

UNIGENOME QUERY FORM

Sequencing Services

Date of receiving:

Date of completion:

Query no.:

Client Details:

Client Name: Organisation:

e.mail: Contact No.:

Address:

Sample Details:

Number of Samples/Reactions/Data point: Platform: ☐ 3730xl DNA analyzer

Application :

☐ Sanger Sequencing ☐ Genotyping by Sanger Sequencing ☐ Gene Expression Analysis

Sample Type:

☐ Tissue ☐ Culture ☐ DNA ☐ PCR product ☐ Plasmid ☐ RNA/cDNA

Service Required :

- ☐ SEQ-1: Purified Plasmid/PCR Product Sequencing . ☐ SEQ-2: recombinant E-coli clone sequencing.
- ☐ SEQ-4: Primer Walk sequencing. ☐ MID-R: Microbial identification of Bactreia/Yeast/Fungus with MID report.
- ☐ MID-S: Sequencing data of 16S, 18S, 28S and ITS region. ☐ MID-C: Microbial identification of Bactreia/Yeast/Fungus with Contig report.

Customize Servies:

- ☐ SNP GENOTYPING: SnaPshot Assay. ☐ Microsatellite Genotyping on ABI 3730XL.
- ☐ Gene Expression Analysis: SYBR Green assay or Taqman Assay

Extra Service Required:

- ☐ Bead Based Purification of PCR Product ☐ Gel-Extraction: Purification of PCR product from Agarose gel.

Information required from client :

In Service SEQ-1:

- ☐ Specified volume of the product ☐ Specified concentration of product and primer ☐ Tm of the primer
- ☐ Purified ☐ Unpurified

In Service SEQ-2: ☐ Vector used ☐ Insert length ☐ Unversal Primer to be used.

Clones in Form of: ☐ Stab ☐ Glycerol stock

In Service SEQ-4:

- ☐ Specified volume of the product ☐ Specified concentration of product and primer ☐ Tm of the primer ☐ Purified
- ☐ Unpurified ☐ Size of the fragment to be sequenced using primer walking sequencing.

In Service MID-S/C/R:

Type of Micro-organism.

- ☐ Pathogenic ☐ Non-pathogenic ☐ Aerobic ☐ Anaerobic ☐ Media to be used ☐ Growth Conditions
- ☐ Specific Media by Costumer

Conserved region to be Sequenced:

- ☐ 16s rRNA ☐ 18S rRNA ☐ 28S rRNA ☐ ITS region ☐ Algae Identification ☐ Mitochondrial Gene Based Identification

Culture Form:

- ☐ Stab ☐ Glycerol stock ☐ Cell Pellet

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SNP genotyping SnapShot assay:

- ☐ Client is providing Ready to Run plate?
- ☐ SNP information ☐ Level of Multiplexing Information. ☐ Labelled Dye information. ☐ Amplicon Size information.
- ☐ Client is providing Amplicon.
- ☐ Amplicon size information ☐ SNP Information per sample
- ☐ Sequence of amplicon in which SNP is to be detected with SNP location. ☐ Reference Sequence
- ☐ Client is providing DNA samples.
- ☐ Quality Report of Isolated DNA. ☐ Primer information for amplification of locus in which SNP is to be identified.
- ☐ SNP information per sample.

Microsatellite genotyping assay:

- ☐ Client is providing Ready to Run plate?
- ☐ Allelic information. ☐ Level of Multiplexing. ☐ Dye used for Multiplexing. ☐ Amplicon size information.
- ☐ Client is providing Labelled amplicon.
- ☐ Allelic Information. ☐ Flouroscent Labelled Dye information. ☐ Multiplexing Information. ☐ Amplicon size information.
- ☐ Client is providing DNA samples.
- ☐ Quality Report of Isolated DNA. ☐ Primer information for amplification with standardized condition for each primer.
- ☐ Sizing information.

Gene Expression Analysis:

- ☐ Client is providing tissue
- ☐ RNA samples. ☐ RNA Intigrity Number should be above 6 ☐ Client want to perform absolute quantification.
- ☐ Relative quantification. ☐ Client is providing control sample. ☐ Gene Information both
- ☐ Test Gene, House-keeping gene with primer information ☐ Validated condtions for amplification of Test and House-keeping gene.

Deliverables required by client in Costumized projects:

- In Service SEQ-1 & 2: ☐ Chromatogram & FASTA FILE ☐ PDF Files
- In Service SEQ-4: ☐ Chromatogram & FASTA FILE ☐ PDF Files ☐ Sequencing data with Primer walk Report.
- In Service MID-S/C/R: ☐ Chromatogram & FASTA FILE ☐ PDF Files ☐ Sequencing data with contig report
- ☐ Sequencing data with MID Report.

SNP genotyping SnapShot assay:

- ☐ Raw data files only. ☐ Raw data with SNP analysis report consist of SNP calling peaks with standard curve and SNP list.

Microsatellite genotyping assay:

- ☐ Raw data files only. ☐ Raw data and compiled report consist of allelic information status of sample with peak area and Peak.

Gene Expression Analysis:

- ☐ Complied summary report consist of delta-delta CT value, fold changes value, melt curve and total protocol performed report.

Additional Information from Client for the Experiment:

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Estimated budget:

Remarks:

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