

**UCLA Technology Center for Genomics & Bioinformatics**  
  
Next Generation Sequencing Service Request

650 Charles E Young Drive South, CHS 38-123

Los Angeles, CA 90095-1735

Phone: (310) 206-3945

Please submit this service request form to [sequencing@mednet.ucla.edu](mailto:sequencing@mednet.ucla.edu) prior to delivering your DNA/RNA samples

on dry ice to CHS 38-123.

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| REQUESTOR INFORMATION | | | |
| Principal Investigator: Leonid Kruglyak | Phone: 310.825.5486 | Email: lkruglyak@mednet.ucla.edu | |
| Institution/Department: UCLA Human Genetics | | | Dept. Code: 1440 |
| Street Address: 695 Charles E Young Dr S Gonda Building RM. 5309 | | | |
| City: Los Angeles | State: CA | Zip Code: 90095 | |
| Research Coordinator: Joshua Bloom | Phone: 609-375-5678 | Email: jbloom@mednet.ucla.edu | |
| Is PI a JCCC Member? x Yes  No | | | |
|  | | | |

*Please fill out completely and in detail in order to avoid processing delays.*

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| **EXPERIMENTAL INFORMATION** |
| Date of Request: July 1st, 2020 |
| Project Name: Detection of covid viral rna using SwabSeq, version 21 |
| Project Description:  We have a library for the NextSeq (Mid Output) of 20uL total at 4nM (more precise quantitation on tube). We would like to run the NextSeq mid ouptput 150-cycle kit. We want to run single-end **26** cycles, with two index reads that are both **10** bp long. We want to load our library at 1.5 pM.  In addition to the sample for the NextSeq, there are three tubes of sequencing primers for the NextSeq run which are absolutely critical:  -1) One tube consists of a pooled primer mix for sequence read 1, it is a mix of 60uL of read1 primers at 20uM final concentration. You should load 52uL of this primer mix into reservoir 20.    -2) Another tube consists of a pooled primer mix for the i7 read (index read 1), it is a mix of 100uL of i7 primers at 20uM final concentration. You will load 85uL of this primer mix into reservoir 22.  3) Another tube consists of a pooled primer mix for the i5 read (index read 2), it is a mix of 100uL of i5 primers at 20uM final concentration. You will load 85uL of this primer mix into reservoir 22.  It is also important that you do NOT check the custom primer box.  Additionally, we request receiving BCL files from this run. |
| Service Requested:  Miseq |
| Application System:  Illumina HiSeq 2000/2500  MiSeq  NextSeq500 Mid Output  NextSeq500 High Output   Hiseq3000  Novaseq S2  Novaseq S4 |
| Sample Submitted:  gDNA  Small RNA  mRNA  Total RNA  DNA Library  ChIP Library   Other - please specify  Amplicon  If you choose ‘Other’ as your sample type, please complete the Biosafety questionnaire on the last page. |
| If customer made library, which kit was used: Custom amplicon protocol from Octant and Sri Kosuri |
| Sample/Library Purification Method: AMPURE XP beads |
| Reference Genome/Species: none |
| Concentration Measured By:  Nanodrop  Qubit  Bioanalyzer  qPCR  Other: |
| Requested Library Prep:  Single Read  Paired End  Barcoded  Other: NO |
| Depth of Coverage Required/Number of Reads: 1 nextseq midoutput kit worth of reads |
| Read Length (e.g., 1X50, 1x75, 1x100, 2X50, 2x75, 2X100, 2x150, 2x250): 1x26 |

*If samples submitted have not been QC’d, additional charges will apply. If traces are available, please attach to this form.*

 Please check this box if you want to pick up any leftover samples. Otherwise, we will dispose of them after data is delivered.

\* We prefer you enter your sample name without spaces, slashes or other special characters. Dashes or underscores are acceptable.

**Bio-Safety Level 2 Facility Questionnaire - Mandatory**

The CMC BSL2 Facility accommodates researchers using biological materials from various sources that may contain known or unknown human pathogens. In order to insure safe and appropriate working conditions for all users of the facility, accurate and complete information about the agents you propose to use is needed to maintain appropriate biosafety standards.

Please fill out this form COMPLETELY and have it signed by the principal investigator before experiments begin. The CMC staff will review the form as part of the training and facility access process, and keep it on file. IF NEW BIOHAZARDS ARE ADDED at a future date, IT IS YOUR RESPONSIBILITY TO UPDATE THIS FORM.

**Do you have current Institutional Biosafety Committee (IBC) approval or Institutional Review Board (IRB) approval for this project? (Check all that apply)**

**Yes.** Attach a copy of the IBC and/or IRB approval letter.

**IBC and/or IRB Approval Pending.**  Access cannot be granted until approval is obtained. Contact the EH&S Biosafety Office at extension x63929 or e-mail at [biosafety@ehs.ucla.edu](mailto:biosafety@ehs.ucla.edu).

**Exempt. Verify exemption with EH&S. Attach copy of IBC letter of exemption.**

**No ICB/IRB Approval Needed.**

**List type of materials to be used, and sources** (i.e., mouse spleen cells, human peripheral blood mononuclear cells, cells from an animal en-grafted with human cells, viruses etc.); for cell lines, describe cell origin.

**Does the sample contain any known infectious agent(s)?** **Yes**  **No**

If yes, list infectious agents (*must be listed on your IBC approval letter with the proper containment indicated)*:

**Were the cells genetically engineered?** **Yes \_\_\_ No** \_\_\_

If yes, how were they genetically engineered? Was a gene therapy virus (adenovirus, retrovirus, lentivirus, herpesvirus, etc.) used to transfer genetic information to the cells?

If yes, describe method in detail, attach vector map and show packaging cell line.

I have read above questions carefully and certify the information provided to be correct.

**PI or Supervisor Signature: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Researcher Signature: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**