(For office use only)

UNIGENOME QUERY FORM
NGS_DNA

Date of receiving: ....

Date of completion: ....

Query no.: ....

Client Details:

Client Name: .... Organisation: ....

e.mail: .... Contact No.: ....

Address: ....

....

Project Details:

Scientific Name: .... Number of samples: ....

Type of Sample: ☐ Tissue ☐ DNA ☐ Body fluid ☐ Bacterial Culture

Platform: ☐ MiSeq ☐ Ion Gene Studio S5 Plus ☐ Novaseq 6000

Application: ☐ Reference based ☐ De novo based

Genome Information: ☐ Genome available ☐ Genome size (Specify) ....

Services type & deliverables :

☐ **Whole Genome Sequencing**

- ☐ **Denovo**
  - ☐ Summarized genome assembly statistics
  - ☐ Assembled genome contigs/scaffolds
  - ☐ Functional annotation of gene
  - ☐ Gene prediction
  - ☐ SNP discovery (only possible if more than one sample or homology based)
  - ☐ SSR identification
  - ☐ GO analysis
  - ☐ Pathway analysis
- ☐ **Reference based**
  - ☐ Alignment report summarizing mapping results
  - ☐ Build consensus sequence
  - ☐ Percentage of gene coverage
  - ☐ SNP discovery
  - ☐ SSR identification

☐ **Plasmid, Fosmid, Phage and small genome sequencing**

- ☐ **Denovo**
  - ☐ **Summarized assembly statistics**
  - ☐ **Assembled genome**
  - ☐ **Functional annotation of gene**
  - ☐ **Gene prediction**
- ☐ **Reference based**
  - ☐ Alignment report summarizing mapping results
  - ☐ Build consensus sequence
  - ☐ Percentage of genome coverage

☐ **Metagenomics**

- ☐ **16S rDNA Metagenome analysis**
  - ☐ **Phylogenetics studies**
  - ☐ **Microbial community abundance and identification**
  - ☐ **Taxa identification**
  - ☐ **Analysis of dominant population**
  - ☐ **Comparative analysis (if more than two samples)**
- ☐ **Whole Metagenome analysis**
  - ☐ **Phylogenetics studies**
  - ☐ **Microbial community abundance and identification**
  - ☐ **Taxa identification**
  - ☐ **Functional annotation**
  - ☐ **Analysis of dominant population**
  - ☐ **KEGG pathway analysis**
  - ☐ **SEED analysis**
  - ☐ **Comparative analysis (if more than two samples)**

☐ **Amplicon sequencing**

- ☐ **Denovo**
  - ☐ Summarized assembly statistics
  - ☐ Assembled genome
  - ☐ Functional annotation of gene
  - ☐ Gene prediction
- ☐ **Reference based**
  - ☐ Alignment report summarizing mapping results
  - ☐ Build consensus sequence
  - ☐ Percentage of genome coverage

☐ **Re-sequencing**

☐ Mapping results ☐ Consensus sequence ☐ SNP discovery and annotation ☐ InDel detection and annotation

For any specific analysis, kindly mention below:

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Estimated Budget: ....

Remarks: ....

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