**Date:** **NGS ID:**

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| **CUSTOMER DETAILS**  |
| **Name:** |       |
| **Institute Name / Department** |       |
| **Address:** |       |
|  |       |
| **Contact Number:** | (Office)       (Mobile)       |
| **Email Address:** |       |
| **Principal Investigator / Supervisor:** |       |
| **Project Name:** |       |

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| **SAMPLES INFORMATION. Please elaborate on the nature of samples.** |
| **Species** | Choose an item.**If ‘Others’ is selected, please specify:**       |
| **Genome Size** |      **bp; If reference genome is available, please provide GenBank Accession #**      |
| **Sample Type** | **[ ] gDNA [ ] PCR product;** please specify amplicon size:     **[ ] Total RNA [ ] Purified mRNA [ ] Small RNA** **[ ] Custom Made Library** *(Please complete the section on ‘Library Information’ on Page 4 and 5)***[ ] Others; please specify:**       |
| **No. of Sample(s)** |       |
| **Condition of Samples/Custom Made Library** | **[ ]** Dissolved in water **[ ]** Dissolved in 10mM Tris HCL, pH7.5-8.5 **[ ]** Others, please specify:     Treated by Rnase: [ ] Yes [ ] No |

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| **PROJECT INFORMATION** |
| **Please elaborate on the objectives/aims of this NGS Project. Please provide as much detail as possible to help us understand what your needs are.**       |

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| **NGS SERVICE INFORMATIOM** |
| **Service Required** | **[ ]  Library Preparation, Sequencing & Standard Bioinformatics Analysis****[ ]  Sequencing only *(Please complete section under ‘Output Requirements’ and ‘LIBRARY INFORMATION’’)*****[ ]  Bioinformatics *(Please complete section under ‘BIOINFORMATICS AND DATA ANALYSIS’)*** | **[ ]  gDNA/RNA Extraction****[ ]  Library Preparation only** |
| **Application** | Choose an item.**If ‘Others’ is selected, please specify:**       |  |
| **Output****Requirements** | [ ]  **Amount of data required per sample;**      **gb or**       **million reads.**[ ]  **Desired coverage;**      **X**[ ]  **No. of lanes required**;       **lane** [ ]  **No. of SMRT cells required**;       **SMRT cells**[ ]  **Others:** please specify:      |
| **Results Delivery** | [ ]  **Illumina BaseSpace account**; email address:      [ ]  **Hard Disk** *\*additional charges apply, please speak to your product specialist before selecting this option* | [ ]  **FTP link download** |
|  |

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| **BIOINFORMATICS AND DATA ANALYSIS** |
| **What are your requirements for Bioinformatics and Data Analysis?**       |
| **SAMPLES INFORMATION** |
| *Please fill up the following table with all available information you have on your samples.*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Sample Name** | **No. of Tubes** | **Sample Conc (ng/ul)** | **Sample Vol (ul)** | **Total Quantity (ug)** | **Preparation Method** | **Purity(A260/280, A260/230)** | **Additional Information** |
| *(e.g)* | *Sample001* | *2* | *50ng/ul* | *20ul* | *1ug* | *Trizol* | *1.8* | *Please combine tubes* |
| *(e.g)* | *Sample002* | *1* | *75ng/ul* | *50ul* | *3.75ug* | *Trizol* | *1.9* | *-* |
| 1 |       |       |       |       |       |       |       |       |
| 2 |       |       |       |       |       |       |       |       |
| 3 |       |       |       |       |       |       |       |       |
| 4 |       |       |       |       |       |       |       |       |
| 5 |       |       |       |       |       |       |       |       |
| 6 |       |       |       |       |       |       |       |       |
| 7 |       |       |       |       |       |       |       |       |
| 8 |       |       |       |       |       |       |       |       |
| 9 |       |       |       |       |       |       |       |       |
| 10 |       |       |       |       |       |       |       |       |
| 11 |       |       |       |       |       |       |       |       |
| 12 |       |       |       |       |       |       |       |       |
| 13 |       |       |       |       |       |       |       |       |
| 14 |       |       |       |       |       |       |       |       |
| 15 |       |       |       |       |       |       |       |       |
| 16 |       |       |       |       |       |       |       |       |
| 17 |       |       |       |       |       |       |       |       |
| 18 |       |       |       |       |       |       |       |       |
| 19 |       |       |       |       |       |       |       |       |
| 20 |       |       |       |       |       |       |       |       |
|  |  |  |  |  |  |  |  |  |

 |
| **LIBRARY INFORMATION (this section is only applicable for client who are sending in prepped library for sequencing service)** |
| **Library Details***Please fill up the following tables with all available information you have on your library.*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Library Name** | **No. of Tubes** | **Library Conc (ng/ul)** | **Library Vol (ul)** | **Total Quantity (ug)** | **Fragment Size** | **Pooled Library?** **(Yes/No)** | **Additional Information** |
| *(e.g)* | *Library001* | *2* | *50ng/ul* | *20ul* | *1ug* | *725bp* | *Yes* | *-* |
| 1 |       |       |       |       |       |       |       |       |

**IMPORTANT NOTE!** For client using Custom Primers:1. Please submit at least 20ul of 100uM for all primers for each sample submitted.
2. Please give a unique Primer ID for each of your primers and label them clearly.
3. Full cost of failed run will be charged if FAS determine that any run failure is due to the usage of Custom Primers.
4. Please indicate if your custom primers are known to have conflict with Illumina Primers.

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| **Library Preparation Kit**  |      (*Brand and Name of Library Prep Kit used*) |
| **No. of Index Reads** | [ ]  No index[ ]  Single-Indexed[ ]  Dual-Indexed |
| **Length of Index Reads** | [ ]  6bp (Illumina TruSeq)[ ]  8bp + 8 bp (Illumina Nextera)[ ]  Others:      *(Please provide Index sequences for de-multiplexing for first submission of other indexes)* |
| **Primer Type** | [ ]  Illumina TruSeq[ ]  Illumina Nextera[ ]  Custom/Others*(Please complete the following section on ‘Custom/Others Primers Details’)* |

**Illumina Primers Details**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Pooled Library Name** | **No. of Sample** | **Sample ID** | **1st Index Read ID** | **1st Index Read Sequences** | **2nd Index Read ID** | **2nd Index Read Sequences** | **Additional Information** |
|       | 1 |       |       |       |       |       |       |
| 2 |       |       |       |       |       |       |
| 3 |       |       |       |       |       |       |
| 4 |       |       |       |       |       |       |
| 5 |       |       |       |       |       |       |
| 6 |       |       |       |       |       |       |
| 7 |       |       |       |       |       |       |
|  | 8 |       |       |       |       |       |       |
|  | 9 |       |       |       |       |       |       |
|  | 10 |       |       |       |       |       |       |

**Custom/Others Primers Details**

|  |  |
| --- | --- |
| **Conflict with Illumina Sequencing Primers** | [ ]  Yes.[ ]  No.[ ]  Not sure. |
| **Read 1** | Primer ID:       |
| Primer Sequence:       |
| Primer Concentration:       |
| **Read 2** | Primer ID:       |
| Primer Sequence:       |
| Primer Concentration:       |
| **Index Read** | Primer ID:       |
| Primer Sequence:       |
| Primer Concentration:       |

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