

Government of India
Bhabha Atomic Research Centre
Nuclear Agriculture and Biotechnology Division
Plant Cell Culture Technology Section

Ref: NABTD/2018/ 127257

June 28th, 2018

Sub: Invitation of quotations for Whole Transcriptome Sequencing services of six banana samples on Illumina Platform

1. Quotations are invited for Whole Transcriptome Sequencing services of six banana samples on Illumina Platform as per enclosed technical details.
2. The bidder shall quote for sequencing of complete mRNA samples and related bioinformatics analysis as per enclosed technical details.
3. The bidder should have experience in Whole Transcriptome Sequencing services and should provide a list of publications as evidence with the quotation.
4. Quotation must include PAN/TIN/ ST No. etc of the firm/ supplier. Excise duty and taxes applicable has to be indicated separately. Necessary tax exemption certificate shall be provided if applicable.
5. The sequencing work has to be completed within 15 months from date of issue of work order. The samples will be provided in a lot of two at a time. The bidder has to receive the material at the North Gate reception of Bhabha Atomic Research Centre, Trombay, Mumbai-400085 (Maharashtra).
6. The quotation must be sent in a sealed envelope (by speed post) super scribed as “for Whole Transcriptome Sequencing services of six banana samples on Illumina Platform (Attn. Himanshu Tak)” indicating the reference and due date.
7. The quotation must reach to “The Head, Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai-400085 (Maharashtra) by 20th July, 2018.
8. Director, BSG, BARC reserve the right to accept or reject any quotations without assigning any reason.

Technical specifications:

1. Quality control assessment of total RNA (provided by us in RNA stabilizing tubes).
2. Ribosomal RNA depletions by ribo-depletion kit.
3. Proposed platform: Illumina Hiseq 2500
4. Sample number: 6
5. Data requirement: 50 million reads/sample (approximately 5Gb of data per sample).

Scope of work:

1. Sequencing technology : Illumina SBS
2. Details: Illumina HiSeq 2500 paired ends run; 2X150 bp.
3. Bio-analyzer plot has to be used at every step to ensure mRNA quality, enrichment success, fragmentation sizes, and final library sizes. The size distribution of the sequencing library has to be determined by gel electrophoresis. Both picogreen and qPCR has to be used for measuring the quantity of the library before sequencing.
4. After the library has been constructed, paired end run has to be performed on Illumina 's HiSeq 2000/2500 platform to obtain 2X150 bp reads.
5. Detailed bioinformatics and differential gene expression data to be provided :-

- NOS data analysis (bioinformatics) should include:-
 - Sequence analysis quality QC
 - Base quality score distribution
 - Sequence quality score distribution
 - Average base content per read
 - Read length distribution
 - GC content distribution of reads
 - PCR amplification/read duplication related metrics
 - Enrichment of specific sequences (overrepresentation of sequences)
 - Biasing of k-mers. At least 80% sequence should have Q30 value. Low quality sequence reads to be excluded from the analysis.
6. Differential expression analysis with functional annotation of differentially expressed genes, pathway analysis, heatmaps etc.
 7. Additional analysis such as Volcano plot, Hierarchical cluster, Gene ontology analysis pathway analysis, raw and normalized data count, up-regulated and down-regulated genes information with heat maps etc should be carried out.
 8. Data files to be submitted in external storage devices/ hard-disks.

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28-6-18

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Himanshu Tak
Scientific Officer-E
NABTD(BSG)
BARC

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Through

Head, NABTD, BARC

डॉ. वि.पि. वेणुगोपालन / Dr. V. P. VENUGOPALAN
सह-निदेशक (अ). जैव-विज्ञान वर्ग एवं
ASSOCIATE DIRECTOR (A), BIO-SCIENCE GROUP &
अध्यक्ष, नाभिकीय कृषि एवं जैव-पौद्योगिकी प्रभाग
HEAD, NUCLEAR AGRICULTURE & BIOTECHNOLOGY DIVISION
भाभा परमाणु अनुसंधान केंद्र / BHABHA ATOMIC RESEARCH CENTRE
भारत सरकार / GOVERNMENT OF INDIA
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