgrade to existing panels designed for an increased plex detection in the future.		

7.	The system should also be capable of simultaneous detection of RNA and protein within the same tissue section.		
8.	The slides should have large 15 x 20 mm imageable area per slide to analyze large tissue sections and be able to process 2 to 4 slides per run.		
9.	System should contain custom optics with > 20X magnification with > 0.9NA objective with 50 nm precision in the xy plane		
10.	System should acquire 3-dimensional spatial information via Z stacking across the whole tissue thickness.		
11.	There should be pre-validated custom panel design support from system manufacturer. Customizable spike in of 7 to 50 RNA targets to pre-validated panels and de novo custom RNA targets must be available providing faster path to discovery while retaining flexibility to fit specific needs.		
12.	System must have commercially available Multi-modal cell segmentation; a process provides accurate cell boundaries detection. This method of cell segmentation uses cell membrane and morphology marker protein images, machine-learning augmented cell segmentation algorithm and transcript-based segmentation refinement to achieve precise single-cell segmentation in morphologically intact tissue		
13.	Manufacturer should offer comprehensive and easily accessible software suited to analyze and interpret acquired data in the cloud. Custom analysis modules and pipelines should be available and integrated into the solution all while leveraging the compute power of the cloud.		
14.	The output data should show cell-feature matrix, full transcript localization, segmentation boundaries, initial clustering results, and morphology images, and should be ready for off-instrumentexploration.		
15.	The accompanying software for data visualization should allow immediate interactivity includingoverlays of transcripts at subcellular resolution, morphology images, segmentation results, cluster localization and neighborhood analysis.		
16.	The cloud based data analysis capabilities must include foundational modules to run: QC normalization, Dimension reduction, UMAP/tSNE calculation and visualization, Cell typing (with marker identification), Spatial clustering. Additional data analysis modules will also be available for Differential expression, Cell proximity, signaling pathway analysis, Ligand-receptor co-expression, Protein data analysis.		
17.	The system should generate data within industry standard file formats, allowing scientists the freedom to use third party analysis tools.		
18.	Electrical Requirements: Input Voltage: 240 V Nominal Temp: 18 C to 28C Humidity: 20% to 60% preferred range		
19	The manufacturer support team should provide comprehensive customer support, starting with site preparation, installation and training, followed by sustained support on all aspects of the workflow.		