Dear Genomics and Microbiome Core Facility (GMCF) investigators:

The GMCF team would like to thank you for using our core facility! We are about to enter the year 2026 and would like to report on some changes to our workflows and new capabilities. As you will see, we have added new instruments and capabilities, but we are saying goodbye to some instruments too. See below for a list of changes to our capabilities. We look forward to continuing to support your research efforts going forward. Please reach out to any of us with questions/comments/requests. Just a reminder that project requests can be submitted through Bookitlab (https://core.bookitlab.com/rush-GMCF/Login).

Please also look for our updated sample and **data retention policy**, which includes storage of all samples for 3 months after completion unless you ask for longer and archiving of Illumina data in Basespace after 6 months. PacBio data will be available for download for 7 days after completion and then archived. Data retrieval from archive will, unfortunately, incur additional charges. Please reach out to our Rush Research Bioinformatics Core (RRBC; rrbc@rush.edu) for help with data analysis, data storage/transfer, submission to the NCBI Sequence Read Archive (SRA), and more.

Finally, please note that the GMCF and RRBC will be closed on Dec 24th, 2025 and will re-open January 2nd, 2026. This will be relevant for shipping of samples – please delay shipments until next year.

Best wishes and holiday greetings from the GMCF!

Changes include:

(1) We have **acquired a new Illumina DNA sequencer – the Illumina MiSeq i100+.** This instrument replaces the old MiSeq instrument, and has many advantages, including: (1) 4X faster runtime, (2) higher quality, particularly for 2x300 sequencing runs, (3) room-temperature reagents (no dry ice!), (4) greater tolerance for amplicons, (5) lower cost per sequence, and (6) greater flexibility in flow cell size. The i100+ instrument has four flow cell sizes of 5M, 25M, 50M and 100M clusters. Current read lengths are 2x150, 2x300 and 2x500, but not all read-lengths are available on all flow cells. The 2x500 flow cell is a major advance, allowing for longer amplicons to be sequenced. The 2x500 chemistry is only available with 25M cluster flow cells. One major difference between the i100+ instrument and the prior MiSeq is the use of patterned flow cells. This increases the robustness of the instrument, but also makes the instrument susceptible to index hopping. Therefore, only unique dual index (UDI) libraries should be sequenced on the instrument. Libraries generated from combinatorial indices (CDI) may lead to improper assignment of sequence data to barcodes. We suggest avoiding CDIs.

(2) We have **discontinued** service for the old **Miseq** (including Nano, V2, and V3 flow cells). Due to the discontinuation of the old MiSeq and MiniSeq (see below), we will no longer be processing amplicon sample with **Fluidigm CS linkers**. We have replaced CS1 and CS2 linkers for amplicons with sIDTP5 and sIDTP7 linkers (see below). All incoming amplicons should have unique dual indexes (UDI) – we are using IDT barcodes with up to 1536 UDI combinations available. Please reach out to us to ensure your 1st stage amplicon library preparation that are compatible with UDI barcoded adapters.

sIDTP5_[ForwardPrimer]: CTACACGACGCTCTTCCGATCT + [FP]

sIDTP7_[ReversePrimer]: CAGACGTGTGCTCTTCCGATCT + [RP]

(3) We will be **discontinuing** service for the Illumina **MiniSeq**, but the instrument will be available for use until it breaks. Libraries with combinatorial indices (CDIs), rather than UDIs, can be sequenced on the MiniSeq. Maximum output for mid-output flow cells is 8M clusters (2x150).

(4) We have **discontinued** service for the **NovaSeq6000** instrument (including SP 2x250 flow cells). We have options to replace this (below); please reach out to us for help in choosing the best platform for your work.

a. Illumina NovaSeq X with 2x150 (1.5B, 10B or 25B cluster flow cells). The 1.5B cluster flow cell has 2 lanes of approximately 750M clusters each. The 10B cluster flow cell has 8 lanes of approximately 1250M clusters each. The 25B cluster flow cell has 8 lanes of approximately 3200M clusters each. Please contact us to help decide on the best sequencing option for you.
b. Illumina NovaSeqX with 2x300 on the 1.5B (billion) cluster flow cell (2 lanes of 750 M clusters each).
c. Illumina MiSeq i100+ with 2x300 sequencing for 5M, 25M or 50M cluster outputs.
d. Illumina MiSeq i100+ with 2x500 sequencing for 25M cluster outputs.
e. Complete Genomics G-800 instrument with 1x600 base sequencing on a 1.6B cluster flow cell (4 lanes of 400 M clusters each)

(5) We have **acquired** a new DNA sequencer from **Complete Genomics – the G-800** (https://www.completegenomics.com/products/sequencing-platforms/dnbseq-g800/). This sequencer has expected quality scores in the Q40 range (rather than Q30) and has individual reads of 600 bases (currently single direction, 1x600). Further increases in read-length are expected. Complete Genomics suggests improved coverage in difficult-to-sequence genomic regions. Standard Illumina libraries can be converted (by GMCF) to be compatible with

Complete Genomics. Each instrument can run two flow cells independently. Available flow cell sizes include:

a. 1x100 – 1.8B clusters
b. 2x100 – 1.8B clusters
c. 2x150 – 1.8B clusters
d. 1x600 – 1.6B clusters

(6) We have **acquired** a new liquid-handling robot from **Volta Labs** called the **"Callisto Sample Prep System"** (https://www.voltalabs.com/product). While this instrument can make PacBio, Oxford Nanopore, Illumina and Complete Genomics libraries, we specifically acquired this instrument to help with hybridization capture protocols. Currently the instrument can perform IDT capture protocols, with Twist captures coming soon. We will be happy to conduct a wide range of off-the-shelf and custom capture protocols, including: whole exome sequencing (WES), whole transcriptome capture – particularly effective for damaged (e.g., FFPE) human DNA, viral captures, etc. Please reach out to us for any projects of interest.

(7) We have **acquired** two **Singulator 200 devices** from **S2 genomics** (https://s2genomics.com/singulator-platform/). This instrument is a "…flexible, automated solution for the rapid dissociation of solid tissue into high-quality, viable single cells or intact nuclei compatible with numerous single-cell genomics applications." As a reminder, we have two platforms for single-cell RNAseq library preparation, including the 10X Chromium X device and associated chemistries, as well as the Illumina Single Cell Prep (formerly Fluent). For spatial transcriptomics, we operate the 10x Visium platform with a CytAssist device and work closely with the UIC spatial core facility for projects needing the 10x Xenium platform.

(8) We are currently running **full-length 16S ribosomal RNA gene amplicon sequencing** protocols using the **PacBio Kinnex** chemistry (https://www.pacb.com/technology/kinnex/). We have developed a custom, adaptable two-stage PCR protocol that can be deployed for amplicons in the range of 1000-2000 bp. Turn-around time is slower than with Illumina sequencing, but data are very high quality (Q30-Q40) and total output from a single SMRT cell on a PacBio Revio instrument is on the scale of 40M reads. The GMCF can provide you with portions of a run (minimum 10%), just as we do for Illumina sequencing. For amplicons <1000 bp, we recommend using Illumina chemistry.

(9) We will be adding a new **charge for development of new primer sets**. Adapting new primer sets is labor intensive and requires the use of one or more agarose gels. Thus, we will be charging one-time flat fees of $50 per new primer set when temperature optimization is necessary and $25 per new primer set when investigators provide us with established annealing temperatures.

(10) We will be adding a new **charge for whole genome amplification** for amplicon sequencing projects and genome/metagenome projects. We have found that some samples with very low or undetectable DNA can benefit from whole genome amplification, either using repliG kits (Qiagen) or primary template-directed amplification (PTA; Bioskryb) kits. For WGA protocols, DNA can be used directly for PCR amplification though it may need additional endonuclease treatment for shotgun metagenomics as well. PTA is not recommended if long-read sequencing is desired. Although effective, these protocols are expensive due to the cost of reagents. We will be introducing costs associated with sample processing using WGA and PTA as well as endonuclease treatment. Please reach out to us for more information.

(11) And finally, a note about invoices. While we do not require POs prior to sending an invoice, if your institution requires a PO# to be your invoice please provide that PO# to us. That way we can ensure that it is listed in the project when you accept the quote. Also, **we have begun to accept payments by credit card**. If this is an option for you, please reach out after receiving your Bookitlab invoice and we can have an e-invoice issued through authorize.net for secure credit card payments.

Contact Information

Laboratory	Name	Email	Title	Focus areas
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