



Center for Computational Biology and Bioinformatics (CCBB) 2022

CCBB services: **Transcriptomics**

- RNA-Seq, UMI-based RNA-Seq, High Throughput RNA-Seq ("Drug-Seq"), smallRNA-Seq (miRNA-Seq)
- Single cell RNA-Seq, immune profiling - V(D)J, Visium Spatial transcriptomics (10x Genomics)

RNA-Seq (standard Level 1 services: ~3 to 5 business days)

Requirements:

- 1) Read targets reached (e.g. ~ 20 million reads per sample; human genome) for each of your samples in the study
- 2) Number of sample submitted are less than 20
- 3) Sample metadata (sample conditions and comparisons to be done) shared with CCBB prior to sequencing
- 4) 3 or more biological replicates per condition in your experiment
- 5) Reference genomes considered as standard: human, mouse, rat

Level 1 services: CCBB effort level - 2 hours

Standard analysis using nf-core/rnaseq workflow: Alignment to reference genome using STAR, raw gene counts (FeatureCounts), differential gene expression analyses (DESeq2, R) along with PCA plot, MultiQC summary file with several QC plots/tables).

Level 2 services: CCBB effort level - 5 hours

- Outlier removal and re-analysis
- Multiple sets of standard analysis
- Analysis involving non-standard genomes
- Custom differential gene expression
- Differential gene expression analysis on publicly available datasets
- Comparisons/inclusion of older datasets for re-analysis
- Advaita functional analysis
- GSEA or SetRank analysis

Level 3 services: **Consult CCBB first!** CCBB effort level no more than 8 hours - short term collaboration less than one month

- Large datasets with more than 20 samples

- Multiple sets of standard analysis
- Differential gene expression analysis on publicly available datasets
- Comparisons/inclusion of older datasets for re-analysis
- Advaita functional analysis for multiple datasets
- GSEA or SetRank analysis for multiple datasets

UMI-based RNA-Seq (~3 to 5 business days)

Requirements: Same as for RNA-Seq analysis

standard services: CCBB effort level - 5 hours

Standard analysis using nf-core/rnaseq workflow: Removal of ribosomal RNA using SortMeRNA, Alignment to reference genome using STAR, deduplication of the reads based on both mapping and UMI barcode information to address PCR duplicates using the UMI-tools, raw gene counts (featureCounts), differential gene expression analyses (DESeq2, R) along with PCA plot, MultiQC summary file with several QC plots/tables).

High Throughput RNA-Seq ("Drug-Seq") (standard Level 1 service: ~3 to 5 business days)

Level 1 services: CCBB effort level - 2 hours

Standard services: inline-barcode based demux (96 samples)

Level 2 services: CCBB effort level - 5 hours

UMI-based RNA-Seq analyses (described above) to identify significantly differentially expressed genes

Level 3 services: **Consult CCBB first!** CCBB effort level no more than 8 hours - short term collaboration less than one month

- Outlier removal and re-analysis
- Multiple sets of standard analysis
- Custom differential gene expression
- Comparisons/inclusion of older datasets for re-analysis
- Advaita functional analysis
- GSEA or SetRank analysis

SmallRNA-Seq (miRNA-Seq) (standard Level 1 services: ~3 to 5 business days)
CCBB services and effort levels similar to RNA-Seq data analysis.

Single cell RNA-Seq, V(D)J, Visium Spatial transcriptomics (10x Genomics)
Consult CCBB first to determine the effort level and timeline to complete analysis

- CellPlex
- Single cell RNA-Seq (cellranger/Seurat analysis)
- Single cell V(D)J (cellranger analysis)
- Visium Spatial transcriptomics (spaceranger analysis)
- More complex experimental designs

[Email to ccbb@scripps.edu](mailto:ccbb@scripps.edu) to set up a consultation meeting for additional service(s)

Additional services: Consult CCBB to get a quote/estimation of effort in hours. CCBB service hourly charges apply.

- Software development, custom pipeline implementation
- Re-analysis of older dataset
- Analysis for public dataset
- Specific figures/tables for publications; writing methods section or contribution for scientific papers/grant proposals
- Functional Analysis using Advaita/GSEA/SetRank
- Letter of Support for grants
- GEO/SRA submissions