

## UC San Diego Center for Computational Biology & Bioinformatics

### Scope of Work

2021

### ChIP-Seq/ATAC-Seq Analysis

UCSD Internal rate: \$180/hour

Non-profit rate: \$261/hour

For-profit rate: \$522/hour

Costs below shown for UCSD internal rate

#### Primary Analysis

1. Raw data quality control (method: FASTQC)
2. Alignment of raw data to genome (method: Bowtie or STAR)
3. Quality control of aligned data (method: RSeQC)
4. Peak calling (method: HOMER/MACS)

Cost: ChIPseq: \$90/sample for  $\leq 20$  samples ; \$45/sample for any additional samples above 20 (bulk rate)

ATACseq: \$360/sample

#### Secondary Analysis

1. Assessment of experimental design and analysis design
2. Differential peak calling (method: Homer, DESeq2, limma, DiffBind)
3. Functional enrichment analysis & pathway analysis

Cost: \$3,600-\$7,200 depending on complexity of design

#### Data Overlay

1. Assessment of second data set and methods for data overlay (~\$180-\$900)
2. Correlate results and other dataset (~\$1,800-\$4,500)
3. Overlay results and other dataset on significantly dysregulated pathways (~\$900-\$1,800)

#### Deliverables:

1. Consultation meeting to discuss experimental design, biological questions, and analysis
2. Results files from all analyses outlined
3. Open-source code from all analyses
4. Summary PowerPoint presentation of all results
5. Post-analysis meeting to discuss results