

ILLUMINA LIBRARY SUBMISSION

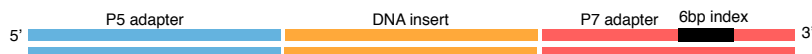
☒ **HISEQ**

☐ **MISEQ**

Order#:	4033	Name:	Kieran Samuk
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Lab:	Mohamed Noor		

IMPORTANT NOTES:

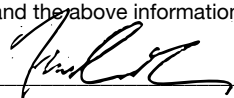
- Unless specified otherwise, leftover samples will be discarded two months after the sequencing is completed.
- Please attach your DUGSIM order form to this submission form when submitting your samples.
- An incomplete submission form will result in a delay with your order.
- If you are on campus please make arrangements ahead of time to drop off your sample(s) by emailing sequencing@duke.edu
- Data will be distributed through our sftp server. Data will be available on our server for 30 days after it has been delivered.
- Default loading concentration for all libraries is 6-12 pM depending on type and QC. Molarity will be estimated using a combination of Qubit and Bioanalyzer/Tapestation trace.
- If custom sequencing primers are provided, they will be spiked-in the Illumina primers.
- Unless specified otherwise, we will assume that libraries are single-indexed with 6bp Illumina barcodes and Illumina sequencing primers will be used. We will assume that the library and index topology is as following:



See library requirements at: <http://tinyurl.com/hazn8sl>

I have read and understand the above information.

Signature: _____





Date: 04/03/2017

INTERNAL USE

Date:		<input type="checkbox"/> Tube/package integrity
Received by:		<input type="checkbox"/> Completed forms
Location:		<input type="checkbox"/> #tubes
		<input type="checkbox"/> Volumes
		<input type="checkbox"/> Sample names

Customer-prepared libraries (Please print this page multiple times if you have more than 10 libraries)

Code (1)	Library type (2)	Label (3)	Conc. (ng/ul)	Vol. (μl)	Size (bp) (4)	Is it a pool?
KS-L1	ddRAD	pseudoobscura Plate 1	24.7	47		<input checked="" type="checkbox"/>
KS-L2	ddRAD	pseudoobscura Plate 2	20.8	47		<input checked="" type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>
						<input type="checkbox"/>

- Code:** Your initials-L-number (e.g. GC-L1, GC-L2, GC-L3); Mark each tube (cap and side) with its code when submitting your materials.
- Library type:** Library type+manufacturer you have prepared.
- Label:** This is to help you to keep track of your sample, so choose a label that's meaningful to you. This is optional.
- Size:** Expected average insert size + adapters size (bp).

If your libraries are barcoded or if you are submitting pools, please complete and send <http://seqweb.gcb.duke.edu/documents/SeqIndexTemplate.xlsx> to sequencing@duke.edu.
 Rename the file such as: <order>_<yourname>_SeqIndex.xlsx

PLEASE CHECK LIBRARY REQUIREMENTS AT:

<http://tinyurl.com/hazn8sl>



PLEASE SHIP YOUR SAMPLES ON **DRY ICE** TO THE FOLLOWING ADDRESS:

Att: Illumina Sequencing

GCB Sequencing and Genomic Technologies

Rm 119 Biology Bldg

Duke University

130 Science Dr

Durham, NC, 27708

USA

Checklist

Please make sure you have included to your submission:

- ☒ A copy of your order from DUGSIM
- ☒ The completed library submission form
- ☒ The completed index information if necessary (emailed to sequencing@duke.edu)



Please review carefully our sample requirements to make sure you send us enough material for library preparation.



Please do not send samples without an order number and the requested information above. If you do not provide us with complete information, we may not be able to process your order in a timely manner.