

## Self-Prepared Illumina Library Submissions

### Submitting Your Order

Consultation is required for this service. Before initiating your experiment, contact [Melissa Stephens](#) to discuss project specifics, receive a quote, and coordinate scheduling. Once your request is confirmed and scheduled, follow the instructions for self-prepared libraries below.

### Confirmed and Scheduled Requests

Core Facility will perform its own evaluation of the library to confirm (1) concentration, (2) molarity, (3) average fragment length, and (4) functionality using a combination of Qubit Assay, Bioanalyzer analysis, and KAPA qPCR Library Quantification kit for Illumina.

1. Schematic of library structure: Submit a diagram that illustrates the position of adapters, barcodes, and read primers relative to the insert.
2. Adapter and index sequences: Submit the excel spreadsheet listing the P5 and P7 adapter and index sequence within the adapter.
  - Custom sequencing primers: If applicable, provide the sequence of each.
3. Library Information: Submit an excel spreadsheet listing the Library Pool ID, concentration (ng/ul), molarity (nM), volume provided (ul), and an average fragment size (bp).
  - If the sample is a multiplexed library pool, list the individual library ID and the index sequence in separate columns within a separate spreadsheet.
4. iLab Core Facility Management: Reserve a sample drop-off day/time. *iLab sends us a notification about scheduled reservations. Do not send us a separate email.*
  - Go to [InsideND](#), search for iLab Core Facility Management, and sign in using University of Notre Dame credentials.
  - Schedule a reservation **24 hours in advance** by selecting a day and time from the Sample Processing Calendar and attach your completed Excel Submission Form. Within the reservation, include the email of other lab members who should be consulted or notified with results.
    - *REQUIRED: If you can not make your reservation, cancel it as soon as possible and select a new time slot.*
    - *Recommendation: Coordinate within your lab to reduce multiple deliveries to a single drop-off reservation whenever possible.*
5. Deliver a self-prepared library (20 ul of 10 nM) in a 1.7 mL microcentrifuge tube labeled with Library ID, your initials, and date (MM-DD-YYYY).
  - Custom sequencing primers: If applicable, provide 20 ul of 100 uM of each in separate 1.7 mL microcentrifuge tubes labeled with Primer ID, your initials, and date (MM-DD-YYYY).
6. Deposit the sample inside the cooler outside of the facility door on your reserved day and time.

### Library Storage

End users are expected to review sequencing data and report issues as soon as possible. Excess (or leftover) library volume is discarded six months after sequencing data is initially shared. *If you would like the excess library volume returned, indicate at the time of submission and provide a recipient's name and shipping address.*