SHIPPING CONDITIONS OF YOUR SAMPLES

IMPORTANT

You are about to send biological samples to IntegraGen for genomic service project. Your samples are very important, and we want to process them with the greatest care in order to return you quality data that makes the IntegraGen brand.

We thank you in advance for respecting the conditions below. This is the only guarantees of success for youR research.

1. Information of the Sample Form

Before sending the sample, you must complete the "Sample Form" document that you received by email. This document contains the information for the proper shipment of your samples. It also contains the project number which is associated with your request (PJAAMMXXX format). **This project number must be written in the sample shipping package and in any request related to its execution.**

If you do not have this number, your project may not be created yet, so please do not send your samples and contact your sales representative at services@integragen.com.services@integragen.com.

*According to GDPR regulations, we would like to remind you that samples should be sent **anonymously**. Any reference to the name, surname, date of birth or others that identify the sample must not be written either on the tube or on the form. If the sample can be identified, we will send the samples back to the sender.*

2. Shipping and packaging format

2.1 DNA extracts, RNA extracts or prepared libraries

- ✓ You must send the samples in 96-well plate with conical and transparent bottom, any other format will be refused upon receipt, except in special cases described below;
- ✓ The samples must be organized in columns, imperatively from the A1 well;
- ✓ Do not leave any empty column or empty line at the beginning or between my samples. All wells must be filled consecutively. Column by column. That is, A1, A2, A3 ... A8, B1, B2 ...
- ✓ Do not leave empty well interposed in a column;
- ✓ **Do not insert more samples than the number of samples specified in the quotation and the associated purchase order**;

- ✓ Make sure that the order and coordinates of the samples on the plate correspond to those documented in the “Sample Form”;
- ✓ Please inform exactly the volumes of each sample. A minimum volume of 20µL is required for all types of samples and projects. In order to avoid any confusion, and any suspicion of a problem occurring during transport of the package, the volume of a sample indicated on the form must be perfectly consistent with the volume
- ✓ Be sure to perfectly seal your plate with a transparent and thermoresistant adhesive film.
- ✓ Identify the plate with the project number provided by Integragen and available in the Sample Form (in PJAAMMXXX format).

- **<u>Recommended plates references</u>**:

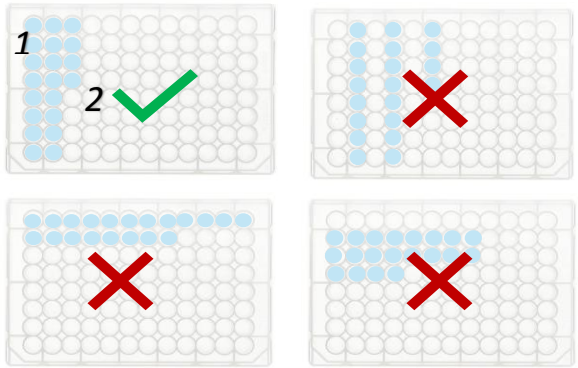
  - ✓ AB-0800 PCR plate, 96 wells, skirted: ThermoFisher Scientific™
  - ✓ AB-0900 PCR plate, 96 wells, segmented, semi-skirted: ThermoFisher Scientific™

- **<u>Recommended thermoresistant film references</u>:**

  - ✓ AB-0558 Adhesive films for PCR plates: ThermoFisher Scientific™

- **<u>Special case</u>**: For 1 to 8 samples shipments, packaging in individual tubes of 1.5ml is accepted. Each tube must be properly and legibly identified with non-erasable pen, thus avoiding ambiguity and errors. These tubes will be stored in a proper and sealed box avoiding leakage.

Examples of a plate containing 20 samples:



2.2 Other types of samples: blood tubes, plasma, frozen samples, slides, saliva samples ...

- ✓ Verify that the packaging of the samples corresponds to the project and attendant as such (e.g. total blood or PBMC, slides or FFPE tissue);
- ✓ Ensure a clear, legible, and anonymous identification of all samples;
- ✓ Make sure the identifiers match with those documented in the "Sample Form";
- ✓ Send the samples in an appropriate rack or box, allowing secure transport and easy identification corresponding perfectly to the information of the "Sample Form";
- ✓ Do not send loose samples in plastic bags.

Examples :

- Blood tubes or plasma tubes: 10 x 10 cardboard box
- FFPE slides in boxes, grouped by patient, and necessarily along with a circled H&E slide with circled tumor area;
- Identify the project number (PJAAMMXXX) on the primary packaging;

3. Package

- ✓ Ensure samples are sent at the appropriate temperature (this temperature varies according to sample type and may be room temperature or dry ice). Also, guarantee the correct storage during shipping, so, if necessary, use proper package, bubble wrap and correct sealing.
- ✓ You MUST ship the following samples in dry ice:
    - RNA
    - Plasma
    - Frozen tissue
- ✓ If dry ice is mandatory, please, guarantee to add enough to maintain the samples frozen for 48 to 72 hours, and ship the package preferentially earlier in the week;
- ✓ Clearly identify the sender on the package mentioning

Full name
Address
Institution / Department / Laboratory
Project number (PJAAMMXXX)

- ✓ Ideally, if you have an electronic Sample Form (e-Sample Form); print the packing label available online and I stick it on the shipment
- ✓ As a reminder, the shipping address for the samples is:

INTEGRAGEN
SERVICES GENOMIQUES
Hélène RAMBUR
5, rue Henri-Auguste Desbruères
Génopole 1, Porte 840
91000 EVRY
Telephone contact 01 60 91 09 13
helene.rambur@integragen.com

Reception hours :

Monday to Thursday from 8h15 am to 12h00 pm – and from 1h00 pm to 5h00 pm

Friday from 8h15 am to 12h00 pm – and from 1h00 pm to 4h00 pm

4. Return of samples

From 02/04/2024, any DNA or RNA residues received will be systematically destroyed within 30 days of delivery of the results (or batch of results for projects with several results).

If you have any questions, please contact our sales department at services@integragen.com.

Recommendations / QC of samples before sending

Preparation of libraries from genomic or circulating DNA

Type of technology	Quality required	Quantity to be supplied	Concentration	Volume
Whole Genome PCR free Sequencing	Intact DNA	>= 600 ng	>= 30 ng/µl	>= 20 µl
Whole Genome PCR Sequencing	Intact DNA	>= 50 ng	>= 2,5 ng/µl	>= 20 µl
Whole exome Sequencing	Intact DNA	>= 200 ng	>= 10 ng/µl	>= 20 µl
Whole exome Sequencing FFPE DNA	DV500 >= 50%	>= 200 ng	>= 10 ng/µl	>= 20 µl
Targeted Sequencing	Intact DNA	>= 200 ng	>= 10 ng/µl	>= 20 µl
WGEM seq	Non-degraded DNA / extracted from silica column	>= 200 ng	>= 10 ng/µl	>= 20 µl
RREM seq	Non-degraded DNA / extracted from silica column	>= 200 ng	>= 10 ng/µl	>= 20 µl
Human Methylone targeted sequencing	Non-degraded DNA / extracted from silica column	>= 200 ng	>= 10 ng/µl	>= 20 µl
Ct DNA prep	160bp mean size DNA, no gDNA traces	>= 10 ng	>= 0,5 ng/µl	>= 20 µl

All DNA must be RNA-free - All DNAs must be quantified by a method equivalent to fluorescence quantification Qubit (Life Technologies)

Preparation of libraries from tRNA

Type of technology	Quality required	Quantity to be supplied	Concentration	Volume
mRNAseq	RIN score >= 5.0	>= 200 ng	>= 10 ng/µl	>= 20 µl
totalRNA seq including globin and ribosomal RNA depletion	DV200 >= 30	>= 400 ng	>= 20 ng/µl	>= 20 µl
3' Tag RNA-seq input FFPE	FFPE	>= 100 ng	>= 5 ng/µl	>= 20 µl
3' Tag RNA-seq input non FFPE	RIN score >= 5.0	>= 50 ng	>= 2,5 ng/µl	>= 20 µl
RNAseq with exonic capture	DV200 >= 30	>= 100 ng	>= 5 ng/µl	>= 20 µl

All RNAs must be DNA-free - All RNAs must be quantified by an electrophoretic migration method (Fragment Analyzer- Agilent type)

All-ready prepared librairies for « SEQUENCING ONLY » project

Type of technology	*Quality required*	*Concentration*	*Volume*
Library compatible with Illumina sequencer	Without the presence of adapter dimers	Depends on the number of lines	Depends on the number of lines

IntegraGen adds up to 10% PhiX per line depending on the diversity of the library or pool of libraries.

All libraries shipped must first be quantified using an electrophoresis migration method (Fragment Analyzer type - Agilent).

Format 10B: minimum volume of library (or pool of libraries) to be supplied depending on its concentration and the number of lanes required.

Type FC	cc° nM library	vol lib min µl for 1 lane	vol lib min µl for 2 lanes	vol lib min µl for 3 lanes	vol lib min µl for 4 lanes	vol lib min µl for 5 lanes	vol lib min µl for 6 lanes	vol lib min µl for 7 lanes	vol lib min µl for 8 lanes
10B	***5***	25	25	25	30	37,5	45	53	60
10B	***6***	25	25	25	25	31	38	44	50
10B	***7***	25	25	25	25	28	34	39	45
10B	***8***	25	25	25	25	25	30	35	40
10B	***9***	25	25	25	25	25	26	31	35
10B	***10***	25	25	25	25	25	25	26	30
10B	***11***	25	25	25	25	25	25	26	30
10B	***12***	25	25	25	25	25	25	26	30
10B	***13 and >13***	25	25	25	25	25	25	25	25

Format 25B: minimum volume of library (or pool of libraries) to be supplied depending on its concentration and the number of lanes required.

Type FC	cc° nM library	vol lib min µl for 1 lane	vol lib min µl for 2 lanes	vol lib min µl for 3 lanes	vol lib min µl for 4 lanes	vol lib min µl for 5 lanes	vol lib min µl for 6 lanes	vol lib min µl for 7 lanes	vol lib min µl for 8 lanes
25B	***5***	25	25	30	40	50	60	70	80
25B	***6***	25	25	28	38	47	56	66	75
25B	***7***	25	25	25	33	41	49	57	65
25B	***8***	25	25	25	28	34	41	48	55
25B	***9***	25	25	25	25	31	**38**	44	50
25B	***10***	25	25	25	25	28	34	39	45
25B	***11***	25	25	25	25	25	30	35	40
25B	***12***	25	25	25	25	25	26	31	35
25B	**13**	25	25	25	25	25	26	31	35
	14	25	25	25	25	25	25	26	30
25B	***15***	25	25	25	25	25	25	26	30
25B	***16***	25	25	25	25	25	25	26	30
25B	***17 and >17***	25	25	25	25	25	25	25	25

If you have any questions about this section, please contact *services@integragen.com*

Infinium SNP or MethEpic analysis from genomic DNA

Type of technology	Quality required	Quantity to be supplied	Concentration	Volume
Infinium SNP	Integrated DNA	>= 500 ng	>= 50 ng/µl	>= 10 µl
Infinium MethEpic	Integrated DNA	>= 1000 ng	>= 50 ng/µl	>= 10 µl
Infinium MethEpic FFPE	To be assessed on receipt with Illumina FFPE QC Kit	>= 1000 ng	>= 50 ng/µl	>= 10 µl

All DNA must be RNA-free - All DNAs must be quantified by a method equivalent to fluorescence quantification Qubit (Life Technologies)