Equipment Run Charges

Equipment	Price	Units
ABI 7900HT Real-time PCR	$20.00	per run
Agilent Bioanalyzer 2100	$12.00	per run
Auto MACs	$10.00	per hour
Genome Sequencer FLX 454	$1,000.00	per run
Gentle MACs Dissociator	$10.00	per hour
OpenArray NT Cycler System	$16.00	per hour
SOLiD Covaris S2	$25.00	per hour
Synergy HT Multi-Detection Microplate Reader	$10.00	per hour

Sequencing

Agilent Bioanalyzer (labor included): The Agilent 2100 Bioanalyzer is a microfluidics-based platform for sizing, quantification and quality control of DNA, RNA, proteins and cells on a single platform. Results are delivered within 30-40 minutes. This is an essential QC check prior to microarray analysis.

RNA Nano Chip	$58.00/chip
RNA Pico Chip	$58.00/chip

Microarrays: Pricing is for Gene-Expression microarrays. Other formats may be requested.

4X44K Feature Gene Expression Arrays	$350.00/sample
Labor (typically, 5 hours/project)	$60.00/hour

Capillary Sequencing (labor included): Sanger Sequencing.

Instrument-Ready Samples	$4.00 per sample
Reaction/Cleanup/Capillary Electrophoresis	$6.00 per sample

Autopure LS: Automated DNA extraction from fresh or frozen blood, buffy coat, cell suspensions, saliva and cultured cells using PureGene Chemistry. Empty tubes charged as samples.

1-5 ml samples:	$10.00 each
5-10 ml samples:	$18.00 each

Real-Time PCR, OpenArray: High throughput, real-time PCR for gene expression, genotyping or digital PCR using SYBR Green and Taq-Man chemistry on pre-configured gene panels or completely customized content. Each OpenArray plate contains 3072 reactions of 33 nl each.

Custom Materials, designed in conjunction w/ Life Technologies	Variable Pricing (approx. $650/plate)
Labor	$60.00/hour

Liquid Handling Automation: Tecan Freedom EVO or Qiagen BioRobot Universal available to automate liquid handling operations such as reaction setup, sample dilutions, cherry-picking, normalization, DNA and RNA extractions. Hourly charge applies to protocol development and operation.

Labor $60.00/hour

Illumina Veracode Genotyping: Illumina's Golden Gate chemistry is ideal for larger genotyping projects due to efficient multiplexing and content is completely customizable. Prices based on Illumina's list costs and subject to change.

Multiplex	# of Samples	# of Kits with same OPA	Price Per Sample	Approx. Labor/Kit	Price Per SNP	Price Per Kit
48 plex	480	1	$10.50	$840.00	$0.28	$6,384.00
	960	2	$8.89		$0.24	$5,531.00
	≥1,440	>3	$6.83		$0.19	$4,446.00
96 plex	480	1	$12.48	$840.00	$0.16	$7,429.00
	960	2	$10.56		$0.14	$6,415.00
	≥1,440	>3	$8.64		$0.12	$5,401.00
144 plex	480	1	$17.28	$840.00	$0.14	$9,963.00
	960	2	$14.62		$0.12	$8,560.00
	≥1,440	>3	$12.10		$0.10	$7,228.00
192 plex	480	1	$23.04	$840.00	$0.14	$13,005.00
	960	2	$19.50		$0.12	$11,134.00
	≥1,440	>3	$16.13		$0.10	$9,356.00
384 plex	480	1	$38.40	$840.00	$0.11	$21,115.00
	960	2	$30.72		$0.09	$17,060.00
	≥1,440	>3	$19.20		$0.06	$10,977.00

Next Generation Sequencing

Price includes reagents, consumables and a minimum of an hour of labor for library construction, emulsion PCR and sequence run. Prices may vary according to unforeseen sample issues and subsequent troubleshooting.
Please contact Eve Farias-Hesson, PhD @ (303) 270-2650 or farias-hessone@njhealth.org for an estimate for a project with a large number of samples or to obtain a quote for a grant proposal.

454 GS FLX Titanium Sequencing

454 FLX Titanium Expected Run Results PTP 70 x 75

No of Regions per PTP	Reads per region (x 10^3)	Throughput per region	Total Reads per PTP	Throughput per PTP
2	450 -650	180 - 280 Mb	~1,000,000	360 - 560 Mb
4	160 - 250	60 - 110 Mb	~800,000	240 - 440 Mb
8	80 - 120	30 - 55 Mb	~800,000	240 - 440 Mb
16	25 - 40	10 - 20 Mb	~512,000	160 - 320 Mb

454 GS FLX Titanium Sequence run

Service[1,2]	Price
454 FLX 2 region PTP sequence	$8,000
454 FLX 4 region PTP sequence	$9,000
454 FLX 8 region PTP sequence	$11,000
454 FLX 1/2 region PTP sequence	$4,000
454 FLX 1/4 region PTP sequence	$2,250
454 FLX 1/8 region PTP sequence	$1,375
emPCR[3]	
SV emPCR titration (4x)	$600
Library Construction[4]	
Short fragment removal (per sample)	$25
Library Quality assessment (per chip)	$60
Shotgun library (gDNA) construction	$550
Library Construction Training	
Per hour	$100

1- Additional information on pricing is available upon request for the 16 region PTP.
2- Partial PTP regions are available, however, the sequence run will be started upon obtaining the complete number of samples for running a full PTP plate.
3- An additional small volume emulsion PCR titration fee may apply if a sample requires troubleshooting.
4- Please contact us for an estimate of amplicon and paired-end library construction.

SOLID 5500xl

Library construction for DNA, RNA and ChIP samples are available. Please contact us for a cost estimate.

Service	Description	Pricing unit	Expected reads	Price
Library quality assessment	post-library QC	per chip	N/A	$45
Library Construction Training	DNA, mRNA, ChiP	hour	N/A	$100
SOLiD 5500xl sequencing	single read 75bp	per lane	170 Million	$1,270
SOLiD 5500xl sequencing	mate-pair 65 x 65bp	per lane	340 Million	$1,570
SOLiD 5500xl sequencing	paired end 75 x 35bp	per lane	340 Million	$2,184

1- Price per lane is subject to change if different users request individual ePCR per lane. Please contact us to get a project cost estimate.
2- Lane run is available, however, sequence run will be started upon obtaining the complete number of samples for running a full flowchip.

Ion Torrent (PGM)

Expected sequence run results

Chip	Throughput
314 chip	10Mb
316 chip	100Mb
318 chip	1Gb

Service	Price
Library Construction	
Fragment library	$240
100bp read length	
314 chip	$562
316 chip	$762
318 chip	$962
200bp read length	
314 chip	$912
316 chip	$1,112
318 chip	$1,312
Library Construction Training	
Per hour	$100.00

Bioinformatics Analysis

Analysis of data generated by the Center for Genes, Environment, and Health varies from basic analysis, which produces the output files typical for a given application, to complex characterization of the genes or loci implicated by the experimental study. Fees shown below apply for basic analyses, using typical pipelines, with the output level and form as detailed. The list of options may vary as additional pipelines are developed. For analysis needs that involve the creation of custom analysis scripts or implementation of programs to investigate specific questions of the data, support will be available at the bioinformatics analysis hourly rate; please contact Sonia Leach, PhD, the Director of Bioinformatics @ (303) 270-2568 or leachs@njhealth.org to discuss the details of your project.

These projects will be charged at the bioinformatics analysis rate of $65 per hour.

Basic Analysis Support

DNA-seq (Whole Genome, Exon, or Targeted)

Analysis Option	Description	Estimated Set-Up and Computation Time	Relevant Output Files	Fee
Mapping to sequenced genome†	Platform-specific mapper or Bowtie	~1-24 hours	Mapping and quality control statistics, *.bam file of aligned reads	$50 per library
SNP Detection and Annotation	Platform-specific or samtools identification of SNPs. Determination of functional consequence (missense, non-sense, non-coding, etc.), Human using SeattleSeq, otherwise Annovar for genomes with known gene models	~2-8 hours for SNP detection. Annotation time depends on number of SNPs and program used.	*.gff or *.vcf file describing SNPs. Tab delimited text file describing effect of variant (and whether in dbSNP for Human)	$100
Small InDel Detection and Annotation	Detection of insertions (~<20bp) or deletions (<10kb). Determination of functional consequence (missense, non-sense, non-coding, etc.), Human using SeattleSeq, otherwise Annovar for genomes with known gene models	~2 hours for detection, ~1 hour for annotation.	*.gff or *.vcf file. Tab delimited text files describing effect of variant (and whether in dbSNP for Human)	$100

DNA-seq (Whole Genome, Exon, or Targeted) Cont.

Analysis Option	Description	Estimated Set-Up and Computation Time	Relevant Output Files	Fee
CNV Detection and Annotation	Determination of copy number variation, with filtering against known segmental duplications	~2 hours	List of genes within CNV segment, and *.gff file describing CNV	$100
Large Indel Detection and Annotation	Determining large insertions and deletions	~1 hour	List of genes within indel, and *.gff file describing indel	$100

†Mapping to specialized sequence reference file will require special consideration

RNA-seq

Analysis Option	Description	Estimated Set-Up and Computation Time	Relevant Output Files	Fee
Mapping to sequenced genome†	Platform-specific mapper	~1-24 hours	Mapping and quality control statistics, *.bam file of aligned reads	$50 per library
Mapping using TopHat	Alternative 3rd party mapping algorithm, with or without reference gene models, identifies splice junctions. Especially for Illumina reads	~6-24 hours	Mapping and quality control statistics, *.bam file of aligned reads	$50 per library
Differential Expression using DESeq	Generates counts of mapped data for reference gene model (e.g. Ensembl), differential expression test by negative binomial	~3 hours	List of Ensembl transcripts with fold changes and p-values, *.bedgraph file	$75
Differential Expression and Transcript Assignment using Cufflinks/Cuffdiff	Assembles transcripts, estimates abundances, tests for differential expression by t-test	~10 hours	List of assembled transcripts (Ensembl id if known) with FPKM, fold changes, p-values, and Microsoft Excel macro-enabled file to explore results in IGV, *.bedgraph file	$100

ChIP-seq

Analysis Option	Description	Estimated Set-Up and Computation Time	Relevant Output Files	Fee
Mapping to sequenced genome†	Platform-specific mapper or Bowtie	~2-10 hours	Mapping and quality control statistics, *.bed file	$50 per library
Peak Calling using MACS	Determination of peaks with or without a control sample	~ 1 hour	*.bed file with list of peaks	$75
Peak Calling using ChIPDiff	Determination of peaks and differential enrichment between two samples	~1 hour	*.bed file with list of peaks	$75

Functional Characterization

Analysis Option	Description	Estimated Set-Up and Computation Time	Relevant Output Files	Fee
Ingenuity Systems IPA Pathway Analysis (Self run)	Given list of genes, determine over-represented pathways	~2 hours	List of over-represented pathways with p-values and genes annotated to them	$20 per hour
Ingenuity Systems IPA Pathway Analysis (Center staff run)	Given list of genes, determine over-represented pathways	~2 hours	List of over-represented pathways with p-values and genes annotated to them	$50 per hour
DAVID Functional Annotation	Given list of genes, perform batch annotation, gene-term enrichment (Gene Ontology, Protein interactions, functional domains, disease associations, pathways, sequence features), and determine over-representation	~1 hour	Gene annotation and list of over-represented pathways with p-values	$50 per hour

Microarray Analysis

Analysis Option	Description	Estimated Set-Up and Computation Time	Relevant Output Files	Fee
Partek Genomics Suite (Self run)	Determines list of significantly differential genes	~2 hours	List of genes and p-values	$20 per hour
Partek Genomics Suite (Center staff run)	Determines list of significantly differential genes	~2 hours	List of genes and p-values	$50 per hour

Other Bioinformatics Analysis

Hourly Bioinformatics Analysis	$65 per hour

FlexiVent

Run by CGEH Staff	$50.00/hour
Self Run *	$35.00/hour
Data Analysis and Interpretation	$50.00/hour
FlexiVent Training	$30.00/hour

**Must be trained on using FlexiVent and receive approval from Center staff.*
There is a 8 animal minimum for FlexiVent.
Contact Leah Teeter to schedule FlexiVent @ (303) 270-2650 or teeterl@njhealth.org

Outside institutions will be charged 58.5%, which is the current NIH indirect rate.
A 10% administrative fee will be added to all supplies purchased through the Center.

Please contact the Genetics Core for pricing as charges vary per application, and number of submitted samples.

Before submitting your DNA/RNA sample, please confirm that:

DNA Sample Requirements-

- DNA must be double stranded. If possible, please submit a well-labeled gel image to indicate that the sample is not degraded and is within the concentration range determined by spectrophotometry.
- DNA should not be the result of whole genome amplification (or other similar process which may compromise representativity).
- DNA should not be degraded

- DNA should contain no particulate matter, organic solvents, salts or proteins.
- DNA should have an OD 260/280 ratio ≥ 1.8.
- Your sample has the minimum amount of DNA for sample preparation. A minimum of 10ug of DNA is recommended for preparing mate-pair libraries of microbial genomes, 20ug for preparing mate-pair libraries of human genome, and 1ug for fragment or paired-end libraries.
- Your sample is in TE buffer (e.g., Qiagen EB) with a minimal concentration of 50 ng/uL (DNA).

RNA Sample Requirements-

- RNA should not be degraded
- RNA should have an RNA integrity number (RIN) greater than 9.
- Whole transcriptome library construction input:
    - 100-500ng of poly(A) RNA or 250-650ng of rRNA-depleted total RNA
    - Suspended in 10uL Nuclease-free water
    - Absent of contaminating rRNA

Library ready for ePCR Sample Requirements-

- Your sample is in TE buffer (e.g., Qiagen EB) with a minimal concentration of 5ng/ul.
- Provide a brief workflow of the library sample preparation.
- Inform origin of adaptors used for making libraries (e.g. IDT HPLC purified oligos).
- If barcoding libraries, inform sequence and barcode series (DNA/RNA) used for preparing each library submitted for sequencing. If sequencing using our SOLiD 5500xl instrument, in order to obtain color balance during sequencing we recommend design experiments to use at least one of the full sets of four barcodes (e.g. barcodes 1-4, 5-8, 9-12, 13-16, 17-20, etc).
- Provide, if available, Bioanalyzer file containing results for the final libraries.