



umcg
Genetica
Genome Analysis Facility

Title: Guidelines for delivery of prepared samples for Next-Generation Sequencing

Protocol number: GAF S012

Version: Version 2

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Author: J.J. de Boer-Bergsma

Introduction

To ensure a successful and rapid processing of the prepped samples, the samples need to meet various criteria. There are also special demands with respect to the format of the sample delivery. All criteria are described in this guideline.

This document describes an overview of important issues for delivery and there is pointed out what has to be delivered.

What the Genome Analysis Facility needs

1. Clearly labelled sample

Present the sample in a 1,5 or 2 ml tube. To avoid miscommunication, all prepped samples has to be clearly labelled. Use printed labels on the side of a tube and make sure the following information is mentioned:

- The name the research center or research group / project
- An unique sample ID (the GAF does not accept patient names)
- Date of delivery
- Concentration in nM

Accepted characters in the sample ID are:

- a – z
- A – Z
- 1 – 9
- 0
- _ (under score)

2. Clear information about sample pools and barcodes

When delivered material consist out of multiple samples combined into one sample pool, a sample sheet is needed. This xls-file needs the following additional information: barcode type (e.g. RPI, AGI), barcode number and barcode sequence: "RPI12 CGTACC". By composing the pools make sure that the nucleotides per position are equally divided over the samples. How smaller the pool, the more important this is.

3. Analyzed capillary electrophoresis output

For the product check, determining the concentration and the quality control of your prepared sample is a measurement needed. We highly recommend using a capillary electrophoresis system such as the BioRad Experion or the Caliper GX.

Measuring and analysis for Experion output data is described in protocol GAF S013. Measuring and analysis for GX output data is described in protocol GAF S022.

3.1. Fragment length

In data analysis of the measuring make sure that the fragment length of the prepped sample is suitable for the experiment. This parameter can differ between experiments and will be pointed out by detailed appointments made before submitting the sample.

Typical used fragments are for single-read runs: 300 bp-350bp. For (exome) paired-end runs: 330 bp-380 bp. These lengths include the extended adapter sequences.

3.2. Sample quality

For a successful clustering the prepped sample following issues are important:

- The concentration of the sample is between 5 nM and 15 nM
- There is no contamination of primer-dimer

Sample delivery information

Deliver the samples on dry ice to the Genome Analysis Facility or send your samples by courier to the Genome Analysis Facility laboratory at the Department of Genetics, UMCG. The shipment should be placed in boxes containing a sufficient amount of dry ice. To avoid any delay during the weekend, please ship the material at the beginning of the week.

Before submitting your samples, please contact the Genome Analysis Facility

Delivery Address: Genome Analysis Facility
 Dept. Genetics UMCG
 Hanzeplein 1, Ingang 47 Oostersingel
 Room E2.030
 9713GZ Groningen
 The Netherlands

Phone number: +31 (0)50-3617100

Email: p.van.der.vlies@umcg.nl