Data Processing Questionnaire for Analysis and Interpretation for

ddRADseq

Study Objectives: Please specify the aim of the project.

## Project Background: Brief description of the project.

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

## Please specify the species below

|  |  |  |  |
| --- | --- | --- | --- |
| Species | Human (Homo sapiens) | hg38 (GRCh38) (recommend) |  |
| Mouse (Mus musculus) | mm10 (GRCm38) |  |
| Other Please specify (Species without Reference Genome) | |  |

## Standard deliverables:

|  |  |  |  |
| --- | --- | --- | --- |
| **Analysis Item** | **Package** | **Y/N** | **If yes, any specific requirements?** |
| Sequencing quality control | FastQC |  |  |
| Alignment for Known Reference Genome | bwa |  |  |
| Alignment files for unknown Reference Genome | Stacks |  |  |
| Variant Calls (Known and Unknown Species) | Stacks |  |  |
| Population genetic statistics | Stacks |  |  |

Clearly specify sample population if you interested in population specific Stats.

For example:

sample\_01 parent

sample\_02 parent

...

sample\_16 progeny

|  |
| --- |
|  |

## \*If any specific version of genome sequence, annotation file, or software/packages/tools for data analyze is needed, please specify it below:

|  |
| --- |
|  |

## If any other customized analysis item(s) is needed, please provide the detailed requirements below, our bioinformatics team will evaluate the feasibility.

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|  |

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