CELLSCRIPT™
RNA for Translation in Cells

EZ-QC™ mRNA Cap 1 Efficiency Assay Kit

Cat. No. **ONE240910**

INTRODUCTION

The EZ-QC™ mRNA Cap 1 Efficiency Assay Kit allows one to quantitate the percentage of Cap 1 vs Cap 0 5'-cap structures in their mRNA production product. The 5' RNA cap consists of an N7-methylated guanine nucleoside joined to the RNA via a 5' to 5' triphosphate linkage. This reaction is catalyzed by mRNA Capping Enzyme (e.g., ScriptCap™ Capping Enzyme) and produces a Cap 0 cap structure. Cap 0 caps can be converted into Cap 1 caps by the additional treatment of an mRNA 2'-O-Methyltransferase (e.g., ScriptCap 2'-O-Methyltransferase) which catalyzes the 2'-O-methylation of the ribose sugar of the first base of the RNA transcript (see below). Most Cap 1 mRNAs are expressed at higher levels in cells, relative to their Cap 0 counterparts since the Cap 1 helps to identify the mRNA as "self" RNA in cells and thus not elicit an innate immune response against the mRNA.[1,2]

Primary transcript (uncapped) IVT RNA lacks a cap structure.

(5') $pppN_1pN(pN)_x$-OH (3')

Capped RNAs (Cap 0 and Cap 1) contain an additional N7-methylated guanosine linked by a 5' to 5' triphosphate bridge to the 5'-end of the IVT RNA.

$\mathbf{m^7G(5')ppp}(5')N_1pN(pN)_x$-OH (3')

Where m^7G represents the 7-methylguanosine cap nucleoside, ppp represents the triphosphate bridge between the 5' carbons of the cap nucleoside and the first nucleotide of the primary RNA transcript, and $N_1pN(pN)_x$-OH (3') represents the primary RNA transcript, of which N_1 is the most 5' nucleotide. In Cap 1 RNA, this nucleotide contains a 2'-O-methyl group on the ribose moiety.

$m^7G(5')ppp(5')\mathbf{m^{2'\text{-}O}N_1}pN(pN)_x$-OH (3')

The EZ-QC mRNA Cap 1 Efficiency Assay Kit reaction labels the mRNA 5'-caps with Cyanine5 Hydrazide (Cy5™). The mRNA 5'-uncapped ends are not labeled. The labeled mRNA is then hydrolyzed with an RNase mixture releasing Cy5-labelled Cap 1 and Cap 0 cap cores which are resolved using polyacrylamide gel electrophoresis and analyzed using a fluorescent gel imager to measure the relative amounts of Cap 1 to Cap 0 present in the sample, thus allowing one to forego tedious and expensive capping efficiency determination methods such as HPLC and mass spectrometry (see example schematic on page 2).

Note: cap structures containing a 3'-O-methyl group on the capping G nucleotide, such as Anti-Reverse Cap Analog (ARCA) and some GpppAG cap analogs, cannot be labeled using the EZ-QC mRNA Cap 1 Efficiency Assay chemistry and thus cannot be assayed with this kit.

For determination of total percent capped RNA content, CELLSCRIPT also offers the EZ-QC XBG mRNA Capping Efficiency Assay Kit (for mRNA containing a Xenopus β-globin [XBG] 5' UTR) and the EZ-QC mRNA Capping Efficiency Assay Kit (for mRNA any known 5' UTR sequence) as well as the EZ-QC mRNA Poly(A) Tail Length Assay Kits for complete mRNA characterization.

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Example Schematic

Cap 0 mRNA

$m^7G(5')ppp(5')N_1pN(pN)_x$-OH (3')

↓

Cy5-Labelled Cap 0 mRNA

Cy5•$m^7G(5')ppp(5')N_1pN(pN)_x$-OH (3')

↓

RNase Treatment of Cy5-Labelled Cap 0 mRNA

Cy5•$m^7G(5')ppp(5')N_1p$ + Np + Np + ...

Cap 1 mRNA

$m^7G(5')ppp(5')m^{2'-O}N_1pN(pN)_x$-OH (3')

↓

Cy5-Labelled Cap 1 mRNA

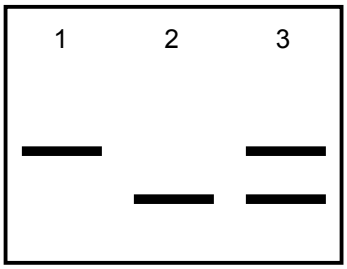
Cy5•$m^7G(5')ppp(5')m^{2'-O}N_1pN(pN)_x$-OH (3')

↓

RNase Treatment of Cy5-Labelled Cap 1 mRNA

Cy5•$m^7G(5')ppp(5')m^{2'-O}N_1pNp$ + Np + Np + ...

PAGE Analysis



1) Released Cap 0 cap core: **Cy5**•$m^7G(5')ppp(5')N_1p$ Dinucleotide molecule

2) Released Cap 1 cap core: **Cy5**•$m^7G(5')ppp(5')m^{2'-O}N_1pNp$ Trinucleotide molecule

3) Mixed sample of Cap 0 & Cap 1 cap cores

MATERIALS

Materials Supplied

Important **Upon receipt of the kit, remove the reagents and store at the indicated temperatures.**

EZ-QC™ mRNA Cap 1 Efficiency Assay Kit Contents (10 reactions) Sufficient for 10 experimental and 10 control reactions.		
Kit Component	Reagent Volume	Storage Temperature
1 M Sodium Acetate	20 µl	Ambient
4 mM Sodium Sulfite	20 µl	Ambient
10 mM Sodium Periodate	40 µl	4°C
80/20 Cap 1 Control Mix Contains a mix of 80% Cap 1 and 20% Cap 0 mRNAs	60 µl	–20°C
5 mM Cyanine5 Hydrazide in DMF	20 µl	–20°C
EZ-QC™ RNase T1 in 50% glycerol and 50 mM Tris-HCl, pH 7.4	20 µl	–20°C
EZ-QC™ RNase I in 50% glycerol, 50 mM Tris-HCl, pH 7.5, 100 mM NaCl and 0.1 mM EDTA	24 µl	–20°C
Cap 1 Stop/Loading Dye 95% formamide, 0.4 mM EDTA and 40 µg/ml Basic Fuchsin	350 µl	–20°C
RNase-Free Water	875 µl	–20°C

For more information, consult the appropriate safety data sheet (SDS) at www.cellscript.com.

Materials Required, but not Supplied

- Purified capped mRNA. See Technical Appendix, section A, for specifications for mRNA <750-nt in length.
- Materials for polyacrylamide gel electrophoresis. See Technical Appendix, section B, for suggested gel and buffer recipes.
- RNAClean XP beads (Beckman Coulter) for mRNA clean-up.
  See the Technical Appendix, section A, for an alternative purification option.
- 70% ethanol
- 0.2-ml polypropylene thermocycler-compatible tubes with caps or 96-well 0.1-ml PCR plate with microseal plastic films. **Note:** Cy5 hydrazide is provided in DMF, which is incompatible with polystyrene-based consumable materials.
- Materials and equipment for polyacrylamide gel visualization, imaging and quantification capable of Cy5 emission detection. See the Technical Appendix, section C, for Syngene® G:Box-specific parameters.

SPECIFICATIONS

Unit Definitions

One standard reaction from the EZ-QC mRNA Cap 1 Efficiency Assay Kit treats 12-24 pmoles of capped RNA.

Functional Testing

The EZ-QC mRNA Cap 1 Efficiency Assay Kit is functionally tested by treatment of Cap 0 and Cap 1 control mRNAs, resolved on a 15% polyacrylamide (14.6% acrylamide, 0.4% Bis-acrylamide), TBE gel, and quantified using GeneTools software of the captured gel image using a Syngene G:Box.

Contaminating Activity Assays

All components of the EZ-QC mRNA Cap 1 Efficiency Assay Kit are free of detectable RNase and DNase activities except for the inherent activity of the EZ-QC RNase T1 and EZ-QC RNase I.

BEFORE YOU START: IMPORTANT TIPS

♦ **RNA Source**:

RNAs can be capped post-transcriptionally (enzymatically) using a Capping Enzyme and 2'-O-Methyltransferase (e.g., CELLSCRIPT's ScriptCap Cap 1 Capping System, mScript™ Standard mRNA Production System or INCOGNITO™ mScript N1meΨ- or Ψ-mRNA Production Systems) after mRNA production. **Note:** the EZ-QC mRNA Cap 1 Efficiency Assay Kit does not distinguish between capped and uncapped RNAs. For determination of total percent capped RNA content, CELLSCRIPT also offers the EZ-QC mRNA Capping Efficiency Assay Kit (distinguishes between total capped [Cap 0 + Cap 1] and uncapped RNAs) as well as the EZ-QC XBG mRNA Capping Efficiency Assay Kit (for mRNA containing a Xenopus β-globin [XBG] 5' UTR).

♦ **Maintaining an RNase-Free Environment (prevention of contamination of the stock mRNA sample)**:

Highly stable RNases are ubiquitous, including on human skin.

Creating an RNase-free work environment and maintaining RNase-free solutions is critical for successful work with RNA.

We strongly recommend to:

– Use RNase-free tubes and pipette tips.

– Always wear gloves when handling kit components or samples containing RNA and change gloves frequently, especially after touching potential sources of RNase contamination such as doorknobs, pens, pencils and human skin. Do not touch any kit component or tube containing RNA with an ungloved hand.

– Keep all kit components tightly sealed when not in use. Keep all tubes containing RNA tightly sealed during the incubation steps.

PROCEDURE

A. Reagent and Sample Preparation

1. Thaw and bring all reagents except the EZ-QC RNases, 80/20 Cap 1 Control Mix and mRNA to room temperature. Vortex mix and spin down prior to use. Store the EZ-QC RNases, 80/20 Cap 1 Control Mix and mRNA on ice prior to use.

2. **During all subsequent steps, care should be taken to protect samples from light during incubation steps and prior to gel loading.**

3. Dilute the 10 mM Sodium Periodate 1:10 in RNase-Free Water to 1 mM concentration (e.g., 1 µl of 10 mM Sodium Periodate + 9 µl of water). Make a fresh dilution of Sodium Periodate each time the assay is set up.

B. EZ-QC mRNA Cap 1 Efficiency Labeling Reaction

1. For each reaction, treat 12-24 pmoles in 6 µl of capped mRNA or 6 µl of 80/20 Cap 1 Control Mix in separate reactions by performing the following procedure:

   Per well in a 96-well plate, combine the following reagents at room temperature in the order indicated below:

EZ-QC mRNA Cap 1 Efficiency Labeling Reaction	
Component	Amount
RNase-Free Water	1 µl
1 M Sodium Acetate	1 µl
1 mM Sodium Periodate (diluted from 10 mM)	2 µl
12-24 pmoles * capped mRNA and in a separate reaction, 80/20 Cap 1 Control Mix Supplement the remaining reagent volume with RNase-Free Water	6 µl
Total Volume	10 µl

   * Estimating amount of input mRNA

   pmol/µg ssRNA = 10^6 / (estimated length of the RNA in nucleotides x 330)

   for example for a 1,700-nt RNA: 10^6 / (1,700 x 330) = 1.8 pmol/µg

2. Pipet to mix and briefly spin down. Incubate at room temperature for 30 minutes, protected from light.

3. Add 1 µl of 4 mM sodium sulfite to each well. Pipet to mix. Incubate at room temperature for 10 minutes, protected from light.

4. Add 1 µl of 5 mM Cy5 hydrazide to each well. Pipet gently to mix. Briefly centrifuge if necessary. Incubate at room temperature for 1 hr, protected from light.

   Caution: Cy5 hydrazide is supplied in solution in DMF, which is incompatible with polystyrene consumables.

C. EZ-QC mRNA Cap 1 Efficiency Cleanup Reaction

1. Perform cleanup of the labeled mRNA using RNAClean XP beads (Beckman Coulter). See Technical Appendix, section A, for an alternate cleanup method.
2. Allow beads to warm to room temperature.
3. Vortex the beads prior to use. Add 21.6 µl of RNAClean XP beads to the completed labeling reaction.
4. Pipet the samples up and down 15 times until thoroughly mixed. Let sit at room temperature for 5 minutes.
5. After the 5-minute incubation, place on magnetic plate for 5 minutes. Without disturbing the pellet, carefully aspirate the solution off the samples and discard it.
6. With samples still magnetized, dispense 150 µl of 70% ethanol into each well. Incubate at room temperature for 30 seconds. Carefully aspirate and discard the supernatant.
7. Repeat the ethanol wash step. With samples still magnetized, dispense 150 µl of 70% ethanol into each well. Aspirate and discard the supernatant. Carefully remove any residual ethanol using a 20 µl pipette.
8. Remove from the magnet. Air-dry the bead pellets at room temperature for 10 minutes.
9. Add 17 µl of RNase-Free Water to each well, and pipet the samples up and down ≥10 times being careful to thoroughly resuspend the beads.
10. Incubate at room temperature for 10 minutes then magnetize for 5 minutes at room temperature.
11. Transfer 15 µl of the eluate to a new well. Proceed to the RNase Treatment Reaction.

D. EZ-QC mRNA Cap 1 Efficiency RNase Treatment Reaction

1. Make a fresh dilution of RNase T1, 1:16 in RNase-Free Water (1 µl of RNase T1 + 15 µl of water).

   Per well in the 96-well plate, combine the following reagents:

EZ-QC mRNA Cap 1 Efficiency RNase Treatment Reaction	
Component	Amount
RNAClean XP bead eluate	15 µl
RNase T1 (1:16 dilution)	1 µl
RNase I	1.2 µl
Total Volume	17.2 µl

2. Pipet to mix each sample, seal the plate and incubate the reactions at 37°C for 1 hour in a thermo-cycler with a heated lid.

3. Upon reaction completion, add 17 µl of the Cap 1 Stop/Loading Dye to each well.
   Samples can be stored at –20°C for up to one week prior to polyacrylamide gel electrophoresis and remaining sample can be run a second time within the same one week time window.

4. While the reactions are incubating, prepare a 15% acrylamide/1X TBE gel.
   See Technical Appendix, section B, for gel and buffer recipes.
   Precast 15% Mini-PROTEAN® TBE-Urea Gel: Bio-Rad #4566053/4566055, may also be used.

   a) Blow out unpolymerized acrylamide from the wells immediately after comb removal.
   b) Pre-run the gel at 300 volts constant voltage for 20-30 minutes. **Not required for precast gel**.
   c) Blow out the wells just prior to sample loading.

5. Load 15 µl of each stopped reaction mix to the appropriate lanes for PAGE.
   Optional: The Basic Fuchsin dye in the Cap 1 Stop/Loading Buffer will not migrate into the gel. An alternative loading dye, which migrates into the gel, can be run in an empty adjacent well to aid in visualization of the electrophoresis progress allowing one to determine when to stop the gel by dye migration as opposed to by time alone. See Technical Appendix, section D, for migration information for alternative dyes Orange G, Bromophenol blue and Xylene cyanol.

6. Run the gel at 300 volts (constant voltage) for 30 minutes.
   a) The cap cores will run toward the bottom of the gel.
      Run the gel no longer than 30 minutes to prevent running the cap cores off of the gel.
      If using a **precast** 15% Mini-PROTEAN® gel, run the gel no longer than **25 minutes** to prevent running the cap cores off of the gel.
   b) The Basic Fuchsin dye in the Cap 1 Stop/Loading Buffer will diffuse out of the wells and will not enter the gel. See Technical Appendix, section D, for migration information for alternative dyes Orange G, Bromophenol blue and Xylene cyanol.

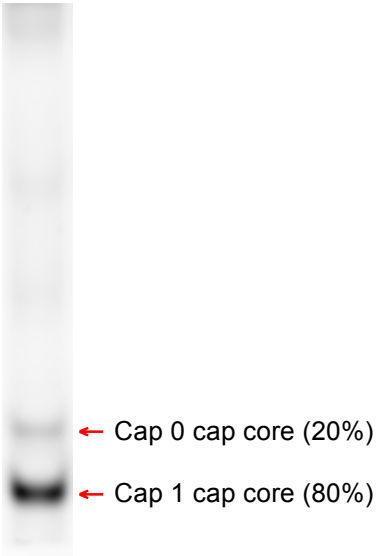
7. Visualize/image the gel under settings appropriate for Cyanine5 detection (typically at 705 nm emission). See Technical Appendix, section C, for Syngene G:Box-specific parameters. Quantitate relative band intensities % Cap 1 and % Cap 0 (system specific). The calculated relative band intensities of the 80/20 Cap 1 Control Mix (80% Cap 1 and 20% Cap 0) can be used to validate the accuracy of your system. Calculate the relative intensity of the Cap 1 and Cap 0 bands only. Do not include any backgrounds bands in the calculation, which may be visible on the gel image (see Example Data Figure 2).

Example Data:

Figure 1A, B

Due to charge differences on the released cap cores, the trinucleotide Cap 1 cap core migrates faster than the dinucleotide Cap 0 cap core. 1A) 15% acrylamide, 1X TBE gel. 1B) Densitometric data from the PAGE gel using a Syngene G:Box Gel Documentation System.

1A



1B

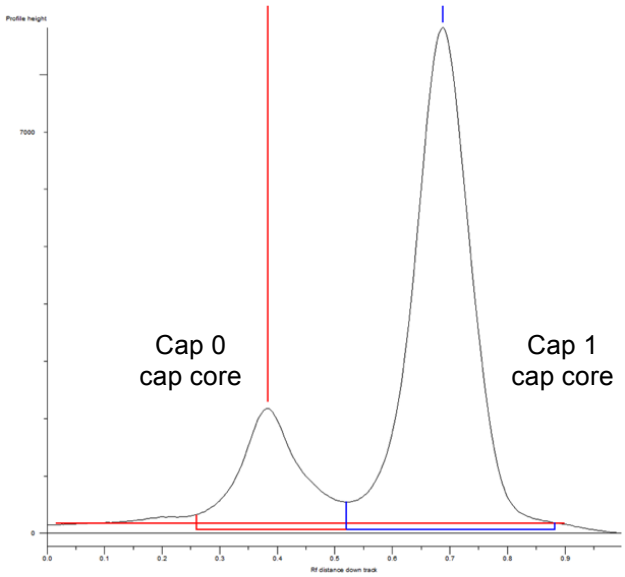
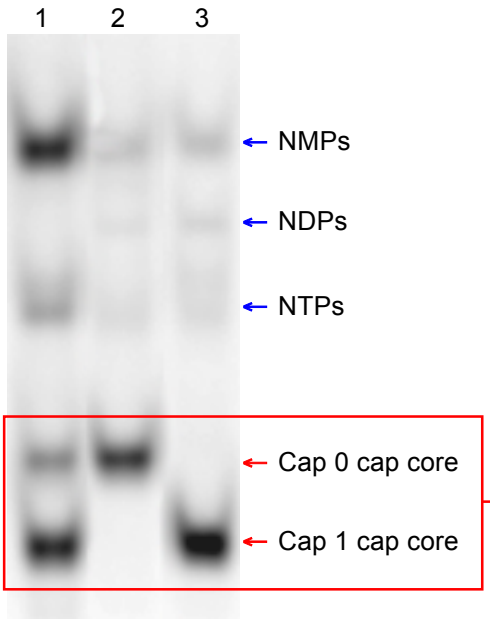


Figure 2

The EZ-QC mRNA Cap 1 Efficiency labeling reaction labels all nucleotides containing vicinal hydroxyl groups. This includes not only the N7me-guanine cap nucleotide which is part of the desired labeled cap core(s), but also the 3'-most base of the mRNA and any leftover nucleotides (from the IVT, capping or tailing reactions), which carried through in the labeled mRNA purification step. These will appear as irrelevant background bands. Calculate the relative intensity of the Cap 1 and Cap 0 bands only. Do not include any backgrounds bands in the calculation.



Only calculate using these bands.

15% acrylamide, 1X TBE gel

1) 70% Cap 1 + 30% Cap 0 mixture

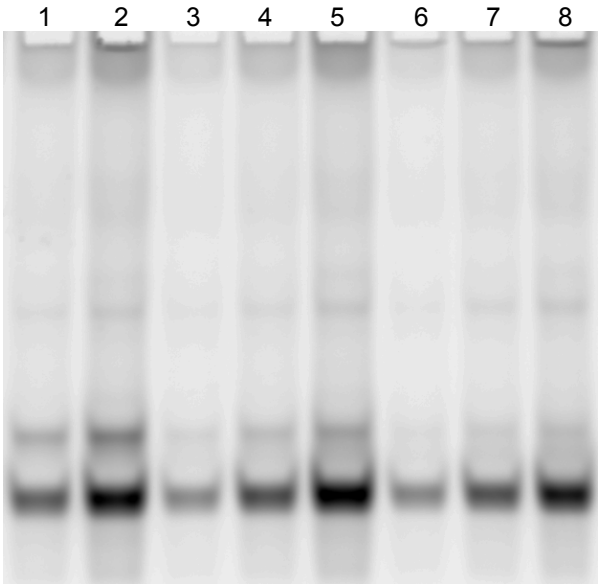
2) 100% Cap 0

3) 100% Cap 1

Figures 3A, B, C

The standard EZ-QC mRNA Cap 1 Efficiency Assay reaction uses 12-24 pmol of input mRNA. The intensity of the cap core bands will vary based on the amount of input mRNA used, however the gel imaging software (e.g., Syngene G:Box Gel Documentation System and GeneTools software) will still be able to quantitate the relative band intensities.

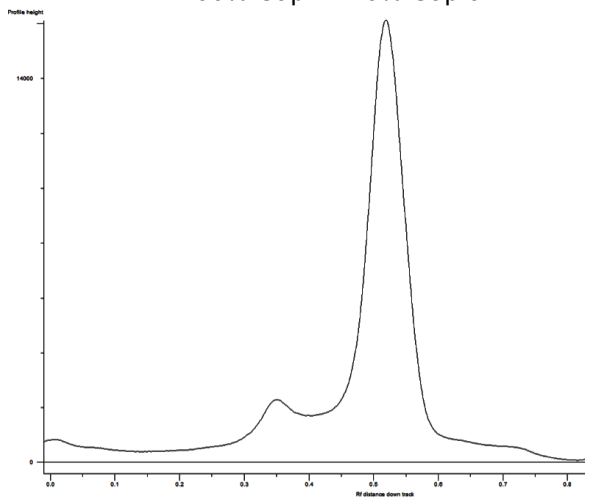
3A



Lane	Cap 1 Content	Cap 0 Content	input mRNA
1	80%	20%	12 pmol
2	80%	20%	24 pmol
3	90%	10%	6 pmol
4	90%	10%	12 pmol
5	90%	10%	24 pmol
6	95%	5%	6 pmol
7	95%	5%	12 pmol
8	95%	5%	24 pmol

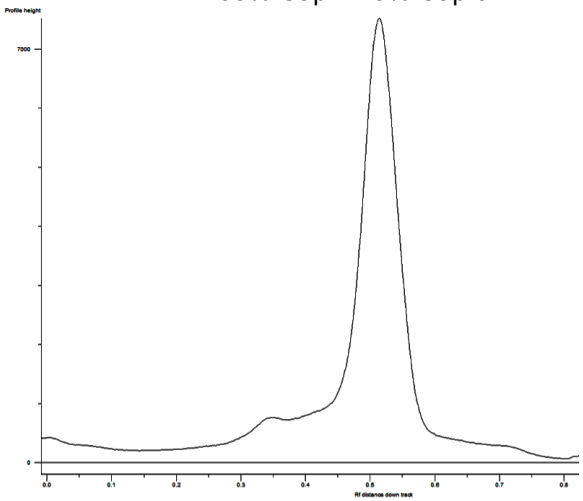
3B

Lane 5 Chromatogram
90% Cap 1 / 10% Cap 0



3C

Lane 7 Chromatogram
95% Cap 1 / 5% Cap 0



TECHNICAL APPENDIX

A. Alternate Purification Method of Labeled mRNA

Bead purification provides optimal purification and recovery of labeled mRNA allowing for the use of minimal amounts of input mRNA. However, if desired, standard non-bead, precipitation-based methods can be performed to purify the labeled mRNA. Standard inputs of 12-24 pmol per reaction may be used, but the precipitated pellet may be small, invisible to the eye, or appear as a smear. For mRNA shorter than 750-nt, input amounts of labeled mRNA >24 pmol may be necessary to obtain a visible precipitated pellet. The recovery efficiency of mRNAs shorter than 250-nt will be reduced with this method.

1) Transfer each labeled 12 µl reaction to a 0.5 ml tube.
2) To each reaction, add 1 volume (12 µl) of 5 M ammonium acetate.
3) Mix well and incubate on ice for 15 minutes.
4) Pellet the RNA by centrifugation at >10,000 x g for 15 minutes at 4°C.
5) Carefully remove the supernatant with a pipette and gently rinse the pellet with 150 µl of 70% ethanol.
6) Carefully remove the ethanol with a pipette without disturbing the mRNA pellet.
7) Air dry the mRNA pellet.
8) Resuspend the mRNA in 15 µl RNase-Free Water.
9) Proceed directly to the RNase Treatment Reaction (Step D).

B. Polyacrylamide Gel

Recommended polyacrylamide gel:
10 or 15-well, 1X TBE, 15% acrylamide (14.6% acrylamide, 0.4% Bis-acrylamide), 0.2 µm-filtered.

5X TBE: 450 mM Tris, 450 mM boric acid, 10 mM EDTA

C. Syngene G:Box Parameters

Excitation filter: Red LED Module (M) 627/41

Emission filter: filt705M 705/10

Integration Parameters

Baseline correction
- Method = Rolling disk
- Disc Radius (pixels) = 1000
- Offset = Yes

Peak Detection
- Minimum width = 7
- Minimum height = 3
- Minimum % Volume = 1
- All peaks same width = unchecked

Savitsky-Golay filter = 3

Invert bands such that bands appear black on a white background.

D. Alternate Gel Loading Dye Migration

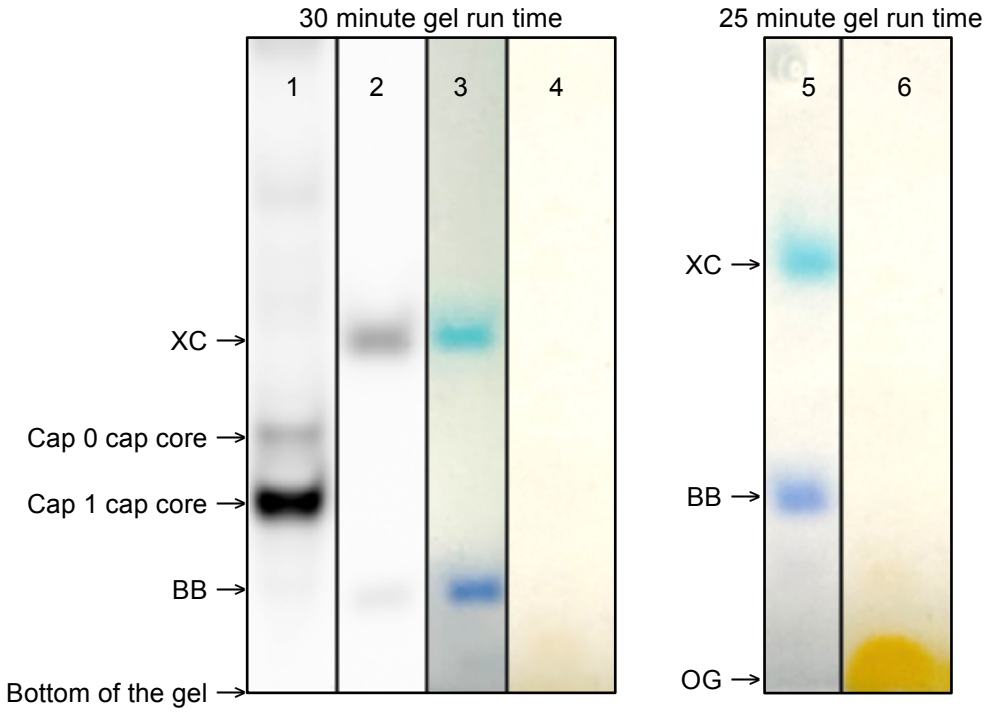
The standard EZ-QC mRNA Cap 1 Efficiency Assay 15% polyacrylamide gel run time is 30 minutes at 300 volts (constant voltage). Under these parameters, the Cap 1/Cap 0 bands of interest will migrate near the bottom third of the gel. Some loading dyes fluoresce in the Cy5 detection range and thus appear as background bands when imaging the gel. To prevent this, the Cap 1 Stop/Loading Dye contains basic fuchsin which serves for sample loading verification, but since it will not enter the gel, it can not be used to visualize the electrophoretic progress of the gel. Loading an alternative dye in an adjacent empty well on the gel can overcome this limitation.

Alternative dyes Orange G (**OG**), Bromophenol blue (**BB**) and Xylene cyanol (**XC**) have been characterized for this purpose.

Orange G: migrates faster than the Cap 1/Cap 0 bands of interest, Bromophenol blue and Xylene cyanol. It will run off of the gel in 30 minutes but be visible as it's running off the gel at 25 minutes of run time.

Bromophenol blue: migrates faster than the Cap 1/Cap 0 bands of interest and Xylene cyanol. It will remain on the gel at 30 minutes of run time (approximately 1 cm from the bottom of the gel). It will appear as a very faint background band in the Cy5 detection range.

Xylene cyanol: migrates slower than the Cap 1/Cap 0 bands of interest. It will appear as an easily visible background band in the Cy5 detection range.



Lane 1) Cap 1/Cap 0 bands of interest shown under Cy5 detection using Cap 1 Stop/Loading Dye.
Lane 2) Bromophenol blue and Xylene cyanol dyes-only shown under Cy5 detection.
Lanes 3 & 5) Bromophenol blue and Xylene cyanol dyes-only shown under visible light.
Lanes 4 & 6) Orange G dye-only shown under visible light.

TROUBLESHOOTING

Symptom	Solution
Experimental bands are not visible but the 80/20 Cap 1 Control Mix bands are	Insufficient amount of input mRNA was used. • If performing bead-based clean up, ensure that ≥12 pmol of mRNA are used for the assay. • Requantify the mRNA stock to ensure that 12-24 pmol of mRNA are used for the assay. Loss of purified mRNA pellet. • If performing precipitation-based clean up, pellets from 12-24 pmol of mRNA may be difficult to see by eye and may be lost during cleanup if not handled carefully. Repeat the reaction taking special care at this step. The overall capping efficiency of the mRNA prep was low. • The kit detects levels of Cap 1 relative to Cap 0, not relative to the total mRNA content. If the overall percent capped mRNA content is low, fewer cap core molecule are labeled resulting in a weak signal. To determine total percent capping, use the EZ-QC mRNA Capping Efficiency Assay Kit or the EZ-QC XBG mRNA Capping Efficiency Assay Kit (for mRNA containing a Xenopus β-globin [XBG] 5' UTR).
Experimental and the 80/20 Cap 1 Control Mix bands are not visible	Reaction failure. • Repeat the reaction using fresh input mRNA. • Sodium periodate was not reactive. Repeat the reaction with a fresh dilution of the sodium periodate stock.
Background bands are visible higher in the gel than the area of the Cap 1/Cap 0 bands of interest	The Cy5 labeling reaction will label all nucleic acid molecules containing vicinal hydroxyl groups. This includes the 3'-most base of the mRNA and any carried over nucleotides (NTP, NDP, NMP) that were part of the transcription or capping or tailing reactions, which were not removed during the labeled mRNA clean up step. The presence of these bands does not change the accuracy of the assay and they should be disregarded during the quantitation analysis step.
Background bands are visible in the area of the Cap 1/Cap 0 bands of interest	A background band appearing slightly above the Cap 1 or Cap 0 bands of interest can be an indication of a low efficiency N7-methylation reaction on the capping G nucleotide which would have been catalyzed by the Capping Enzyme. • Use the cumulative signal intensity of both bands as the calculated intensity of the appropriate cap core band for quantitation calculations. • If desired, the mRNA can be recapped to complete the N7-methylation. Verify that the *S*-adenosyl-methionine used for this step is still intact.

Continued on next page.

TROUBLESHOOTING

Symptom	Solution
The percentage Cap 1/Cap 0 calculated by the imaging software doesn't seem to match with what is observed by visual inspection of the gel image	The dynamic range of the imaging detector has been exceeded during the imaging process. The gel was over-exposed such that the most intense bands are out of the quantification range. Under-exposure of the gel may also impact quantitation. • Ensure that gel imaging exposure times are such that no pixels are saturated and that bands are adequately exposed.
	Depending on the amount of input mRNA used for the assay, and depending on how efficient the Cap 1 methylation reaction was during RNA capping, there can be little to no Cap 0 present in the mRNA prep. For mRNA preps with ≥95%, but <100% Cap 1 content, detection of the Cap 0 band may depend on the sensitivity of the gel imaging equipment.
Only background bands are visible, cap core bands are not visible, band migration is toward the bottom of the gel	Gel composition and/or running buffer composition may be incorrect. • Use the gel and buffer formulations described in Technical Appendix, section B.

RELATED PRODUCTS

– Cap-Clip™ Acid Pyrophosphatase
– EZ-QC™ mRNA Capping Efficiency Assay Kit
– EZ-QC™ mRNA Poly(A) Tail Length Assay Kit
– EZ-QC™ XBG mRNA Capping Efficiency Assay Kit
– INCOGNITO™ T7 mScript™ Complete N1meΨ-mRNA Production System
– INCOGNITO™ T7 mScript™ Complete Ψ-mRNA Production System
– INCOGNITO™ T7 mScript™ N1meΨ-mRNA Production System
– INCOGNITO™ T7 mScript™ Ψ-mRNA Production System
– ScriptCap™ Cap 1 Capping System
– ScriptCap™ m^7G Capping System
– ScriptCap™ 2'-O-Methyltransferase
– T7 mScript™ Complete Standard mRNA Production System
– T7 mScript™ Standard mRNA Production System V2

REFERENCES

1. Daffis, S. et al., (2010) Nature 468, 452.
2. Devarkar, S.C. et al., (2016) PNAS 113, 596.

The performance of this product is guaranteed for one year from the date of purchase.

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