



Illumina NovaSeqX Submission Form

PO #:

NOTE: Please indicate special instructions (pooling schemes, combination of projects in one lane, etc) in the Comments section below. Email chains with Facility personnel will NOT qualify as evidence of instruction in case of disputes.

UofC Clients mark "N/A"

Contact Information	Date (mm/dd/yyyy)	
	Principal Investigator	Principal Investigator Email / Phone
	Department	Cancer Center Member? <input type="checkbox"/> Yes <input type="checkbox"/> No
	Experiment Contact	Experiment Contact Email / Phone
	Billing Administrator	Billing Administrator Email / Phone

Sample Preparation and Delivery



Use 1.5 Eppendorf tubes
Total RNA: 13 ul at 100ng/ul

Write Simple, Unique Labels
"Initials-number"

Email Us with and Sample Details
genomics@bsd.uchicago.edu

Mail/Drop-Off Samples
9:00am-4:00pm M-F
Use dry ice for mailing

Project Information	Sample Species:		
	<input type="checkbox"/> Human	<input type="checkbox"/> Mouse	<input type="checkbox"/> Rat <input type="checkbox"/> Other:
	Number of Tubes Submitted: (minimum 12 samples)		Have the samples been treated with DNase? <input type="checkbox"/> Yes <input type="checkbox"/> No
	(Note: DNase treatment mandatory for Ribo-Zero)		
Please Submit Excel Sheet Listing Sample Labels			
Library Type & Sequencing: NovaSeq Special			
<input type="checkbox"/> Oligo-dT mRNA directional PE100 ~25-30M clusters/smpl* ~50-60M PE reads/smpl*	<input type="checkbox"/> Oligo-dT mRNA directional PE100 ~50-60M clusters/smpl* ~100-120M PE reads/smpl*	<input type="checkbox"/> Ribo-Zero depletion PE100 ~50-60M clusters/smpl* ~100-120M PE read/smpl*	
* estimated cluster totals +/- 10% NOTE: additional charges will be applied for any dilutions, cleanups or DNase treatments performed by the Core.			

****Please describe the source of the RNA (There is a big difference in processing RNA from quiescent cells versus tissue culture tumor cell lines in terms of mRNA content that affects the specifics of processing the samples on our end):**