Government of India
Bhabha Atomic Research Centre
Molecular Biology Division

Ref: ~~MBD/2021~~ MBD/I/14559/2022 **03 February 2022**

Sub: Invitation of quotation (Two-part Bids) for Transcriptome Sequencing, small RNA sequencing and Bioinformatics Analysis for *E.coli* cells on illumina platform

1. Quotations are invited for the **Transcriptome Sequencing, small RNA sequencing and Bioinformatics Analysis for *E.coli* cells** on illumina platform as per the attached specifications (annexure-I).
2. **Technical and financial bids should be sent in two separate envelopes** as per the guidelines of two bid tender procedure.
3. Bacterial cells will be provided to the firm/company under dry ice conditions which will be used by the supplier for RNA isolation, ribodepletion, next Generation RNA sequencing compatible library preparation, small RNA library preparation, transcriptome sequencing, small RNA seqeuncing and bioinformatics analysis (of Transcriptome Sequencing, small RNA). Details of the work are given in annexure-I.
4. The company/firm should collect the samples from Bhabha Atomic Research Centre, Trombay, Mumbai.
5. Both RAW and PROCESSED data and results of analysis should be provided as soft copy.
6. Bidder shall quote for the fabrication of these components without material supply.
7. The quotation must include the PAN, GST no. of the firm/supplier. Taxes and excise duties shall be quoted separately. Form AF shall be provided wherever necessary.
8. The quotations should be on printed letter head, in original, and must reach to **Head,** Molecular Biology Division by **Date: 28 Februrary, 2022. Technical and financial bids should be sent separately in two sealed envelopes by speed post only** super scribed with the above reference number and the due date. The address on the envelop should read

   The Head,
   Molecular Biology Division,
   Bhabha Atomic Research Centre,
   Mod. Labs, Trombay, Mumbai 400 085.
   Attention: Ms. Shruti Mishra
9. The bidder shall deliver the finished components after approval by the appropriate authority, **within four months from the date of final work order** issued to the bidder.
10. The finished components shall be delivered by the bidder at Molecular Biology Division, Mod labs, Bhabha Atomic Research Centre, Trombay, Mumbai 400 085.
11. 100 % payment will be made only after the satisfactory completion of the work for all the samples.
12. Head, MBD, BARC reserves the right to accept/reject any or all the quotations without assigning any reason.

Shruti Mishra
SO/D
mshruti@barc.gov.in

Through,

Head, MBD
For kind approval
(Encl: Specifications, Scope of work, terms and conditions)

11/2/22

To,
Web display and notice board

Dr. Hasan Ozaran Misra
अध्यक्ष / Head
आण्विक जैविक प्रभाग / Molecular Biology Division
भारत सरकार / Government of India
भाभा परमाणु अनुसंधान केंद्र / Bhabha Atomic Research Centre
ट्रॉम्बे, मुंबई - ४०० ०८५ / Trombay, Mumbai - 400 085

Annexure-I

Specifications for Transcriptome Sequencing, small RNA sequencing and Bioinformatics Analysis for *E.coli* cells on illumina platform

1. **Technology to be used: Illumina Hi-Seq Platform**
2. **Application: Transcriptome sequencing, small RNA sequencing, Bioinformatic analysis**
3. Sample Type: Bacterial cells
4. No of sample: 15
5. Bacterial cells will be provided to the firm/company under dry ice conditions. The supplier has to pick up the samples from user site (provision of at least 4 times sample pick up should be there and is invoked in case of split samples or if the sample fails the quality control)-bidder must mention the requirement in the quotation.
6. RNA has to be isolated from bacterial cells as per the below mentioned specifications: Qubit 1ug/20ul low TE buffer OR Nanodrop 1.5ug/20ul low TE buffer, 260/280 Ratio: Above 2.0 and 260/230 Ratio: Above 1.0.
7. Extracted RNA form biological samples will be used by the supplier for
    a. Transcriptome sequencing
    b. Small RNA sequencing
    c. Steps in between - Ribodepletion, small RNA QC, RNA QC, small RNA library preparation, RNA library preparation for transcriptome, next generation small RNA Sequencing and Next Generation RNA Sequencing.
8. **All the methods/kits followed should be disclosed by the company at the time of submitting the quotations**.
9. Library QC using Qubit, Tape station and qPCR to be used for measuring the quality and quantity of the library before sequencing.
10. Read Length and Data: 150x2 or > 150 x 2 for RNA Sequencing to generate 60 million reads (30 million Paired End Reads) per sample with at least 10 GB data per sample
11. At least 90 % reads should have QC value (Phred Quality Scores) >30, Low quality reads should be excluded from the analysis
12. Data analysis should include the following
    - Average base content per read
    - GC content distribution of reads
    - Read length distribution
    - Sequence quality score distribution
    - Base quality score distribution
13. Bioinformatics data analysis for should include entire analysis as mentioned below
14. Bioinformatics data Analysis for Transcriptome/RNA Sequencing (The detailed bioinformatics pipeline including the softwares used should be mentioned in the quote; otherwise the bid will be solemnly rejected):
    - Primary Statistics report - QA/QC results should be generated using FASTQC Tool
    - Read statistics reports,
    - Adapter sequence removal and contamination sequence removal (tRNA, rRNA)
    - Read Alignment statistics report from RNA sequencing experiments should be generated using HiSat (hierarchical indexing for spliced alignment of transcripts) Alignment Tool.
    - Differential Gene Expression Reports across different conditions using DeSeq Tool or DEseq2 whichever is applicable.
    - Transcript annotation results (Gene Ontology and Pathway Analysis), Gene set enrichment analysis (GSEA) using latest updated Uniprot /KEGG Databases.

- Transcript wise expression matrix across all samples using HTSeq Tool (tool to quantify gene expression), to deal with reads that align to or overlap with more than one feature and for accurate read count generation.
- Heatmap generation using RScript Tool.
- PCA plots, hierarchical clustering, and t-SNE, volcano plots, MDS plot for graphical representation should be provided
- SNP Analysis using STAR + GATK
- Support for uploading data in required format in public databases
- Data should be maintained on the server for at least 3 months after the project completion.

15. Bioinformatics data Analysis for small RNA Sequencing (The detailed bioinformatics pipeline including the softwares used should be mentioned in the quote; otherwise the bid will be solemnly rejected):
    - Primary Statistics report - QA/QC results should be generated using FASTQC Tool
    - Read statistics reports,
    - Adapter sequence removal and contamination sequence removal (tRNA, rRNA)
    - Read Alignment statistics report from RNA sequencing experiments should be generated using HiSat (hierarchical indexing for spliced alignment of transcripts) Alignment Tool.
    - Differential Gene Expression Reports across different conditions using DeSeq Tool or DEseq2 whichever is applicable.
    - Small RNA identification and annotation (known and novel miRNA reports)
    - Small RNA abundance matrix and RPM
    - Small RNA differential expression analysis
    - Small RNA target identification
    - Heatmap generation of top 20 up and down regulated small RNA using RScript Tool.
    - Support for uploading data in required format in public databases
    - Data should be maintained on the server for at least 3 months after the project completion.
16. Vendor should own in-house sequencing facility in India. Illumina CS Pro certified vendor only will be considered.
17. Samples (Tissue, RNA, library etc.) should not be sent out of India.
18. Proof of Publications: Minimum 500 publications should be cited for NGS Analysis, Minimum 3 NGS publications list from BARC should be attached with quotation.
19. Proof of lab facility: Illumina installation certificate in India should be provided, partner/collaborator company installation certificate located abroad will not be considered.
20. Establishment of firm: Firm should be established in India 20 years before with NGS lab and experience in handling NGS projects. The company should have good experience/ record in conducting such experiments before with proof of publications, purchase/work order and successful completion certificate for 'RNA-seq and bioinformatics analyses' from 5 independent scientists (at least 3 from BARC) in last two years in writing.
21. Quotation should be on firm's letter head with GST Number, PAN Number and CST Number mentioned clearly.
22. All the quotations will be evaluated based on the technical competence and past experience in the similar projects by the bidding companies. Each technically suitable offer will be evaluated by the indenter by audio and video conferencing, if needed.
23. Data should be delivered through secured server & HDD only. To maintain data confidentiality, firm should not write data in CDs/DVDs. Both Raw and processed data and results of analysis should be provided as soft copy
24. Time line to complete the project with complete analysis (including bioinformatics part) should be written clearly and should not exceed more than 4 months.

5. The details of progress of experiment will be intimated to the customer/scientist and further processing in case of any issues will be based on the instructions of the customer only.
26. Failure to submit quotation as per the technical specification will deprive the concerned firm from consideration. Bidders must clearly mention all the above technical specification, term and conditions in the quotation, failing which the quotation will be rejected.
27. DAE-BARC reserves the right to disqualify any bidder without certifying any reason.
28. **Submission of a point by point compliance sheet mentioning bidder's specifications against all the specifications mentioned in the tender document with proper documentary/literature evidence is mandatory,** failing which the quotation will be rejected.