

ProtoScript® First Strand cDNA Synthesis Kit

NEB #E6300S/L

30/150 reactions

Version 3.0_1/20

Table of Contents

Quality Controls	2
First Strand cDNA Synthesis Protocols	2
General Information for Successful cDNA Synthesis.....	3
Troubleshooting Guide	4
References	4
Appendix	4
Ordering Information.....	5
Revision History	5

Kit Components:

All kit components can be stored for one year at -20°C except where noted.

M-MuLV Enzyme Mix (10X)

M-MuLV Reaction Mix (2X)

Oligo d(T)₂₃ VN* (50 μM)**

Random Primer Mix (60 μM)**

Nuclease-free H₂O

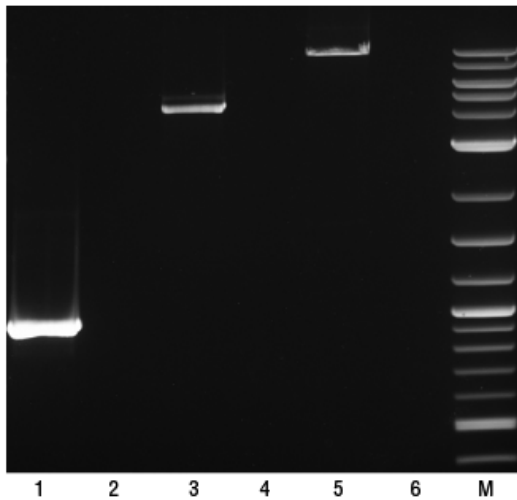
*V = A, G or C; N = A, G, C or T

**Contains 1 mM dNTP

Introduction

ProtoScript First Strand cDNA Synthesis Kit features two optimized mixes, M-MuLV Enzyme Mix and M-MuLV Reaction Mix. M-MuLV Enzyme Mix combines M-MuLV Reverse Transcriptase and murine RNase Inhibitor, while M-MuLV Reaction Mix contains dNTPs and an optimized buffer. The kit also contains two optimized primers for reverse transcription and nuclease-free water. An anchored oligo-dT primer [d(T)₂₃VN] forces the primer to anneal to the beginning of the polyA tail. The optimized Random Primer Mix provides random and consistent priming sites covering the entire RNA template including both mRNAs and non-polyadenylated RNAs. The first strand cDNA product generated is more than 10 kb (Figure 1).

Figure 1:



First strand cDNA synthesis was carried out with 1X M-MuLV Enzyme Mix at 42°C using 2 µg of human spleen total RNA. Negative control reactions were carried out with 1X M-MuLV Reaction Mix. A fraction of the first strand cDNA product was used to amplify sequences specific for three different messenger RNAs using 1X LongAmp Taq 2X Master Mix (NEB #M0287). Lane 1: 1.1 kb of beta-actin gene. Lane 2: noRT control of 1.1 kb of beta-actin gene. Lane 3: 4.7 kb of Xrn-1 gene. Lane 4: noRT control of 4.7 kb of Xrn-1 gene. Lane 5: 9.8 kb of guanine nucleotide exchange factor p532. Lane 6: noRT control of 9.8 kb of guanine nucleotide exchange factor p532. Marker M is 2-Log DNA Ladder (NEB #N3200).

Quality Controls

The performance of ProtoScript First Strand cDNA Synthesis Kit is tested in an RT reaction using human Jurkat total RNA with primer d(T)₂₃VN. The sensitivity of the kit is verified by the detection of GAPDH transcript in 20 pg total RNA after 35 cycles. The length of cDNA achieved is verified by the detection of a 5.5 kb amplicon of the p532 gene.

First Strand cDNA Synthesis Protocols

Thaw system components and put on ice. A control reaction without reverse transcriptase is recommended to examine the DNA contamination in the samples.

1. Mix RNA sample and primer d(T)₂₃VN in two sterile RNase-free microfuge tubes.

COMPONENT	VOLUME
Total RNA	1–6 µl
d(T) ₂₃ VN (50 µM)	2 µl
Nuclease-free H ₂ O	variable
Total Volume	8 µl

2. Denature RNA for 5 minutes at 70°C. Spin briefly and put promptly on ice. This step is optional. However, it improves the cDNA yield for long messenger RNAs and GC-rich RNA regions.
3. Add the following components to one tube.

M-MuLV Reaction Mix	10 µl
M-MuLV Enzyme Mix	2 µl

To the negative control tube, add the following:

M-MuLV Reaction Mix	10 µl
H ₂ O	2 µl

4. Incubate the 20 µl cDNA synthesis reaction at 42°C for one hour. **If Random Primer Mix is used, an incubation step at 25°C for 5 min is recommended before the 42°C incubation.**
5. Inactivate the enzyme at 80°C for 5 minutes. Dilute reaction to 50 µl with 30 µl H₂O for PCR. The cDNA product should be stored at –20°C. For downstream PCR amplification, the volume of cDNA product should not exceed 1/10 of the PCR reaction volume.

General Information for Successful cDNA Synthesis

Template RNA

- Intact RNA of high purity is essential for sensitive RT-PCR detection. RNA should have a minimum A_{260}/A_{280} ratio of 1.7 or higher.
- Either total RNA or mRNA can be used in the reverse transcription reaction. Total RNA is generally sufficient for most RT-PCR analyses. However, if desired mRNA can be easily obtained using a PolyA Spin mRNA Isolation Kit (NEB #S1560) or Magnetic mRNA Isolation Kit (NEB #S1550).
- The amount of RNA required for detection depends on the abundance of the transcript of interest. In general 1 ng to 1 μ g total RNA or 0.050–100 ng mRNA are recommended.

First Strand cDNA Synthesis Reaction:

- Denaturation of RNA and primer at 70°C for 5 minutes can remove secondary structures that may impede long cDNA synthesis. However, this step can be omitted in some cases (unpublished results).
- We recommend incubation at 42°C for one hour for maximum yield and length. However, many targets can be detected after a much shorter incubation time. For example, 5 minutes incubation is enough for a 2 kb cDNA synthesis.

Choice of Primers for Reverse Transcription:

- Oligo d(T) priming is preferred for most applications because it ensures that all cDNA copies terminate at the 3' end of the mRNA and produces the longest contiguous cDNA. An anchored oligo-d(T) primer [d(T)₂₃VN] forces the primer to anneal to the start of the polyA tail, thereby preventing priming at internal sites in the polyA tail (1). However, two other priming choices are possible if desired.
- The Random Primer Mix is an optimized mix of hexamer and d(T)₂₃VN primers. It provides random priming sites covering the entire RNA templates including both mRNAs and non-polyadenylated RNAs (such as ribosomal RNAs). The Random Primer Mix yields shorter cDNAs on average and can be used for the detection of multiple short RT-PCR products. Random Primer Mix offers good performance in a wide range of RNA templates.
- When a gene-specific primer is used in a cDNA synthesis reaction, the cDNA product can be used only for amplification of that transcript. This priming method gives good results when the amount of RNA is limiting (below 10 ng) and only one particular cDNA is desired.

Recommended primer concentration:

PRIMER	OLIGO d(T) ₂₃ VN	RANDOM PRIMER MIX	SPECIFIC PRIMER
Final concentration	5 μ M	6 μ M	0.1–1 μ M

Troubleshooting Guide

PROBLEM	SOLUTION(S)
Low yield of cDNA	<ul style="list-style-type: none">• Check the integrity of the RNA by denaturing agarose gel electrophoresis (2)• RNA should have a minimum A_{260}/A_{280} ratio of 1.7 or higher. Ethanol precipitation followed by a 70% ethanol wash can remove most contaminants such as EDTA and guanidinium. Precipitation with lithium chloride can remove polysaccharides (2).
	<ul style="list-style-type: none">• Phenol/chloroform extraction and ethanol extraction can remove contaminant proteins such as proteases (2)
	<ul style="list-style-type: none">• Some target RNA may contain strong pauses for RT; Use random priming instead of $d(T)_{23}VN$
	<ul style="list-style-type: none">• Use sufficient amount of RNA

References

1. Liao, J. and Gong, Z. (1997) *Biotechniques* 23, 368-370.
2. Sambrook, J. and Russel, D.W. (2001). *Molecular Cloning: A Laboratory Manual*, (3rd ed.), (pp. 8.46–8.53 and 11.37–11.42). Cold Spring Harbor: Cold Spring Harbor Laboratory Press.

Appendix

Supplied Components:

1X M-MuLV Enzyme Mix:

- 0.5 units/ μ l M-MuLV Reverse Transcriptase
- 1.0 unit/ μ l Murine RNase Inhibitor

1X M-MuLV Reaction Mix:

- 50 mM Tris-Acetate (pH 8.3)
- 75 mM KOAc
- 3.1 mM $Mg(OAc)_2$
- 0.5 mM dNTPs each

Ordering Information

NEB #	PRODUCT	SIZE
E6300S/L	ProtoScript First Strand cDNA Synthesis Kit	30/150 reactions

COMPANION PRODUCTS

NEB #	PRODUCT	SIZE
S1560S	polyA Spin mRNA Isolation Kit	100/500 units
S1550S	Magnetic mRNA Isolation Kit	1,600/8,000/8,000 units
S1419S	Oligo d(T) ₂₃ Magnetic Beads	25 mg
E6400S	ProtoScript <i>Taq</i> RT-PCR Kit	30 reactions
M0314S/L	Murine RNase Inhibitor	3,000/15,000 units
S1330S	Random Primer Mix	1.0 A ₂₆₀ units
M0287S/L	LongAmp <i>Taq</i> 2X Master Mix	100/500 reactions
M0270S/L	<i>Taq</i> 2X Master Mix	100/500 reactions

Revision History

REVISION #	DESCRIPTION	DATE
1.0		
2.0		2/13
2.1		11/14
2.2		11/16
2.3		12/17
3.0	Update to new manual format	1/20

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New England Biolabs, Inc., 240 County Road, Ipswich, MA 01938-2723 Telephone: (978) 927-5054 Toll Free: (USA Orders) 1-800-632-5227 (USA Tech) 1-800-632-7799 Fax: (978) 921-1350 e-mail: info@neb.com