**Date:**

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

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| **SAMPLES INFORMATION. Please elaborate on the nature of samples.** |
| **Nature of Sample****[ ]  gDNA [ ]  PCR product**Please indicate: (i) Size       in bp / kb / Mb / Gb, and (ii) Sequencing depth:       **X** coverage**[ ]  Total RNA** Please indicate: (i) Data output, per sample       in Mb/ Gb, or  (ii) Amount of reads, per sample:       (e.g. 5,000, 1 Mil or etc.) **[ ]  Custom made libraries;** please indicate: (i) estimated library or the insert size:      (ii) Library kit information (brand, catalog name, protocol, etc.):      (iii) Primer/ Barcode (MID) sequence information if any:     **[ ]  Others;** please specify:     Please indicate: (i) Data output, per sample       in Mb/ Gb, or (ii) Amount of reads, per sample:       (e.g. 5,000, 1 Mil or etc.) **No. of Samples:**       |
| **Sample Origins**[ ]  **Human** [ ]  **Animal**, please provide species      [ ]  **Plant**, please provide species      [ ]  **Microbe**, please provide species      [ ]  **Others**, please provide species       | **Reference Genome Available?****[ ]  Yes.** Please provide GenBank Accession #     . Or please provide reference file as a separate attachment.**[ ]  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.** *E.g. “I would like to sequence several strains of the target organism, and compare these to a known reference to identify differences between them. I am interested in SNPs but not structural variations”.*      |
| **Application** | [ ]  **Whole Genome *de novo* Sequencing**[ ]  **Whole genome Re-Sequencing**[ ]  **Exome Sequencing**[ ]  **Custom capture / Targeted Sequencing**[ ]  **Transcriptome *de novo* Sequencing**[ ]  **Transcriptome Re-Sequencing** [ ]  **Small RNA Sequencing** | [ ]  **MBD sequencing**[ ]  **ChIP sequencing**[ ]  **Whole Genome Bisulfite Sequencing**[ ]  **Metagenome 16 rDNA Sequencing**[ ]  **Metagenome Shotgun Sequencing**[ ]  **Sample QC only**[ ]  **Others:** please specify:      |
| **NGS Platform**  | [ ]  **HiSeq 2000** [ ]  **GS- FLX Plus**[ ]  **HiSeq 2500** [ ]  **Ion Torrent- PGM / Ion Proton**[ ]  **HiSeq X Ten** [ ]  **PacBio RS II**[ ]  **MiSeq** [ ]  **Others:** please specify:     [ ]  **GS- FLX Titanium** |
| **Run Type** | **Type of read;** [ ]  **Single- Read**[ ]  **Paired- End**[ ]  **Others:** please specify:      | **Size;** [ ]  **50bp (only applicable for HiSeq2500 and MiSeq)**[ ]  **100bp (only applicable for HiSeq2000)**[ ]  **150bp (only applicable for HiSeq2500, HiSeq X Ten, MiSeq)**[ ]  **300bp (only applicable for MiSeq)** |
| **Run Output** | **Illumina;** [ ]  **No. of lanes** (1 to 8):     [ ]  **One flow cell (HiSeq2500 only)**[ ]  **Throughput base;** please specify:      **Gb** [ ]  **Others:** please specify:      | **GS-FLX;**[ ]  **1/2 region PTP** [ ]  **1/4 region PTP** [ ]  **1/8 region PTP** [ ]  **Others:** please specify:      |
| **Library Information – please indicate the Exome Capture kit/ Library Preparation kit you wish to use for the project?** *E.g. Sureselect V5/ Nextera DNA/Mate Paired end library etc.*  [ ]  **I am not sure about that right now, please advise.** |
| **NGS Approach - do you have any preferred NGS approach that you wish to use for the project?** *E.g. fragment (shotgun) sequencing only, or paired-end/mate-pair sequencing only, or combination approach.* [ ]  **I am not sure about that right now, please advise.** |

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| **BIOINFORMATICS AND DATA ANALYSIS** |
| **What are your requirements for Bioinformatics and Data Analysis?** *A detailed answer would help us provide an accurate proposal and quotation***.**     [ ]  **I am not sure about that right now, please advise.** |

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| **PROJECT TIMELINES** |
| **When do you plan to commence on this NGS project?**      [ ]  **I am not sure about that right now.** |
| **Where have you sent your NGS projects to previously?**[ ]  **N/A, I am new to this.**[ ]  **My collaborator’s core facility, please specify:**      [ ]  **Others, please specify:**       |