**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:

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| --- | --- | --- | --- | --- | --- |
| 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 | Strongly Recommended | ≥6 μg | ≥8 (Animal)  ≥7 (Plant) | ≥20ng/μL | OD260/280>2.0  No degradation or DNA contamination |
| Required | ≥3 μg | ≥8 (Animal)  ≥7 (Plant) |
| 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 choose 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 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. |

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| **Standard Analysis** |
| Data Quality Control: filtering reads containing adapter or with low quality |
| Summarize the length distribution of small RNA |
| Analyze common and specific sequences between two samples |
| Align small RNA to reference genome |
| Identify known miRNA |
| Identify rRNA, tRNA, snRNA, snoRNA and Non-coding RNA |
| Identify repeat associated small RNAs (repeat annotation information of the reference genome should be provided) |
| Align small RNA to mRNA, exon and intron |
| Predict novel miRNAs and their secondary structures by Mireap from unannotated small RNAs |
| Analyze the expression pattern of known miRNAs |
| Analyze the base bias of miRNA |
| Classify and annotate of small RNAs |
| **Advanced Analysis** |
| Analyze correlation of miRNA expression among samples (≥2 samples) |
| Analyze differentially expressed miRNA and cluster analysis among samples (≥2 samples) |
| Predict target gene of miRNA |
| Gene ontology analysis of DEGs and pathway enrichment analysis of DEGs |

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| **Standard Analysis of conjunction analysis between mRNA and miRNA** |
| Cluster analysis of the common gene between Differential Expression mRNA and Differential Expression miRNA downstream target mRNA. |
| GO enrichment analysis of the common gene between Differential Expression mRNA and Differential Expression miRNA downstream target mRNA. |
| KEGG enrichment analysis of the common gene between Differential Expression mRNA and Differential Expression miRNA downstream target mRNA. |
| Interaction analysis between Differential Expression mRNA and Differential Expression miRNA. |