**Official Quotation**

Quote No: VAR\_QUOTE\_NUM

Date Issued: 4 February 2020

Validity: 30 days

VAR\_CLIENT\_NAME

VAR\_CLIENT\_EMAIL

VAR\_CLIENT\_SCHOOL

We are pleased to quote the following:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Project | No. | Part Number/ Description | Qty. | Unit Price  (USD) | Line Total  (USD) |
| SAM\_NUM\_1 microbial samples (*VAR\_SPECIES*)  De novo Service | 1 | SERVICE\_NAME  (lib prep & seq & analysis,  DATA\_OUTPUT G/sample) | SAM\_NUM\_1 | VAR\_UP\_1 | TOTAL\_1 |
| 4 | Date Release via FTP | 1 | Free | |
| **Total** | | USD TOTAL\_FINAL | | |

**Technical Terms:**

1. Overview of Service

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| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | Purified genomic DNA sample from tissues |
| Sample Number | SAM\_NUM\_1 |
| Data Output | DATA\_OUTPUT G/sample |
| Bioinformatics | Standard bioinformatics analysis-de novo for microbe |
| Turnaround Time | TAT working days starting after we receive the library preparation confirmation from client |

2. Technical notes for library preparation:

|  |  |
| --- | --- |
| **Types of service** | **Library types** |
| Bacteria draft map | 350bp insert library |
| Bacteria fine map | 350bp insert library & 6kb mate-paired library |
| Bacteria complete map | 10Kb SMRT Bell Library |
| Fungus draft map | 350bp insert library |
| Fungus fine map | 350bp insert library & 20kb SMRT Bell library |

3. Sample Requirements

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| --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | Concentration | Purity |
| Genomic DNA/HMW DNA | Strongly Recommended | ≥2 or 12 μg | ≥20 μL | ≥50ng/μL | OD260/280=1.8-2.0 |
| Required | ≥1 or 11 μg | ≥20μL | 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 choose 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.

4. Bioinformatics:

**draft map of bacteria genome**

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| --- |
| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome preliminarily assembles |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repetitive sequences, non-coding RNAs |
| Gene function annotation: NR, GO, COG, KEGG, and Pfam. |

**Fine map of bacteria genome**

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| --- |
| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome advanced assemble |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs, CRISPR, prophage analysis, gene island analysis |
| Gene function annotation: KEGG, SwissPort, NR, GO, and COG |

**Complete map of bacteria genome**

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| --- |
| Standard Analysis |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome advanced assemble |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs, CRISPR, prophage analysis, gene island analysis |
| Gene function annotation: KEGG, SwissPort, NR, GO, COG |
| Genome cycle graph |

**Fungal genome survey**

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| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome preliminarily assembles |
| Genome survey: genome size, GC distribution, repeat rate, & heterozygosity rate |

**Draft map /fine map of fungi genome**

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| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome advanced assemble |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs |
| Gene function annotation: NR, GO, KOG, and KEGG |

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| **Advanced analysis** |
| Analysis of pathogenicity (for animal): secondary metabolite gene cluster, secretory protein prediction, TNSS, PHI, VFDB, ARDB, and TCDB. |
| Analysis of pathogenicity (for plant): secondary metabolite gene cluster, secretary protein prediction, TNSS, PHI, CAZy, TCDB. |