

## UC San Diego Center for Computational Biology & Bioinformatics

### Scope of Work

2020

### ChIP-Seq/ATAC-Seq Analysis

*UCSD Internal rate: \$180/hour*

*Non-profit rate: \$261/hour*

*For-profit rate: \$362/hour*

#### 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: 0.5 hours/sample for  $\leq 20$  samples ; 0.25 hours/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 (method: Hypergeometric test in TopGene)

*Cost: 15-40 hours depending on complexity of design*

#### Data Overlay

1. Assessment of second data set and methods for data overlay (~2-5 hours)
2. Correlate results and other dataset (~10-25 hours)
3. Overlay results and other dataset on significantly dysregulated pathways (~5-10 hours)
4. Differential network analysis (~25-40 hours)

*Cost: Hourly*

#### 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