**Date:**

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| **CUSTOMER DETAILS** | |
| **Name:** |  |
| **Institute Name / Department** |  |
| **Address:** |  |
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| **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:** |