

ddPCR 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/>

QX200 Droplet Digital PCR System (<https://www.bio-rad.com/en-us/product/qx200-droplet-digital-pcr-system?ID=MPOQQE4VY>)

- 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 Steve Shema in the Core to discuss your experimental design and how to submit your samples.
- 3) Complete sample submission form provided to you by Core.
 - a) Sample volumes should be: 11ul supermix, 1.1ul DNA, 1.1ul each primer/probe and water up to a total volume of 22ul.
 - b) Spin down plate, seal and bring to Core on ice.
 - c) Confirm delivery time with Core staff via e-mail.
- 4) Submit a service request for ddPCR on the iLab website
 - a) Select your service from the drop-down menu (ddPCR)
 - b) 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.
 - c) Select Assay type from drop-down (Evagreen or probe)
 - d) Make sure to click "Confirm".
- 5) We do charge for this service. All the consumables for the instruments are furnished by us and we charge \$6/sample.

Bio-Rad contacts:

Mario Aragon, Technical Rep, to discuss any details of your experiment.
mario_aragon@bio-rad.com

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.