

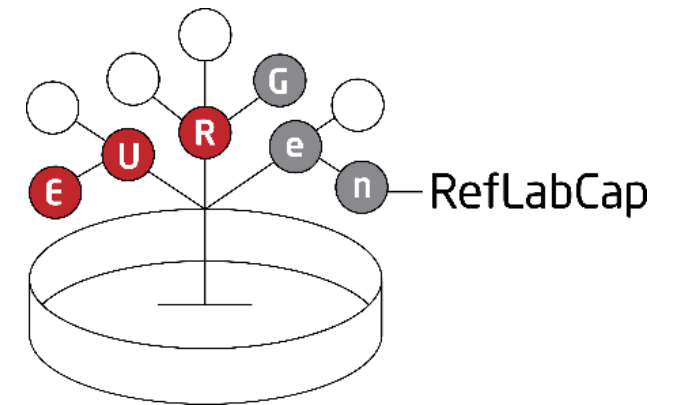
# EURGen-RefLabCap

## Best practice workshop – Nanopore sequencing

Second day

Wednesday, 6 December 2023

09:00 – 17:00 CET



# Previously...

First day (virtual) – Thursday 30 November 2023, 9:00 - 12:30 CET

- Biochemical principles of Oxford Nanopore Technologies
- Comparison between ONT and Illumina sequencing
- State-of-the-art – literature on ONT sequencing applied to microbiology research and public health surveillance
- DNA extraction and library preparation for ONT sequencing
- Troubleshooting ONT runs
- Introduction of bioinformatics analyses of ONT data
- Explanation regarding purchase of Nanopore sequencer and reagents

# Agenda for today

## Second day (physical) – Wednesday 6 December 2023, 9:00 - 17:00 CET

9:00 – 9:10: Introduction and agenda for the day (Ana Rita Rebelo, DTU)

9:10 – 10:00: Overview of the DNA extraction protocol and preparation for lab work (Ana Rita Rebelo, DTU)

10:00 – 14:00: Laboratory work – DNA extraction (including *ad hoc* lunch)

14:00 – 15:30: Laboratory work – DNA quality control with Qubit

*15:30 – 16:00: Coffee break*

16:00 – 16:30: Other options for DNA quality control (Niamh Lacy-Roberts and Jette Sejer Kjeldgaard, DTU)

16:30 – 17:00: Q&A, wrap-up (Ana Rita Rebelo, DTU)

*17:00: Bus to the restaurant*

Ana Rita Rebelo  
*anrire@food.dtu.dk*

# Overview of the DNA extraction protocol

# DNA extraction

We will use protocol:

## INSTRUCTION MANUAL



### Monarch<sup>®</sup> HMW DNA Extraction Kit for Tissue

NEB #T3060S/L

5/50 preps

Version 2.1\_4/21

The full protocol has 33 pages. What's important for us:

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And then pages 25-33:

- Homogenization of HMW DNA
- Measuring & Analyzing HMW DNA
- Troubleshooting

# DNA extraction

We will not use the big protocol.

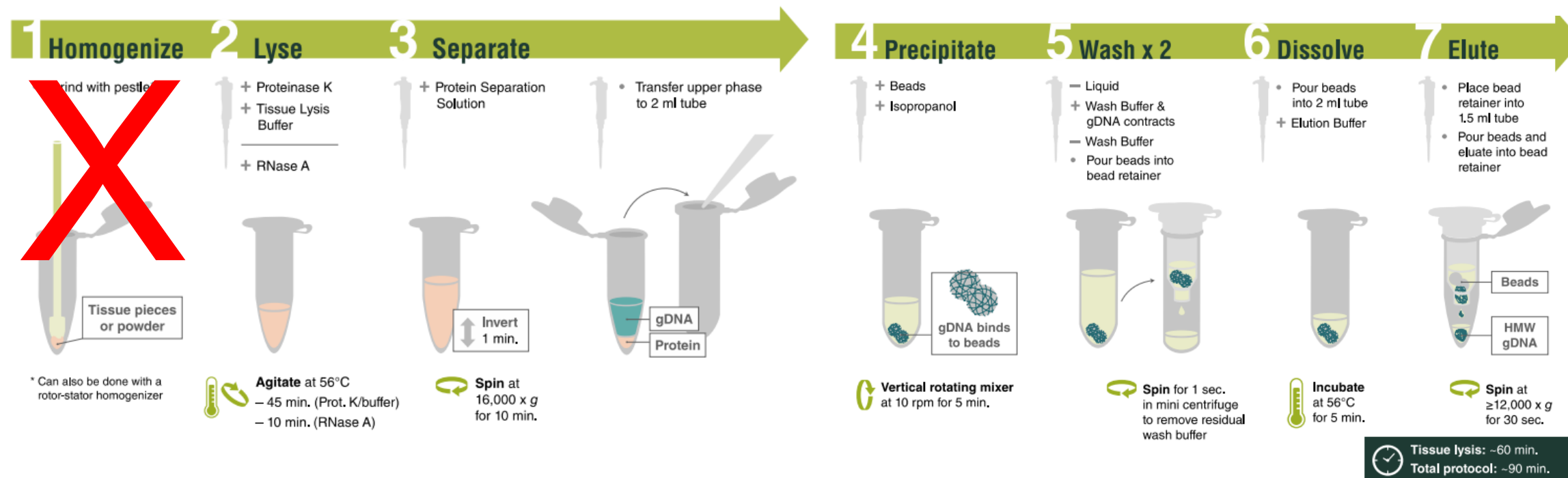
We prepared a 6-page shortened protocol with the most important information.

This short protocol has been optimized at DTU:

- input material and amount (e.g. bacterial colonies from agar plates instead of ON liquid culture)
- volumes of some reagents (e.g. lysozyme)
- agitation times and speeds
- centrifugation times and temperatures



Figure 2: Workflow for Tissue Samples



# DNA extraction

<https://www.youtube.com/watch?v=B4x4oQBrscU&t=214s>

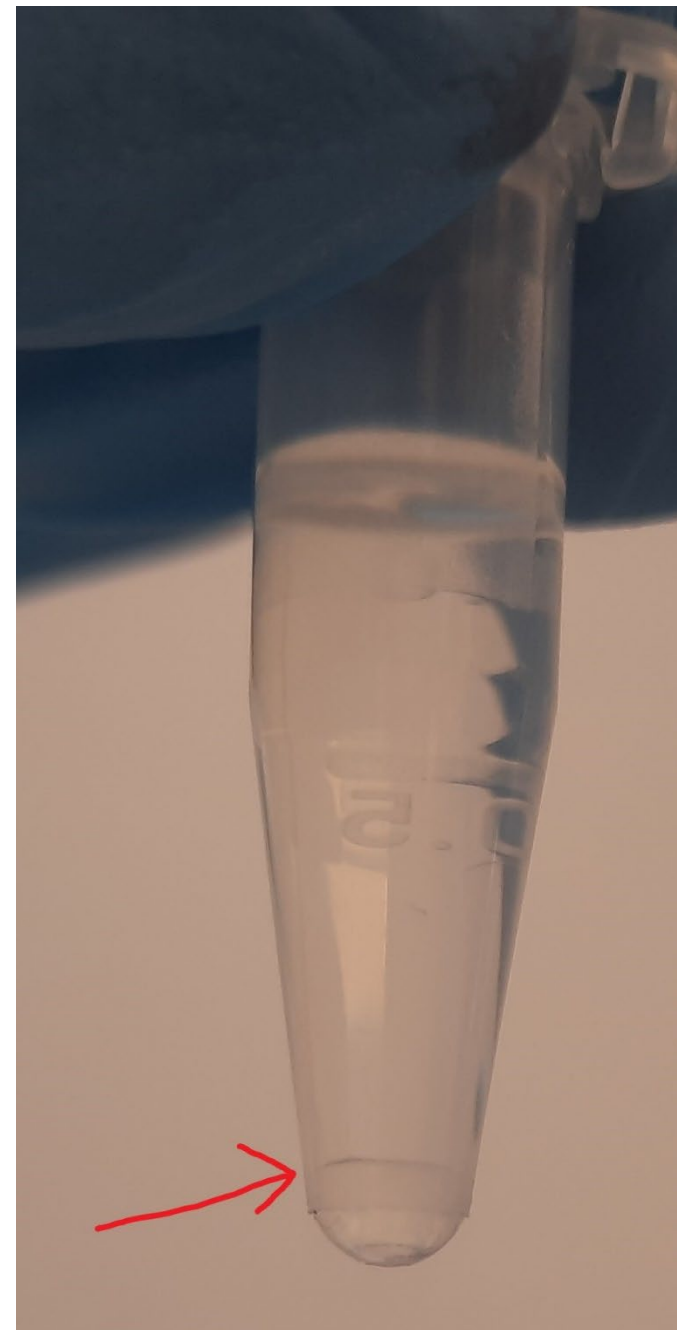
# DNA extraction

Very important:

- manual inversions need to be gentle
- it's probable that you will need to centrifuge longer for phase separation
- inversions after adding the isopropanol needs to be **extra gentle – 5-6 seconds** per inversion
- **If you're unsure about what to discard (beads? eluate?) - ask**

# DNA extraction

How the phase separation will look:



# DNA extraction

How the DNA will look wrapped around the beads:



Ana Rita Rebelo  
*anrire@food.dtu.dk*

# Overview of DNA quality control with Qubit

We will use protocol:

 invitrogen

USER GUIDE

## Qubit™ dsDNA HS Assay Kit

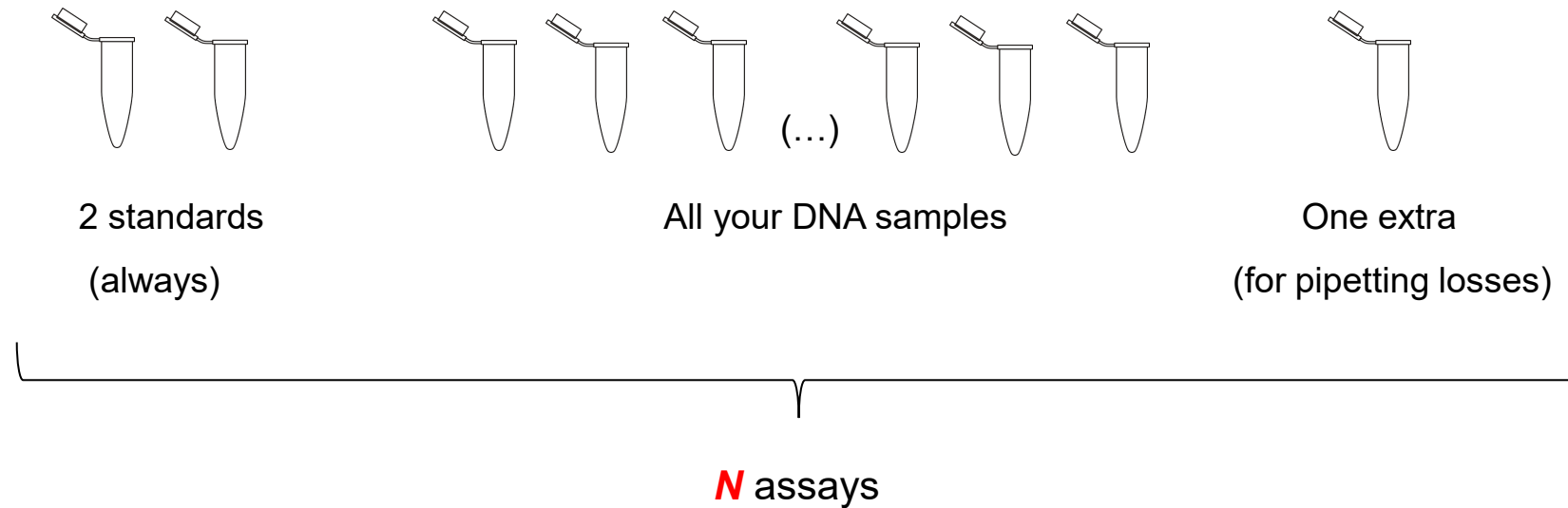
Catalog Numbers Q32851, Q32854

Pub. No. MAN0002326 Rev. C.0

We will not use the big protocol (8 pages).

We prepared a 2-page shortened protocol with the most important information.

## PREPARING THE WORKING SOLUTION:

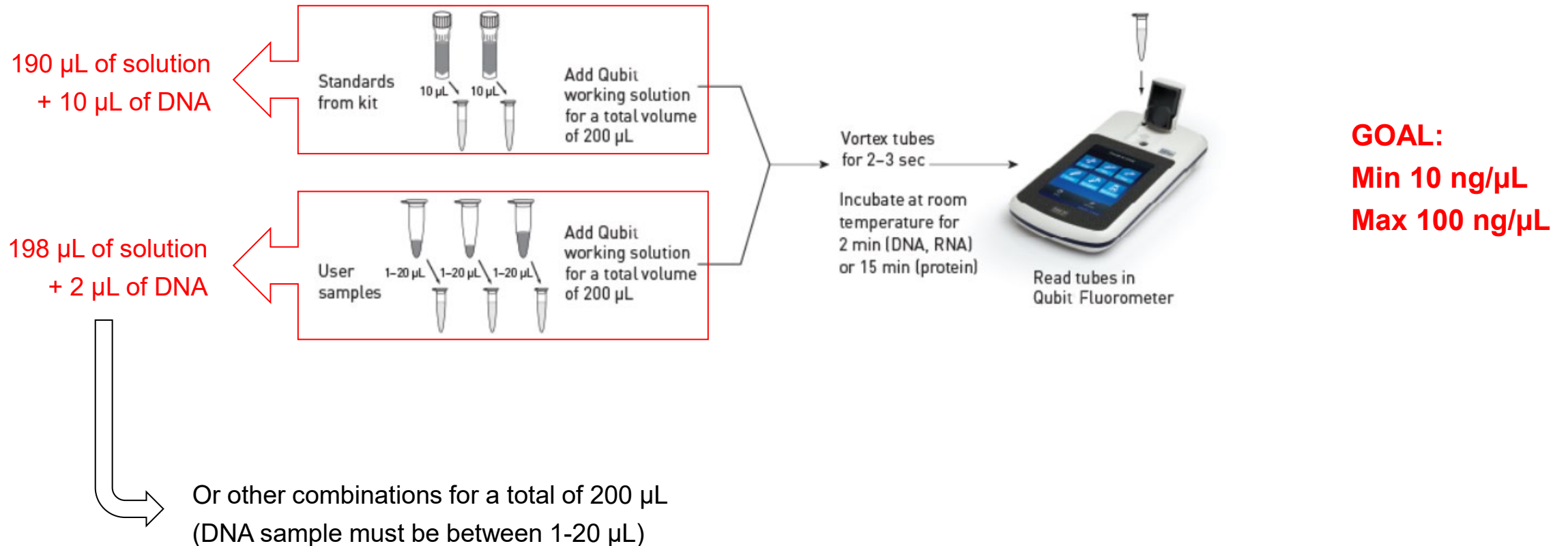


Volume of reagent to use = ***N***  $\mu\text{L}$

Volume of buffer to use = ***N***  $\times 199 \mu\text{L}$



## DISTRIBUTING WORKING SOLUTION AND DNA:



Niamh Lacy-Roberts and Jette Sejer Kjeldgaard

*nlac@food.dtu.dk*

*jetk@food.dtu.dk*

# DNA Quality Control

# Which quality control (QC) is performed for sequencing(!?)

**DNA quantity**

**DNA integrity**

**DNA purity**

For WGS/NGS we have two check points:

1. DNA Quality Control (DNA QC)
2. Library Quality Control (Library QC)

# Why is it important to quality control DNA?

- It is important that you check your input DNA for quality before and during library preparation.
- Low molecular weight, incorrectly quantified and/or contaminated DNA can have a significant impact on downstream processes and your sequencing runs.
- Chemical impurities such as detergents, denaturants, chelating agents and high concentrations of salts should be avoided as these may affect the efficiency of enzymatic steps.
- Other contaminants such as single stranded DNA, RNA, proteins, dyes and beads may also reduce the efficiency of steps in the library preparation.

# Why is it important to quality control DNA?

- It's important that the nanopores are kept filled with DNA to minimize the time they are idle between strands – for maximum sequencing yield.
- The less DNA goes into the flow cell, the less DNA is captured by the pores. This means the pores will be searching for DNA for longer, and if the pores are not always sequencing throughput may be compromised. Shorter fragments can also have a similar effect.
- Therefore, you can measure:
  - Mass (concentration in ng/ul)
  - Quality (purity)
  - Fragment Length
- ONT recommends the Qubit fluorometer to determine the mass of the sample, for quality use nanodrop and for fragment size you could use: gels (e.g. Bio-Rad CHEF system), Agilent devices (e.g. Bioanalyzer or Tapestation), or FEMTO Pulse from AATI.

# Measuring concentration with Qubit

- Quantifies 1  $\mu$ l DNA per sample
- Broad range (0.01 – 5  $\mu$ g/mL) and High sensitivity dsDNA kits (1 – 500 ng/mL)
- Should be accurate in the presence of RNA, salts, solvents, proteins, and free nucleotides

Image at <http://vitechltd.vn/en/qubit-4-fluorometer-with-wifi.html>

# Measuring quality with Nanodrop

- Quantifies 1  $\mu$ l DNA per sample
- Also measures concentration (but always refer to qubit for concentration over [nanodrop](#))
- ONT recommends that sample DNA has a 260/280  $\sim$  1.80 and a 260/230  $\sim$  2.0-2.2.
- A 260/280 which is higher than  $\sim$ 1.8 indicates the presence of RNA.
- A 260/280 which is lower than  $\sim$ 1.8 can indicate the presence of protein or phenol.
- A 260/230 significantly lower than 2.0-2.2 indicates the presence of contaminants, and the DNA may need additional purification.

Image at  
<https://www.fishersci.com/shop/products/nanodrop-one-spectrophotometer-wifi-qubit-4-fluorometer/13400525>

# Measuring fragment length

- Nanopore sequencing devices generate reads that reflect the lengths of the fragments loaded into the flow cell.
- To have control over the size of the fragments generated in the library prep, it is important to begin with high molecular weight (HMW) DNA.
- The shearing of HMW DNA can be minimised by:
  - Using wide-bore pipette tips to handle the gDNA
  - Mixing gently but thoroughly by flicking the tube, as opposed to vortexing or pipetting
  - Avoiding unnecessary freeze-thaw cycles
  - Avoiding pH <6 and >9
  - Avoiding high temperatures, which can lead to degradation
- Conventional agarose gels cannot resolve DNA fragments greater than 15–20 kb, but the molecular weight of starting material can be measured by [pulsed-field gel analysis](#).



# Assessing fragmentation

- The quality of the fragmented material may be assessed by different methods e.g. [Agilent Bioanalyzer](#).
- Quantifies 1 µl DNA per sample – up to 12,000bp
- Takes 30 minutes, 12 samples at a time

Image at

[https://community.nanoporetech.com/docs/prepare/library\\_prep\\_protocols/input-dna-rna-qc/v/idi\\_s1006\\_v1\\_revb\\_18apr2016/assessing-input-dna](https://community.nanoporetech.com/docs/prepare/library_prep_protocols/input-dna-rna-qc/v/idi_s1006_v1_revb_18apr2016/assessing-input-dna)

Thanks for listening!

**Any Questions?** 😊

[EURGen-RefLabCap@food.dtu.dk](mailto:EURGen-RefLabCap@food.dtu.dk)

**Thank you on behalf of the  
EURGen-RefLabCap team**