राष्ट्रीय पादप जीनोम अनुसंधान संस्थान

(जैव प्रौद्योगिकी विभाग, विज्ञान एवं प्रौद्योगिकी मंत्रालय, भारत सरकार का स्वायत्त अनुसंधान संस्थान)

NATIONAL INSTITUTE OF PLANT GENOME RESEARCH

(An Autonomous Institution of the Department of Biotechnology, Ministry of Science and Technology, Government of India)

अरूणा आसफ अली मार्ग, पो. बाक्स नं. 10531, नई दिल्ली–110067

Aruna Asaf Ali Marg, Post Box Number 10531, New Delhi-110067

संख्या: 9/2015-16/रा.पा.जी.अनु.सं./एस एण्ड पी

दिनांक: 06/10/2015

विषय / Subject: मुहरबंद कोटेशन का निमंत्रण / Invitation of Sealed Quotations

Sealed Tenders are invited on behalf of Director, NIPGR from the authorized service providers for **Bisulfite Sequencing**, as per the following specifications for our Institute.

Technical specifications and requirements

1. The work will involve whole genome library preparation and sequencing of Bisulphite converted 12 rice samples using Illumina platform with 90-100bp paired-end sequencing chemistry.
2. Need to generate minimum of 110 million high quality reads for each library that should give at least 10 GB clean high quality filtered data with average depth of 12X per base per DNA strand.
3. The bisulphite conversion efficiency should be more than 99% and for that appropriate control evidence should be provided. The number of clonal duplicates should be less than 5%.
4. Need to carry out following bioinformatics analysis of sequence data generated for all the samples, which includes:
    - Quality checking of sequence reads.
    - Mapping/alignment of sequence reads onto reference (Nipponbare) Rice Genome Annotation Project TIGR/MSU version 7.0 and cultivar specific assembled pseudomolecule (will be specified later) using data-specific aligner. The alignment summary result should mention overall statistics (including Total, aligned, uniquely aligned, unaligned, percent of reads for each sample) for both the references.
    - Assessment and integration of biological replicates for significant and reproducible methylation pattern and the same should be considered thereafter for a separate following analysis (evaluation of fraction of reads mapped to genome before and after biological replicate assessment).
    - All the following analysis should be done for CG, CHG and CHH sequence contexts for all the samples.
    - Calculation of global and chromosome wise Methylation Level using standard statistical methods/tests. Distribution of mCs on the sense and antisense strands of rice chromosomes for each sequence context. The sliding window size of 50 kb and the step size of 25 kb should be used.
    - Methylation patterns should be characterized in following functional regions: TEs, and genic regions including the promoter (2kb upstream of the transcriptional start site, TSS), gene body (the entire transcribed region), and the transcriptional termination region (TTR, 2kb downstream of transcriptional termination site.
    - Gene body should be further divided into untranslated regions (UTRs), coding regions (CDs) and introns for methylation pattern.
    - Methylation level should also be calculated across TE, including their gene body and flanking sequences using an overlapping sliding window of 5% of the sequence length at a step of 2.5% of the sequence length.
    - Structural and functional annotation of methylated regions, such as but not limited to transposable elements, telomeric sequences and centromeres and each identified target region peak should be annotated.
    - Identification and annotation of Single Methylation polymorphism (SMPs), differentially-methylated regions (DMR) among the all samples.

Cont. 2

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- Methylome comparison between all samples.
- Gene set enrichment analysis of differentially methylated genes and functional analysis at GO and pathway level. Gene Ontology (GO) and pathway analysis of Promoter-methylated, Body-methylated and Un-methylated genes for all the samples (graphical).

Visualizations and Deliverables:

- All the above analysis separately in tab delimited file.
- Chromosome-wide distribution of methylation in 100kb windows (tab delimited file and graphical).
- List of methylated sites in chromosomes at CGH/CHH/CG context with methylation values (tab delimited file).
- Methylation levels in different types of genes (protein-coding, RNA coding, pseudo genes and transposons) and repeats (inverted and tandem repeats) at three sequence contexts (CGH, CHH, CG) (tab delimited file and graphical).

5. All the information such as description of all the step and protocol, used reference databases/websites and files, QC details, all the raw and high quality filtered data for each library should be provide in appropriate storage device or via ftp download.
6. The company should maintain the confidentiality of the work. All the terms and conditions, including sample requirement and turnaround time should be clearly mentioned.
7. Vendor should provide in-house Illumina Hiseq 2000/2500 facility certificate explicitly on the name of Company (it should not be in lease or tie up).
8. Samples should not be outsourced outside of India at any stage.
9. Vendor has to provide DSIR, NABL accreditation letter.

You are therefore requested to please send your offer in **two bid system** indicating the maximum discount offered. The quotations must accompany a Demand Draft amounting to ₹ 28,000/- (Rupees Twenty Eight Thousand only), being the EMD in the name of Director, NIPGR, New Delhi and must be sent in a **Sealed Envelope** duly super-scribed on top of envelope as "**Quotation for Bisulfite Sequencing**" so as to reach to the undersigned latest by **26/10/2015 (3:00 p.m.)**, the same shall be opened on same day at **3:30 p.m.**

धन्यवाद,

(क्रय एवं भंण्डार अधिकारी)

Encl: Terms & Conditions (Annex – I)

Annexure – I

नियम और शर्तें:

- The quotations must accompany a Demand Draft amounting to ₹ 28,000/- (Rupees Twenty Eight Thousand only), being the EMD in the name of Director, NIPGR, New Delhi. In the event of non fulfillment of work awarded / withdrawal of quotations, the EMD will be forfeited by the Institute. The EMD shall be released upon completion of work to the satisfaction of Indentor Scientist.

- The rates quoted by you for the said services shall be valid for a period of one year from the date of issue of Work Order and no requests for any increase in the rates will be entertained during the contract period. No advance payment will be made.

- The Director, NIPGR reserves the right to amend any of the terms and conditions contained in the Tender Document or reject any or all applications (offers) or not to award the contract to the lowest bidder without giving any notice or assigning any reason thereof. The decision of the Director, NIPGR in this regard will be final and binding.

- Payment will be released after completion of work to the satisfaction of the Indentor Scientist and after deduction of tax at source as per Rules.

- The bids will be accepted in respect of those companies having successfully completed one similar work costing not less than ₹ 11,20,000/- or two similar works each costing not less than ₹ 7,00,000/- or three similar works each costing not less than ₹ 5,60,000/- and having annual financial turnover of ₹ 14,00,000/- during the last three financial years. Similar works means, work related to sequencing / analysis of similar samples in Government National Laboratories / Institutions / Universities and reputed Organizations, engaged in the area of Research & Development. Intending tenderers must enclose documents such as Completion Certificates and Work / Supply orders / certified Balance Sheet / ITR Returns for three last financial years.

(क्रय एवं भंण्डार अधिकारी)