**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 SE50,  Q30≥85%) | 1 | SERVICE\_NAME  (lib prep& seq & analysis)  (20M raw reads/sample) |  |  |  |
| 2 | Date Release via FTP | 1 | Free | |
| **Total** | | USD | | |

**Technical Terms:**

1. Overview of Service

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| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | Total RNA Sample |
| Sample Number | SAM\_NUM\_1 |
| Library Type | 18~40 bp insert sRNA library |
| Bioinformatics | VAR\_ALY |
| Turnaround Time | VAR\_TAT working days starting after we receive the library preparation confirmation from client |

1. Sample Requirements

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| --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount/Volume | RIN | Concentration | Purity |
| Total RNA sample | Required | ≥2 μg | ≥7.5 (Animal)  ≥7 (Plant and Fungus), smooth base line | ≥50 ng/μL | OD260/280>2.0,  OD260/230 ≥ 2.0, No degradation or DNA contamination |
| Animal Fresh Tissue | Strongly Recommended | ≥600 mg | - | - | - |
| Required | ≥300 mg |
| Plant Fresh Tissue | Strongly Recommended | ≥1.6 g | - | - | - |
| Required | ≥800 mg |
| Cells | Strongly Recommended | ≥5×107 | - | - | - |
| Required | ≥1×107 |
| Saliva | Volume | ≥2-5mL | - | - | - |
| Blood Sample | Volume | ≥8mL | - | - | - |
| FFPE slides | Thickness | 5um~10um | - | - | - |
| Area | > 0.5cm2 |
| Quantity | 5-10 slides |

Note:

1. Detailed requirements can be referred to the Sample Information Form(SIF).
2. Samples not meeting Novogene’s specifications can be designated by the customers as to be processed “at risk”. If library preparation failed, only the cost for library preparation will be charged. The turnaround time could be extend depending on circumstance.
3. The above-mentioned sample requirement is for post-QC samples. Please send us excess samples to account for nucleic acid used for QC experiments.
4. If the customer chooses to opt out certain procedures in Novogene standard QC pipeline, the samples will be graded as “Hold” or “Fail”.
5. Amplified cDNA samples will be subjected to different QC standard.
6. Bioinformatics Analysis

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| **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 |
| Summary of Length Distribution |
| Common and Specific Sequence Summary |

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| **Only Mapping Analysis** |
| 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 low quality nucleotides |
| Statistic Summary of Data Quality: Amount of data output, Error rate, Q20%, Q30% and GC content, etc |
| Summary of Length Distribution |
| Common and Specific Sequence Summary |
| Mapping Clean Reads to Reference Genome |

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| --- | --- |
| **Standard Analysis (miRNA)** | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | |
| Summary of Length Distribution | |
| Common and Specific Sequence Summary | |
| Mapping Clean Reads to Reference Genome | |
| Functional Classification and Annotation of small RNA | Identification Known miRNA |
| Non-coding Transcripts Annotation |
| Repeat Sequence Annotation  (Annotation of the reference genome should be provided) |
| Exon and Intron Annotation |
| Novel miRNA Prediction |
| miRNA Base Edit | |
| miRNA Family Analysis | |
| miRNA Expression Quantification | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | |
| Differential Expression Analysis (**Only for Compared Groupings**) | |
| Target Gene Prediction of Known and Novel miRNA | |
| Functional Analysis of **Differentially Expressed Genes** (**Only for Compared Groupings**) | Gene Ontology (**GO**) Enrichment Analysis |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |