**Official Quotation**

VAR\_CLIENT\_NAME

VAR\_CLIENT\_EMAIL

VAR\_CLIENT\_SCHOOL

Quote No: VAR\_QUOTE\_NUM

Date Issued: 5 September 2019

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 | Strongly Recommended | ≥4 μg | ≥20μL | ≥6.8 (Animal)  ≥6.3 (Plant/Fungi) | ≥20 ng/μL | OD260/280>2.0  No degradation or DNA contamination |
| Required | ≥2 μg | ≥20μL | ≥6.8 (Animal)  ≥6.3 (Plant/Fungi) |

**For circRNA Library**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | RIN | Concentration | Purity |
| Total RNA sample | Strongly Recommended | ≥10 μg | ≥20μL | ≥7 (Animal)  ≥6.5 (Plant/Fungi) | ≥20ng/μL | OD260/280>2.0  No degradation or DNA contamination |
| Required | ≥5 μg | ≥20μL | ≥7  (Animal)  ≥6.5 (Plant/Fungi) |

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 Quality |
| Distribution of Sequencing Error Rate |
| Distribution of A/T/G/C Base |
| Statistic Summary of Sequencing Quality. Including amount of data output, error rate, Q30 and GC content, etc. |

|  |  |
| --- | --- |
| **Standard Analysis** | |
| **QC** | 1. Data Quality Control: filtering reads containing adapter or with low quality |
| 1. Statistics of Data Production and Quality |
| 1. Alignment with Reference Genome |
| **circRNA**  **Identification** | 1. Length Distribution of circRNAs |
| 1. Sources of circRNAs |
| 1. Distribution of circRNA in the Chromosomes |
| **Differential Expression of circRNAs** | 1. Expression Quantification Analysis of circRNAs |
| 1. TPM Distribution of circRNAs |
| 1. Differential Expression Analysis of circRNAs (>2 sample groups) |
| **Enrichment Analysis** | 1. GO Enrichment Analysis |
| 1. KEGG Enrichment Analysis |
| **Prediction of miRNA targets** | 1. Finding miRNA targets from circRNAs |