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QUOTATION NOTICE

Ref. No.: **WBDST/DC/CONSUMABLE/26-27/1**

Date: 18.05.2026

Quotation for the following items are invited from authorized parties for supplying the under noted items for the **WBDST project Memo No. 65(Sanc.)/STBT-11012(11)/16/2024-ST SEC, under Prof. Dipankar Chakraborti at Department of Genetics**. Suppliers are hereby requested to submit their quotations including the current GST registration certificate, PAN no., copy of registration certificate with statutory authorities and other credentials **within 7 days** from the publication of this notice in a sealed envelope addressed to the undersigned. **Please provide a tender complete in all aspects, otherwise, it won't be considered.** The authority reserves the right to accept/reject any quotation without showing any reason thereof.

Sl. No.	Description	Specification	Sample	Qty.
1.	Next generation sequencing services of whole transcriptome of plant samples	Service Required: Reference based RNA sequencing (Transcriptome including lnc RNA analysis) Sample Type: Whole leaf samples Sample family: Theaceae Sample collection location: Bagdogra Dist. Darjeeling, DTRDC Kurseong (Sample transport (in dry ice) costs should be included) Platform: Illumina Novaseq6000 or other latest versions Library type: PE150 Depth/sample: 100 Million reads/Sample Bioinformatics: Yes Bioinformatics Analysis Required: • Individual raw and processed samples FASTQ files • Individual raw and processed samples QC report (Trimmomatic analysis is required) • Summary of rRNA filtration • Reference based analysis (FASTA), using tea genome • Transcript CDS (FASTA) and Protein (FASTA) based on evidential gene/transdecoder analysis. • Transcript absolute counts of individual samples • FPKM normalized transcript counts of individual samples • The principal component analysis (PCA) plot showing variation between samples.	Leaf Samples	2



		• Sample to sample distance cluster plot based on their euclidean distance using the regularized log transformed count data • The DESeq2 result with complete set of upregulated and down-regulated gene/transcript counts, unadjusted p-value, adjusted p-value, fold change, log2foldchange, q statistics should be provided in.xls format. NOTE: DESeq2 result need to be filtered based on the following 6 cutoffs, and shared as a provisional report 1. FDR <0.05 AND LOG2FC 2 2. FDR <0.05 AND LOG2FC 1.5 3. FDR <0.05 AND LOG2FC 1 4. Uncorrected p value <0.05 AND LOG2FC 2 5. Uncorrected p value <0.05 AND LOG2FC 1.5 6. Uncorrected p value <0.05 AND LOG2FC 1 Annotation using BLASTX against a. NCBI's NRDB (based on client's specified Taxonomy ID), b. UniProt c. InterproScan / eggNOG d. KEGG Automatic Annotation Server • Heatmap of 200 most variable transcripts • MA plot (based on suggested statistical test and LogFC) • Volcano plot (based on suggested statistical test and LogFC) Gene Set Enrichment Analysis (GSEA) based on the availability of the suggested closest genome in the reference database		
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Yours faithfully,

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