**Official Quotation**

VAR\_CLIENT\_NAME

VAR\_CLIENT\_EMAIL

VAR\_CLIENT\_SCHOOL

Quote No: VAR\_QUOTE\_NUM

Date Issued: 16 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 Human  Target Region Sequencing (Illumina Platform PE150, Q30≥80%) | 1 | Target Region Sequencing  (target region capture & lib prep & seq & analysis,  DATA\_OUTPUT G raw data/sample) |  |  |  |
| 2 | Data Release via FTP | 1 | Free | |
| **Total** | | USD | | |

**Technical Terms:**

1. Overview of Service

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| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | Purified genomic DNA Sample |
| Sample Number | SAM\_NUM\_1 |
| Target Region Capture | Agilent Sure SelectXT Custom 1Kb-499Kb |
| Bioinformatics | VAR\_ALY |
| Turnaround Time | VAR\_TAT working days starting after we receive the library preparation confirmation from client (2-3 months for kit ordering is excluded) |

1. Sample Requirements

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| --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | Concentration | Purity |
| Genomic DNA | Required | ≥400 ng | ≥20 μL | ≥20 ng/μL | OD260/280=1.8-2.0  No degradation or RNA contamination |
| MDA product/Single Cell Ampified DNA | Required | ≥1 μg | ≥20 μL | ≥20 ng/μL | Smear phenotype for MDA products from single cell and genomes  No gDNA Degradation  No Protein /RNA Contamination |
| Genomic DNA from FFPE | Required | ≥0.8 μg | ≥20 μL | ≥20 ng/μL | OD260/280=1.8-2.0  No degradation or RNA contamination |
| Fresh Tissue | Strongly Recommended | ≥600 mg | - | - | - |
| Required | ≥300 mg |
| Cells | Counts | ≥5×107 | - | - | - |
| Saliva | Volume | ≥4 mL | - | - | - |
| Blood | Volume | ≥1 mL | - | - | - |
| Serum/Plasma | Volume | ≥4 mL | - | - | - |
| FFPE slides | Thickness | 5 μm~10 μm | - | - | - |
| Area | >1 cm2 |
| Quantity | ≥ 10 slides |
| Paraffin tissue block | Amount | ≥0.2 g | - | - | - |
|

Note:

1. Detailed requirements can be referred to the Sample Information Form (SIF).
2. Samples not meeting these 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.
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. |

Note：although we do data filtering on our side for data quality control, data released will be unfiltered raw data if not specified.

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| **Standard Analysis (Human)** |
| Data Quality Control: filtering reads containing adapter or with low quality |
| Alignment with Reference, Statistics of Sequencing Depth and Coverage |
| SNP and InDel Calling, Annotation and Statistics |
| Somatic SNP/InDel/CNV Calling, Annotation and Statistics (paired tumor samples) |