Data Processing Questionnaire for Analysis and Interpretation for Hi-C

1. Study Objectives: Please specify the aim of the project.
2. **Project Background: Brief description of the project.**
3. Expected deliverables: Please choose the deliverables below and/or specify any additional items/requirements

Please specify the species below:

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| --- | --- | --- |
| Standard species | Human (Homo sapiens) | Hg38 |
| Hg19(GRCh37) |
| Mouse (Mus musculus) | mm10 (GRCm38) |
| Others (or Species without Reference Genome) |  |  |

Please specify the restriction enzyme below:

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Standard deliverables:

|  |  |  |  |
| --- | --- | --- | --- |
| Analysis Item | Package | Y/N | If yes, any specific requirements? |
| Sequencing quality control | FastQC |  |  |
| Statistics for Hi-C contacts | juicier |  |  |
| Hi-C contacts | juicier/  Juicebox |  |  |
| Contact domains | juicier/  arrowhead |  |  |
| Chromatin loops | juicer/hiccups |  |  |
| Hi-C scaffolding | SALSA |  |  |

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

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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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1. **Sequencing details: Eg. Sequencing primer detail etc.**
2. References: Please attach and or provide links of the relevant references as per your project.