

Exhibit A: University of Michigan DNA Sequencing Core Services, Pricing and Information for External Clients

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The University of Michigan DNA Sequencing Core (“UMDSC”) provides analytical services to UMich-affiliated researchers (“internal clients”) and non-UMich-affiliated researchers (“external clients”). This document is an appendix to the BRCF Service Agreement, and lists the services provided to external clients of the UMDSC, including the prices of those services as of the above revision date. Please refer to the following URL to obtain the latest revision of this document:

http://seqcore.brcf.med.umich.edu/sites/default/files/DNASC_ExhA.pdf

Revisions to the UM DNA Sequencing Core’s Exhibit A (henceforth referred to as simply “Exhibit A”) will be made periodically at our discretion, and may include price changes or changes in service. Such revisions become effective when the revised Exhibit A becomes available on the above URL, and at that time it supersedes all previous versions of Exhibit A. No further notification will be given to preexisting external clients, beyond replacement of the Exhibit A at the above URL. It is the responsibility of the external client to check for the latest Exhibit A when preparing to request services from the UMDSC. A Service Agreement, signed in association with one version of Exhibit A, will remain in effect and unrevised in event a revised Exhibit A goes into effect.

The University of Michigan DNA Sequencing Core offers nucleic acid analysis services as listed in the following table. For definitions or for detailed information on the services, please consult with staff members of the UMDSC, or refer to the UMDSC’s web site (<http://seqcore.brcf.med.umich.edu>).

Sanger Sequencing:

Sanger Sequencing, standard <i>(Rush service is not offered to External clients.)</i>	\$3.87/rxn
Sanger Seq, full 96-well plates <i>(Will be charged for any empty wells)</i>	\$3.10/rxn
Sanger Seq, Reduced Service <i>(Full 96-well plate only. Please consult Core staff before attempting to use this service.)</i>	\$2.90/rxn
Sanger Seq, Sec Structure DNA <i>(siRNA, hairpin)</i>	\$7.74/rxn
Sanger Sequencing, Large DNA Sanger Seq, large projects	\$15.48/rxn <i>Contact us</i>

Fragment Analysis:

FragAnalysis, Instrument Use	\$74.82/run
FragAnalysis, CE Loading Plate <i>(Sorry, no shipment or deliveries)</i>	\$46.44/plate
FragAnalysis, IdentifilerPlus	\$45.15/rxn

qPCR Instrument Usage:

qPCR Instrument Usage <i>(Run one SIBR Green or Taqman 96- or 384-well plate, client-prepared)</i>	\$25.80/run
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Sequenom MassARRAY Services:

Sequenom Pinset, reagents only <i>(Pinset is 24 reactions, each of which is 1 sample tested against 1 multiplex)</i>	\$407.64/pinset
Sequenom Quadrant reagents only <i>(Quadrant is 96 reactions, each of which is 1 sample tested against 1 multiplex)</i>	\$1032.00/quadrant
Sequenom HalfChip reagents only <i>(HalfChip is 192 reactions, each of which is 1 sample tested against 1 multiplex)</i>	\$1831.80/half chip
Sequenom FullChip reagents only <i>(FullChip is 384 reactions, each of which is 1 sample tested against 1 multiplex)</i>	\$3328.20/full chip
EpiTyper reagents only <i>(Priced as fraction of a chip)</i>	\$967.50/chip
Sequenom technician time <i>(e.g. assay design, sample processing, reaction spotting, data analysis)</i>	\$116.10/hour

PyroMark pyrosequencing services:

FullPlate reagents, std labor	\$774.00/plate
PartialPlate reagents, std labor <i>(24 wells)</i>	\$374.10/plate
PyroMark technician time <i>(Extra effort beyond standard processing labor)</i>	\$116.10/hour

Illumina BeadArray services:

Illumina kits at market price

BeadArray technician time	\$78.69/hour
BeadArray reagents and supplies <i>(Per 96-well plate)</i>	\$331.53/plate
BeadArray Scanning <i>(Instrument usage)</i>	\$15.48/hour

Illumina Sequencing services, Library generation:

Standard Genomic libraries	\$131.58/library
96-well Genomic libraries <i>(High throughput automated process, in development)</i>	\$43.86/library
Ultra-low input genomic lib	\$158.67/library
PCR-free genomic libraries	\$154.80/library
10x Genomics Long-Contig lib	\$1324.83/library
Exome captures, pools	\$684.99/pool
Non-Stranded mRNA polyA lib <i>(Discontinued by Illumina 12/31/2017)</i>	167.70/library
Stranded mRNA polyA libraries	\$156.09/library
Stranded mRNA Ribo-reduced lib	\$367.65/library
SMARTer stranded low input <i>(Client supplies Ribo-Gone kit if needed)</i>	\$269.61/library
smRNA-seq libraries	\$250.26/library
10x Genomics Single-cell RNA <i>(Limited availability to External clients; must be performed on-site and scheduled in advance!)</i>	\$2220.09/library
Library QC/Normalize/Pooling	\$28.38/library
Pool assessment for loading	\$61.92/pool
Illumina Library Tech time <i>(Extra services for custom projects)</i>	\$125.13/hour

Illumina Sequencing Services on the HiSeq 2500 - 2 lanes per flow cell:

HS 2500v2 Single-end, 50 RAPID	\$1350.63/lane
HS 2500v2 Paired-end, 50 RAPID	\$2129.79/lane
HS 2500v2 Paired-end 100 RAPID	\$2818.65/lane
HS 2500v2 Add 50nt RAPID run <i>(Custom projects only)</i>	\$558.57/lane

Illumina Sequencing Services on the HiSeq 2500 and HiSeq 4000 - 8 lanes per flow cell:

HS 2500 v4 Single-end, 50	\$1264.20/lane
HS 2500 v4 Paired-end, 50	\$2000.79/lane
HS 2500 v4 Paired-end, 125	\$3027.63/lane
HS 2500 v4 Add 50nt to v4 run	\$518.58/lane
HS 4000 Single-end, 50	\$1255.17/lane
HS 4000 Paired-end, 50	\$2009.82/lane
HS 4000 Paired-end, 75	\$2150.43/lane
HS 4000 Paired-end, 150	\$2961.84/lane
HS 4000 Add 50nt to HS4000 run <i>(Custom projects only)</i>	\$521.16/lane

Illumina Sequencing Services on the NextSeq 500 and MiSeq- 1 lane per flow cell:

NextSeq Mid-Output 150 cycle	\$1713.12/lane
NextSeq Mid-Output 300 cycle	\$2547.75/lane
NextSeq High-Output 75 cycle	\$2079.48/lane
NextSeq High-Output 150 cycle	\$3770.67/lane
NextSeq High-Output 300 cycle	\$5837.25/lane
MiSeq 300 cycle Micro	\$910.74/lane
MiSeq 300 cycle Nano	\$763.68/lane
MiSeq 500 cycle Nano	\$919.77/lane
MiSeq 150 cycle v3	\$1566.06/lane
MiSeq 500 cycle v2	\$2065.29/lane
Duo cBot RAPID kit	\$273.48/each
Drive, 1T	\$96.75/each
Illumina Lanes Tech time <i>(Extra services for custom projects)</i>	\$113.52/hour

MicroArray Services:

(Note: Except as noted below, all Affymetrix microarrays provided by customer; prices are for processing costs ONLY)

Life Technologies/Affymetrix Gene Expression:

Std GeneChip cartridge GE proc	\$405.06/sample
Std GeneAtlas 4-strip GE proc.	\$358.62/sample
Std GeneTitan plate GE proc.	\$232.20/sample
<i>(Plates are available in 16-, 24- and 96-array formats)</i>	
Low-input GeneChip GE proc.	\$410.22/sample
Low-input GeneAtlas strip proc	\$374.10/sample
Low-input GeneTitan plate proc	\$274.77/sample
GeneChip, hyb scan only	\$130.29/sample
Tech Time	\$188.34/hour

Life Technologies/Affymetrix SNP Typing:

GeneChip SNP typing proc.	\$446.34/sample
GeneChip SNP hybrid only	\$165.12/sample
GeneTitan SNP typing proc.	\$52.89/sample
OncoScan CNV/SNP typing	\$903.00/sample
<i>(Includes the cost of the arrays)</i>	

Targeted qPCR Arrays:

Qiagen RT2 array processing	\$354.75/plate
<i>(Qiagen 96- or 384-well plates)</i>	
LifeTech OpenArray mRNA proc.	\$258.00/array
LifeTech OpenArray miRNA proc.	\$270.90/array
<i>(Accessories are billed at market prices.)</i>	

DNA Isolation Services:

Whole blood DNA Isolation	\$30.96/sample
DNA Isolation, Saliva	\$20.64/sample
Aliquot/transfer DNA	\$1.42/sample
Quantitate DNA (BULK)	\$1.03/sample

DNA and RNA Quality Control Service:

*Agilent Bioanalyzer 2100 - Submission requests are **per chip**. We cannot bill for partial chips.*

Bioan DNA 1000, 7500 or 12000	\$99.33/chip
Bioan DNA High Sensitivity	\$132.87/chip
Bioan RNA 6000 Nano	\$96.75/chip
Bioan RNA 6000 Pico	\$104.49/chip
Bioan Small RNA	\$104.49/chip

Agilent TapeStation 2200

TapeStation Standard DNA 1000	\$25.80/sample
TapeStation High-Sens DNA 1000	\$29.67/sample
TapeStation Genomic DNA	\$30.96/sample
TapeStation RNA 6000	\$27.09/sample
TapeStation High-Sens RNA 6000	\$27.09/sample
Qubit DNA/RNA quantification	\$3.87/sample

Please note the following for all services:

The UM DNA Sequencing Core will process samples on a first-come, first-served basis, but samples from external clients will be processed at lower priority than internal clients. For the Pacific Biosciences sequencer, HHMI Investigators have priority equal to that of UM researchers. Prospective customers must register with the UM DNA Sequencing Core via our computer system (see the "PI Administration" section of Core's web site, URL listed above). All samples must be entered into our computer system, and must be properly labeled with our tracking number(s) *before* they are delivered to this Core. We reserve the right to discard any samples that are not properly labeled. The Core does not return unused samples or portions of samples after completion of work; they are discarded.

Prices listed in this document are those charged to external clients, as determined by the method of billing employed by the University of Michigan Financial Operations. If a client pays using funds from a "shortcode" within the UM Financial Operations, that client will be charged the rate for internal clients, and the prices listed in this document are not applicable. If a client pays by any other method, then the prices listed in this document are applicable. No exception to this policy will be made for any actual or perceived affiliation the client may have with the University of Michigan, nor for any collaborative agreement the client may have with a University of Michigan employee, faculty, student, officer or agent.

An analysis performed by the UMDSC can fail for many reasons, including failures on the Core's part (e.g. instrument malfunction, Core technician error) and failures on the Customer's part (e.g. misquantitated nucleic acids, misdesigned experiment, impure samples). We will, to the best of our ability, assess whether a failed analysis is due to a failure on the part of the Core, and we reserve the right to decide whether to repeat an analysis or to refuse to perform such a repeat, based on our assessment. We will not be held liable for analytical failures arising due to errors or problems in the Client's laboratory. We will not bear the cost of repeat runs unless we initiated the repeat of our own accord, or they subsequently prove that the Core was at fault in the original failure. Determination of the cause of failure is based solely on our judgment. The decision of the Core Director on cause of failure and/or our liability for the cost of a repeat is final.