Questionnaire for Data Processing, Analysis, and Interpretation for RNA-seq

## 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 by clicking the checkbox or provide other resource.

|  |  |  |  |
| --- | --- | --- | --- |
| Standard species | Human (Homo sapiens) | hg38 (GRCh38) (recommend) | [ ]  |
| hg19 (old version) | [ ]  |
| Mouse (Mus musculus) | mm10 (GRCm38) | [ ]  |
| Rat (Rattus norvegicus) | Rnor\_6.0 | [ ]  |
| Pig (Sus scrofa) | Sscrofa11.1 | [ ]  |
| Macaque (Macaca mulatta) | Mmul8.0.1 | [ ]  |
| Turkey (Meleagris gallopavo) | UMD2 | [ ]  |
| Fruit fly (Drosophila melanogaster) | DM6 | [ ]  |
| Other species |  | [ ]  |

##  Standard deliverables:

|  |  |  |
| --- | --- | --- |
| **Analysis Item** | **Y/N** | **If yes, any specific requirements?** |
| QC Statistics | [x]  |  |
| Sequence alignment | [x]  |  |
| Summary of alignment quality | [x]  |  |
| Normalized count | [x]  |  |
| Gene feature counting | [x]  |  |
| DEanalysis | Sample correlation (Pearson correlation) | [x]  |  |
| Heatmap |  |
| Principle Component Analysis |  |
| MA plot |  |
| Volcano plot |  |
| Analysis result (DE table etc.) |  |
| GO/KEGG (if annotation available) | GO Analysis | [ ]  |  |
| KEGG Analysis  | [ ]  |  |

### Optional deliverables **(each item is additional charges and may affect turnaround time, please request specific pricing from PM team)**:

|  |  |  |
| --- | --- | --- |
| Analysis Item | Y/N | If yes, any specific requirements? |
| Alternative splicing events: rMATS | [ ]  |  |
| Interaction network: STRING | [ ]  |  |
| ANNOVA analysis | [ ]  |  |

\*If Differential gene expression analysis is chosen, please specify the detailed group comparison information below:

For example:

Group A: Sample 1, 2, 3

Group B: Sample 4, 5, 6

Group C: Sample 7, 8, 9

Group D: Sample 10, 11, 12

Group A vs. Group B, Group C vs. Group D

|  |
| --- |
|  |

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

|  |
| --- |
|  |

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