**Official Quotation**

VAR\_CLIENT\_NAME

VAR\_CLIENT\_EMAIL

VAR\_CLIENT\_SCHOOL

Quote No: VAR\_QUOTE\_NUM

Date Issued: 29 January 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*)  PacBio Whole Genome Sequencing | 1 | HMW DNA extraction & PFGE QC | SAM\_NUM\_1 |  |  |
| 2 | SMRTbell DNA Library preparation | SAM\_NUM\_1 |  |  |
| 3 | Sequencing  (DATA\_OUTPUT SMRT cells/sample)/ (DATA\_OUTPUT G raw data/sample) | SAM\_NUM\_1 |  |  |
| 4 | Date Release via FTP | 1 | Free | |
| **Total** | | USD | | |

**Technical Terms:**

1. Overview of Service

|  |  |
| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | Purified genomic DNA sample |
| Library Type | 10kb/20kb SMRTbell DNA Library |
| Sample Number | SAM\_NUM\_1 |
| Data Output | DATA\_OUTPUT G raw data/sample |
| Bioinformatics | VAR\_ALY |
| Turnaround Time | VAR\_TAT working days starting after we receive the library preparation confirmation from client |

2. Sample Requirements

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample Type | Amount (Qubit) | Volume | Concentration (Qubit) | Note |
| HMW Genomic DNA | ≥10μg | ≥50 μL | ≥100 ng/μL | Purity and concentration should be measured by Qubit  OD260/280=1.8-2.0  No degradation or RNA contamination |
| Bacteria | Required | 0.2g | -- | - |
| Fungus | Required | 1g | -- |
| Plant  Fresh Tissue | Required | 2g | - |
| Animal  Fresh Tissue | Required | 2g | Note: it is recommended at least 3g in case of insects with ordinary size, such as beetles. |

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 FFPE DNA, MDA product will be subjected to different QC standards as appeared on the final QC report sent by Novogene.

3. Bioinformatics Analysis

|  |
| --- |
| **Data Quality Control** |
| Polymerase Read Statistics |
| Subreads Statistics |

|  |
| --- |
| **Standard Analysis** |
| Data quality control |
| Sequence Alignment |
| Structural Variant (SV) detection |
| Variation Annotation |