**Exhibit A: University of Michigan DNA Sequencing Core** *Revised 28-Aug-17*
**Services, Pricing and Information for External Clients** *Effective 01-Sep-17*

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** | **$3.87/rxn** |
| *(Rush service is not offered to External clients.)* | |
| **Sanger Seq, full 96-well plates** | **$3.10/rxn** |
| *(Will be charged for any empty wells)* | |
| **Sanger Seq, Reduced Service** | **$2.90/rxn** |
| *(Full 96-well plate only. Please consult Core staff before attempting to use this service.)* | |
| **Sanger Seq, Sec Structure DNA** | **$7.74/rxn** |
| *(siRNA, hairpin)* | |
| **Sanger Sequencing, Large DNA** | **$15.48/rxn** |
| **Sanger Seq, large projects** | *Contact us* |
| Fragment Analysis: | |
| **FragAnalysis, Instrument Use** | **$74.82/run** |
| **FragAnalysis, CE Loading Plate** | **$46.44/plate** |
| (*Sorry, no shipment or deliveries)* | |
| **FragAnalysis, IdentifilerPlus** | **$45.15/rxn** |
| qPCR Instrument Usage: | |
| **qPCR Instrument Usage** | **$25.80/run** |
| *(Run one SIBR Green or Taqman 96- or 384-well plate, client-prepared)* | |
| Sequenom MassARRAY Services: | |
| **Sequenom Pinset, reagents only** | **$407.64/pinset** |
| *(Pinset is 24 reactions, each of which is 1 sample tested against 1 multiplex)* | |
| **Sequenom Quadrant reagnts only** | **$1032.00/quadrant** |
| *(Quadrant is 96 reactions, each of which is 1 sample tested against 1 multiplex)* | |
| **Sequenom HalfChip reagnts only** | **$1831.80/half chip** |
| *(HalfChip is 192 reactions, each of which is 1 sample tested against 1 multiplex)* | |
| **Sequenom FullChip reagnts only** | **$3328.20/full chip** |
| *(FullChip is 384 reactions, each of which is 1 sample tested against 1 multiplex)* | |
| **EpiTyper reagents only** | **$967.50/chip** |
| *(Priced as fraction of a chip)* | |
| **Sequenom technician time** | **$116.10/hour** |
| *(e.g. assay design, sample processing, reaction spotting, data analysis)* | |

PyroMark pyrosequencing services:

| | |
|---|---|
| **FullPlate reagents, std labor** | **$774.00/plate** |
| **PartialPlate reagnts,std labor** | **$374.10/plate** |
| *(24 wells)* | |
| **PyroMark technician time** | **$116.10/hour** |
| *(Extra effort beyond standard processing labor)* | |

Illumina BeadArray services:

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|---|---|
| *Illumina kits at market price* | |
| **BeadArray technician time** | **$78.69/hour** |
| **BeadArray reagnts and supplies** | **$331.53/plate** |
| *(Per 96-well plate)* | |
| **BeadArray Scanning** | **$15.48/hour** |
| *(Instrument usage)* | |

Illumina Sequencing services, Library generation:

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

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

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|---|---|
| **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** | **$558.57/lane** |
| (*Custom projects only)* | |

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** | **$521.16/lane** |
| (*Custom projects only)* | |

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

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|---|---|
| **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** | **$113.52/hour** |
| *(Extra services for custom projects)* | |

Pacific Biosciences Sequencing services:

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|---|---|
| **PacBio shearing and QC** | **$114.81/sample** |
| **PacBio DNA library preparation** | **$603.72/sample** |
| (*Additional reagents may be required, in certain cases. Discuss with Core staff.)* | |
| **BluePippin Isolation** | **$143.19/sample** |
| **PacBio Technician time** | **$96.75/hour** |
| **PacBio SMRT Cell sequencing** | **$548.25/SMRT cell** |

MicroArray Services:

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

*Life Technologies/Affymetrtix*

| | |
|---|---|
| **Std, GeneChip cartridge** | **$331.53/sample** |
| **Std, GeneAtlas 4-array strip** | **$296.70/sample** |
| **Standard, GeneTitan plate** | **$201.24/sample** |
| *(Plates are available in 16-, 24-and 96-array formats)* | |
| **Low-input, GeneChip cartridge** | **$286.38/sample** |
| **Low-input, GeneAtlas strip** | **$265.74/sample** |
| **Low-input, GeneTitan plate** | **$214.14/sample** |
| **GeneChip, hyb scan only** | **$104.49/sample** |
| **GeneAtlas, hyb scan only** | **$39.23/sample** |
| **GeneTitan, hyb scan only** | **$53.83/sample** |
| **GeneChip SNP typing** | **$374.10/sample** |
| **GeneChip SNP typing, hyb only** | **$55.47/sample** |
| **Axiom (GeneTitan) SNP typing** | **$34.83/sample** |
| **OncoScan CNV and SNP typing** | **$986.85/sample** |
| *(Includes the cost of the arrays)* | |

Targeted qPCR Arrays:

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|---|---|
| **Qiagen RT2 Profiler prep** | **$314.76/plate** |
| *(Qiagen 96- or 384-well plates are billed at market prices plus external client surcharge.)* | |
| **Life Tech OpenArray prep** | **$165.12/array** |
| **Life Tech OpenArray miRNA prep** | **$193.50/array** |
| *(Life Tech arrays and accessories are billed at market prices plus external client surcharge.)* | |

DNA Isolation Services:

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|---|---|
| **Whole blood, fresh** | **$52.24/sample** |
| **Buffy coat** | **$36.76/sample** |
| **Whole blood, frozen** | **$63.21/sample** |
| **Buffy coat, frozen** | **$42.57/sample** |
| **Saliva, in Oragene tube** | **$25.16/sample** |

| | |
|---|---|
| **Subaliquot, transfer, dilution** | **$2.19/sample** |
| **Quantify, Nanodrop or Qubit** | **$2.19/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** | **$90.30/chip** |
| **Bioan DNA High Sensitivity** | **$118.68/chip** |
| **Bioan RNA 6000 Nano** | **$87.72/chip** |
| **Bioan RNA 6000 Pico** | **$92.88/chip** |

Agilent TapeStation 2200

| | |
|---|---|
| **TapeStation Standard DNA 1000** | **$23.86/sample** |
| **TapeStation High-Sens DNA 1000** | **$26.32/sample** |
| **TapeStation Genomic DNA** | **$26.32/sample** |
| **TapeStation Standard RNA 6000** | **$24.00/sample** |
| **TapeStation High-Sens RNA 6000** | **$24.51/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.