EXTERNAL PRICE LIST–VALID THROUGH JUNE 30, 2016

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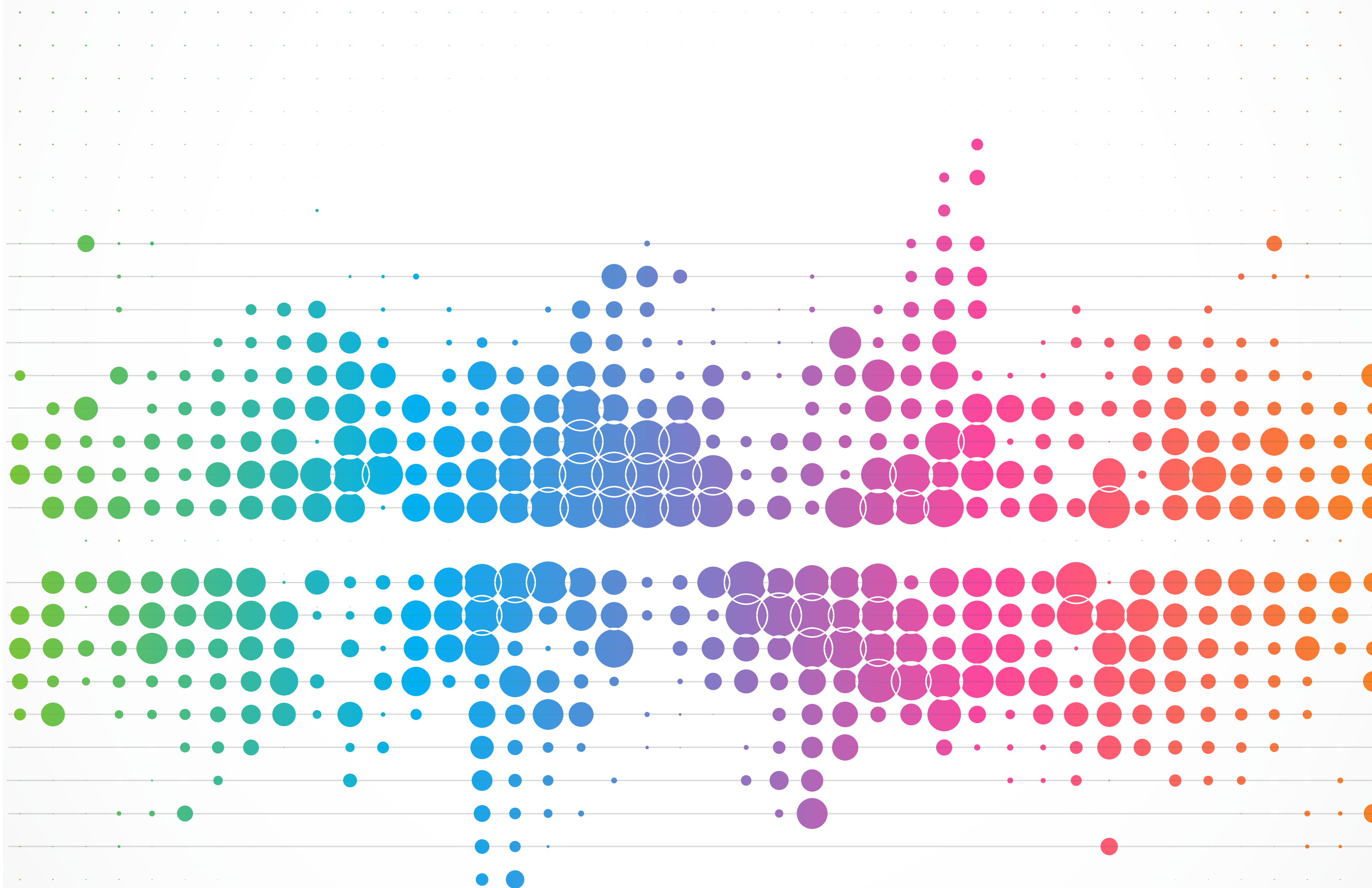

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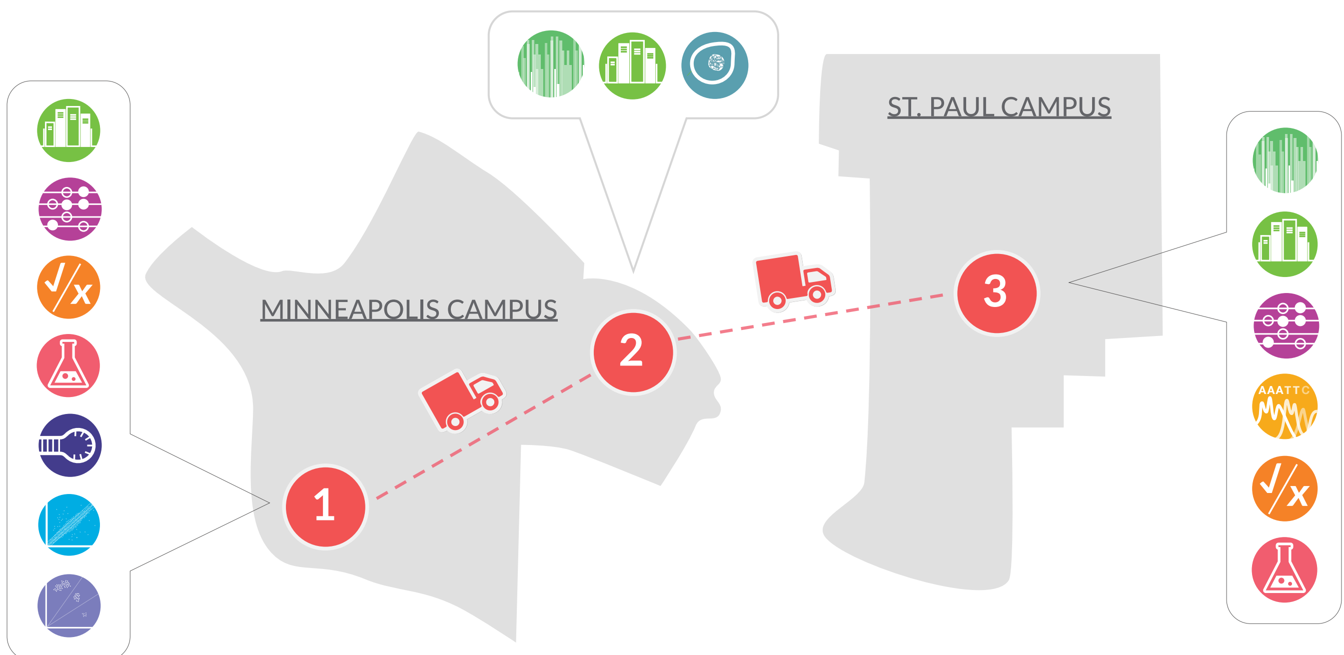

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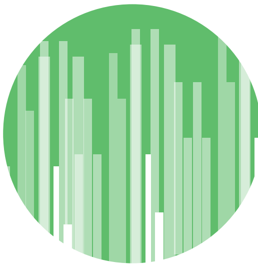


NEXT-GENERATION SEQUENCING

The UMGC provides next-generation sequencing (NGS) using Illumina instruments: the HiSeq 2500 and its smaller sibling, the MiSeq. Our three HiSeq sequencers support applications that require > 100M reads per lane, whereas our four MiSeqs power studies that require fewer than 20M reads per lane.

INSTRUMENTS

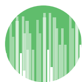
Our HiSeq 2500s ("Watson", "Crick" and "Franklin") and Illumina MiSeqs provide a range of capabilities, differing in terms of their output, speed, turnaround time, and read lengths. In this section, NGS instrument options are explained. (See the NGS Library Creation section below for applications). In addition to sequencing on Illumina instruments, UMN scientists are able to outsource long-read sequencing on the Pacific Biosciences RS II instrument at the Mayo Clinic (please inquire).

SINGLE-VS. PAIRED-READ

Illumina sequencers can be run in single-read (SR) or paired-end (PE) mode. In single-read runs, sequencing proceeds from only one direction of molecules (the "forward" direction), whereas in paired-end runs, sequencing is carried our sequentially on both ends of each molecule ("forward" and "reverse"). SR runs are described with the nomenclature "1 x read length in bp", (e.g. "1x50 SR"). PE runs are described with the nomenclature "2 x read length in bp" (e.g. "2x50 PE").

READ LENGTH

"Read length" refers to the number of bases of sequence generated during a sequencing run. For SR runs, this is the length of the single read, whereas in PE runs, it refers to the length of *each* of the two paired runs. The read length options we offer are constrained by available reagent kits from Illumina. Note, however: the read-lengths listed below are not an exhaustive list of all possibilities. If you are interested in a "flavor" of sequencing that is not shown, please contact us.



HISEQ 2500 HIGH-OUTPUT SEQUENCING ON "FRANKLIN"

HiSeq 2500 instruments can be run in two different modes: "High-output" or "Rapid Run". High-output mode utilizes 8-lane flow cells in combination with "version 4 chemistry", whereas Rapid Run mode uses 2-lane flow cells with "Rapid" SBS chemistry. Only our most recently acquired HiSeq 2500 ("Franklin") is capable of running in High-output mode.

OUTPUT: For single-read lanes, we deliver ≥ 220 million reads in the forward direction, and for paired-end lanes, we produce ≥ 220 million reads in both forward and reverse directions (resulting in ≥ 440 million single reads in all).

BENEFITS: High-output mode provides almost twice as many reads per lane than rapid-run mode, at a lower cost per lane, resulting in a cost per read about half that of Rapid Run mode.

DRAWBACKS: Thanks to the use of 8-lane flow cells, it can take considerably longer for a high-output mode run to be "filled" with enough samples for a run to proceed. As a result, project turnaround in high-output mode can be longer than in rapid-run mode.

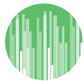
QUESTIONS?

Contact Aaron Becker: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
HiSeq 2500 High-output Mode – Single-read.			
50-bp Single-read (1x50 SR).[1]	*1-any*	*lane*	*$1,455.52*
100 bp Single-read (1 x 100 SR).[2]	*1-any*	*lane*	*$1,910.61*
HiSeq 2500 High-output Mode – Paired-end.			
50-bp Paired-end (2x50 PE).[3]	*1-any*	*lane*	*$2,332.12*
125-bp Paired-end (2x125 PE).[4]	*1-any*	*lane*	*$3,362.39*

NOTES

1. Output ≥ 220,000,000 x 50 bp = 11 Gb.
2. Output ≥ 220,000,000 x 2 x 50 bp = 22 Gb.
3. Output ≥ 220,000,000 x 100 bp = 22 Gb.
4. Output ≥ 220,000,000 x 2 x 125 bp = 55 Gb.



HISEQ 2500 RAPID RUN SEQUENCING ON "WATSON" & "CRICK"

Two of our HiSeq 2500s ("Watson" and "Crick") use Illumina's "Rapid" SBS chemistry on two-lane flow cells.

OUTPUT: For single-read lanes, we deliver ≥ 120 million reads in the forward direction, and for paired-end lanes, we produce ≥ 120 million reads in both forward and reverse directions (resulting in ≥ 240 million single-reads in all).

BENEFITS: With only two flow cell lanes to scan, Rapid Runs are fast, enabling quicker turnaround and the longest read lengths available (250 cycles). Moreover, with only two lanes to occupy, Rapid Run flow cells are easier to "fill", with less delay incurred waiting for samples to be submitted for sequencing. As a result, project turnaround in Rapid Run mode can be shorter, especially for sequencing read lengths that are less commonly requested.

DRAWBACKS: Due to the smaller surface area of Rapid Run lanes, output is lower — and cost per read higher — than High-output mode.

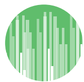
QUESTIONS?

Contact Aaron Becker: next-gen@umn

SERVICE	SCALE	UNIT	PRICE
HiSeq 2500 Rapid Run Mode – Single-read.			
50-bp Single-read (1x50 SR).[1]	*1-any*	*lane*	*$2,048.82*
100-bp Single-read (1x100 SR).[2]	*1-any*	*lane*	*$2,468.67*
HiSeq 2500 Rapid Run Mode – Paired-end.			
50-bp Paired-end (2x50 PE).[3]	*1-any*	*lane*	*$2,857.42*
100-bp Paired-end (2x100 PE).[4]	*1-any*	*lane*	*$3,540.07*
150-bp Paired-end (2x150 PE).[5]	*1-any*	*lane*	*$4,379.74*
250-bp Paired-end (2x250 PE).[6]	*1-any*	*lane*	*$5,399.92*

NOTES

1. Output ≥ 120,000,000 x 50 bp = 6 Gb.
2. Output ≥ 120,000,000 x 100 bp = 12 Gb.
3. Output ≥ 120,000,000 x 2 x 50 bp = 12 Gb.
4. Output ≥ 120,000,000 x 2 x 100 bp = 24 Gb.
5. Output ≥ 120,000,000 x 2 x 150 bp = 36 Gb.
6. Output ≥ 120,000,000 x 2 x 250 bp = 60 Gb.



MISEQ SEQUENCING

The Illumina MiSeq is a "desktop" sequencer specialized for quick, lower-output runs on single-lane flow cells.

OUTPUT:
Nano runs ≥ 1 million reads.
Micro runs ≥ 4 millions reads.
Version 2 chemistry ≥ 8 millions reads.
Version 3 chemistry ≥ 16 million reads.

BENEFITS: With only a single lane to scan, the MiSeq has the quickest run per cycle of any Illumina instrument, and consequently, achieves the longest read length (paired-end 300 cycles). The MiSeq is therefore ideal for targeted sequencing of long amplicons, including microbial 16S sequencing. Turnaround time on the MiSeq is also theoretically faster than on other Illumina instruments (although in practice, queues may develop on the instrument). Our expedited 2x300-bp run is designed for projects requiring guaranteed 1-week turnaround.

DRAWBACKS: Cost per read is significantly higher on the MiSeq platform than on HiSeq instruments.

QUESTIONS?

Contact Aaron Becker: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
MiSeq Nano – Paired-end.			
150-bp Paired-end (2x150 PE).	*1-any*	*lane*	*$1,064.69*
250-bp Paired-end (2x250 PE).	*1-any*	*lane*	*$1,223.14*
MiSeq Micro.			
150-bp Paired-end (2x150 PE).	*1-any*	*lane*	*$1,454.29*
MiSeq. Version 2 – Single-read.			
50-bp Single-read (1x50 SR).	*1-any*	*lane*	*$1,380.14*
MiSeq. Version 2 – Paired-end.			
150-bp Paired-end (2x150 PE).	*1-any*	*lane*	*$1,686.89*
250-bp Paired-end (2x250 PE).	*1-any*	*lane*	*$1,843.90*
MiSeq. Version 3 – Paired-end.			
75-bp Paired-end (2x75 PE).	*1-any*	*lane*	*$1,492.09*
300-bp Paired-end (2x300 PE).	*1-any*	*lane*	*$2,390.52*
300-bp Paired-end (2x300 PE). Expedited.	*1-any*	*lane*	*$3,698.95*

NGS LIBRARY CREATION

The true power of next-generation sequencing derives from the diversity of library creation methods available. There exist hundreds of NGS library creation methods tailored to different experimental approaches, with numerous commercial kits and variations for each method. It is impossible for us to list all of these various methods as "standard" services, with a fixed price and established expectations for turnaround and performance for each. However, we encourage researchers to contact us with requests for protocols they do not find here, as we are able to provide many of these as "custom" services. Here, we simply list the subset of "standard" and "high-throughput" workflows that are offered as routine services.

DNA

DNA-Seq methods that differ in terms of the DNA fragmentation method, genome size of interest, use of PCR amplification in library creation, and the use of "mate-pair" technology. All of the protocols listed in this section utilize Illumina reagents and protocols.

TRUSEQ NANO MANUAL: this is a "standard" NGS workflow: 1) acoustic shearing of DNA, 2) enzymatic repair/ligation of adaptors, and 3) PCR amplification.

TRUSEQ NANO AUTOMATED: following manual acoustic shearing, libraries are created in an automated fashion on the NeoPrep robot. For Neoprep runs, samples must be submitted in sets of 16 samples.

NEXTERA: this "transposase" method does not involve physical fragmentation of gDNA, instead using direct incorporation of Illumina adaptors via "tagmentation".

NEXTERA MATE-PAIR: combines a first round of specialized Nextera-based intra-molecular circularization, followed by shearing and traditional TruSeq library creation, to generate "jumping libraries" of fragments that originate from a known distance apart in the original gDNA.

NEXTERA XT: tailored to small genomes, such as those of bacteria. In both Nextera and Nextera XT methods, PCR is used to amplify successful tagmented molecules.

PCR-FREE: designed to avoid GC-bias associated with methods such as TruSeq and Nextera.

QUESTIONS?

Contact Elyse Froehling: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
TruSeq Nano DNA Library Creation.			
Input DNA requirements: 100 ng for insert size of 350 bp, 200 ng for insert size of 550 bp.	1-any	sample	$105.16
TruSeq Nano DNA Library Creation. Automated on Illumina NeoPrep.			
Input DNA requirements: 100 ng for insert size of 350 bp, 200 ng for insert size of 550 bp.	16-any	sample	$72.35
Nextera Library Creation.			
Standard Scale. 50 ng of input DNA needed.	1-24	sample	$153.29
High Scale. 50 ng of input DNA needed.	25-any	sample	$141.00
Nextera Mate-pair Library Creation.			
Gel Free. Standard Scale.[1]	1-any	sample	$337.69
Gel Plus. Standard Scale.[1]	1-any	sample	$743.02
Nextera XT Library Creation.			
1 ng of input DNA for a library insert size of 350 bp. 2 ug of input DNA for a library insert size of 550 bp.	1-24	sample	$90.47
	25-any	sample	$79.83
PCR-Free Library Creation.			
1 ug of input DNA for a library insert size of 350 bp. 2 ug of input DNA for a library insert size of 550 bp.	1-any	sample	$152.95

NOTES

1. There are two different approaches to Nextera Mate-pair Library Creation: Gel-Free vs Gel-Plus. The Gel-Free protocol, which does not include fragment sizing, requires 1 µg of DNA, is more robust, and yields a higher diversity of fragments with a broader range of fragment sizes. The Gel-Plus protocol, which includes gel-based fragment sizing, requires 4 µg of DNA, and allows the selection of a narrower range of fragment sizes.

RNA

RNA-Seq (NGS of double-stranded cDNA generated by reverse-transcription of RNA) has become the standard method for genome-wide gene expression analysis, largely replacing microarray-based methods. We provide several different services for RNA-Seq library creation.

Prices listed include the costs of library QC, but do not include the cost of QC of the input material, which is an obligatory step. (See the QC section for details).

CLASSIC: using total RNA as input, involves removal of rRNA from total RNA via oligo-dT purification of mRNA, followed by random-primed reverse-transcription, second-strand cDNA synthesis, and subsequent library creation from the resulting dsDNA. Note that this protocol is becoming obsolete, and is offered for clients who wish to generate data that is backwards-compatible. In order to ensure forward-compatibility, new RNA-Seq projects should use the STRAND-SPECIFIC RNA-SEQ protocol.

STRAND-SPECIFIC: like classic RNA-Seq, this protocol begins with total RNA input and oligo-dT purification, but preserves information about the strandedness of transcripts. Strand-specific RNA-Seq libraries can be created manually, or in an automated fashion on the NeoPrep robot. For NeoPrep runs, samples must be submitted in sets of 16 samples.

STRAND-SPECIFIC WITH RIBOZERO: in cases where polyadenylation cannot be used to selectively remove rDNA from total RNA, Strand-specific RNA-Seq with RiboZero uses sequence-specific pull-down to remove rRNA sequences.

SMARTer cDNA SYNTHESIS: in cases where limiting quantities of RNA are an issue, we provide SMARTer cDNA methods for combined amplification and cDNA creation from as little as 1-2 ng of RNA, using oligo-dT or universal priming of reverse transcription. Please inquire for further details of the workflow.

RIBOSOMAL REDUCTION: subtractive hybridization removal of rRNA is helpful in cases where universal RNA priming is involved, or for organisms without polyadenylated RNA.

SMALL RNA: The expression of microRNA can be studies using the Small RNA Library Creation. Please inquire for further details of the workflow.

TRUSEQ RNA ACCESS: targeted RNA-Seq is a useful approach to the study of degraded RNA Please inquire for further details of the workflow.

QUESTIONS?

Contact Elyse Froehling: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
Classic RNA-Seq *Input mass of ≥ 1 ug of total RNA.*	*1-any*	*sample*	*$148.99*
Strand-specific RNA-Seq Library Creation. Manual. *Input mass of ≥ 1 ug of total RNA.*	*1-any*	*sample*	*$128.74*
Strand-specific RNA-Seq Library Creation. Automated on Illumina NeoPrep.[1] *Input mass of ≥ 100 ng of total RNA.*	*16-any*	*sample*	*$95.35*
Strand-specific RNA-Seq Library Creation with RiboZero. *Input mass of ≥ 1 ug of total RNA.*	*1-any*	*sample*	*$201.34*
Clontech SMARTer cDNA Synthesis. *Input mass of 1-2 ng of total RNA.*	*1-24*	*sample*	*$119.39*
	25-any	*sample*	*$108.91*
Clontech SMARTer Universal Low cDNA Synthesis. *Useful for degraded RNA. Must be combined with ribosomal reduction of rRNA sequences.*	*1-any*	*sample*	*$169.69*
Ribosomal Reduction *We use RiboZero rRNA removal kits available for several different species. Please inquire for availability for your spceis of interest.*	*1-24*	*sample*	*$128.32*
	25-any	*sample*	*$118.74*
Small RNA Library Creation. *1 ug of total RNA input can be submitted or alternatively, you can submit the entire fraction of isolated small RNA from 1 ug total RNA.*	*12-59*	*sample*	*$197.44*
	60-any	*sample*	*$174.53*
TruSeq RNA Access. Degraded RNA.	*1-24*	*sample*	*$303.10*
	25-48	*sample*	*$280.78*
	49-any	*sample*	*$262.70*

NOTES

1. The RNA-Seq protocol on the NeoPrep is scheduled for commercial release by Illumina in Quarter 1 of 2016. Please inquire for availability.

DNA METHYLATION

Next-generation sequencing is a powerful means to profile DNA methylation at the single-nucleotide resolution, when it is combined with bisulfite conversion of DNA either before or after library creation.

Exposure of DNA to sodium bisulfite results in the conversion of cytosine (C) – but not methylated cytosine (C*) – to uracil (U). Subsequent amplification of DNA during PCR converts U to T. Consequently, bisulfite conversion results in the change of C residues in DNA to T, leaving *C unchanged. Once such conversion has been accomplished, the original methylation state – C or C* – can be read out as the presence of a C vs T at a given CpG site.

QUESTIONS?

Contact Aaron Becker: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
Reduced Representation Bisulfite Sequencing (RRBC).			
A "traditional" DNA methylation library creation method utilizing bisulfite conversion after standard DNA shearing-based library creation. The method uses kits and protocols from New England Biolabs.	*1-12*	*sample*	*$272.18*
	13-48	*sample*	*$194.14*
	49-any	*sample*	*$164.42*

NOTES

1. There are a large variety of other methods for the measurement of DNA methylation in DNA, including whole-genome methods, methods based on sequence capture of CpG islands, and targeted methods. Please inquire for more details.

DNA SEQUENCE CAPTURE ENRICHMENT – AGILENT/NIMBLEGEN/IDT BAITS

Sequence capture ("Seq-Cap") is used to enrich genomic regions of interest, thereby reducing downstream NGS coverage and cost. Capture baits are oligos – custom or pre-designed stock products – that are used in the hybridization step. Baits are available from several different vendors.

Seq-Cap projects include two costs: 1) Library creation (labor and generic reagents) and 2) Baits (baits and vendor-specific library creation reagents). In the table on the right, we show the labor costs for Seq-Cap using baits from Agilent, Nimblegen, or IDT. For the additional cost for baits, see please inquire.

QUESTIONS?

Contact Ann Bohac: bohac001@umn.edu

SERVICE	SCALE	UNIT	PRICE
Seq-Cap Library Creation: Agilent/NimbleGen/IDT.			
Standard Scale.	*1-16*	*sample*	*$174.64*
High Scale.	*17-48*	*sample*	*$144.99*
Very High Scale.	*49-any*	*sample*	*$121.34*
There are more bait options offered by vendors than we can list here. Please contact us for more information.			

CHIP-SEQ

Illumina ChIP-Seq Library Creation is performed in collaboration with researchers, who are responsible for the chromatin immunoprecipitation aspects of ChIP-Seq projects, and provide immunoprecipitated DNA to the UMGC for subsequent processing.

QUESTIONS?

Contact Elyse Froehling: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
Illumina ChIP-Seq Library Creation.			
Standard Scale.	*1-24*	*sample*	*$204.59*
High Scale.	*26-any*	*sample*	*$166.38*
5 - 10 ng of ChIP DNA input is recommended.			

16S/18S AMPLIFICATION

PCR amplification of the 16S or 18S rRNA gene forms the basis for studying microbial diversity. The UMGC provides two workflows: a UMGC-developed dual-indexing approach, and the Earth Microbiome Project protocol. Studies in the UMGC comparing the two protocols have demonstrated greater accuracy and precision with our dual-indexing approach (please inquire).

UMGC DUAL-INDEXING: In the first step, the 16S or 18S target is amplified using identical PCR primers for all samples. In the second step, amplicons are tailed using minimal cycles of overlap-extension PCR, to add functional sequencing adaptors and sample-specific bar-coding indexes for multiplexing.

EMP: The Earth Microbiome Project (EMP) protocol is a single PCR amplification protocol (availabe for 16S V4 region only) that uses a large library of different PCR primers (each with different indexes) to enable multiplexing of amplicons.

TURNAROUND: Standard turnaround (submission to NGS data release) is typically within 4-6 weeks of sample submission. In cases where a more rapid turnaround is required, our expedited service may be available, with data returned in 7 days or less from the time of submission.

QUESTIONS?

Contact Allison MacLean: micbiom@umn.edu

SERVICE	SCALE	UNIT	PRICE
16S/18S. UMGC Dual-indexing. *Price per sample. Variable regions available include: V1-V3, V4, V4-V6, V5-V6, and fuingal 18S (V9). Turnaround from sample submission to sequencing data release between 4-6 weeks.*	*1-any*	*sample*	*$12.65*
16S/18S. UMGC Dual-indexing. Expedited. *Price per 96-well plate (One rate no matter how many wells of plate are filled). Turnaround from sample submission to sequencing data release ≤ 7 days. This rate must be paired with Expedited MiSeq 300-bp Paired-end (2x300 PE) run, and is subject to availability at time of request (please inquire).*	*1*	*up to 94 samples*	*$1,146.77*
Earth Microbiome Project Protocol (V4). *Price per sample. V4 region only. Turnaround from sample submission to sequencing data release between 4-6 weeks.*	*1-any*	*sample*	*$9.84*

LIBRARY MANIPULATION

Library creation by clients themselves is a good method for researchers to decrease costs. In order to help researchers be successful in their own library creation efforts, the following DNA manipulation services are available “à la carte”.

QUESTIONS?

Contact Elyse Froehling: next-gen@umn.edu

SERVICE	SCALE	UNIT	PRICE
DNA Shearing. Covaris. *This rate includes Agilent DNA sizing.*	*8-any*	*sample*	*$36.63*
Caliper XT Size Selection. DNA. *This rate includes Agilent DNA sizing.*	*1-any*	*sample*	*$91.68*
Library Pooling. 96-well plate.	*1-2*	*plate of 96*	*$107.69*
	3-4	*plate of 96*	*$81.47*
	5-any	*plate of 96*	*$58.52*

GENE EXPRESSION

The UMGC offers quantitative analysis of gene expression via array-based, PCR-based, and molecular counting methods. Details and pricing for sequencing-based transcriptome analysis (RNA-Seq), and for single-cell gene expression, are described in the Next-generation Sequencing (above) and Single-cell Genomics sections, respectively.

ILLUMINA ARRAY EXPRESSION

Illumina manufactures "BeadChip" microarrays for direct-hybridization, whole transcriptome gene expression analysis of human. Human HT-12v4 arrays contain 47,000 probes derived from the National Center for Biotechnology Information RefSeq Release 38, and are designed for parallel analysis of 12 human RNA samples.

QUESTIONS?

Contact Darrell Johnson: exprn@umn.edu

SERVICE	SCALE	UNIT	PRICE
Illumina Array Expression. HT-12v4. *Array hybridization only for samples that have been labeled by researchers themselves.*	*1-any*	*sample*	*$77.43*
Illumina Array Expression. Human HT-12v4.	*12-36*	*sample*	*$302.58*
	48-96	*sample*	*$260.91*
	108-any	*sample*	*$231.93*

NANOSTRING NCOUNTER

The NanoString nCounter is a single-molecule counting device for the digital quantification of up to 800 different genes in a single multiplexed reaction. The technology uses molecular "barcodes", each of which is color-coded and attached to a single probe corresponding to a gene of interest, in combination with solid-phase hybridization and automated imaging and detection. Panels of barcoded probes are called "CodeSets".

Unique features of nCounter analysis include direct hybridization to RNA (no reverse-transcription required), exquisite discrimination of closely-related miRNA species, and simple, spreadsheet-based digital output.

QUESTIONS?

Contact Darrell Johnson: exprn@umn.edu

SERVICE	SCALE	UNIT	PRICE
nCounter Expression Analysis. Processing. *Price excludes CodeSet cost, but includes labor, instrument time, and "universal" reagents.[1]*	*12-any*	*sample*	*$46.43*

NOTES

1. Because the range of content options on the nCounter evolves rapidly, please contact the UMGC (and peruse the NanoString website) for details on the availability and pricing of pre-designed nCounter CodeSets.

QUANTITATIVE REAL-TIME PCR (Q-PCR) IN 384-WELL FORMAT

The UMGC offers quantitative Real-time PCR in 384-well format using the Applied Biosystems 7900HT instrument. Users may submit their own 384-well plates to be amplified and detected on the ABI 7900HT, or they may elect to use the UMGC's full-service real-time Q-PCR platform, which is based on Roche's Universal Probe Library (UPL) technology.

ROCHE UNIVERSAL PROBE LIBRARY: a library of 165 short hydrolysis probes designed such that virtually any gene will contain one or more appropriate probes. Designing a gene-specific "Taqman" assay is thus quick and inexpensive, as only (inexpensive) primers are required that flank the hydrolysis probe.

The UMGC offers a service for design and functional verification of such Roche UPL Taqman assays, as well as a full-service, RNA-to-expression level analysis. This involves the iterative design, synthesis, and functional validation (PCR efficiency determination) of up to 3 primer-probe assays per target gene. Validation includes a multi-point determination of amplification efficiency.

SERVICE	SCALE	UNIT	PRICE
Design & Validation of Roche UPL primer-probe assay.	*1-3*	*gene*	*$88.23*
	4-8	*gene*	*$93.06*
	9-any	*gene*	*$61.10*
Quantitative Real-time PCR Analysis with UPL Probe.	*8-32*	*data point*	*$10.78*
	16-32	*data point*	*$4.64*
	40-any	*data point*	*$3.57*
Quantitative PCR. ABI 7900 Run, Client-submitted Plate.	*1-any*	*plate of 384*	*$50.19*
Reverse-transcription of RNA.	*1-any*	*sample*	*$16.87*
Taqman Assay Validation. 96-well Plate.	*1-any*	*plate of 96*	*$75.11*

QUESTIONS?

Contact Darrell Johnson: exprn@umn.edu

HIGH-THROUGHPUT Q-PCR ON FLUIDIGM BIOMARK HD

The Fluidigm BioMark HD is a microfluidic, high-throughput instrument for real-time Q-PCR of up to 9,216 reactions in a single run. The heart of the platform is a microfluidic chip called an "Integrated Fluidic Circuit (IFC)" into which are deposited amplification-ready templates (e.g., cDNA) and gene-specific assays (e.g., Taqman). The IFC performs automatic mixing of templates and assays in nanoliter amplification wells, followed by real-time PCR and data capture on the BioMark HD.

High-throughput IFCs can be run at the UMGC in two formats (# templates vs # assays): 1) 96.96 (9216 reactions), 2) 48.48 (2304 reactions). A third IFC also exists – the "FLEXsix IFC" – contains six independent 12.12 arrays that can be run independently, for small-scale experiments or pilot runs.

Use of the Fluidigm BioMark involves two costs from among those listed in the table on the right:

1) the IFC itself, 2) Chip processing.

Chip processing may be performed by the UMGC (high-throughput IFCs), or by clients themselves, who therefore pay only for the intrument access (FLEXsix IFC).

SERVICE	SCALE	UNIT	PRICE
Fluidigm BioMark HD Chip Processing.			
By client.	*1-any*	*run*	*$458.89*
By UMGC.	*1-any*	*run*	*$1,027.59*
Fluidigm BioMark IFCs.			
FLEXsix Chip and Loading Reagents.[1]	*1-any*	*each*	*$952.28*
48.48 (samples.assays).	*1-any*	*each*	*$987.62*
96.96 (samples.assays).	*1-any*	*each*	*$3,167.99*
Fluidigm DELTAgene Assays.			
Real-time Q-PCR assay.	*12-any*	*gene*	*$96.91*
Wet-lab tested.[2]	*12-any*	*gene*	*$242.27*

NOTES

1. The FLEXsix IFC is designed for smaller-scale, pilot, and optimization experiments, and contains six independent 12.12 (samples.assays) arrays of reactions chambers that can be run simultaneously, or in separate runs.

2. Each gene-specific DELTAgene assays provide adequate material for up to 100 IFCs. Wet-lab tested assay have been functionally validated by Fluidigm.

QUESTIONS?

Contact Darrell Johnson: exprn@umn.edu

GENOTYPING

The UMGC provides genotyping services at several different scales, from single-SNP (Uniplex) to genome-wide approaches (Illumina Infinium). Here, we also list methods for the analysis of structural variation (fragment analysis).

ILLUMINA INFINIUM

Illumina Infinium BeadChips are designed for moderate-scale (3,000 SNPs) to genome-wide-scale (> 5M SNPs) genotyping of either custom or predesigned content.

The cost of a custom Infinium project involves the design and synthesis (by Illumina) of a custom oligonucleotide pool (OPA). The Infinium family of products includes a wide variety of predesigned BeadChips from both Illumina and academic consortia.

Pricing for an Infinium project includes two different components: 1) BeadChip kit consisting of stock or custom SNP microarrays and processing reagents, and 2) the cost of BeadChip processing, assessed per sample.

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
Illumina Infinium 12-sample/24-sample BeadChip Processing. *Samples must be submitted in multiples of 12 or 24 samples, depending on the BeadChip format.*	*12-48*	*sample*	*$33.72*
	60-192	*sample*	*$21.39*
	204-768	*sample*	*$12.02*
	780-any	*sample*	*$8.64*
Illumina Infinium 4-sample/8-sample BeadChip Processing. *Samples must be submitted in multiples of 4 or 8 samples, depending on the BeadChip format.*	*8-48*	*sample*	*$76.90*
	56-96	*sample*	*$23.83*
	104-384	*sample*	*$19.49*
	432-any	*sample*	*$11.67*

AGENA BIOSCIENCE IPLEX

Agena Bioscience iPLEX genotyping (formerly known as Sequenom iPLEX genotyping) is a low-to-moderate multiplex, custom genotyping platform ideal for the analysis of between 5-500 SNPs.

One iPLEX "multiplex" can contain anywhere from 1-36 SNP "assays", and is run in one "well" against a single DNA sample. Samples are submitted to iPLEX genotyping in 96-well plates, each of which is run against one of more multiplexes.

One 384-well "plate" of iPLEX genotyping may therefore consist of any of the following experimental designs:

1) one 96-well plate of samples vs four iPLEX multiplexes, 2) two 96-well plates of samples vs two iPLEX multiplexes, or 3) four 96-well plates of samples vs one iPLEX multiplexes.

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
iPLEX Assay Design & Validation. *There is no charge for assay design. Once designed and validated, adequate material is on hand for an unlimited number of future genotyping reactions.*	*1-any*	*SNP*	*$29.49*
iPLEX Genotyping/Allelotyping. *The iPLEX genotyping service includes automated and manual calling of genotyping clusters and return of results in a finished format (Excel).*	*1-any*	*plate of 384*	*$1,847.91*
iPLEX Genotyping/Allelotyping. *Excludes reagents. This service is used in combination with Agena's pre-designed iPLEX panels. Please inquire for more details.*	*1-any*	*run*	*$903.31*

UNIPLEX

Uniplex genotyping using Taqman chemistry is useful for the analysis of sets of fewer than 4-6 SNPs, for follow-up of SNPs whose performance in other platforms has been unsatisfactory, or for simple validation of results. Pricing for a uniplex genotyping project includes two different components: 1) acquisition of a Taqman assay, and 2) the cost of genotyping *per se*, which is assessed per 384-well plate. Taqman assays are ordered from Thermo Fisher Scientific (ABI), which maintains a library of hundreds of thousands of predesigned assays for human, mouse, and other organisms, and the UMGC offers validation (amplification efficiency across a dilution series of model template) for Taqman assays. Custom Taqman assays are also available (please inquire).

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
Taqman Assay Acquisition.			
Small scale (188 ul), which is adequate for the genotyping of 1500 samples. Price includes shipping. Other scales are available. Please inquire.	*1-any*	*each*	*$344.30*
Taqman Genotyping.			
Low Scale.	*1-2*	*plate of 384*	*$284.58*
Standard Scale.	*3-4*	*plate of 384*	*$161.39*
High Scale.	*5-8*	*plate of 384*	*$144.71*
Very High Scale.	*9-any*	*plate of 384*	*$116.68*

STRUCTURAL VARIATION

In addition to SNP detection, we provide capillary electrophoresis services to support the analysis of more complex polymorphisms (e.g., short tandem repeats (STRs)) via the measurement of fragment length polymorphisms (FLPs). We use the ABI 3730xl capillary electrophoresis platform (the same used in our Sanger sequencing services), enabling highly multiplexed FLP detection, and a lower cost per data point. Due to the high-throughput nature of the ABI 3730xl, the unit of submission is a plate of samples. Researchers can purchase fragment sizing standards themselves, and submit amplicons + standards ready for loading onto the instrument, or may opt to have the UMGC add sizing standards as well as load samples. Although not listed here, the UMGC can also provide a full-service FLP analysis, including amplification. Due to the customized nature of most multiplexed FLP assays, please inquire for the cost of such analysis.

QUESTIONS?

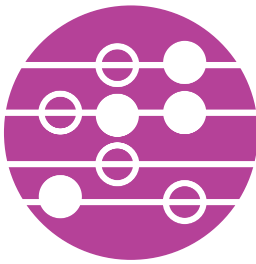
Contact Patrick Warner: warne436@umn.edu

SERVICE	SCALE	UNIT	PRICE
Fragment Analysis.[1]	*1-any*	*plate of 96*	*$234.80*
Fragment Analysis. Instrument Run.[2]	*1-any*	*plate of 96*	*$137.34*

NOTES

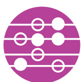
1. UMGC provides and adds sizing standards to user-supplied amplicon pools.

2. Researcher provides amplicon pools containing sizing standards, ready for loading onto capillary electrophoresis instrument.



EPIGENOMICS

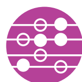
Although there are a wide variety of methods for studying epigenetic phenomena in a high-throughput fashion, among the most widely used is the measurement of DNA methylation profile, achieved via array- or sequencing-based platforms. Here, we list services for array-based DNA methylation analysis. For next-generation sequencing-based DNA methylation services, see the Next-generation Sequencing section.



BISULFITE CONVERSION

Exposure of denatured DNA to sodium bisulfite results in the conversion of the base cytosine (C) – but not methylated cytosine (C*) – to uracil (U). Subsequent amplification of treated DNA by PCR (or any other DNA polymerase based method) converts U to T. Consequently, bisulfite conversion results in the change of C residues in DNA to T, leaving *C unchanged. Once such conversion has been accomplished, C/C* ratios can be measured as T/C ratios, using any tools designed for quantification of DNA variants. Bisulfite conversion is therefore a critical first step in many technologies for the study of DNA methylation. We use Zymo Research Corporation EZ DNA Methylation Kit for bisulfite conversion, either in combination with other services (Illumina 450K DNA Methylation, below), or as a standalone service.

SERVICE	SCALE	UNIT	PRICE
Bisulfite Conversion of DNA. *A submission of 12 samples is the minimum scale accepted.*	*12-24*	*sample*	*$19.73*
	25-48	*sample*	*$15.57*
	96-any	*sample*	*$7.42*
Bisulfite Conversion. *From tissues. Individual Spin column.*	*1-any*	*sample*	*$19.86*



ILLUMINA INFINIUM METHYLATION

The Illumina Infinium HumanMethylation450 BeadChip is based on the Illumina Infinium genotyping platform, and queries individual CpG sites across the human genome by measuring the C/T ratio following bisulfite conversion of DNA, thereby permitting the % methylation of each CpG site to be ascertained. The platform allows researchers to interrogate over 485000 methylation sites per sample at single-nucleotide resolution. Content on the BeadChip was selected by a global consortium of epigenomics experts, and covers 99% of RefSeq genes, with an average of 17 CpG sites per gene region, distributed across the promoter, 5' untranslated region, first exon, gene body, and 3' untranslated region. Array content covers 96% of CpG islands, with additional coverage in island shores and the regions flanking them. All samples submitted for Illumina 450K DNA Methylation analysis must first be bisulfite converted (see Bisulfite Conversion service, above).

SERVICE	SCALE	UNIT	PRICE
Illumina Infinium Human Methylation 450K. *Other scales are available. Please inquire.*	*12-192*	*sample*	*$398.80*

SANGER SEQUENCING

The UMGC provides Sanger sequencing on an Applied Biosystems 3730xl DNA Analyzer. This 96-capillary instrument affords rapid, high-throughput service with read lengths of up to 800-1000 bp (with performance depending on the quality of the template and the sequence context). Our Sanger services are geared to the need for low-cost, rapid, routine sequencing of template-primer reactions assembled by clients ("Classic" service), although we also able to work with clients to optimize difficult-to-sequence regions.

SANGER SEQUENCING

All services use ABI BigDye Terminator version 3.1 chemistry. Primer and template input recommendations are available on our website.

CLASSIC: clients are responsible for combining their DNA template and custom sequencing primer, and the UMGC carries out Sanger chemistry, reaction clean-up, and capillary electrophoresis. Sequence quality from this service is dependent on the purity of submitted template-primer material and the accuracy of template and primer quantification. Classic sequencing is available in both standard throughput (tube) and high-throughput (plate) formats.

QUANT: Clients submit template and primer separately. The UMGC measures the concentration of each, prepares the template-primer cocktail, and carries out Sanger chemistry, reaction clean-up, and capillary electrophoresis. A QC report will be generated and sent to client. Quant sequencing is available in both standard throughput (tube) and high-throughput (plate) formats.

REACTION CLEAN-UP: To further reduce UMGC charges, clients may opt to carry out Sanger reactions themselves, submitting completed reactions for clean-up and sequencing only.

DIFFICULT TEMPLATES: the UMGC runs a panel of alternative reaction conditions in order to find a better reaction cocktail for problematic templates. A QC report is provided with recommendions for future custom sequencing submission.

CUSTOM: Clients may submit custom templates (difficult templates, BACs, giant fragments, high GC, etc.) to be sequenced using a non-standard reaction cocktail. In order to use the custom service, clients must have determined which custom sequencing reaction conditions to select (this is often acheived by accessing our "difficult template" service first).

QUESTIONS?

Contact Patrick Warner: umgcseq@umn.edu

SERVICE	SCALE	UNIT	PRICE
Classic Sequencing. Tube Submission. *Clients submit 12 ul of combined template + primer in a 0.5 ml tube.*	*1-any*	*sample*	*$4.92*
Classic Sequencing. Plate Submission. *A high-throughput service. Clients submit 6 ul of combined template + primer in a 96-well ABI FAST plate. Minimum # samples = 48.*	*48-94*	*sample*	*$3.38*
Quant & Primer Addition Sequencing. Tube Submission. *Clients submit 15 ul of template and primer separately in 0.5 ml tubes.*	*1-any*	*sample*	*$13.11*
Quant & Primer Addition Sequencing. Plate Submission. *Clients submit 15 ul of template in a 96-well ABI FAST plate, and primer separately in a tube. The UMGC is also able to bank client custom primers for routine use.*	*1-94*	*sample*	*$11.57*
Reaction Clean-up & Electrophoresis. *Clients submit 10 ul of Sanger reactions in a 96-well ABI FAST plate. UMGC carries out reaction clean-up and capillary electrophoresis.*	*1-94*	*sample*	*$1.35*
Difficult Template Sequencing. *Template and primer are submitted separately in 0.5 ml tubes.*	*1-any*	*sample*	*$74.10*
Custom Option Sequencing. *12 ul of template and primer are combined and submitted in 0.5 ml tubes.*	*1-any*	*sample*	*$10.60*

NUCLEIC ACID SERVICES

UMGC provides DNA and RNA extraction from a number of sample types, including plant and animal tissue, buccal cells, whole blood of buffy coat preps, and stool or environmental samples. Nucleic acids can be returned to the researcher in barcoded plates or tubes, or retained at the UMGC for on-going projects. In addition, the UMGC offers a variety of sample manipulation services, from sample management (archive, track, transfer, cherry pick) to normalization, quantification and quality control (see Section on Quality Control, below).

DNA EXTRACTION

The assessment of DNA purity and concentration by UV spectroscopy (NanoDrop) and fluorimetry (PicoGreen quantification) is included in the price of most services.

WHOLE BLOOD: The UMGC processes bulk whole blood samples for gDNA using a "salting out" method that have been in place at the UMN's hospital clinic for two decades, and delivers very high yields.

QIAGEN DNeasy: a standard, lower-cost silica-binding purification method that provides DNA of excellent quality for genomic applications.

ORAGENE BUCCAL: Oragene buccal cell collection kits offer pain-free and noninvasive collection that is readily self-administered, suitable for shipment in standard mail, and stable at room temperature.

QUICK-AND-EASY: low-cost extraction suitable for downstream mouse genotyping. The output is a semi-purified DNA prep that compatible with PCR-based assays. The method forgoes quantification and purification in order to achieve the lowest cost possible.

MOBIO POWERSOIL: a "bead-beating" method that uses abrasive beads to break the cell walls of microbes in stool and other samples. This service is typically used in combination with 16S/18S sequencing.

HIGH-THROUGHPUT PLANT: a hombrew method developed at the UMGC for high-throughput extraction of DNA from plant material submitted in 96-well plate format. Please inquire for details.

QUESTIONS?

Contact Nichole Peterson: peter585@umn.edu

SERVICE	SCALE	UNIT	PRICE
Whole blood. 1-3 Vacutainer Tubes. *Yields from 1-3 Vacutainer tubes are typically in excess of 250 ug.*	*1-96* *97-any*	*sample* *sample*	*$27.78* *$17.44*
QIAGEN DNeasy Blood & Tissue Kit. *Yields are typically in the range of 2-10 ug.*	*1-36* *37-any*	*sample* *sample*	*$17.28* *$11.68*
Oragene Buccal Cell Kit. *Please note, the kits are purchased by the researcher through Oragene.*	*1-95* *96-any*	*sample* *sample*	*$37.21* *$30.33*
"Quick-and-Easy" for Mouse Genotyping. *Tissue samples (mouse tail tip, toe or ear clippings) may be submitted in 96-well PCR plates completely covered in 100% ethanol. Please note, this method forgoes certain quantification and purification steps when unnecessary for downstream processing.*	*1-any*	*sample*	*$1.20*
MoBio PowerSoil for Stool, Soil, and Other Environmental Samples. *Yields depend on sample type.*	*1-95* *96-any*	*sample* *sample*	*$28.35* *$15.16*
High-throughput Plant Extraction. *Minimum submission is one plate of plant material. Note that a pilot extraction using this homebrew UMGC method will be required for any species or tissue type/format that the UMGC has not yet encountered.*	*1-any*	*plate of 96*	*$730.32*

RNA EXTRACTION

Our staff can isolate total RNA from blood, cells or tissues by methods appropriate to your project. Extracted RNA can also be returned to the client when requested (shipping charges apply). RNA is extracted from client samples by appropriate methods, either TRIzol or column-based extraction, depending on sample type, client choice and end use. For example, clients wishing to profile miRNA expression would be advised to use a TRIzol type extraction because it preserves the small RNA fraction that contains miRNAs better than column methods. Please contact us with any questions or requirements. Initial assessment of RNA purity and concentration is performed by NanoDrop spectrophotometer analysis and Ribo Green Assay which is included in the service. RNA integrity is determined using the Agilent 2100 Bioanalyzer, TapeStation or Caliper GX (optional but highly recommended).

QUESTIONS?

Contact Nichole Peterson: peter585@umn.edu

SERVICE	SCALE	UNIT	PRICE
RNA Extraction Individual PAXgene and Quantification.	*1-24*	*sample*	*$30.76*
	25-any	*sample*	*$25.50*
RNA Extraction with RiboPure Bacterial Kit and Quantification.	*1-36*	*sample*	*$27.05*
	37-any	*sample*	*$21.45*
RNA Extraction. PureLink and Quantification.	*1-36*	*sample*	*$22.46*
	37-any	*sample*	*$16.86*
RNA Extraction. RiboPure. With RNAlater-ICE. *Tissue of Cultured Cell Kit with RNAlater-ICE.*	*1-36*	*sample*	*$32.06*
	37-any	*sample*	*$26.46*
RNA Extraction. RNeasy Blood & Tissue Kit.	*1-36*	*sample*	*$17.55*
	37-any	*sample*	*$11.95*
Tissue Lysis. *Will be used together with either RNA or DNA extraction of Tissue samples.*	*1-48*	*sample*	*$8.84*
	49-any	*sample*	*$3.66*
RNA Extraction. RNeasy Plus Universal Mini Kit.	*1-36*	*sample*	*$16.19*
	37-any	*sample*	*$10.59*
GLOBINclear mRNA Reduction. Human.	*8-24*	*sample*	*$56.19*
	32-any	*sample*	*$29.48*

DNA AND RNA MANIPULATION

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
DNA Normalization. 96-well Plate.	*1*	*plate of 96*	*$150.82*
	2-4	*plate of 96*	*$108.86*
	5-any	*plate of 96*	*$87.52*
DNA Resuspension.	*1-any*	*sample*	*$1.63*
RNA Sample Pull, Drydown. Normalization.	*1-any*	*sample*	*$7.56*

SAMPLE MANIPULATION

A prerequisite for many projects is the manipulation of sample collections prior to analysis. We have liquid handling robots for manipulating plates of samples in a high-throughput fashion, and systems for maintaining large sample collection in 2D-barcoded tubes in a format that enables semi-automated sample tracking and retrieval using specialized robots.

Please inquire for further details of these workflows.

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
Plate Transfer.	*1-any*	*plate of 96*	*$30.50*
Sample Normalization. For samples associated with projects.	*1-24*	*sample*	*$2.31*
Sample Pull. *2D Barcoded Tube and other.*	*1-any*	*plate of 96*	*$78.81*
Sample Pull. Dispensed Fixed Volume. *Into 96-well plate.*	*1-94*	*plate of 96*	*$4.02*
	95-384	*plate of 96*	*$3.14*
	385-any	*plate of 96*	*$2.31*
Sample Pull. Normalization. *Into 96-well plate.*	*1-any*	*sample*	*$3.27*

WHOLE GENOME AMPLIFICATION

We use QIAGEN's REPLI-g whole genome amplification technology to provide high yields of whole genomic DNA from small or precious samples, including single cells.

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
Whole Genome Amplification.			
8-10 ug Yield.	*1-any*	*sample*	*$9.53*
30-40 ug Yield.	*1-any*	*sample*	*$15.76*

QUALITY CONTROL

Nucleic acid quantification and molecular sizing tools form the foundation of many UMGC workflows, and can also be accessed as standalone services, listed below.

DNA SIZING

The integrity of DNA can be observed through capillary electrophoretic sizing, a high-throughput, sensitive, and high-resolution alternative to the running of agarose gels. The success of NGS library creation is determined by inspection a capillary electrophoretic profile of the library. The UMGC uses three different platforms for capillary electrophoresis of DNA: 1) Agilent 2100 Bioanalyzer, 2) Agilent 2200 TapeStation, and 3) Caliper GX.

QUESTIONS?

Contact Patrick Warner: warne436@umn.edu

SERVICE	SCALE	UNIT	PRICE
Caliper DNA QC. High Sensitivity Chip. *The Caliper GX DNA High Sensitivity chip provides quantitative sizing in the range of 50–5000 bp, at a concentration range of between 0.01–0.5 ng/ul per fragment.*	*16-any*	*sample*	*$11.82*
DNA Sizing. *Agilent TapeStation/BioAnalyzer.*	*1-any*	*sample*	*$10.30*

RNA SIZING

The integrity of RNA can be observed through capillary electrophoretic sizing, a high-throughput, sensitive, and high-resolution alternative to the running of denaturing agarose gels. The UMGC uses three different platforms for capillary electrophoresis of DNA: 1) Agilent 2100 Bioanalyzer, 2) Agilent 2200 TapeStation, and 3) Caliper GX.

QUESTIONS?

Contact Patrick Warner: warne436@umn.edu

SERVICE	SCALE	UNIT	PRICE
Caliper RNA QC.	*16-any*	*sample*	*$8.19*
RNA Sizing. Agilent TapeStation/BioAnalyzer.	*1-any*	*sample*	*$7.30*

SEX DETERMINATION

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

SERVICE	SCALE	UNIT	PRICE
Taqman-based Human Sex-Typing. 384-well Plate.	*1-any*	*plate of 384*	*$117.06*

QUANTIFICATION OF DNA OR RNA

Quantification of nucleic acids can be achieved via UV spectroscopy or via the use of fluorometry (in combination with DNA (PicoGreen) or RNA (RiboGreen)-binding dyes). The NanoDrop instrument for UV quantification consumes only 1-2 ul of material, and provides a measure of DNA purity (260/280 and 260/230 ratios), but is not able to accurately quantify impure nucleic acids, and is incapable of quantifying dilute DNA or RNA. PicoGreen and RiboGreen quantification are therefore the gold standards for specific quantification of DNA and RNA, respectively.

SERVICE	SCALE	UNIT	PRICE
NanoDrop Quantification.	*1-any*	*sample*	*$0.33*
PicoGreen DNA Quantification.	*1-any*	*sample*	*$2.40*
RiboGreen RNA Quantification.	*1-any*	*sample*	*$5.06*

QUESTIONS?

St. Paul—Patrick Warner warne436@umn.edu

Mpls.—Tsuleng Lyfoung, lyfou006@umn.edu

GENOTYPING QUALITY CONTROL OF DNA

High-throughput quality control for genotyping involves functional assays called “QC1”, “QC2”, and “QC3”. Unlike simple DNA quantification, which may fail to detect DNA impurities, these functional assays predict performance of DNA in genotyping. These assays are also useful for quantifying DNA that may be chemically pure, but of mixed origin (e.g., human buccal DNA that contains microbial DNA contamination). Another use for these assays is ensuring that fragmented DNA is of adequate length for PCR amplification.

SERVICE	SCALE	UNIT	PRICE
QC1. *a non-allelic Q-PCR assay that measures the quantity of PCR_amplifiable human DNA.*	*1-any*	*plate of 96*	*$79.21*
QC2. *An end-point Taqman SNP genotyping assay that is a sensitive indicator of sample-to-sample cross-contamination.*	*1-any*	*plate of 96*	*$87.76*
QC3. 96-well Plate. Primer Probe Sets (UPL). *The QC3 test is the same test as QC1, but designed for non-human DNA samples. Depending on the species to be tested, the UMGC may already have a QC3 Taqman assay designed.*	*1-any*	*plate of 96*	*$95.12*

QUESTIONS?

Contact Shalane Porter: genotype@umn.edu

NGS LIBRARY QC

The UMGC welcomes client-submitted NGS libraries, but requires UMGC quantification and quality control assessment of such libraries, to ensure that the resulting sequence data is acceptable. Client library QC involves three bundled assays: 1) PicoGreen quantification, 2) quantitative capillary electrophoretic sizing (Agilent), and functional quantification (KAPA Biosystems Q-PCR).

SERVICE	SCALE	UNIT	PRICE
KAPA Library QC. *For libraries prepared outside of the UMGC.*	*1-any*	*sample*	*$62.46*

QUESTIONS?

Contact Elyse Froehling: next-gen@umn.edu

UMGC DIRECTORY

ADMINISTRATION

Director	Dr. Kenneth Beckman	kbeckman@umn.edu
Research Associate	Dr. Daryl Gohl	dmgohl@umn.edu
Lab Operations Manager, Minneapolis	Dinesha Walek	walek001@umn.edu
Lab Operations Manager, St. Paul	Nichole Peterson	peter585@umn.edu
General Operations Manager	Karina Sartorio	bunje001@umn.edu

NEXT-GENERATION SEQUENCING AND LIBRARY CREATION

Illumina Next-generation Sequencing (HiSeq 2500, MiSeq)	Aaron Becker	next-gen@umn.edu
Standard Library Creation	Elyse Froehling	next-gen@umn.edu
Custom Library Creation	Ann Bohac	bohac001@umn.edu.
Microbiome	Allison MacLean	micbiom@umn.edu

EXPRESSION ANALYSIS

Illumina Array Expression	Darrell Johnson	exprn@umn.edu
NanoString nCounter	Darrell Johnson	exprn@umn.edu
Fluidigm BioMark	Darrell Johnson	exprn@umn.edu
Q-PCR	Darrell Johnson	qpcr@umn.edu

GENOTYPING

Illumina Infinium Genotyping & Infinium Methylation	Shalane Porter	genotype@umn.edu
Agena Bioscience iPLEX	Shalane Porter	genotype@umn.edu
Taqman	Shalane Porter	genotype@umn.edu
Fragment Analysis on 3730xl	Patrick Warner	warne436@umn.edu

SINGLE-CELL GENOMICS

Fluidigm C1	Jerry Daniel	danie786@umn.edu

SANGER SEQUENCING

Sanger Sequencing	Patrick Warner	umgcseq@umn.edu

NUCLEIC ACID SERVICES

Nucleic Acid Services	Nichole Peterson	peter585@umn.edu
Quality Control (Minneapolis)	Tsuleng Lyfoung	lyfou006@umn.edu
Quality Control (St. Paul)	Patrick Warner	warne436@umn.edu
Oligonucleotide Synthesis	Cody Hoffmann	oligo@umn.edu

RNAI

RNAi Clones	Cody Hoffmann	rnai@umn.edu