Nanostring nCounter User Guide (FY21)

CCR Genomics Core

Location: Building 37, Room 2135

Core e-mail: ncilecdnacore@mail.nih.gov

Core website: https://genomics.ccr.cancer.gov/

1) To request core services and to schedule equipment you must be registered under your PI as a member in our iLab website (https://nci.corefacilities.org/account/login). Log-in using your NIH credentials (NIH Username and password, not your PIV card) as an internal NCI user (even if you are from a different institute).

   a) If you are a new member, register as a member under your PI from the drop-down list. Please note that you will not be able to register unless your PI is already in system with a CAN number. Contact the Core manager (liz_conner@nih.gov) if your PI is not listed.

2) Contact at Inna Dzekunova Nanostring Technologies to order your code sets. Make sure to indicate that you will be working with the CCR Genomics Core as we provide the Master kits.
   e-mail: idzekunova@nanostring.com
   Cell: 443-844-0815

3) Once your code set arrives, you can make an appointment with us for the day you would like to set up your hybridization. Reservation can be made Monday -Thursday only between 1-3 PM. Keep in mind that samples are run in groups of 12 and that we can only process 36 samples in one day. Everything up to the hybridization step will be done by you.

4) On the day of your reservation, you will come to our lab and set up your hybridization. We have the buffer for your master mix and strip tubes. Just follow your protocol which should be included in the Nanostring-provided thumb drive. We will need the thumb-drive to upload your RLF to the digital analyzer.

5) Place your strip tubes, capped, labeled 1-12 into thermal cycle at the appropriate hybridization temperature indicated in your protocol and notify staff that you have finished. All post-hybridizations steps will be done by us. Results are typically generated are emailed or placed in your data destination folder within 24 h of the hybridization set up.

6) Complete the service request for Nanostring on the iLab website
   a) Enter sample names into the “Sample Grid.” Copy and paste sample names into the sample grid rather than uploading an excel file or typing in sample names. Make sure to click “Confirm”.
   b) Sample names cannot be longer than 31 characters or contain any of these characters + \ / [ ] ; : ‘ “ { } | < >. Keep it simple.

c) Remember to include the name of your RLF.
d) Staff can enter iLab request for you if you provide the RLF and samples names to us in an e-mail.

7) We do charge for this service. All the consumables for the instruments are furnished by us and we charge $24/sample for NCI and $48/sample for NON-NCI users.

8) **NOTE NCI CCR USERS**: Nanostring reagents (code sets) are eligible for 50% OSTR subsidy. Please request subsidy directly at the STARS subsidy site. Upon approval of the subsidy request, please forward this email outlining our charges to Ashley Jordre (ashley.jordre@nih.gov), as proof of purchase. Please include the OSTR Subsidy ID# in the subject line. Contact either David Goldstein (goldsted@mail.nih.gov) or Mariam Malik (malikm@mail.nih.gov) if you have questions.

Help with data analysis & nSolver™ Analysis Software contact Amy Wahba at Nanostring:
Mobile: (803)767-1874
Email: awahba@nanostring.com

Check out NanoString's latest tips and tricks below!

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nSolver and data analysis

- Follow our training curriculum to expedite your analysis!

Sample Prep and QC

- Guidelines for purified RNA and lysates from fresh/frozen samples
- Tips for microRNA in plasma, serum, and biofluids.

Useful tips from outside NanoString

- An overview of RNA isolation
- RNA yield and storage considerations.

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The CCR Genomics Core would like to remind our customers that it is important to acknowledge the core in scientific publications, posters, and presentations that include data derived from the facility. Proper acknowledgment provides a visible measure of the impact of the core and is thus essential for our existence both for our continued funding and leadership support. It also helps tremendously in our future effort to secure additional instruments and services. Acknowledgment at the authorship-level would be strongly appreciated when extensive collaborative efforts are involved. Please send us a reprint of the paper, or an e-mail including the reference information for any publication in which the CCR Genomics Core is acknowledged.

An example of Acknowledgement:

[Insert name of services(s) here] was conducted at the CCR Genomics Core at the National Cancer Institute, NIH, Bethesda, MD 20892.