RAPiD GENOMICS
DNA Genotyping & Genetic Data Analysis

Capture-Seq Sample Submission Requirements

Thank you for your business and we look forward to receiving your samples. Rapid Genomics' pricing is based on the assumption that submitted samples can begin processing upon arrival. Any sample submissions not meeting the requirements below will be subject to project delay and surcharges. If you have any questions regarding these guidelines, or anything else, please do not hesitate to contact us at genotyping@rapid-genomics.com.

Please ship all samples to:

Rapid Genomics LLC
(Project ABC_010101*[1]*)
747 SW 2nd Avenue
Ste 354, IMB# 14
Gainesville, FL 32601
U.S.A.
Phone: +1 (352) 273 - 2196

*1 Make sure you substitute ABC_010101 for the correct code that was assigned to your project.

Completing the provided Plate Layout file

A Plate Layout file containing information about your samples should be completed prior to shipping. **Samples will not be accepted before the completed Plate Layout has been digitally submitted**. Please note that the default format for the Plate Layout is row-based, but you may sort the file so that it becomes column-based. RAPiD Genomics cannot confirm that sample locations are correctly oriented. Incorrect completion of the Plate Layout will result in data assigned incorrectly to each sample. As such, please ensure that your sample locations, both plate and well position, are accurate. See the example below for an explanation of the sample location code.

ABC_010101_P01_WA01[*2] = Project ABC_010101, Plate 1, Well A01

*2 In the plate layout provided by RAPiD Genomics, ABC_010101 will be replaced by the code assigned to your project.

Sample Quantifications

Concentrations should be estimated using a double-stranded dye intercalating method such as Qubit or PicoGreen.

Concentration & Volume

If possible, normalize samples to 50 ng/μL but send no less than 30 ng/μL and no more than 75 ng/μL. Sample volumes should never be less than 35 μL and never more than 180 μL. Rapid Genomics recommends a minimum of 1 μg of DNA per sample (if possible send more than 1 μg). A gel image of the DNA is also required. We recommend four random samples per extraction batch using a 2% agarose gel. If you cannot provide samples in these conditions see Exceptions for Concentration below and contact us prior to shipping.

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Labware & Shipping Conditions

All samples should be shipped in 96-well plates sealed with **strip caps** and packaged in protective material. Cut plates will not be accepted. Each plate should be clearly marked with the project number as well as the plate number corresponding to the Plate Layout file. Samples submitted in tubes are not accepted. We recommend this semi-skirted plate with these strip caps. Fully-skirted and non-skirted plates are highly susceptible to damage during shipping and should be avoided. RAPiD Genomics is not responsible for samples damaged during shipment. Samples can be shipped at room temperature, with dry ice or ice packs, but dry ice is preferred. We do not recommend shipping samples with foil/plastic sealers as they almost always partially unseal during shipping and samples cross-contaminate**.**

Exceptions for Concentration

If you cannot send 1 μg of DNA, send the samples in exactly 35 μL, drying or diluting them as needed. Note that after quantification we will normalize the entire plate to a single starting ng input. Therefore, if most samples on a plate are present at low input, the whole plate will be normalized to a lower reaction input. Lowering the starting DNA input often requires increased PCR cycles during library preparation, which may negatively impact data quality when compared to higher DNA inputs. If a few samples on the plate have low input, the whole plate will be normalized to a higher reaction input and all DNA available might be used for these samples. RAPiD Genomics cannot guarantee success under these conditions and might be unable to repeat samples that fail library preparation.

Shearing & Processing of Degraded DNA

Shearing is performed on a plate basis and assumes high molecular weight DNA (i.e. not degraded). The default procedure will be to shear the plate following our standard protocol, which yields fragments of 200-400bp. Shearing of degraded DNA will result in over-shearing of the sample, which jeopardizes data quality. When submitting plates, please indicate in the submission spreadsheet plates that are not to be sheared. If a plate contains a combination of samples that do and do not require shearing, a plate reformatting surcharge will be added to the project (see below). Please contact us prior to shipping if the project requires modification of shearing profile (on a per plate basis).

Surcharges for additional plate formatting & manipulation

If samples arrive outside the above required guidelines, a surcharge will be billed for performing the following corrections:

- Plate reformatting – $250.00 per plate.
- Sample concentration or dilution – $250.00 per plate.
- Quantification for re-submission of samples – $2.50 per sample.