STEPS AND RECOMMENDATIONS FOR SEQUENCING CUSTOMERS (MICROARRAY CUSTOMERS SEE OTHER SECTION):

STEP 1: PAPERWORK/PREPARATION FOR SEQUENCING SUBMISSIONS (EXTERNAL CUSTOMERS ONLY):

New external customers, please do the following to get started:

a) Fill out a new customer form with billing information. Email the completed form to wibr-genome@wi.mit.edu. The new customer form can be found here: http://jura.wi.mit.edu/genomecorewiki/index.php/Forms

b) Once your lab is registered (we will notify you), you will be able to access the database for submission in order to register yourself as a user here: http://jura.wi.mit.edu/gtc/sequencing/samplesubmission/samplesubmission.php Questions or problems related to the submission database should be directed to Sumeet Gupta at sgupta@wi.mit.edu

All external customers please contact your Accounts Payable department in advance of each submission, to obtain a purchase order number. If you need a quote, please email us at wibr-genome@wi.mit.edu or call us at 617-258-8803. Blanket purchase orders are preferred, if you plan to submit multiple projects over time.

STEP 2: PREPARATION OF SAMPLES:

SUBMISSION OF SAMPLES FOR LIBRARY PREPARATION (PRE-PREPARED LIBRARIES, SEE BELOW)

Samples may be in any buffer that does not contain trace amounts of phenol or EDTA. We will save and return any unused input material to you after the libraries have been successfully prepared, and we will archive your unused library as well.

Input Recommendations for Library Preparation

Sample Type	Sonication/Fragmentation*	Fragment Size (bp)	Input requirements (ng)**	Volume (ul)
Genomic	Required	200-400	500 to 1,000	<50
ChIP	NA	NA	10 to 50	<50
RNA	NA	NA	100 to 1,000	<50

*Unless special arrangements are made with us in advance, we will assume that your genomic DNA sample has been fragmented, by sonication or otherwise, prior to submission. We generally recommend that sonications target a size range of 200-400 bp.

**We can work with less if necessary, but it is best if you elute your DNA in 50 ul or less if you believe we may need to use all of it.

SUBMISSION OF PRE-PREPARED SEQUENCING LIBRARIES:

We typically need 10-20 ul of each library at 5 ng/ul or greater. You can submit them full strength; we will dilute as necessary. If your library is less concentrated than 5 ng/ul, don't worry. We'll quantify it to make sure you have enough to sequence. Typically there is plenty, but we will let you know if there is not enough sample to achieve quality results. We will archive your leftover library, so you won't lose any.

STEP 3: WHICH LIBRARY PREP PROTOCOL SHOULD I CHOOSE?

Typically the "DNA-Basic" option is fine for samples with at least 1 ug of starting material to work with. The Basic protocol is an automated protocol using the IntegenX Apollo system. Users with less input material (such as ChIP samples) are best off choosing our "DNA-Premium" option, which is optimized for low input and done by hand. Premium is also an option for those with higher amounts of input.

RNA-Seq customers may select either the "RNA-Basic" or "RNA-Premium" library prep service. The Basic protocol is an automated protocol using the IntegenX Apollo system. The Premium protocol is a manual protocol based on the Illumina TruSeq kits. Both can generate high quality libraries, though it should be noted that the Basic libraries are "strand-specific," while the Premium libraries are not. The Basic option also allows for ribo-zero RNA enrichment instead of PolyA enrichment.

Library Prep Protocol Recommendations

Sample Type	Directional Data?	Recommended Library Prep Options
Genomic	NA	DNA-Basic (Automated)
Genomic	NA	DNA-Premium (Manual)
ChIP	NA	DNA-Premium (Manual)
RNA - polyA enriched	YES	RNA-Basic
RNA - polyA enriched	NO	RNA-Premium
RNA- ribo-zero enriched	YES	RNA-Basic w/ ribo-zero add-on

*Prices listed are for internal customers from WI and MIT only. External customers pay 30% surcharge unless otherwise arranged.

STEP 4: ONLINE SUBMISSION OF SEQUENCING LIBRARIES:

Please complete the online submission form:
http://jura.wi.mit.edu/gtc/sequencing/samplesubmission/samplesubmission.php

Every sample should have its own ID number, even if you plan to multiplex them. We will individually QC each sample for you, and pool them according to our measurements. If you have a sample which is pre-pooled, that's OK. Just be sure to let us know the barcodes contained within your pool.

Once you submit your samples online, you will obtain a Genome Tech Core ID (GTC ID) number for each of your samples. Every tube/sample should have its own ID number, regardless of whether we will be multiplexing them. GTC ID numbers have the following format: L##_### (ex: L23_123). After your submission, you will receive a confirmation email, which also lists the samples and ID numbers, for your records. Please retain the confirmation email. It contains a link for you to follow the status of your samples throughout the sequencing process here at Whitehead.

Please write your name GTC ID numbers on the tubes. We prefer 1.5 ml tubes.

STEP 5: DROP-OFF OR SHIPPING

You may drop off samples to us in person in room 325, or ship them on dry ice (see below). Please do not ship to us without first contacting someone in the lab, to make sure that we are here to receive your package. Please email wibr-genome@wi.mit.edu or call 617-258-8803 prior to shipping. Do not rely on voicemail. Please wait until you hear back from someone.

When you are ready, you may hand deliver or ship your samples to:

Whitehead Institute Genome Technology Core
9 Cambridge Center, Room 325
Cambridge, MA 02142

STEP 6: HOW TO CHECK THE STATUS OF YOUR SAMPLES AFTER SUBMISSION

After you submit your samples, you will receive an email receipt. The email will also provide a link which you can use to keep track of your samples as they move through the various steps of the sequencing process. The link is: http://jura.wi.mit.edu/gtc/status/seqsamplestatus.php

STEPS AND RECOMMENDATIONS FOR MICROARRAY CUSTOMERS (SEQUENCING CUSTOMERS SEE OTHER SECTION):

STEP 1: PAPERWORK/PREPARATION FOR MICROARRAY SUBMISSIONS (EXTERNAL CUSTOMERS ONLY)

Please contact us in advance of submitting any microarray projects, for approval. Wibr-genome@wi.mit.edu

New external customers, please fill out a new customer form with billing information. Email the completed form to wibr-genome@wi.mit.edu. The new customer form can be found here: http://jura.wi.mit.edu/genomecorewiki/index.php/Forms

All external customers, please contact your Accounts Payable department in advance of submission, to obtain a purchase order number. If you need a quote, please email us at wibr-genome@wi.mit.edu or call us at 617-258-8803. Blanket purchase orders are preferred, if you plan to submit multiple projects over time.

STEP 2: PREPARATION OF SAMPLES FOR MICROARRAY SUBMISSION

We typically use 100 ng – 1 ug of total RNA in 3 ul as input for microarray sample preparation, so your RNA should be at least 33 ng/ul. We can work with less if necessary, but it is best if you elute your RNA in as little volume as is practical to avoid having to dry down. Any buffer that does not contain trace amounts of phenol or EDTA is acceptable. We will save and return any unused input material and microarray-ready samples to you after the arrays have been done.

STEP 3: FILL OUT AND EMAIL THE SUBMISSION FORM

Please fill out and email the microarray submission form to wibr-genome@wi.mit.edu. The form can be found here: http://jura.wi.mit.edu/genomecorewiki/index.php/Forms

Please note that due to contractual obligations, we are not able to purchase Affymetrix arrays for customers outside of the WI/MIT community. External customers should order arrays and ship them along with samples. Affymetrix may also be able to ship your order to us directly.

STEP 4: DROP-OFF OR SHIPPING

You may drop off samples to us in person in room 325, or ship them on dry ice (see below). Please do not ship to us without first contacting someone in the lab, to make sure that we are here to receive your package. Please email wibr-genome@wi.mit.edu or call 617-258-8803 prior to shipping. Do not rely on voicemail. Please wait until you hear back from someone.

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