



Illumina NovaSeq X Submission Form

Core-generated ChIPseq, Whole-Genome seq, Exome seq libraries

PO #:

UofC Clients mark "N/A"

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.

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

gDNA: 200-400ng, max 30ul

ChIP: 1-10 ng , in max 40 ul

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

Write Simple, Unique Labels

"Initials-number"

Email Us

genomics@bsd.uchicago.edu

Mail/Drop-Off Samples

9am - 4pm; M-F

Project Information	Sample Species		
	<input type="checkbox"/> Human	<input type="checkbox"/> Mouse	<input type="checkbox"/> Rat <input type="checkbox"/> Other:
	Number of Tubes Submitted		
	Library Type		
	<input type="checkbox"/> ChIP	<input type="checkbox"/> gDNA (WGS)	<input type="checkbox"/> Exome <input type="checkbox"/> Other:
Please Submit Excel Sheet Listing Sample Labels			
	" 7	V O V	total output: 1.1 - 1.2B clusters per lane
	<input type="checkbox"/> h- <input type="checkbox"/> h-		
	<input type="checkbox"/> ck <input type="checkbox"/> h-		

Comments: