**Official Quotation**

VAR\_CLIENT\_NAME Quote No: VAR\_QUOTE\_NUM

VAR\_CLIENT\_EMAIL Date Issued: 28 November 2019

VAR\_CLIENT\_SCHOOL 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 PCR product samples  1. Amplicon Sequencing  (Illumina PE250,  Q30≥75%), or  2. Re-sequencing  (Illumina PE150,  Q30≥80%) | 1 | PCR product  If amplicon, specify region here  i.e. 16S V4 sequencing  (PCR-free library preparation & sequencing,  DATA\_OUTPUT M raw reads/sample or DATA\_OUTPUT Gb raw data/sample) | SAM\_NUM\_1 |  |  |
| 2 | Date Release via FTP | 1 | Free | |
| **Total** | | USD | | |

Note: For Re-sequencing, PE250 (Q30≥75%) only provided upon request, please consult with PS for Re-sequencing PE250.

**Technical Terms:**

1. Overview of Service

|  |  |
| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | Purified PCR product (Length) |
| Sample Number | SAM\_NUM\_1 |
| Library Type | PCR-free library |
| Data Output | DATA\_OUTPUT M raw reads/sample or DATA\_OUTPUT Gb raw data/sample |
| Bioinformatics | Data quality control |
| Turnaround Time | VAR\_TAT working days upon next day after the library preparation confirmation from client |

1. Sample Requirements

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount  (Qubit) | Volume | Concentration | Purity |
| PCR product (Single library) | Required | ≥1.5 μg | ≥20 μL | ≥20 ng/μL | OD260/280=1.8-2.0  No degradation or RNA contamination |
| PCR product (Mixed library) | Required | ≥200 ng | ≥20 μL | ≥10 ng/μL | OD260/280=1.8-2.0  No degradation or RNA contamination |

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” and will be subjected to billing regardless of data quality. 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. Special samples such as MDA product will be subjected to different QC standards as appeared on the final QC report sent by Novogene.
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. |