

UC San Diego Center for Computational Biology & Bioinformatics

Scope of Work 2021 DNA-seq Analysis

UCSD Internal rate: \$180/hour

Non-profit rate: \$261/hour

For-profit rate: \$362/hour

Costs below shown for UCSD internal rate

*For whole genome sequencing, compute and storage cost is passed directly to the investigator. Compute cost averages ~\$45/sample for GATK germline variant calling and ~\$60/pair of samples for MUTECT somatic variant calling.

**HIPAA-compliant compute is available through iDASH

(<https://idash.ucsd.edu/cyberinfrastructure>) or Amazon Web Services

(<https://aws.amazon.com/compliance/hipaa-compliance/>) for an additional compute cost (~\$135/sample for GATK on AWS).

Primary Analysis

1. Raw data quality control (method: FASTQC)
2. Alignment of raw data to genome (method: BWA)
3. Quality control of aligned data (method: RSeQC)
4. Variant calling (method: GATK or MUTECT)
5. Variant annotation (method: ANNOVAR and myVariant.info)

Cost: Whole exome primary analysis \$180/sample; Whole genome primary analysis \$360/sample (inclusive of compute cost for < 20 samples. >20 samples compute passed directly to customer and bulk rate of \$7,200-\$14,400 plus compute for <200 samples)

Secondary Analysis

1. Variant prioritization (method: custom variant filtering and prioritization) (\$90/sample)
2. Functional enrichment analysis, pathway analysis and data overlay of variants on significantly dysregulated pathways (method: Hypergeometric test in ToppGene) (\$90/sample)

Other options

1. Assessment of second data set and methods for data overlay (~\$180-\$900)
2. Correlate variants with other data types (~\$1,800-\$4,500)
3. Overlay DNA-seq results on significantly dysregulated pathways (~\$900-\$1,800)
4. Structural variants (custom pricing)
5. Copy number variants (custom pricing)
6. Custom algorithms and pipelines (custom pricing)

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. Post-analysis meetings to discuss results