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Poly(A) RNA Selection Kit
User Guide

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Table of Contents

1. Overview

Lexogen's Poly(A) RNA Selection Kit is suited for rapid and highly specific isolation of polyadenylated RNA from total RNA samples.

Total RNA is briefly denatured and the polyadenylated 3' ends present in most mRNAs are hybridized to oligo(dT) beads. Any RNA without poly(A) stretches, such as 28S and 18S ribosomal RNAs and tRNAs, will not be captured by the oligo(dT) beads and hence be removed during subsequent washing steps.

A typical downstream application for polyadenylated RNAs is Next Generation Sequencing (NGS). We recommend preparing libraries for RNA-Seq using the CORALL Total RNA-Seq Library Prep Kit (Cat. No. 095). It is necessary to elute the poly(A) RNA from the beads before continuing with the CORALL Total RNA-Seq Library Prep protocol.

This Poly(A) Selection Kit protocol is validated for use with input amounts ranging from 1 ng - 100 µg of total RNA input. The input amount depends on the intended application and also determines the amount of oligo(dT) beads required. In general, use 10 µl Magnosphere MS150/Oligo(dT) Beads for up to 5 µg of total RNA input. Higher inputs require higher bead volumes (see Appendix B, p.16). With this kit a total of 500 µg total RNA (100x 5 µg) or 1,000 µg total RNA (10x 100 µg) can be purified.

For preparation of RNA samples for Lexogen's CORALL Total RNA-Seq Library Prep Kit, we recommend using a minimum input of 200 ng total RNA. This will enable full quantification capability of poly(A) selected RNA.

ATTENTION: Lower input amounts down to 1 ng can also be used for poly(A) selection prior to CORALL Total RNA-Seq Library Preparation. Adjustments to elution volume are advised (see Appendix B, p.16) and we recommended to proceed directly to library preparation.

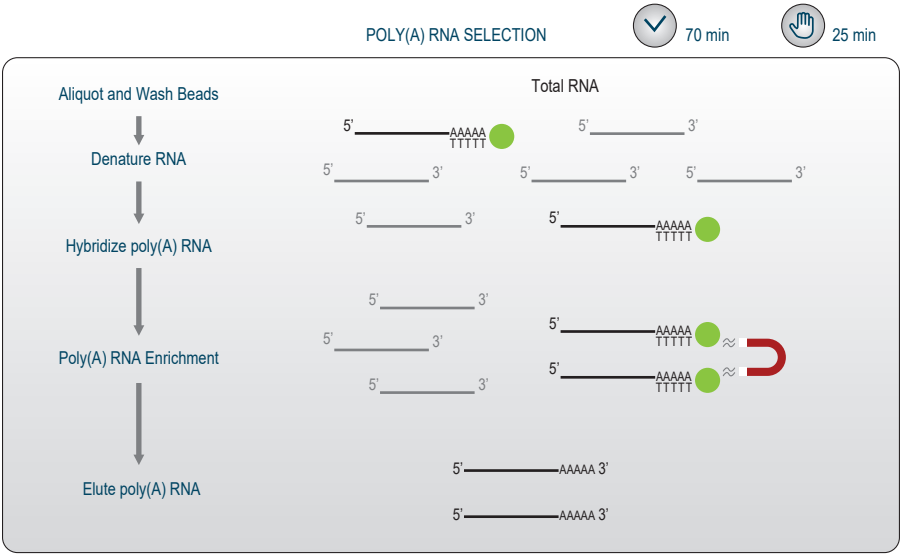

Figure 1. Schematic overview of the poly(A) RNA selection.

2. Kit Components and Storage Conditions

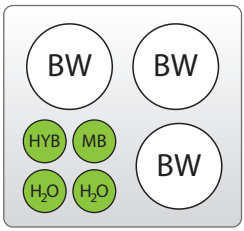

Figure 2. Location of kit components.

Kit Component	Tube Label	Volume*	Storage
Magnosphere MS150/Oligo(dT) Beads	**MB** ●	1,100 µl	+4 °C
RNA Hybridization Buffer	**HYB** ●	1,100 µl	+4 °C
Molecular Biology Grade Water	**H_2O** ●	2,750 µl	+4 °C
Bead Wash Buffer	**BW** ○	38,500 µl	+4 °C

*including a 10 % surplus

The kit is shipped at room temperature, upon receipt please store it at +4 °C. Before use, check the contents of **BW** ○ which may precipitate during shipping. If a precipitate is visible or the content appears turbid, incubate at 37 °C until buffer components dissolve completely.

3. User-supplied Consumables and Equipment

Check to ensure that you have all of the necessary materials and equipment before beginning library preparation. All reagents, equipment, and labware must be free of nucleases and nucleic acid contamination.

Equipment

- Magnetic rack / plate e.g., for 1.5 ml tubes: BcMag Magnetic separator-24, article# MS-03 from Bioclone; for 96-well plates: 96S Super Magnet Plate, article# A001322 from Alpaqua, Dynamag™-96 Side/Side Skirted. Magnets, article # 12331D/12027 from Thermo Fisher.
- Benchtop centrifuge (rotor compatible with 1.5 ml tubes or 96-well plates).
- Calibrated single-channel pipettes for handling 1 µl to 1,000 µl volumes.
- Thermomixer for 1.5 ml tubes or 96-well plates (dry bath incubator with shaking function).
- UV-spectrophotometer to quantify RNA.

Labware

- Suitable low binding pipette tips (pipette tips with aerosol barriers recommended).
- 1.5 ml tubes or PCR plate / tubes, low binding, certified ribonuclease-free.
- Vortex mixer.

Optional Equipment

- Automated microfluidic electrophoresis station (Agilent Technologies 2100 Bioanalyzer).
- Benchtop fluorometer and appropriate assays (for RNA quality control).
- Agarose gels, dyes, and electrophoresis rig (for RNA quality control).

The complete set of materials, reagents, and labware necessary for RNA selection and quality control is not listed. Consult Appendix A, p.14 and Appendix B, p.16 for more information on RNA quality and quantity. Consult Appendix C, p.17 for information on RNA quantification methods.

4. Guidelines

RNA Handling

- RNases are ubiquitous, and special care should be taken throughout the procedure to avoid RNase contamination.
- Use commercial ribonuclease inhibitors (i.e., RNasin, Promega Corp.) to maintain RNA integrity when storing samples.
- Use a sterile and RNase-free workstation or laminar flow hood if available. Please note that RNases may still be present on sterile surfaces, and that autoclaving does not completely eliminate RNase contamination. Well before starting a library preparation, clean your work space, pipettes, and other equipment with RNase removal spray (such as RNaseZap, Ambion Inc.) as per the manufacturer's instructions. **ATTENTION:** Do not forget to rinse off any RNAZap residue with RNAse-free water after usage! Residues of RNAZap may damage the RNA.
- Protect all reagents and your RNA samples from RNases on your skin by wearing a clean lab coat and fresh gloves. Change gloves after making contact with equipment or surfaces outside of the RNase-free zone.
- Avoid speaking above opened tubes. Keep reagents closed when not in use to avoid airborne RNase contamination.

Bead Handling

- Beads are stored at +4 °C and must be resuspended before usage. Beads can be resuspended by pipetting up and down several times or by vortexing. When resuspended, the solution should have a uniform brown color with no visible clumping on the walls or bottom of the tube.
- Beads may stick to certain pipette tips, in which case removing the beads from the inside of the tip may be impossible. Avoid resuspending by repeated pipetting, and instead resuspend by vortexing if this occurs with your tips.
- Beads are superparamagnetic and are collected by placing the plate / tube in a magnetic 96-well plate or a magnetic stand. The time required for complete separation will vary depending on the strength of your magnets, tube / well thickness, viscosity of the solution, and the proximity of the tube / well to the magnet. Separation time may need to be adjusted accordingly. When fully separated, the supernatant should be completely clear, and the beads collected at one point or as a ring along the wall of the tube / plate, depending on the magnet that was used.
- Do not remove the plate / tube from the magnetic stand when removing the supernatant,

as the absence of the magnet will cause the beads to go into suspension again.

- Always store beads in an upright position to ensure that they are covered by liquid.
- In general, beads should not be centrifuged during the protocol. However, should drops of fluid stay on the side of the reaction tube (e.g., after mixing by vortexing), centrifugation at 2,000 x g for 30 seconds should be carried out before placing the tube / plate on the magnetic rack.
- Allowing the beads to dry out can damage them. Always keep the beads in suspension except for the short period after withdrawing the supernatant but before adding the next reagent. Beads can be resuspended by vortexing, but make sure that beads are not deposited on the tube / well walls above the level of the liquid, where they can dry during incubation. If necessary, stuck beads can be collected by centrifuging the tube / plate briefly with a suitable benchtop centrifuge.

General

- Always spin down the tubes before opening! This prevents spillage and cross contamination.
- Unless explicitly mentioned, all steps should be carried out at room temperature (RT) between 20 °C and 25 °C. Results may be negatively impacted if the protocol is performed at temperatures outside of this range. While reaction set-up is often performed at RT, incubation temperatures are explicitly defined and must be strictly adhered to.
- Ensure that adequate volumes of all reagents and the necessary equipment are available and set to the proper temperatures before beginning the protocol.
- Pre-heat thermomixers (dry bath incubators) well in advance.
- Perform all pipetting steps with calibrated pipettes and always use fresh tips. Pipette carefully to avoid foaming as some solutions may contain detergents.
- Equilibrate all necessary buffers at room temperature or as indicated in the preparation tables at the beginning of each step of the detailed protocol. Mix reagents well by vortexing or pipetting repeatedly, and centrifuge briefly with a benchtop centrifuge to collect contents before use.
- When using multi-channel pipettes, always include a 10 % surplus per reaction in order to have enough solution available for all reactions.

5. Detailed Protocol

Preparation

Aliquot and Wash Beads	Denature RNA	Hybridize Poly(A) RNA	Elute Poly(A) RNA
MB ● – stored at 4 °C **HYB** ● – stored at 4 °C **BW** ○ – stored at 4 °C	**Total RNA** – thawed on ice **H_2O** ● – stored at 4 °C	**BW** ○ – stored at 4 °C	**H_2O** ● – stored at 4 °C
Magnetic rack / plate	Thermocycler 60 °C, 1 min 25 °C, ∞	Thermomixer 1,250 rpm, set to 25 °C	Magnetic rack / plate Thermomixer / Thermo-cycler 70 °C, 1 min

Aliquot and Wash Beads

Lexogen's Poly(A) RNA Selection Kit uses Magnosphere MS150/Oligo(dT) beads from JSR Life Sciences. Magnetic beads must be washed before use. All steps are performed at room temperature.

ATTENTION: Volume modifications apply for steps 1, 3 - 6, and 10 - 11, when using input amounts >5 µg total RNA, and for elution at step 12 when using ≤500 ng total RNA (see Appendix B, p.16).

1. Mix the beads (**MB** ●) well. Transfer 10 µl of the resuspended beads per poly(A) selection for up to 5 µg total RNA into a new 1.5 ml tube. Beads can be washed as a batch (maximum of 50 µl beads) if multiple poly(A) selections are required. **REMARK:** For higher total RNA input amounts see Appendix B, p.16 for modifications.
2. Place the tube in a magnetic rack and let the beads collect for 5 minutes or until the supernatant is completely clear (depends on the magnet strength). Remove and discard the supernatant with a pipette while the tube remains in contact with the magnet.
3. Remove the tube from the magnetic rack and add 75 µl Bead Wash Buffer (**BW** ○) per poly(A) selection. Resuspend the beads and transfer the tube to the magnetic rack. Let the beads collect for 5 minutes; remove and discard the supernatant.
4. Repeat this washing step once (for a total of two washes).
5. Resuspend the beads in 10 µl RNA Hybridization Buffer (**HYB** ●) per sample. Pipette and mix carefully to avoid introducing air bubbles.

Denature RNA

RNA samples are briefly heated to resolve secondary structures and promote efficient hybridization. For information on appropriate amounts of total RNA input see Appendix B, p.16.

6	Dilute up to 5 µg of total RNA to a volume of 10 µl with RNase-free water.
7	Denature RNA samples using a thermocycler at 60 °C for 1 minute and then hold at 25 °C. **ATTENTION:** Do not cool samples excessively or place denatured RNA on ice. If no thermomixer is available, incubate in a thermocycler (with vortex & spin down) every 10 minutes.

Hybridize Poly(A) RNA

The denatured total RNA is incubated with the washed beads, which specifically bind polyadenylated RNAs. RNAs lacking a poly(A) tail are then washed away, leaving only purified poly(A) RNA hybridized to the beads.

8	Add the 10 µl of denatured RNA to 10 µl of washed beads and incubate using a thermomixer at 25 °C for 20 minutes with 1,250 rpm agitation.
9	Transfer the tube onto a magnetic rack and let the beads collect for 5 minutes (or until the supernatant is clear). Remove and discard the supernatant.
10	Remove the tube from the magnetic rack and add 100 µl Bead Wash Buffer (**BW** ○). Resuspend the beads and mix well. Incubate using a thermomixer at 25 °C for 5 minutes with 1,250 rpm agitation. Collect the beads by placing the tube onto a magnetic stand for 5 minutes or until the supernatant is completely clear. Remove and discard the supernatant.
11	Repeat this washing step once (for a total of two washes).

RNA Elution

The poly(A) RNA is eluted from the oligo(dT) beads by heating in water.

12	Completely remove the supernatant from the last wash (step 11) and resuspend the beads in 25 µl of Molecular Biology Grade Water (**H_2O** ●). **REMARK:** Reduce the elution volume to 12 µl if total input amount was ≤500 ng, or higher mRNA concentration is desired.
13	Incubate for 1 minute at 70 °C.

14	Immediately transfer the tube onto a magnetic rack and let the beads collect for 5 minutes (or until the supernatant is clear).
15	Transfer the clear supernatant into a fresh tube. The supernatant now contains the poly(A) selected RNA that can be used for quality control, concentration determination, and further downstream applications. **ATTENTION:** Avoid bead carryover. ☞ Safe stopping point. The poly(A) selected RNA can be stored at -20 °C at this point.
16	For long term storage we recommend adding Tris, pH 7.0 to the isolated poly(A) RNA to final concentration of 10 mM Tris, pH 7.0 (i.e., add 2.5 µl of 100 mM Tris pH 7.0 if the RNA was eluted in 25 µl). Furthermore, addition of RNase inhibitor (e.g., RNasin) can be recommended for long-term storage of poly(A) RNA (see Appendix A, p.14).

6. Short Procedure

ATTENTION: Spin down solutions before opening tubes or plates!

70 min Poly(A) Selection

Standard Input (>500 - 5 µg)	Lower Input (≤500 ng)	High Input (50 - 100 µg)
Aliquot and Wash Beads		
☐☐ Wash 10 µl beads (**MB** ●) twice with 75 µl **BW** ○.		☐☐ Wash 50 - 100 µl beads (**MB** ●) twice with ≥200 µl **BW** ○.
☐ Withdraw supernatant.		
☐ Resuspend beads with 10 µl **HYB** ●.		☐ Resuspend beads with 50 - 100 µl **HYB** ●.
Denature RNA		
☐ Prepare total RNA in a volume of 10 µl.		☐ Prepare total RNA in a volume of 50 - 100 µl.
☐ Incubate for 1 min at 60 °C, hold at 25 °C.		
Hybridize Poly(A) RNA		
☐ Add denatured RNA (10 µl) to washed beads (10 µl).		☐ Add denatured RNA (50-100 µl) to washed beads (50-100 µl).
☐ Incubate for 20 min at 25 °C / 1,250 rpm.		
☐☐ Wash 2 x for 5 min at 25 °C / 1,250 rpm with 100 µl **BW** ○.		☐☐ Wash 2 x for 5 min at 25 °C / 1,250 rpm with ≥200 µl **BW** ○.
☐ Withdraw supernatant.		
Elute Poly(A) RNA		
☐ Add 25 µl **H_2O** ●.	☐ For ≤500 ng: Add 12 µl **H_2O** ●.	☐ For >5 µg: Add up to 50 µl **H_2O** ●.
☐ Incubate for 1 min at 70 °C.		
☐ Place on magnet for 5 min or until supernatant is clear.		
☐ Transfer the clear supernatant into a fresh tube. ☞ Safe stopping point.		

7. Appendix A: General RNA Requirements

RNA Integrity

The integrity of an RNA sample can be assessed with a variety of methods. We recommend the use of a microfluidics assay such as the RNA6000 series for the 2100 Bioanalyzer (Agilent Technologies Inc.). However, RNA quality can also be assessed with denaturing agarose gel electrophoresis if such a device is not available. Most microfluidics platforms will carry out an automated peak analysis and generate a quality score (RIN or RQN), and we recommend a RIN score of 8 or greater for optimal full-length poly(A) RNA selection. Typically such samples have easily detectable rRNA peaks and a comparatively low abundance of short RNAs, which can arise from both intact short transcripts as well as from RNA degradation. Poly(A) RNA can also be isolated from lower quality RNA, but this may lead to 3'-bias in subsequent reactions. **ATTENTION:** RNA isolation methods that quantitatively co-isolate all RNAs below 200 nt (tRNAs, 5S rRNA) may result in lower RIN scores, despite intact 18S and 28 S rRNA peaks.

Potential Contaminants

RNA samples should be free of salts, metal ions, and organic solvents which can be carried over from RNA extraction. Several sources of contamination can be detected with an UV-Vis spectrophotometer. An acceptably pure RNA sample should have an A260/A280 ratio between 1.8 and 2.1. The A260/A230 ratio should be approximately 2. Several common contaminants including proteins, chaotropic salts, and phenol absorb strongly between 220 and 230 nm and can often be identified as peaks in this region. Contamination with any of these generates a lower A260/230 ratio. Phenol has an absorption maximum between 250 and 280 nm which overlaps that of nucleic acid, hance high 230 nm absorbance combined with a biphasic or broad peak between 250 and 280 nm may indicate contamination with phenol rather than chaotropic salts.

Genomic DNA Contamination

Depending on the RNA extraction protocol used, samples may contain significant amounts of genomic DNA (gDNA), which is indistinguishable from RNA on a spectrophotometer. Furthermore, as many of the dyes used in RNA microfluidics assays stain single-stranded nucleic acids much more intensely than double-stranded, low to moderate amounts of gDNA may not be readily visible with an RNA-specific microfluidics assay. We highly recommend examining all RNA samples on a denaturing agarose gel or using a fluorometric assay with DNA- and RNA-specific dyes to check samples for DNA contamination. On an agarose gel, gDNA can appear as either a dark mass which remains in the slot if relatively intact, or as a high molecular weight smear if it has been sheared during extraction.

The best way to avoid gDNA contamination is to use an RNA extraction protocol that does not co-isolate gDNA such as Lexogen's SPLIT RNA Extraction Kit (Cat. No. 008.48). DNase I treatment is

generally not required when poly(A) selection is performed, as genomic DNA will not be captured by the oligo(dT) beads and is therefore, efficiently removed during the washing steps. However, if desired, gDNA can optionally be removed from irreplaceable samples by acidic phenol extraction or DNase I digestion. If samples must be DNase I-treated, heat inactivation should be avoided, and the enzyme should be deactivated by other means such as phenol / chloroform extraction or silica column purification.

RNA Storage

If immediate RNA extraction is not possible, tissue samples can be either flash-frozen with liquid nitrogen or submerged in RNAlater (Life Technologies Inc.) and stored at -80 °C. After extraction, RNA can be stored at -20 °C or -80 °C in 10 mM Tris pH 7.0. Avoid frequent freeze-thaw cycles as RNA might be sheared. Addition of an RNase inhibitor, e.g., RNasin from Promega at a final concentration of 0.4 U/µl, is recommended.

RNA Spike-in Control Mixes

RNA spike-in control mixes such as the ERCC RNA Spike-in Controls (Ambion Inc.) and / or Lexogen's set of artificial spike in transcripts called SIRVs (Spike-in RNA Variant Control Mixes, Cat. No. 025, 050, 051), should be spiked into total RNA before poly(A) selection. As both ERCC control RNAs and SIRVs are polyadenylated they will be isolated with the oligo(dT) beads along with the mRNA. Such control mixes serve as a control and anchor set for the comparison of experiments. Also for some applications such as RNA-Seq they enable the hypothesis-neutral calculation of strandedness, isoform quantitation, and the validation of the performance of isoform-specific RNA-Seq workflows.

8. Appendix B: RNA Amount

High quality mRNA isolation relies on high quality input RNA. The poly(A) content of an RNA sample or tissue varies, but is usually between 1 and 3 % of the total RNA amount. This protocol was tested extensively with various mouse tissues and human reference RNA. Total RNA isolated from kidney, liver, and brain for instance has a higher poly(A) content than total RNA isolated from lung or heart. For Universal Human Reference RNA (UHRR) the amount of poly(A) RNA recovered is about 2 % of the total RNA input.

An important factor in determining the percentage of poly(A) RNA recovered is using the same method for concentration measurement before and after poly(A) enrichment. Determining the total RNA input by NanoDrop measurements and the recovered poly(A) RNA using Bioanalyzer may result in the impression of a low mRNA recovery as the two methods differ significantly in the concentration determination, with the NanoDrop usually giving much higher concentration values.

We typically recommend using up to 5 µg of total RNA input with 10 µl of beads (MB ●). However, 100 µg and 50 µg of total RNA (UHRR) have also been tested with a few protocol adjustments (adjusted oligo(dT) beads (MB ●), Bead Wash Buffer (BW ○), RNA, and HYB ● volumes, see table below).

The lowest RNA input recommended to enable recovery of measurable amounts of poly(A) RNA is 200 ng total RNA. Reducing input below 500 ng requires reducing the elution volume at step 12 to 12 µl. Total RNA input amounts down to 1 ng can also be used for poly(A) selection prior to library preparation with Lexogen's CORALL Total-RNA Seq Library Prep Kit. When using input amounts ≤200 ng of total RNA, we recommend to elute the poly(A)-selected RNA in 12 µl and take 10 µl as input for CORALL.

Universal Human Reference RNA Input (UHRR)	Step 1 Volume of MB	Step 3 / 4 Volume of BW	Step 5 HYB added to MB	Step 6 RNA in Volume	Step 10 / 11 Volume of BW	Step 12 Elution Volume
100 µg UHRR	**100 µl**	≥200 µl	100 µl HYB	100 µl	≥200 µl	50 µl
50 µg UHRR	**50 µl**	≥200 µl	50 µl HYB	50 µl	≥200 µl	25 µl
5 µg UHRR	**10 µl**	75 µl	10 µl HYB	10 µl	100 µl	
2 µg UHRR						
500 ng UHRR						12 µl
100 ng UHRR						
1 ng UHRR						

ATTENTION: Inputs ≤200 ng of total RNA will result in poly(A) RNA that is not quantifiable by usual quality control methods (e.g., Bioanalyzer, Qubit, NanoDrop etc). However, the recovered RNA can be used directly for downstream CORALL library preparation.

9. Appendix C: Quality Control

Quality Control Methods

Quality control of poly(A) RNA can only be reliably performed where the input amount is >200 ng and is best performed using microcapillary electrophoresis. For low- to medium-throughput applications, we recommend the Agilent Bioanalyzer 2100 and RNA 6000 Pico chips (Agilent Technologies, Inc.) or simlar. Typically, 1 µl of eluted poly(A) RNA produced according to the directions in this manual can be analyzed directly on a Pico RNA chip. For high-throughput applications instruments such as LabChip GX II (Perkin Elmer) or 2200 TapeStation (Agilent Technologies, Inc.) are recommended. Depending on the minimum sample loading requirements for each instrument, 1 µl of the eluted poly(A) RNA may be diluted to the required volume (e.g., 2 µl sample for TapeStation RNA 6000 Pico and High Sensitivity R6K kits and 10 µl for LabChip GX II).

ATTENTION: Be advised that poly(A) RNA does not contain 18S and 28S rRNA peaks anymore, hence an RNA integrity number (RIN) or RNA Quality Number (RQN) cannot be calculated.

If microcapillary electrophoresis platforms are not available, very basic quality control can also be performed by separating a small aliquot of the RNA on a polyacrylamide or a denaturing agarose gel. RNA quantification can also be performed with an inexpensive benchtop fluorometer using one of several commercially available assays. We recommend using a Qubit HS RNA assay (Life Technologies, Inc.). Most UV-Vis spectrophotometers are not sensitive enough at these concentrations to accurately quantify low RNA amounts and should be avoided.

Typical Results

The poly(A) content of an RNA sample or tissue varies, but is usually between 1 and 3 % of the total RNA amount. From 5 µg Universal Human Reference RNA (UHRR) around 100 ng poly(A) RNA can be isolated (~2 %).

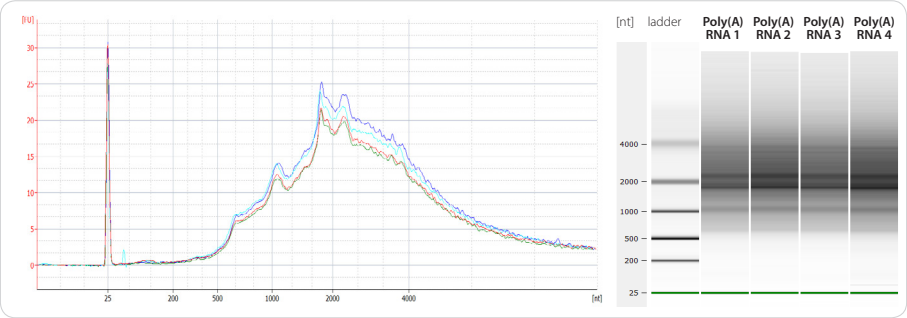

Figure 3. Bioanalyzer traces of 4 independent poly(A) selections from 5 µg Universal Human Reference RNA. Poly(A) RNA was eluted in 25 µl Molecular Biology Grade Water and 1 µl was loaded onto an RNA 6000 Pico chip (Agilent Technologies, Inc.). The concentration of all 4 samples was around 4 ng/µl poly(A) RNA (3.8 ng/µl - 4.1 ng/µl).

The peaks visible in the poly(A) trace (see Figure 3) correspond to high abundant mRNA transcripts. A direct overlay of the poly(A) traces with a diluted total RNA sample confirms that those peaks are not rRNA peaks but in fact are of different nucleotide lengths (see Figure 4).

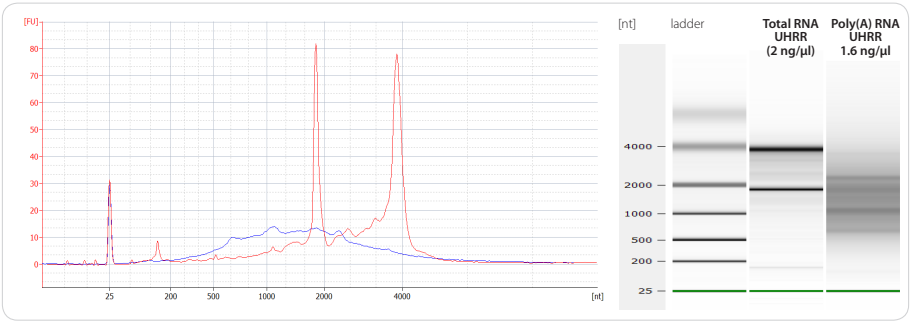

Figure 4. Bioanalyzer traces of Universal Human Reference Total RNA (red trace) and poly(A) selected RNA from 2 µg Universal Human Reference RNA. Poly(A) RNA was eluted in 25 µl Molecular Biology Grade Water and 1 µl was loaded onto an RNA 6000 Pico chip (Agilent Technologies, Inc.). The total RNA was diluted and 2 ng were loaded onto the chip.

10. Appendix D: Revision History

Publication No. / Revision Date	Change	Page
039UG069V104 Jun. 07, 2019	Added notes for use with CORALL Total-RNA Seq Library Prep Kit.	4, 11, 15
	Updated input recommendations.	4, 15
	Short Procedure reformatted.	13
039UG069V103 Dec. 14, 2017	Added note at step 7.	11
	Added safe stopping points.	11-12
	Added adjusted volumes for Bead Wash Buffer.	15
039UG069V102 Dec. 12, 2016	Restructuring of Appendices.	13 - 19
	Figure 4: Comparison of total RNA and poly(A) selected RNA.	17
039UG069V101 Nov. 26, 2015	Initial Release.	

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Associated Products:

025, 050, 051 (Spike-In RNA Variant Controls: SIRV-Set 1, SIRV-Set 2, SIRV-Set 3)
095 (CORALL Total RNA Seq Library Prep Kits))

Poly(A) RNA Selection Kit · User Guide

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