DAICEL arbor biosciences

SERVICE POLICIES

myReads® NGS Service Policies

By placing an order with Daicel Arbor Biosciences ("Arbor") that include myReads service line items, the Client agrees to the myReads service policies and commitments described in this document.

Please read and return a signed copy to **service@arbor.daicel.com.**

Please address any questions to **service@arbor.daicel.com.**

Client name: ____________________ **Signature:** ____________________

Project ID: ____________________ **Date:** ____________________

Project details and requirements

1. "Standard DNA" project type

a. Samples must contain a minimum of 500ng of DNA of a modal fragment length of at least 10kbp and have UV 260:280 ratio of 1.7-1.9. DNA concentration/mass must be measured by spectrometry.
b. Client will receive a Sample Preparation Guide detailing the requirements for their project and sample type.
c. If the sample cannot meet the criteria for Standard DNA projects, the performance commitment is not applicable.
d. Performance commitment:
    i. We will determine the optimal library mass to pool per sample based on the number of samples pooled per capture.
    ii. If, after library preparation, more than 10% of samples do not have sufficient mass to reach this optimal amount, we will repeat library preparation for the samples that do not reach the threshold, if sufficient gDNA remains.
    iii. We will perform one repeat of library preparation. If >10% of samples do not have sufficient mass at this point, we will pool 100%of existing mass.

2. "Degraded DNA" project type

a. There is no minimum mass or other quality requirements for samples, though we recommend sending at least 10ng of gDNA.
b. Arbor will perform an extended QC, which includes total DNA quantification and visualization of sample morphology on the Agilent TapeStation or Bioanalyzer platform. Arbor reserves the right to perform the extended QC on a representative subset of samples.
c. Arbor will adjust the protocols for sample shearing and/or size selection (if required) and/or library preparation based on sample mass and morphology.
d. Arbor makes no performance guarantees for degraded samples.

3. "Ancient DNA" project type

a. There is no minimum mass for samples (either double-stranded or single-stranded configurations)
b. Samples sent for Ancient DNA projects must be low molecular weight (<1kbp).
c. Arbor may perform a long fragment removal prior to library preparation at client request.
d. Arbor makes no performance guarantees for ancient DNA samples.

4. **“Long Insert” project type**
    a. Samples must contain a minimum of 5µg of DNA of a modal fragment length of at least 10kbp and have a UV 260:280 ratio of 1.7-1.9. DNA concentration/mass must be measured by spectrometry.
    b. Client will receive a Sample Preparation Guide detailing the requirements for their project and sample type.
    c. If the sample cannot meet the criteria for Long Insert DNA projects, the performance commitment is not applicable.
    d. Performance commitment:
        i. We will determine the optimal library mass to pool per sample based on the number of samples pooled per capture.
        ii. If, after library preparation, more than 10% of samples do not have sufficient mass to reach this optimal amount, we will repeat library preparation for the samples that do not reach the threshold, if sufficient gDNA remains.
        iii. We will perform one repeat of library preparation. If >10% of samples do not have sufficient mass at this point, we will pool 100%of existing mass.

5. **“Standard RNA” project type**
    a. Samples must contain a minimum of 250ng of RNA for Standard Applications and 2.5µg of RNA for depletion applications. RNA must have a UV 260:280 ratio of 1.9-2.1 and be free from DNA contamination. RNA concentration/mass must be measured by spectrometry.
    b. Client will receive a Sample Preparation Guide detailing the requirements for their project and sample type.
    c. If the sample cannot meet the criteria for Standard RNA projects, the performance commitment is not applicable.
    d. Performance commitment:
        i. We will determine the optimal library mass to pool per sample based on the number of samples pooled per capture.
        ii. If, after library preparation, more than 10% of samples do not have sufficient mass to reach this optimal amount, we will repeat library preparation for the samples that do not reach the threshold, if sufficient RNA remains.
        iii. We will perform one repeat of library preparation. If >10% of samples do not have sufficient mass at this point, we will pool 100%of existing mass.

6. **Expert (catalog), Community, and WGS packages**
    a. Unless Degraded DNA or RNA handling is ordered, samples will be considered Standard DNA or Standard RNA.
    b. Performance commitment for Standard DNA (1d) or Standard RNA (5d) samples apply if conditions are met as above.
    c. Arbor will decide the appropriate plexity for capture when applicable
    d. The appropriate number of reactions of the chosen myBaits kit are included in the sample price when applicable. Additional kits may be purchased separately.

Sample shipment

1. **Arbor will provide a copy of the “Sample Preparation Guide” (SPG) to the Client.**

2. **Client is expected to adhere to the guidelines set forth in the SPG, including but not limited to:**
    a. Never ship 100% of an irreplaceable sample.
    b. Ship gDNA sample fully dried, if at all possible.
    c. Plates containing nucleic acids or libraries must be half- or fully-skirted and seals should be aluminum.
    d. Plates containing specimens for DNA extraction must be the exact brand and type listed in the SPG.
    e. If shipping liquids, tubes must be sealed closed with parafilm and volume should be under 100µL.

3. **Arbor will inspect the shipment upon arrival for integrity of the plastics, seals, and approximate volume.**
    a. If there are issues with the shipment, the Client may replace the samples at the Client’s expense.

4. **Non-compliance with shipping requirements**
    a. If nucleic acid or library samples are received and are found to be in non-compliance with the required shipping format as outlined in the SPG, an invoice with a Plate Organization fee of $500/plate will be sent to the billing address provided by the client. This fee must be paid before QC can commence.
    b. If client opts not to pay the Plate Organization fee, they must organize and pay for return shipping of their samples and may resubmit samples that comply with shipping requirements. The project’s place in the QC queue will not be held if samples are returned.
    c. If client opts not to pay Plate Organization fee and does not organize the return shipment within 30 days, samples will be discarded without further notice.

5. **International shipping permits**
    a. If a permit is required to import one or more of the Client's species into the United States of America, the client is responsible for reporting the species to Arbor and identifying the permit(s) that are required.
    b. Arbor reserves the right to reject the shipment of restricted species.
    c. Arbor, at its sole discretion, may agree to apply for the necessary permits for an additional fee.
        i. Application for a permit does not ensure that it will be granted. Client is responsible for the permit application fee in the event of a permit rejection.
    d. Arbor cannot return CITES-listed or otherwise restricted material.
6. **Ethics documentation for human samples**
    a. We require documentation that the appropriate clearance has been obtained from relevant regulating bodies and stakeholders prior to accepting projects involving human samples (contemporary and ancient).
    b. For projects that involve destructive sampling, we require documentation that clearance has been obtained for this type of work.
    c. Arbor can provide a template for a signed self-certified ethics statement upon request.

Specimens for extraction

1. **Due to the potential effects of upstream sample handling procedures, Arbor cannot guarantee output mass, purity, or integrity of nucleic acids.**
2. **Arbor cannot return any physical specimens provided for nucleic acid extraction unless arrangements are made prior to order placement.**
3. **For samples intended for downstream Standard DNA handling, reduced submission criteria apply for samples to receive performance commitment: the input mass is 100ng instead of 500ng.**
4. **Submission requirements outlined in the SPG must be followed.**
    a. If more mass than maximum specified in SPG or samples arrive in tubes or in plastics other than those specified in SPG, Client will be offered the option to pay additional subsampling and/or reformatting and/or lyophilization fee, as appropriate.
    b. If Client declines to pay the appropriate fee(s), they must organize and pay for return shipping of their samples and may resubmit samples that comply with shipping requirements.
    c. If Client declines to pay for return shipping and/or does not organize the return shipment within 30 days, samples will be discarded without further notice.

QC reports

1. **For all project types, Arbor will provide a QC report to the client.**
    a. Client will receive a QC report consisting of sample names/labels and total DNA or RNA mass measurements upon arrival.
        i. For Standard DNA project types for which gDNA was submitted, total DNA mass after mandatory SPRI purification will also be reported.
        ii. For Standard RNA projects, total RNA mass after mandatory DNase treatment and SPRI purification will also be reported.
    b. Arbor will flag samples that do not meet the minimum requirements, if applicable.
    c. Client may decide to drop the sample(s) from the project, ship supplementary gDNA or RNA for the sample(s), or continue with the sample(s) as-is.
    d. If the client decides to drop the sample(s), the invoice will be adjusted to reflect the actual work performed.
    e. If the client decides to submit additional gDNA or RNA, this can only be done once per project. A new QC report will not be generated.
    f. If the client decides to continue with the samples, 100% of the sample mass will be taken through the entire process, regardless of performance.

Sequencing

1. **Arbor will make every effort to equilibrate samples within capture pools (if applicable) and equilibrate capture pools for sequencing.**
    a. Due to the nature of hybridization capture, performance differences within and between reactions may result in the bias of sequencing data toward or away from certain samples.
2. **Arbor will deliver the total amount of data ordered in Gbp (within 5% of amount ordered), but does not guarantee a particular read depth for individual samples within the project.**
3. **Packages:**
    a. With the exception of the Long Insert packages, all packages include paired-end 150 data and will be sequenced on the instrument and run configuration deemed appropriate by Arbor to minimize turnaround time.
    b. The platforms currently include Illumina NovaSeq and Element Biosciences AVITI.
    c. The default short-read sequencing platform is AVITI.
4. **A la carte:**
    a. Client may choose from the available sequencing instrument and run configurations.
    b. At Arbor's discretion, an a la carte project may be upgraded to a run configuration on the specified instrument and with the same read length that delivers an equal amount or more data.
5. **Full lanes or flowcells**
    a. The output of a full lane or flowcell will be the actual yield of that lane or flowcell.
    b. Arbor may provide a rough estimate of yield expectations for a given configuration, but this estimate is not a guarantee.

Data delivery

1. **Data will be delivered in electronic format in demultiplexed, but otherwise raw/unprocessed, FASTQ files.**
    a. Delivery will be via Globus, SFTP, and/or similar delivery modes, including Arbor's delivery platform, at Arbor's discretion.
    b. Client can request a hard drive to be shipped at client's expense as an alternate form of delivery. No other alternate forms of delivery are available.
2. **Arbor's delivery portal**
    a. Arbor will provide one username and password per myReads project. Client may share the log-in with collaborators to download the data at their discretion.
    b. Arbor will provide a PDF of instructions for how to access the portal and how to generate a wget script (a script for downloading the files via command line on a Unix machine) for batch data download. Download of individual files is also possible.
    c. The downloadable files include:
        i. FASTQ files (R1 & R2 file per sample)
        ii. QC output (FASTQC and/or MultiQC at Arbor's discretion)
        iii. Tabular summary of client sample ID, sequencing ID, index information, read count, data quality per sample
        iv. MD5 checksum
3. **Data will be available for 60 days upon delivery (Globus, SFTP, or similar).**
    a. Arbor will not retain a copy of the data. It is the client's responsibility to ensure the data is downloaded and backed up within the time frame specified.
    b. Where possible, Arbor will inform the client in advance of permanent deletion of data from the server.

Bioinformatics

1. **Customized bioinformatics services are available for some project types on a case-by-case basis.**
2. **Arbor must discuss project-specific needs and goals with Client before agreeing to undertake any Bioinformatics services.**
3. **Arbor will present the Client with a list of customized project deliverables prior to Client placing an order for Bioinformatics services.**
4. **Arbor reserves the right to terminate a Bioinformatics services project in the event that the data collected and/or provided are unsuitable for the types of analysis intended.**

Physical sample storage

1. **Arbor will retain the following materials, if present, for 30 days after the delivery of the data (or other deliverable in cases where the sequencing is not arranged by Arbor):**
    a. gDNA or RNA
    b. Indexed library
    c. Post-capture non-amplified material
    d. Post-capture amplified material
2. **Client may request the retention of other material types (i.e. non-captured fractions, purified gDNA) with agreement from Arbor.**
3. **Client is responsible for providing the following information upon submission of samples if sample return is desired:**
    a. Shipping contact name, address, telephone number, email address, and VAT number (where applicable).
    b. Preferred shipping carrier name and account number (if direct billing is desired) OR billing contact name & address for invoice of shipping fees.
4. **Sample returns will be made on dry ice at the expense of the client. Samples can be dried for an additional fee.**
5. **If return information is not provided upon submission of samples, Arbor will discard all materials 30 days after the delivery of the data.**
6. **Long-term storage is available in increments of 1 year for an additional fee. Long-term storage must be requested before the 30 day post-delivery storage period has elapsed.**
    a. Client may request their materials be returned at any time within a 1 year period. The client is responsible for paying shipping costs.
    b. After the 1 year storage period concludes, Arbor will email the person with whom the project correspondence was performed indicating that the storage period has concluded.
        i. If Arbor does not receive a response within 2 weeks, Arbor will send a follow-up email
        ii. If Arbor receives no response to the follow-up email, the materials will be discarded.
        iii. The client may choose to discard the materials, have the materials returned (for a shipping fee), or to continue storage at Arbor for an additional 1 year (for a storage fee).

General terms and information

1. **The service terms described in this document apply to all myReads NGS services projects.**
2. **Due to inherently unpredictable elements of scientific experiments performed on unknown samples, Arbor does not guarantee project aspects unable to be controlled or predicted, most importantly in the areas of (i) target enrichment performance (such as on-target percentage, unique read complexity, unique read coverage depth, PCR duplicate levels, etc.) and (ii) project completion timelines.**
3. **Any timeline dates provided during the course of the project are intended to be estimates for planning purposes only. Arbor is not liable for loss or damage caused by any perceived delay(s) beyond estimated timelines.**
4. **Projects are handled on a first-come-first-served basis. A spot in the service queue is reserved upon: (i) physical receipt of all project samples at Arbor's facility, and (ii) receipt of official purchase order(s) for the entire project.**
5. **Client is responsible for confirming that the project configuration ordered (including, but not limited to handling type, capture conditions, sequencing length and amount, bait set) correctly matches with their desired configuration. Arbor will execute service projects as ordered.**