Government of India
Bhabha Atomic Research Centre
Nuclear Agriculture and Biotechnology Division

Ref: NABTD/2022/OPA/ P68838

10th November, 2022

Sub: Ultra Deep Whole Genome Resequencing of Soybean and Novel SNP Discovery (60 samples).

Quotations are invited for "Ultra Deep Whole Genome Resequencing of Soybean and Novel SNP Discovery (60 samples)". Refer annexure-B for detailed technical specification.

1. Taxes and excise duties shall be quoted separately. Form AF shall be provided wherever necessary.
2. 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.
3. The quotation must reach the undersigned by **November 30, 2022** and must be sent in a sealed envelope superscribed with the above reference number and due date given above, by SPEED POST only.
4. The address on the envelope should read

   Mrs. Reema Devi Singh
   Nuclear Agriculture and Biotechnology Division
   Bahbha Atomic Research Centre,
   Mumbai 400 085

5. There is no need of inspection.
6. Payment will be made against delivery.
7. The bidder shall deliver the finished components within 10 weeks from the date of firm purchase order issued to the bidder.
8. Associate Director (A), Bio-Science Group, BARC reserves the right to accept/reject any or all quotations without any reason.

10/11/2022

Reema

Mrs. Reema Devi Singh
SO/D, NABTD

Forwarded through:

10.11.22

Dr. P. K. Mukherjee
Head, NABTD
डॉ. मुखर्जी पी.के. / DR. MUKHERJEE P.K.
अध्यक्ष, नाभिकीय कृषि एवं जैव-प्रौद्योगिकी प्रभाग
HEAD, NUCLEAR AGRICULTURE & BIOTECHNOLOGY DIVISION

To,

Web display and notice board.

Annexure-B

Sample type send from user

- Sample Requirement: Genomic DNA
- No. of Samples: 60
- QC: Gel, Nanodrop and Qubit
- Sequencing platform: Illumina NovaSeq 6000
- Library Preparation: Roche Kapa Hyper Plus DNA prep kit for novel SNP Discovery
- Library QC: Bioanalyser and Qubit reports should be submitted
- Read length: 2x150 bp
- Flowcell: NovaSeq/HiSeq
- Total no of reads: 150 million PE reads per sample
- Data analysis:
    - QA/QC results, read statistics report,
    - alignment statistics report after Mapping to two reference genomes,
    - SNP, InDel using GATK,FreeBayes or Deepvariant,
    - SNP, InDel annotation
    - Final Report submission with sample QC, Library QC and Sequencing report with analysis report should be submitted

Mandatory Terms and Conditions for WGS on Illumina/NovaSeq6000

- Participating companies (the service provider) should have their own in-house sequencing platform in India. The bidder should provide proof of in house NGS facility and Bioinformatics analysis facility and expertise of their own, due to confidentiality issues. The user may visit site before issuing work order.
- The firm must generate comparable data. If the generated data in any sample is significantly deviating from other samples, necessary actions (re-analysis and/or re-sequencing) should be made to rectify it, without any additional charges.
- Reference of the previous work records and/or publications in genome resequencing and expertise of the firm in WGS analysis and the services so far completed in that area to other educational and research institutes should be enclosed in a separate list along with complete details of the beneficiaries. At least three satisfactory work completion certificates should be attached.
- The data generated will be kept confidential and should not be shared with a third party.
- The raw data should be provided in a hard-disk.