Questionnaire for Data Processing, Analysis, and Interpretation for

De-novo assembly

## Project Background: Brief description of the project

## Expected deliverables: Please choose the deliverables below and/or specify any additional items/requirements

**Please specify the estimate size of the species**

## Standard deliverables:

|  |  |  |
| --- | --- | --- |
| **Analysis Item** | **Y/N** | **If yes, any specific requirements?** |
| QC Statistics of raw reads (fastqc report) | [x]  |  |
| Assembly statistics, Contig, scaffolds, and intermediate files of SPAdes assembler (small genome) | [x]  |  |

## Optional deliverables for bacteria or archaeal genomes **(each item is an additional charge and may affect turnaround time, please request specific pricing from team)**:

|  |  |  |
| --- | --- | --- |
| **Analysis Item** | **Y/N** | **If yes, any specific requirements?** |
| Taxonomy assignment using [The Genome Taxonomy Database (GTDB)](https://gtdb.ecogenomic.org/) | [ ]  |  |
| Prokka gene structure prediction | [ ]  |  |

If any other customized data analysis request, please describe below.

Please note that it is not guaranteed to be accepted and might incur additional cost.

|  |
| --- |
|  |

## References: Please attach and or provide links of the relevant references as per your project if needed