1. Bioinformatics Analysis

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| **Standard Analysis (human/mouse[Medical Species])** | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | |
| Mapping Clean Reads to Reference Genome | |
| Gene Expression Quantification | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | |
| Differential Expression Analysis (**Only for Grouping with control samples**) | |
| Functional Analysis of **Differentially Expressed Genes** (DEGs) (**Only for Grouping with control samples**) | Gene Ontology (**GO**) Enrichment Analysis |
| Disease Ontology (**DO**) Enrichment Analysis (**Only for Human samples**) |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |
| Reactome Pathway Enrichment Analysis |
| DisGeNET Enrichment Analysis of Differentially Expressed Genes (DEGs) (two or more groups of samples and only for human samples) |
| GSEA Enrichment Analysis of Expressed Genes (two or more groups of samples) |
| Oncogene Functional Annotation analysis |
| Protein Protein Interaction Analysis |
| Structural Analysis | Alternative Splicing (**AS**) Quantification and Differential Expression Analysis (**Only for Grouping with control samples**) |
| SNP/InDel Detection and Annotation Analysis |
| Fusion Gene Analysis (**Only for Grouping with TUMOR or CANCER tissue/cell line**) |