

UC San Diego Center for Computational Biology & Bioinformatics
RNA-seq Analysis
2022

UCSD Internal rate: \$180/hour

Non-profit rate: \$261/hour

For-profit rate: \$522/hour

Estimates below are shown for the UCSD internal rate. All projects are subject to operational charges.

Bulk RNA-seq

Primary Analysis

1. Raw data quality control (method: FASTQC)
2. Alignment of raw data to genome (method: STAR)
3. Gene or transcript level quantification (method: RSEM or Kallisto)

Estimate: \$90/sample for ≤ 20 samples ; \$45/sample for any additional samples above 20 (bulk rate)

Secondary Analysis

1. Assessment of experimental design and analysis design
2. Quality control of read quantification & outlier detection (method: MDS plot)
3. Normalization (method: TMM normalization)
4. Differential expression analysis (method: limma-voom)
5. Functional enrichment analysis & pathway analysis (method: Hypergeometric test and GSEA)
6. Standard figures: MDS plots, MD plots and heatmaps of top 25 DE genes

Estimate: \$3240-\$5400. May be higher for complex experimental designs.

Follow-Up Analysis

Further analysis (such as inclusion of additional datasets, custom visualizations, and other downstream requests) will be scoped on a per-project basis.

Single cell RNA-seq

Primary Analysis

1. Alignment and quantification of raw data using CellRanger (10X Genomics)

Estimate: \$180/sample

Secondary Analysis

1. Quality control
2. Initial clustering analysis using the standard Seurat workflow
3. Cell type predictions using SingleR or equivalent software
4. Cell type identification and relabeling with direction from customer

5. Differential expression comparisons between conditions for all cell types
6. Standard figures: Heatmaps, UMAP plots, feature plots, dot plots, etc.

Estimate: \$3,240-\$5,400 and a storage and compute charge of \$270. May be higher for complex experimental designs.

Trajectory Analysis

Estimate: \$3,240-\$10,800 and a storage and compute charge of \$270.

Follow-Up Analysis

Further analysis (such as inclusion of additional datasets, custom visualizations, and other downstream requests) will be scoped on a per-project basis.

Spatial Transcriptomics

Visium

Primary analysis

1. Alignment and quantification of raw data using SpaceRanger (10X Genomics)

Estimate: \$360/sample

Secondary analysis

1. Quality control
2. Initial clustering analysis using the standard Seurat workflow
3. Cell type predictions using SingleR or equivalent software
4. Cell type identification and relabeling with direction from customer
5. Differential expression comparisons between conditions and/or regions
6. Standard figures: Heatmaps, UMAP and spatial plots, spatial feature plots, etc.

Estimate: \$3,240-\$7,560 and a storage and compute charge of \$270. May be higher for complex experimental designs.

Nanostring GeoMX

Estimate: \$3,240-\$7,560. May be higher for complex experimental designs.