

<b>ERIBA</b>	<b>Checklist for sequencing libraries</b>	SOP nr. ERIBA F009
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Effective date: July 2021	Author: Jennefer Beenen Revision: Diana Spierings	<b>Version 2.1</b>

<b>Date of sequencing run</b>	<input type="checkbox"/> to be determined
<b>Name of pool</b>	
<b>Researcher</b>	
<b>Principal Investigator</b>	
<b>Contact information about QC and pool</b>	Phone: _____ e-mail: _____
<b>Contact information for results</b>	Phone: _____ e-mail: _____
<i>(optional)</i> <b>Project tracking code</b>	

#### Pools Molarity

\_\_\_\_\_ nM  Unknown, will be determined by Sequencing Facility

#### Is quality control of the library pool by the Sequencing Facility required?

Yes  No

#### Molarity to load to flow cell of sequencer

\_\_\_\_\_ pM

#### Percentage to load of control library (PhiX)

\_\_\_\_\_ % of total Molarity

#### NextSeq reagent kit size, (total cycles available per kit)

*Note: A 75 bp kit contains reagents for 92 cycles in total, i.e. the following run length can be used: Read1 74 bp, Index1 9 bp, Index2 9 bp.*

75 bp, (total 92 cycles)  150 bp, (total 166 cycles)  300 bp, (total 316 cycles)

#### Output type

High Output  Mid Output


#### Read type

Single Read  Paired End

#### Run lengths

**IMPORTANT:** Add 1 bp to your indexed read length. Sometimes the sequencer can lag one cycle. (example: index is 8bp, fill in 9bp.)

Read 1	Read 2	Index 1 (i7)	Index 2 (i5)
_____ bp <input type="checkbox"/> N/A	_____ bp <input type="checkbox"/> N/A	_____ bp <input type="checkbox"/> N/A	_____ bp <input type="checkbox"/> N/A

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**Custom recipe**
 Yes     No

If yes, please select name of the recipe:

 LEXOGEN\_NextSeqHighv2-12DK     ERIBA\_NextSeqHighv2-3dk

**Custom primer**
 Yes     No

If yes, please write down the name, applicable sequencing phase, and molarity (preferably 100 µM) of the primer:

Name: \_\_\_\_\_ Molarity: \_\_\_\_\_

**Follow run by BaseSpace?**
 Yes     No

If yes, please enter e-mail address:

\_\_\_\_\_

**Post-run services by the Sequencing Facility**
 Yes     No

If yes, please select what is applicable for this run:

 Demultiplexing.

 Aligning to genome of organism in pool: \_\_\_\_\_

**Please provide us the following by mail (required):**

- This form signed.
- If demultiplexing was checked: Sample names and their corresponding indexes as read during sequencing.
- Regarding the QC files:  
Project tracking information of QC analyses of individual samples and pool.  
Results and calculations of the superpool.

**Sample discarding policy (required)**

Submitted pool with a successful run will be discarded after 6 months. You are responsible for retrieving your pool after sequencing within 6 months if you wish to keep the pool.

 By checking this box, you declare that you have read the 'Sample discarding policy'.

**Sign for acceptance by ordering party:**