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)

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

9/2014/NIPGR/S&P

October 8, 2013

Sub: Invitation of Sealed Quotation

Sir,

We are interested in **Outsourcing of samples** as per the following specifications for our Institute.

Technical specifications and requirements

Number of samples: 4
Organism: Rice
Service: Genome library preparation, whole genome sequencing and bioinformatics analysis.
Plateform: Illumina
Data:

$\geq$ 150 million reads using 2x100 bp PE sequencing giving at least 50X sequence coverage of each sample. Minimum 20 GB clean high-quality filtered data should be generated for each library. The number of clonal/duplicated reads should be less than 5%.

All the information should be provided, including detailed description of all the steps and protocol followed, QC details of all the steps, all the raw and high-quality filtered data from each library in a hard disc.

Bioinformatics analysis:

Need to carry out complete bioinformatics analysis for genome assembly and mapping of sequence data generated for all the four rice samples including the followings:

➢ Quality checking of sequence reads and de novo assembly of contigs.
➢ Mapping/aligning of sequence reads onto the rice reference genome (MSU pseudomolecule version 7.0; http:/rice.plantbiology.msu.edu) and generation of high quality genome assembly and sequences.
➢ Structural and functional annotation of sequences (Protein coding genes, long and small non coding genes, introns, UTRs and Splice variants).
➢ Mining of genome wide high-quality SNPs within the four rice samples along with detailed analysis for the followings:
   ✓ Synonyms and Nonsynonymous SNPs, SNPs in Promoter regions, regulatory regions including miRNA target sites, splicing sites, 5' and 3' UTR, intronic and intergenic regions. Statistical analysis of SNPs must be done.
➢ Analysis and High quality annotation of rearrangements, Small Indel: 1- to 20-bp and Large Indels.
➢ Analysis and annotation of Polymorphism within repetitive sequences (SSR), transposable elements, telomeric sequences and centromeres. Statistical analysis must be done for these.
➢ Copy number variations (CNVs) analysis over protein coding or non-protein coding genes and their identity.

Reference sequence: Good quality reference sequence of Arabidopsis genome is available on http:/rice.plantbiology.msu.edu. Service provider should use the latest version of assembled pseudomolecule sequence available on this site.

You are therefore requested to please send your offer along with a copy of PAN & Tin no. certificate and maximum discount that you will be able to offer in a **Sealed Envelope** duly super-scribed on top of envelope as **"Quotation for Outsourcing of Samples"** so as to reach to the undersigned latest by **28/10/2013 (3:00 p.m.)**, the same shall be opened on **29/10/2013 (11:00 a.m.)**.

Thanking you,

(Purchase cum Stores Officer)