**Official Quotation**

VAR\_CLIENT\_NAME

VAR\_CLIENT\_EMAIL

VAR\_CLIENT\_SCHOOL

Quote No: VAR\_QUOTE\_NUM

Date Issued: 9 April 2020

Validity: 30 days

We are pleased to quote the following:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Project | No. | Part Number/ Description | Qty. | Unit Price  (USD) | Line Total  (USD) |
| SAM\_NUM\_1 samples  (*VAR\_SPECIES*)  (Illumina Platform PE150,  Q30≥80%) | 1 | SERVICE\_NAME  (lib prep & seq & analysis)  (8G/12G raw data/sample) |  |  |  |
| 2 | Date Release via FTP | 1 | Free | |
| **Total** | | USD | | |

**Technical Terms:**

1. Overview of Service

|  |  |
| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | RNA Sample |
| Sample Number | SAM\_NUM\_1 |
| Library Type | 250~300 bp insert **strand specific library** with rRNA removal/**specific circular RNA library** |
| Bioinformatics | VAR\_ALY |
| Turnaround Time | VAR\_TAT working days starting after we receive the library preparation confirmation from client |

1. Sample Requirements

**For lncRNA library:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | RIN | Concentration | Purity |
| Total RNA sample | Required | ≥2 μg | ≥20 μL | ≥6.5 (Animal)  ≥6 (Plant/Fungi)  Smooth base line | ≥50 ng/μL | OD260/280>2.0, OD260/230 ≥ 2.0, No degradation or DNA contamination |

**For circRNA Library**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | RIN | Concentration | Purity |
| Total RNA sample | Required | ≥5 μg | ≥20μL | ≥7 (Animal)  ≥6.5 (Plant/Fungi)  Smooth base line | ≥50 ng/μL | OD260/280>2.0  No degradation or DNA contamination |

Note:

1. Samples not meeting these specifications can be designated by the customers as to be processed “at risk”. Novogene have rich experience with samples ≥200ng and if library preparation failed, only the cost for library preparation will be charged. The turnaround time could be extend depending on circumstance.
2. The above-mentioned sample requirement is for post-QC samples. Please send us excess samples to account for nucleic acid used for QC experiments.
3. If the customer chooses to opt out certain procedures in Novogene standard QC pipeline, the samples will be graded as “Hold” or “Fail”.
4. Special samples such as FFPE RNA, amplified cDNA samples will be subjected to different QC standards as appeared on the final QC report sent by Novogene.
5. Bioinformatics Analysis

|  |
| --- |
| **Data Quality Control** |
| Distribution of Sequencing Error Rate |
| Distribution of A/T/G/C Base Content |
| Data Filtering: Removal of reads with adaptor contamination, uncertain nucleotides(N)with > 10% content and nucleotides of low quality |
| Statistic Summary of Data Quality: Amount of data output, Error rate, Q20%, Q30% and GC content, etc |

|  |  |
| --- | --- |
| **Standard Analysis (for Species with Reference)** | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | |
| Mapping Clean Reads to Reference Genome | |
| circRNA Identification | Length Distribution of circRNAs |
| Sources of circRNAs |
| Distribution of circRNA on the Chromosomes |
| Transcript Expression Quantification | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | |
| Differential Expression Analysis (**Only for Compared Groupings**) | |
| Functional Analysis of **Differentially Expressed circRNA Source Genes** (**Only for Compared Groupings**) | Gene Ontology (**GO**) Enrichment Analysis |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |
| CircRNA Target Gene Prediction | |