



Genomic DNA Specifications for Methylation

The customer is to provide genomic DNA for methylation in the following format:

1. DNA FORMAT

Extraction: any method that yields high molecular weight DNA of high purity (OD260/280 ratio of 1.6 to 2.0).

Quantity: 1ug genomic DNA per samples for 0-96 amplicons, normalized to 50 ng/uL in either H₂O or 5mM Tris. Ship 1ug extra for every additional 96 amplicons.

NOTE: Do not ship less than 15ul per sample and not more than 45ul.

2. PLATE FORMAT OF DNA

Plate samples in 96 well plates:

-Plate: Abgene 0.8ml storage plate, natural color, Abgene (www.abgene.com) catalogue number: AB-0765

-Seal: Matrix ScreenMates 96 Well EVA Cap Mats for 96 Well Plates and 1mL Blocks, Thermo Scientific (www.matrixtechcorp.com) catalogue number: 4411

Sequenom can provide empty plates and seals to the customer by request. Contact the Customer Liaison at services@sequenom.com.

2. TUBE FORMAT OF DNA

We accept samples in a screw-cap leak proof tube with O-rings. Contact the Methylation Project Manager at dbroder@sequenom.com for further information about this format.

3. SHIPPING

Ensure that the plate(s) are completely sealed and frozen in a horizontal orientation. Use a spacer (cardboard or Styrofoam) between plates and use bubble wrap to package the plates.

Ship samples frozen with at least 5 kg dry ice for domestic shipments and at least 10 kg dry ice for international shipments.

Ship only on Monday, Tuesday, or Wednesday for shipments within the U.S. Ship only on Monday for international shipments. Do not ship for receipt on any standard U.S. holidays.

E-mail the Methylation Project Manager, (dbroder@sequenom.com) three days before shipping to confirm the ship date.

E-mail the Methylation Project Manager, (dbroder@sequenom.com) the day the samples are shipped with the shipping courier name and tracking number.

Ship to:

Sequenom, Inc.
ATTN: Genetic Services Laboratory
3595 John Hopkins Court
San Diego CA, 92121
Phone: 858-202-9035

4. INFORMATION SPECIFICATIONS

Sample File

- 4.1.1 E-mail an excel file with the following information and format to the Methylation Project Manager, (dbroder@sequenom.com) unless stated otherwise within contract. A *Sample File Template* can be provided upon request.

- 4.1.1.1 Required Information: Plate ID or Plate Barcode, Sample ID or Barcode, Well ID in three digits (A01, A02 etc.) proceeding left to right, top to bottom, sample concentration in ng/ μ L, Sample volume in μ L and comments.
- 4.1.1.2 Please also include the method that was used to determine sample concentration.
- 4.1.1.2 Please indicate Non-Template Controls as “NTC.”
 - 4.1.1.2.1 **NOTE:** Sequenom will not accept samples without an electronic sample information file.
 - 4.1.1.2.2 Consult with the Methylation Project Manager (dbroder@sequenom.com) for any modification of sample information format.

Example:

Plate_ID	Sample_ID	Well_ID	Conc_(ng/ μ L)	Volume_(μ L)	Comments
ABCD1	1234	A01	50	20	Quant method: picogreen
ABCD1	1235	A02	50	20	Quant method: picogreen
ABCD1	NTC	A03	0	0	
ABCD1	1236	A04	50	20	Quant method: picogreen
ABCD1	1237	A05	50	20	Quant method: picogreen