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Instructions For Use

Cystic Fibrosis Transmembrane Conductance Regulator Gene (*CFTR*) Library Prep Kit for Illumina[®]

NGS Library Prep by Reverse Complement PCR

Version:2REF:IFU-CFTRRevision Date:2022-10-05

Description of the symbols used on the labels

Symbol	Description		
	Manufacturer		
\sum	Use-by date		
LOT	Lot number		
REF	Reference number		
	Upper limit of temperature for storage		
	Temperature limit for storage		
Ĩ	Consult the instructions for use		
Σ	Contains sufficient for < <i>n</i> > tests		
CE	CE-mark		
IVD	In vitro diagnostic medical device		
2X	The box contains 2 index plates		
	Matrix code containing the reference number, lot number and use-by date		





Product and Company Information

Product name: REF: Product use:	Cystic Fibrosis Transmembrane Conductance Regulator Gene (<i>CFTR</i>) Library Prep Kit for Illumina [*] RC-CFTR096-I For <i>In Vitro</i> Diagnostic use
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Product Use

The intended purpose of this assay is NGS library preparation for Illumina[®] sequencing of the human CFTR gene coding exons, including a minimum of 20 bases upstream and downstream of each exon; to aid in the diagnosis of (the congenital predisposition to) cystic fibrosis by detecting sequence variants. This assay also includes 2 intronic hotspot mutations.

The assay is designed for use with DNA extracted from peripheral blood. Specimens should have an absorbance ratio (260/280) of ~1.8, regardless of the extraction method used.

The assay provides reagents for Multiplex Amplicon-based NGS library preparation and is for professional use only.

The kit is based on the patented Reverse Complement PCR technology, providing a safe, robust and simple workflow, combining multiplex amplification in a single reaction, decreasing the risk of PCR contamination and sample swapping.

Kit Content: RC-CFTR096-I (-20 °C storage)

Description	Content
RC-PCR Probe Panel A (REF: PM-CFTR-A)	Tube 24 μL
RC-PCR Probe Panel B (REF: PM-CFTR-B)	Tube 24 μL
2x Master Mix (Hot Start HiFi) (REF: MMHS096)	2 Tubes 1.15 mL
Probe Dilution Buffer (REF: RC-PDB)	Tube 500 μL

To be ordered separately: IDX096-U01D-I or IDX096-U02D-I (max 25 °C storage)

Description	Content
IDX* Primer Plates, dehydrated, coloured, 96 Unique Dual, 10 bp Indexes for Illumina [®]	2x 96-well plate, with Alphanumeric Coding
Caps	2x 12 Domed 8-Cap Strips

*IDX plates are semi-skirted, ABI style PCR Plates, breakable per 8 tubes, containing dehydrated and stabilized Unique Dual Index primer pairs in each well and a red tracking dye, ready to use.

The reagents do not contain any tissues or substances from human or animal origin.





Needed, but not included

Description	Vendor	
Adjustable Pipette Set (P2, P10, P20, P100, P200, P1000)	Multiple Vendors	
TapeStation, Bioanalyzer System, or equivalent, incl. consumables, or optional: agarose gel system	Agilent \degree or other	
Ethanol absolute, mol. biol. grade	Multiple Vendors	
AMPureXP [™] Bead Solution (or similar)	Beckman Coulter	
General plasticware, DNAse free (1.5 mL tubes, pipette tips w/filter)	Multiple Vendors	
Ice or tabletop cooling block	Multiple Vendors	
Mini Spinner for 1.5 mL tubes and 8-well PCR strips	Multiple Vendors	
Magnetic Stand for 1.5 mL Eppendorf tubes	Multiple Vendors	
PCR Grade Water	Multiple Vendors	
Qubit™ Fluorometer including High Sensitivity consumables	Thermo Fisher	
Thermocycler with heated lid (0.2 mL standard PCR tubes) compatible with semi-skirted ABI style PCR plates and option for ramp rate programming of 0.1 °C/sec (or 2% of max).	Multiple Vendors	
The next five items are only necessary when sequencing in-house (not needed in case of sending samples to a core facility)		
NaOH solution (2 N)	Multiple Vendors	
Tris/HCl (200 mM), pH 7	Multiple Vendors	
Low TE (10 mM Tris-HCl (pH 8.0), 0.1 mM EDTA)	Multiple Vendors	
Illumina [®] NGS Sequencing instrument	Illumina [®]	
Illumina [®] Sequencing Reagent kit (300 (2x151) bp run)	Illumina [®]	



Procedure

General precaution

Use a Pre-PCR environment for setting up the RC-PCR. Pooling, cleaning and library preparation should be performed in a Post-PCR environment.

1. Thermocycling program

Тетр	Duration	Ramping rate (from previous step)	Cycles
98 °C	2 minutes	N/A	1 x
98 °C	10 seconds	Max	
58 °C	10 minutes	0.1 °C/sec (or 2% of max)	1 x
72 °C	1 minute	Max	
95 °C	10 seconds	Max	
80 °C	1 second	Max	2 x
58 °C	90 <u>minutes</u>	0.1 °C/sec (or 2% of max)	2 X
72 °C	30 seconds	Max	
95 °C	10 seconds	Max	
80 °C	1 second	Max	34 x
58 °C	2 minutes	0.5 °C/sec (or 10% of max)	54 X
72 °C	30 seconds	Max	

Heated lid at 105 °C.

Double Check: Depending on the instrument, this protocol takes 6-7 hours to complete.



2. Reverse Complement PCR

The target specific RC-probes will be transformed into the functional, tailed and indexed PCR primers, followed by multiplex DNA amplification of the target regions.

2.1 Thaw on ice:

- RC-PCR Probe Panel A (Black cap)
- RC-PCR Probe Panel B (Red cap)
- Probe Dilution Buffer (Blue cap)
- 2x HiFi Master Mix (White cap)

Note: The Master Mix contains isostabilizers and may not freeze completely, even when stored at -15 °C to -25 °C. The Master Mix may contain precipitates when thawed at +2 °C to +8 °C. Always ensure that the Master Mix is fully thawed and thoroughly mixed before use.

2.2. Take two identical IDX PCR plates and cut off the number of strips needed. Mark the plates with 'A' and 'B'.

Note: Register the indexes used (IDX set/strip-column number and well position for each sample).

Note: For each sample, two PCR reactions are needed (Panel A and Panel B). Always use the same well position for the same sample, in order to generate identical indexes for each sample in both panels.

Note: Make sure to use the strips or plates in the right orientation.

- 2.3. Prepare in a fresh 1.5 mL Eppendorf tube the Probe-Polymerase premix panel A, by combining and mixing:
 - 0.2 μL RC-PCR Probe Panel A per reaction (Black cap)
 - 1.8 μL Probe Dilution Buffer per reaction (Blue cap)
 - 4 μL Molecular Grade Water
 - 10 μL Master Mix per reaction (White cap)
- 2.4. Prepare in a fresh 1.5 mL Eppendorf tube the Probe-Polymerase premix panel B, by combining and mixing:
 - 0.2 μL RC-PCR Probe Panel B per reaction (Red cap)
 - 1.8 μL Probe Dilution Buffer per reaction (Blue cap)
 - 4 μL Molecular Grade Water
 - 10 μL Master Mix per reaction (White cap)

Example: 24 samples + 10% extra volume*

- Probe-Polymerase premix:
 - 5.28 μL RC-PCR Probe Panel
 - 47.52 μL Probe Dilution Buffer
 - 105.6 μL Molecular Grade Water
 - 264 µL Master Mix

* It is recommended to allow for a 10% excess when preparing the Probe-Polymerase premix to correct for any pipetting loss. The kit contains extra reagent for this.



- 2.5. Add to each tube of plate A: 16 µL of Probe-Polymerase premix Panel A (from 2.3).
- 2.6. Add to each tube of plate B: 16 µL of Probe-Polymerase premix Panel B (from 2.4).
- 2.7. Add to each well 4 μL of DNA (5 ng/ μL).
- 2.8. Close the tube strips carefully with caps and mix by flicking. Check for a homogeneous pink coloured reaction mix and then spin shortly.
- 2.9. Start the RC-PCR program in the thermal cycler(s) and place the samples in the cycler when the block is between 60 °C and 98 °C. Then close the lid.



Safe stopping point after RC-PCR



3. Pool, Purify and Sequence

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After the PCR, the samples have been amplified and tagged with sample specific indexes and sequencing tails. From this point, PCR products can be pooled together in a single tube, purified by a bead purification to remove primers, primer-dimers and salt.

Note: Before pooling, optionally check 3 µL of the unpurified PCR products on agarose (2%).

- 3.1. Bring the AMPureXP[™] beads solution to Room Temperature.
- 3.2. Perform steps 3.3 to 3.7 for both Panel A and Panel B individually.
- 3.3. Combine 5 μ L RC-PCR products from all the reaction wells from Panel A/B (except negative controls) in a 1.5 mL Eppendorf tube.
- 3.4. Mix well and transfer 40 μL of the pool to a new 1.5 mL Eppendorf tube.
- 3.5. Add 60 μ L Low TE buffer or molecular grade water to the tube (total volume is now 100 μ L).
- 3.6. Beads purification:
 - **a.** Vortex the beads thoroughly to resuspend.
 - **b.** Add 100 μ L beads solution to the 100 μ L pool (from step 3.5) and mix well immediately by pipetting up and down 5 times.
 - **c.** Incubate for 5 minutes, off magnet.
 - **d.** Place the tube on magnet for 3 minutes or for the solution to be fully cleared.
 - e. Remove and discard all liquid carefully without disturbing the beads.
 - f. Add 200 µL (freshly prepared) 75% ethanol, without disturbing the beads.
 - **g.** Wait for 1 minute.
 - h. Repeat steps e., f. and g. for a second ethanol wash step.
 - i. Carefully remove all liquid <u>without leaving traces of ethanol.</u> (Optionally a quick spin can be performed, then place the tube back on magnet and remove excess ethanol)
 - j. Dry with open cap for 2-3 minutes at Room Temperature. **Do not over-dry.**
- 3.7. Elution:
 - **a.** On Magnet: Add 100 μL Low TE buffer to the tube.
 - **b.** Off Magnet: Re-suspend the beads by flicking or short vortexing.
 - c. Incubate for 2 minutes, off magnet.
 - **d.** Put the tube on magnet and wait for 1-3 minutes or for the solution to be fully cleared.
 - e. Carefully bring 90 μL of the clear solution to a new 1.5 mL Eppendorf tube, making sure not to transfer any of the beads.





2x Ethanol wash

The libraries are now ready for quantification and qualification.

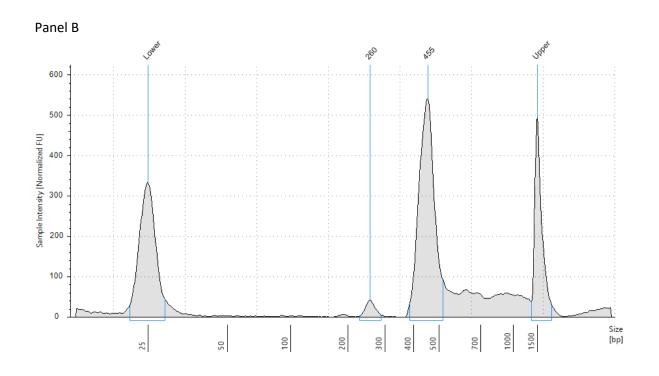
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- 3.8. Determine the final concentration of the libraries by a double Qubit (HS) measurement according to manufacturer's manual.
- 3.9. Verify the libraries on TapeStation or Bioanalyzer, according to the manufacturer's protocol. If needed, dilute the panels. Example: For TapeStation High Sensitivity kit, dilute to $\sim 2 \text{ ng/}\mu L$.

Panel A 23 1000 800 Sample Intensity [Normalized FU] 600 400 200 0 Size 1000 1500 100 200 300 500 400 700 [bp] 50 25

Example of clean libraries on TapeStation:





3.10. Perform sequencing on an Illumina[®] NGS platform, according to the manufacturer's manual.

- a. Read at a minimum of 151-8-8-151.
- The Bed. File is available at: https://nimagen.com/gfx/Human_Genetics/CFTR_customers.txt
- **c.** Using a read depth of 32 000 per sample will, on average, result in a minimum read depth of 100 reads per amplicon.

Note: For technical assistance contact our technical support at techsupport@nimagen.com.

Apply local regulations regarding waste disposal.





Legal Notices: RC-PCR is patent protected (PCT/GB2016/050558, WO2016146968A1) and exclusively licensed to NimaGen B.V. Nijmegen Qubit is a trademark of Thermo Fisher Scientific Inc. AMPureXP is a trademark of Beckman Coulter

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