



Illumina NovaSeq 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

Prepare 13ul at 10nM

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



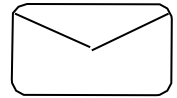
Simple, Unique Labels

"Initials-number"



Email Sample Names & Index Seqs

genomics@bsd.uchicago.edu



Mail/Drop-Off

9:00am-4:00pm M-F

| | | |
|---|--|--|
| 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>Flowcell:</u> <input type="checkbox"/> SP Flowcell (0.88B) <input type="checkbox"/> S1 Flowcell (1.6B) <input type="checkbox"/> S2 Flowcell (4.1B) <input type="checkbox"/> *S4 Flowcell (9.0B) <input type="checkbox"/> 100bp cassette <input type="checkbox"/> 100bp cassette <input type="checkbox"/> 100bp cassette <input type="checkbox"/> 200bp cassette <input type="checkbox"/> 200bp cassette <input type="checkbox"/> 200bp cassette <input type="checkbox"/> 200bp cassette <input type="checkbox"/> 300bp cassette <input type="checkbox"/> 300bp cassette <input type="checkbox"/> 300bp cassette <input type="checkbox"/> 300bp cassette <input type="checkbox"/> 300bp cassette *note: S4 for WGS submissions only!! | |
| | <u>Runtype Requested:</u> | <u>Gel Cut Required:</u> if yes, specify size range for seq: <input type="checkbox"/> yes <input type="checkbox"/> no |
| | <u>Index Length</u> <input type="checkbox"/> 6 bases <input type="checkbox"/> 8 bases <input type="checkbox"/> Dual (8/8) <input type="checkbox"/> Other | <u>Index Manufacturer</u> |
| Comments: (please specify if libraries are non-standard, i.e. low complexity/low nucleotide diversity, repeating elements, etc) | | |