UC San Diego Center for Computational Biology & Bioinformatics
DNA-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.

For whole genome sequencing, compute and storage cost is generally 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)

Estimate:
Whole exome primary analysis: $180/sample inclusive of compute cost
Whole genome primary analysis for < 20 samples: $360/sample inclusive of compute cost
Whole genome primary analysis for >= 20 samples: $6,480-$14,040 plus compute compute passed directly to customer

Secondary Analysis

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

Estimate: $180/sample

Follow-Up Analysis

Further analysis (such as inclusion of additional datasets, correlation of variants with other data types, identification of structural or copy number variants, custom visualizations, and other downstream requests) will be scoped on a per-project basis.