BHABHA ATOMIC RESEARCH CENTRE NUCLEAR AGRICULTURE AND BIOTECHOLGY DIVISION MUMBAI 400 085

Ref.: NABTD/I/16939/2022

Dated: 09/03/2022

Sub.: Transcriptome Sequencing and analysis of soybean leaf samples (24 samples)

- 1. Quotations are invited for Transcriptome sequencing of 24 soybean samples on Illumina Hiseq/Novaseq platform (150 x 2 chemistry) and its analysis including full bioinformatics support up to proper annotation of differentially expressed genes (As per annexure-1).
- 2. <u>Technical and financial bids should be sent in two separate envelopes</u> as per the guidelines of two bid tender procedure.
- 3. The company/firm should collect the samples from Bhabha Atomic Research Centre, Trombay, Mumbai.
- 4. Taxes and excise duties shall be quoted separately. Form AF shall be provided wherever necessary.
 - 5. The quotations are to be strictly in printed letter head and the quotation format should consist of sales tax registration number registered with local ST authority/CST authority, PAN number of the firm, service tax registration number etc.
 - 6. The quotations should be on printed letter head, in original, and must reach to Head, Nuclear Agriculture and Biotechnology Division on or before 30 March, 2022. <u>Technical and financial bids should be sent separately in two sealed envelopes by speed post only</u> super scribed with Attention: Dr. S. K. Gupta and must mention above reference number and the due date. The address on the envelop should read

The Head,

Nuclear Agriculture and Biotechnology Division,

Bhabha Atomic Research Centre,

Mod. Labs, Trombay, Mumbai 400 085

- 7. There is no need of inspection. The bidder shall deliver the finished components within three months from the date of final work order issued to the bidder.
- 8. The finished components shall be delivered by the bidder at Nuclear Agriculture and Biotechnology Division, Mod labs, Bhabha Atomic Research Centre, Trombay, Mumbai 400 085.
- 9. 100 % payment will be made only after the satisfactory completion of the work for all the samples
- 10. Head NA&BTD, BARC reserves the right to accept/reject any or all quotations without any reason.

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(**Dr. S. K. Gupta**) SO/F, NA&BTD Phone: 25590365

Through

To

Cognosali 7 (Dr. T. R. Ganapathi)

Head, NABTD

डॉ. राणपति टी. आर. / DR. GANAPATHI T. R. अध्यक्ष, नाभिकीय कृषि एवं जैव-प्रौद्योगिकी प्रभाग HEAD, NUCLEAR AGRICULTURE & BIOTECHNOLOGY DIVISION भाभा परमाणु अनुसंधान केंद्र. BHABHA ATOMIC RESEARCH CENTRE भारत सरकार / GOVERNMENT OF INDIA ट्रॉबे, मुंबई - 400 085 / TROMBAY, MUMBAI - 400 085.

Web display and Notice Boards.....

Annexure – 1

Ref.: NABTD/I/16939/2022

Dated: 09/03/2022

Technical Specifications for Transcriptome Sequencing and Bioinformatics Analysis for soybean Samples (<u>Two Bid System: Technical and Financial Bid</u>)

- 1. Technology required for sequencing of samples: Illumina NovaSeq 6000/HiSeqXten.
- 2. No of Samples: 24
- 3. **Starting Material:** BARC will give fresh tissues samples as starting material and company must collect samples in two or three batches using dry ice.
- 4. Two separate envelopes should be submitted for TECHNICAL BID and FINANCIAL BID. Technical Bid must include technical compliance (all points as per annexure should be complied with supporting docs (page no should be mentioned), proof of lab facility, installation certificate, Genomics publication list, work orders from Government institutes, satisfactory work completion certificates and company documents.

Please note: Only technically qualified bidders will be considered for financial bid evaluation.

- 5. Quality check of RNA should be provided using gel, nanodrop or qubit.
- 6. Standard library preparation kits should be used for library preparation.
- Data required per sample: Company should provide at least 50 60 million reads per sample. At least 90 % reads should have QC value (Phred Quality Scores) >30, Low quality reads should be excluded from the analysis. Q30 data should be minimum 15 Gb per sample
- 8. Read length for sequencing should be 2 x 150 bp.
- 9. Detailed report for each step should be provided by the company.
- 10. Primary data analysis including data quality check, filtering and trimming.
- 11. Data stats like coverage, N, poor quality reads etc.
- 12. Alignment stats (Alignment should not be less than 80 90%).
- 13. Differential gene expression (DGE should be done among the samples and different groups).
- 14. Gene annotations.
- 15. Core gene set analysis and KEGG Pathways analysis using maximum data bases.
- 16. Heat map, BAM files for each comparison should be provided.
- 17. PCA plots, hierarchical clustering, and t-SNE, volcano plots, Venn Diagram, MDS plot for graphical representation should be provided
- 18. SNP/indel variant calling analysis

- 19. SSR mining for Genic-SSRs
- 20. Detailed analysis report should be provided for each step.
- 21. Company should allow the scientist to visit the lab any time during the experiment and analysis.
- 22. Bioinformatics support should be provided till paper publication followed by data submission in NCBI. Queries raised by reviewer should be addressed immediately.
- 23. Data should be delivered through both secured server and HDD. To maintain data confidentiality, firm should not write data in CDs/DVDs. Both raw and processed data including results of analysis should be provided.
- 24. Samples (Tissue, RNA etc.) should not be sent out of India.
- 25. The vendor must have in-house facility for data generation and analysis. And a proof of inhouse lab facility should be provided. Partner/collaborator company installation certificate located abroad will not be considered.
- 26. The firm should be well established in India and should have good experience/ record in handling NGS projects (generating good quality data and its bioinformatics analysis). The company brochures/authentic company website details should be attached. Record of previous NGS work orders ('RNA-seq and bioinformatics analyses') and their successful completion certificates should be submitted. Also, testimonial of successful completion of NGS projects from the clients/end users should be provided. Vendor should also enclose an updated list of publications of transcriptome analysis and proof of publication (references).
- 27. Quotation should be on firm's letter head with GST Number, PAN Number and CST Number mentioned clearly.
- 28. Time lines to complete the project with complete bioinformatics analysis should be written clearly and should not exceed more than 4months. Further support for *in-silico* analysis for the data generated by this tender, as deemed necessary by the user, should be provided in future till one year after the completion.