

Sample shipment protocol for microbiome DNA isolation services

It is important to follow this protocol when sending samples to the Genomics Core Facility of Erasmus MC to ensure the samples can be processed as efficiently as possible. **Please note that any deviation from this protocol could lead to a delay in the service.**

Frozen samples

- Send at least 1 g of feces preferably taken from multiple sites in the stool.
- Send at least 1 ml of saliva.
- Send at least 1 ml of urine, preferably the pellet spun down at max speed from 50ml urine and resuspended in 1ml of remaining urine.
- Wet swabs (or Copan eSwabs in Amies storage medium) should be in 1ml of storage medium.
- Dry swabs should be in a closed tube.
- Samples should be sent on dry ice.

Genotek OMNIgene GUT tubes and other stabilizers

- Samples in stabilizer should be frozen as soon as possible.
- Samples in stabilizer can be sent at room temperature.
- We will freeze the sample at -80C at our laboratory upon arrival.

Other samples

If you would like DNA isolation from any other type of tissue or material (e.g. blood, cards, biopsies, hair, etc.) please contact us to discuss the possibilities.

General

- Samples should be in tubes in 24, 48 or 96 well format, or in rack format with labeled positions.
- Please make sure to send your samples in the same order as the sample sheet. If this is not possible, samples can be sorted at our facility.

- Clearly label the samples. All samples should be barcoded (or at least contain any kind of identifier).
- For efficient processing of your samples, we recommend you to keep a few guidelines in mind concerning sample IDs. Most genetic software are unable to handle sample IDs including these features and will generate errors. Also tracking systems and Excel might recode sample IDs with these features. In general, we advise to use a combination of numbers and letters, and avoid special characters, symbols and spaces. When making your sample IDs please avoid the following:
 - o Special characters in sample IDs (e.g., 12.34 or 12,34 or 12_34 should be 1234)
 - o Spaces in sample IDs (e.g., 12 34 should be 1234)
 - o Number IDs starting with one or multiple '0's (e.g., 01234 should be either 1234 or a01234)
 - o Duplicate IDs. If a sample has been run twice please add an addition to the IDs (e.g., 1234a and 1234b)
- Complete the following file according the 'Samplesheet file instruction' before sending the samples: 'Samplesheet microbiome DNA isolation'. For instructions on how to fill in the samplesheet, please see appendix 1.
- Send the samplesheet to genomics-isolation@erasmusmc.nl and provide exact time and date of shipment. Only send samples to the Genomics Core Facility, when the samplesheet has been approved. We will notify you upon receiving the samples.
- Do not ship samples on a Friday or Saturday.
- Send the samples to the following address:

Erasmus MC
Genomics Core Facility
Mila Jhamai/Pascal Arp/Michael Verbiest/Ramazan Büyükcelik
Room Ee 575
Westzeedijk 353
3015 AA Rotterdam
The Netherlands
010-7043645 / 010-7043575

For general questions regarding projects, please contact the contract- and project manager dr. Gaby van Dijk (g.m.vandijk@erasmusmc.nl or genomics@erasmusmc.nl).

Appendix 1: Samplesheet file instruction

Our laboratory makes use of a Laboratory Information Management System (LIMS) to track samples and project status. To enable a fast turnaround time of your project we request that you fill in the samplesheet for all samples you are going to send. This sample sheet is formatted in such a way that it can be uploaded directly to the LIMS system. As such it is important that you follow the instructions below carefully, and do not deviate from the given format.

The sample input excel file contains one sheet. The information required in the sample sheet is given below, while an example sheet can be seen in figure 1.

- Sample name/ID
- Container type (32perbag or 36perack or 96perbox)
- Container name (number that's on the container)
- Well location (LIMS needs this information, even when it's not available, will be explained later)
- Acronym of the study
- Quote number (your Erasmus MC contract number)
- Sample type (stool, urine, saliva, swab, eswab, etc)
- Volume (ml or g)

Sample input file								
-TABLE HEADERS-								
Sample/Name	Container/Type	Container/Name	Sample/Well location	LIDP/Acronym	LIDP/Quote number	LIDP/Sample type	LIDP/Volume (ml)	LIDP/Sender
-SAMPLE ENTRIES-								
1	32per bag	DNA 2017 24 OF bag 1	a-1	Test	DNA 2017 24-01	Blood	5	MT
2	32per bag	DNA 2017 24 OF bag 1	b-1	Test	DNA 2017 24-01	Blood	5	MT
3	32per bag	DNA 2017 24 OF bag 1	c-1	Test	DNA 2017 24-01	Blood	5	MT
4	32per bag	DNA 2017 24 OF bag 1	d-1	Test	DNA 2017 24-01	Blood	5	MT
5	32per bag	DNA 2017 24 OF bag 1	e-1	Test	DNA 2017 24-01	Blood	5	MT
6	32per bag	DNA 2017 24 OF bag 1	f-1	Test	DNA 2017 24-01	Blood	5	MT
7	32per bag	DNA 2017 24 OF bag 1	a-2	Test	DNA 2017 24-01	Blood	5	MT
8	32per bag	DNA 2017 24 OF bag 1	b-2	Test	DNA 2017 24-01	Blood	5	MT
-SAMPLE ENTRIES-								

Figure 1. Example samplesheet

Step-by-step instructions

An explanation on how to fill in the sample input sheet is given below. Figure 2 contains an additional graphic step-by-step explanation to make things extra clear, but if any questions remain they can be addressed to Ramazan Büyükelik (r.buyukcelik@erasmusmc.nl).

Step 1

Fill in the sample IDs from the samples in the first container (bag, rack, box) in the column A (Sample/name)

Step 2

In column B (Container/type) you should fill in the container type. In this examples, the client will send 32 tubes with Blood per bag, therefore the container type is 32perbag.



Step 3

In column C (Container/name) fill in the Erasmus MC contract number followed by the number of the bag that correlates to the sample IDs in that bag. Fill in the same number for all 32 samples.

Step 4

In column D (sample/well location) you should fill in the well or rack location. Even though this is not applicable, LIMS needs information in this column. Per 32 samples you should fill in A:1, B:1.....until H:4 (see figure 2). Be sure to use the same annotation as in the example, so A:1 etc.

Step 5

In column E (UDF/acronym) you should fill in the name of your study. If you don't have one, just fill in NA

Step 6

In column F (UDF/Quote number) you should fill in the Erasmus MC contract number.

Step 7

In column G (UDF/Sample type) you should fill in the sample type. Be sure to use only the following options (stool, urine, saliva, swab, eswab, etc). Do not deviate from the format (for example the first letter should be a capital letter, do not change that)

Step 8

In column H (UDF/Volume (ml or g) you should fill in the volume of your sample if applicable. If not, please leave it empty

Step 9

In column I (UDF/Gender) you should fill in the gender of your sample. Only use M, F or NA.

Step 10

Repeat step 1-8 for the other bags and put the information below each other.

Step 11

When finished, make sure that the </SAMPLE ENTRIES> tag is below the last sample.

Step 12

Please give the file your Erasmus MC contract number as a name and save it as an .xlsx file.

Sample input file

Sample input file								
-TABLE HEADER-								
Sample/Volume	Container/Type	Container/Volume	Sample/Well location	UOP/Assaytype	UOP/Date number	UOP/Sample type	UOP/Volume [ml]	UOP/Residue
-TABLE END-								
1	30pwrfrag	[DNA] 2017-04-07 frag 1	a:1	Test	[DNA] 2017-04-07	Blood	5	ml
2	30pwrfrag	[DNA] 2017-04-07 frag 1	b:1	Test	[DNA] 2017-04-07	Blood	5	ml
3	30pwrfrag	[DNA] 2017-04-07 frag 1	a:1	Test	[DNA] 2017-04-07	Blood	5	ml
4	30pwrfrag	[DNA] 2017-04-07 frag 1	b:1	Test	[DNA] 2017-04-07	Blood	5	ml
5	30pwrfrag	[DNA] 2017-04-07 frag 1	a:1	Test	[DNA] 2017-04-07	Blood	5	ml
6	30pwrfrag	[DNA] 2017-04-07 frag 1	f:1	Test	[DNA] 2017-04-07	Blood	5	ml
7	30pwrfrag	[DNA] 2017-04-07 frag 1	g:1	Test	[DNA] 2017-04-07	Blood	5	ml
8	30pwrfrag	[DNA] 2017-04-07 frag 1	h:1	Test	[DNA] 2017-04-07	Blood	5	ml
9	30pwrfrag	[DNA] 2017-04-07 frag 1	a:2	Test	[DNA] 2017-04-07	Blood	5	ml
10	30pwrfrag	[DNA] 2017-04-07 frag 1	b:2	Test	[DNA] 2017-04-07	Blood	5	ml
11	30pwrfrag	[DNA] 2017-04-07 frag 1	c:2	Test	[DNA] 2017-04-07	Blood	5	ml
12	30pwrfrag	[DNA] 2017-04-07 frag 1	d:2	Test	[DNA] 2017-04-07	Blood	5	ml
13	30pwrfrag	[DNA] 2017-04-07 frag 1	e:2	Test	[DNA] 2017-04-07	Blood	5	ml
14	30pwrfrag	[DNA] 2017-04-07 frag 1	f:2	Test	[DNA] 2017-04-07	Blood	5	ml
15	30pwrfrag	[DNA] 2017-04-07 frag 1	g:2	Test	[DNA] 2017-04-07	Blood	5	ml
16	30pwrfrag	[DNA] 2017-04-07 frag 1	h:2	Test	[DNA] 2017-04-07	Blood	5	ml
17	30pwrfrag	[DNA] 2017-04-07 frag 1	a:3	Test	[DNA] 2017-04-07	Blood	5	ml
18	30pwrfrag	[DNA] 2017-04-07 frag 1	b:3	Test	[DNA] 2017-04-07	Blood	5	ml
19	30pwrfrag	[DNA] 2017-04-07 frag 1	c:3	Test	[DNA] 2017-04-07	Blood	5	ml
20	30pwrfrag	[DNA] 2017-04-07 frag 1	d:3	Test	[DNA] 2017-04-07	Blood	5	ml
21	30pwrfrag	[DNA] 2017-04-07 frag 1	e:3	Test	[DNA] 2017-04-07	Blood	5	ml
22	30pwrfrag	[DNA] 2017-04-07 frag 1	f:3	Test	[DNA] 2017-04-07	Blood	5	ml
23	30pwrfrag	[DNA] 2017-04-07 frag 1	g:3	Test	[DNA] 2017-04-07	Blood	5	ml
24	30pwrfrag	[DNA] 2017-04-07 frag 1	h:3	Test	[DNA] 2017-04-07	Blood	5	ml
25	30pwrfrag	[DNA] 2017-04-07 frag 1	a:4	Test	[DNA] 2017-04-07	Blood	5	ml
26	30pwrfrag	[DNA] 2017-04-07 frag 1	b:4	Test	[DNA] 2017-04-07	Blood	5	ml
27	30pwrfrag	[DNA] 2017-04-07 frag 1	c:4	Test	[DNA] 2017-04-07	Blood	5	ml
28	30pwrfrag	[DNA] 2017-04-07 frag 1	d:4	Test	[DNA] 2017-04-07	Blood	5	ml
29	30pwrfrag	[DNA] 2017-04-07 frag 1	e:4	Test	[DNA] 2017-04-07	Blood	5	ml
30	30pwrfrag	[DNA] 2017-04-07 frag 1	f:4	Test	[DNA] 2017-04-07	Blood	5	ml
31	30pwrfrag	[DNA] 2017-04-07 frag 1	g:4	Test	[DNA] 2017-04-07	Blood	5	ml
32	30pwrfrag	[DNA] 2017-04-07 frag 1	h:4	Test	[DNA] 2017-04-07	Blood	5	ml
33	30pwrfrag	[DNA] 2017-04-07 frag 2	a:1	Test	[DNA] 2017-04-07	Blood	5	ml
34	30pwrfrag	[DNA] 2017-04-07 frag 2	b:1	Test	[DNA] 2017-04-07	Blood	5	ml
35	30pwrfrag	[DNA] 2017-04-07 frag 2	a:1	Test	[DNA] 2017-04-07	Blood	5	ml
-SAMPLE END-								

Do not change this part

Fill in your sample IDs

Fill in the container here

Fill in the container names here

Fill in the gender of the samples

Fill in the volumes or weight (estimated) of your samples

Figure 2. Graphic step-by-step explanation

Put this tag below the last sample

Fill in well location as in example

Fill in the study name here

Fill in the Erasmus MC contract number

Fill in the sample type here