



ILLUMINA NovaSeq X Submission Form

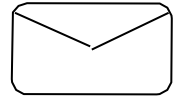
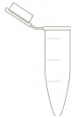
PO #:

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 mL Eppendorf tubes

Simple, Unique Labels

Email Sample Names & Index Seqs

Mail/Drop-Off

Prepare 13ul at 10nM

"Initials-number"

genomics@bsd.uchicago.edu

9am - 4pm M-F

NO PLATES, STRIP TUBES, OR 0.5ml TUBES!!

Project Information	<u>Sample Species</u>	
	<input type="checkbox"/> Human	<input type="checkbox"/> Mouse <input type="checkbox"/> Rat <input type="checkbox"/> Other:
	<u>Number of Tubes Submitted:</u>	<u>Number of Samples per Tube:</u>
	<u>Library Type:</u> *Please note: Success of the experiment will be predicated upon properly completing the below fields:	
	<input type="checkbox"/> High-Complexity <input type="checkbox"/> Low-Complexity	
	<input type="checkbox"/> RNA <input type="checkbox"/> ChIP <input type="checkbox"/> ATAC <input type="checkbox"/> PCR product <input type="checkbox"/> DNA-Whole-Genome <input type="checkbox"/> DNA-Other (please specify in comments)	
	Please Submit Excel Sheet Listing Sample Labels and Index Sequences	
	<u>10B Flowcell</u>	<u>Number of Lanes Needed:</u> (at 1.1 - 1.2B clusters per lane)
Runtype Requested:		
<input type="checkbox"/> PE50 <input type="checkbox"/> PE100		
<input type="checkbox"/> SR100 <input type="checkbox"/> PE150		
<input type="checkbox"/> 29-10-10-89 (10x) <input type="checkbox"/> 52-10-24-52 (10x)		
<u>Index Length</u>	<u>Gel Cut Required:</u> if yes, specify size range for seq:	
<input type="checkbox"/> 8 bases <input type="checkbox"/> Dual (8/8) <input type="checkbox"/> Dual (10/10) <input type="checkbox"/> Other	<input type="checkbox"/> yes <input type="checkbox"/> no	
	<u>Index Manufacturer</u>	
Comments: (please specify if libraries are non-standard, i.e. low complexity/low nucleotide diversity, repeating elements, etc)		