

B) MATERIALS

▲ **CRITICAL** All reagents and equipment must be maintained free of RNase contamination. We strongly recommend that all reagents and kits are purchased at the highest molecular and manufacturing quality and to be reserved for RNA use only. Similarly, we highly recommend that equipment used for RNA-related work be reserved for RNA use only.

B-1) Reagents

- Transgenic *UAS-HA-CD:UPRT* fly lines: *pUAS-HA-CD:UPRT-attB* constructs (containing either a N-terminal HA-tagged *Saccharomyces cerevisiae S.c. CD:UPRT* fusion gene or a *Drosophila* codon-optimized *CD:UPRT* fusion gene) were used to generate second and third chromosome *UAS-CD:UPRT* lines for both the *S.c.CD:UPRT* and optimized *CD:UPRT*. All four fly lines have been deposited with the Bloomington Drosophila Stock Center (<https://bdsc.indiana.edu>): N-terminal HA-tagged *S. cerevisiae UAS-HA-CD:UPRT* (2nd chromosome) (#77119); N-terminal HA-tagged *S. cerevisiae UAS-HA-CD:UPRT* (3rd chromosome) (#77120); N-terminal HA-tagged *Drosophila* codon-optimized *UAS-HA-CD:UPRT* (2nd chromosome) (#77121); N-terminal HA-tagged *Drosophila* codon-optimized *UAS-HA-CD:UPRT* (3rd chromosome) (#77122).
- Transgenic tissue-specific *Gal4* fly lines: the following *Gal4* line was obtained from the Bloomington Drosophila Stock Center: *109(2)80-Gal4* (#8769) to drive the expression of *UAS-HA-CD:UPRT* in the *Drosophila* multi-dendritic neurons (52)
- Schneider's *Drosophila* media
- TRIzol reagent (Invitrogen, cat. no. 15596026) ! **CAUTION** TRIzol is toxic and should be used in a fume hood; wear gloves and a lab coat.
- Chloroform (MP Biomedicals, cat. no. 194002) ! **CAUTION** Chloroform is toxic and should be used in a fume hood; wear gloves and a lab coat.
- Isopropanol (Fisher Scientific, cat. no. BP2618)
- Ethanol (Fisher Scientific, cat. no. BP2818)
- Sodium Acetate
- Sodium Chloride (Invitrogen, cat. no. AM9759)
- Nuclease-free water
- RNeasy Mini Kit (Qiagen, cat. no. 74104)
- RNase-free DNase I (Qiagen, cat. no. 79254)
- 5-EC (5-ethynyl cytosine)
- 5-EUd (5-ethynyl uridine)
- Click-iT® Nascent RNA Capture Kit (Invitrogen, cat. no. C10365)
- Biotin Azide
- THPTA (tris-hydroxypropyltriazolymethylamine) (Click Chemistry Tools, cat. no. 1010)
- Copper (II) sulfate (Sigma Aldrich, cat. no. 451657)
- (+) - Sodium L-Ascorbate (Sigma Aldrich, cat. no. A7631)
- HEPES
- Dynabeads™ MyOne™ Streptavidin T1 (Invitrogen, cat. no. 65601)
- Poly(deoxyinosinic-deoxycytidylic) acid, sodium salt (Poly(dI-dC) • Poly(dI-dC) sodium salt) (Sigma Aldrich, cat. no. P4929)
- Tris-HCl pH 7.5 (Invitrogen, cat. no. 15567-027)
- Ultrapure EDTA, pH 8.0 (Invitrogen, cat. no. 15575-038)
- TWEEN® 20 (Sigma Aldrich, cat. no. P9416)
- RNaseOUT™ Recombinant Ribonuclease Inhibitor (Invitrogen, cat. no. 10777019)
- NuGEN Ovation® Universal RNA-Seq System 1-16 (NuGEN, cat. no. 0343-32)

- 50 • 10X PBS Buffer, pH 7.4 (Ambion, cat. no. AM9624)
- 51 • RNaseH buffer, 10X
- 52 • D-biotin, 50 mM
- 53 • RNase Cocktail™ Enzyme Mix (Invitrogen, cat. no. AM2286)
- 54 • Ribonuclease H (RNase H) (Invitrogen, cat. no. 18021014)
- 55 • Dimethyl sulfoxide (DMSO) (Sigma Aldrich, cat. no. D8418)
- 56 • Zymo DNA Clean & Concentrator-5 kit (Zymo Research, cat. no. D4013)
- 57 • Qubit™ RNA HS Assay Kit (Invitrogen, cat. no. Q32852)
- 58 • EvaGreen® Dye, 20X in Water (Biotium, cat. no. 31000)

59
60
61
62

63 **B-2) Equipment**

- 64 • RNase-free microcentrifuge tubes, 1.5 mL
- 65 • Phase-lock tubes, RNase-free
- 66 • RNase-free microcentrifuge tubes, 5 mL
- 67 • RNase-free Centrifuge tubes, 15 mL
- 68 • RNase-free Centrifuge tubes, 50 mL
- 69 • Qubit assay tubes
- 70 • Thin-walled PCR tubes
- 71 • RNase-free tubes, 0.6 mL
- 72 • Sterile syringe, 1 mL, 3 mL and 5 mL
- 73 • 26 G × 3/8 inch detachable needle
- 74 • Refrigerated centrifuge (Eppendorf)
- 75 • RNase-free pellet pestle grinder
- 76 • Pestle, RNase-free
- 77 • SpeedVac
- 78 • Thermomixer
- 79 • Thermomixer heated cover
- 80 • Thermocycler
- 81 • Vortex
- 82 • Rotator
- 83 • Covaris M-series
- 84 • Qubit 2.0 fluorometer
- 85 • Nanodrop
- 86 • Agilent bioanalyzer
- 87 • Agilent Bioanalyzer DNA high-sensitivity kit
- 88 • Agilent Bioanalyzer's RNA Pico Kit
- 89 • Illumina HiSeq ---- OR NextSeq ----

90

91 **B-3) Software**

- 92 • RNA-seq software
- 93 • Bioanalyzer software
- 94 • Analysis software
 - 95 ○ R
 - 96 ○ R studio
 - 97 ○ Excel

98

99 **B-4) Reagent setup**

- 100 • 5-EC (5-ethynyl cytosine)
- 101 • 5-EUd (5-ethynyl uridine)
- 102 • CuSO₄ (for home-made biotinylation reaction)
- 103 • NA Ascorbate (for home-made biotinylation reaction)
- 104 • Biotin Azide
- 105 • Precipitation Solution Na Acetate, 3M, pH 5.2
- 106 • RNase-free DNase I stock
- 107 • Preparing stock of Component E from Click-iT kit
- 108 • HEPES Buffer, 10X
- 109 • Block & Washing (B&W) Buffer, 2X
- 110 • TNE bead-blocking buffer, 10X: 100 mM Tris.Cl, pH 7.5; 10 mM EDTA, pH 8.0; 2 M NaCl; 20
- 111 mg/ml nuclease-free BSA; and 10 µg/ml poly(deoxyinosinic-deoxycytidylic) acid, sodium salt.
- 112 Aliquot and store up to a year at -20°C.
- 113 • Wash 65-T Buffer: 100 mM Tris.Cl, pH 7.4; 10 mM EDTA, pH 8.0; 1 M NaCl; and 0.1%
- 114 Tween 20. Mix first three items. Store buffer up to a year at room temperature. Add 0.1%
- 115 Tween 20 fresh each time just before use.
- 116 • TNE 2.0-T Buffer: 10 mM Tris.Cl, pH 7.4; 1 mM EDTA, pH 8.0; 2 M NaCl; and 0.1% Tween
- 117 20. Mix first three items. Store buffer up to a year at room temperature. Add 0.1% Tween 20
- 118 fresh each time just before use.
- 119 • TNE 0.2-T Buffer: 10 mM Tris.Cl, pH 7.4; 1 mM EDTA, pH 8.0; 200 mM NaCl; 0.1% Tween
- 120 20. Mix first three items. Store buffer up to a year at room temperature. Add 0.1% Tween 20
- 121 fresh each time just before use.
- 122 • TNE 0.2 Buffer: 10 mM Tris.Cl, pH 7.4; 1 mM EDTA, pH 8.0; and 200 mM NaCl in nuclease-
- 123 free water. Store up to a year at room temperature.
- 124 • Adult tagging solution (Sucrose tagging solution)
- 125 • Larval tagging media (Mocha cap)
- 126 • Embryo tagging media

127

128 **C) PROCEDURE**

129 **5-EC and/or 5-EUd delivery and total RNA extraction**

130 1| Thaw 5-EC (or 5-EUd) stock solution at room temperature.

131 ▲ **CRITICAL** 5-EC tends to precipitate out of solution, especially at higher concentration.

132 Hence, we highly recommend vortexing the stock solution vigorously before diluting it to the

133 required tagging concentration using the appropriate tagging media.

134

135 2| Delivery of 5-EC (or 5-EUd) into Drosophila embryos, larvae or adult stages. Here – see fly

136 delivery protocols or replace with cell culture-specific protocol

137

138

139 **Total RNA purification**

140 ▲ **CRITICAL** From this point on, special care should be taken to maintain RNase-free

141 conditions. Benchtops and pipettes should be thoroughly cleaned with RNaseAWAY. RNase-

142 free tubes and filtered pipette tips should be always used. Gloves should be worn at all times.

143

144 3| Precool microcentrifuge to 4°C.

145

146 4| Thaw TRIzol samples (stored from at -80°C from TRIzol-based total RNA extraction step).

147 Add additional TRIzol or combine similar samples to reach a final volume of 1 mL of TRIzol.

148 Incubate the 1.5 mL microcentrifuge tube for 5 minutes at room temperature (~22°C). Transfer
149 the contents of the microcentrifuge tube to a 2 mL phase lock gel tube.
150 **! CAUTION** TRIzol is toxic and should be used in a fume hood. Wear gloves and a lab coat.
151 **▲ CRITICAL** Make sure to spin down the heavy gel to the bottom of the phase lock gel tube(s)
152 before transferring the TRIzol content to it(them).
153
154 5| Add 200 µL of chloroform. Mix well either by vigorous shaking or vortexing for 15 s. Incubate
155 the phase lock gel tube for 3 minutes at room temperature.
156 **! CAUTION** Wear gloves and use a fume hood when working with chloroform
157 **▲ CRITICAL** The vigorous extended shaking after adding chloroform is important for high RNA
158 yield and quality.
159
160 6| Centrifuge the phase lock gel tube at 12,000g for 15 minutes at 4°C.
161
162 7| Transfer the upper aqueous phase to a new RNase-free 1.5 mL microcentrifuge tube. Add
163 250 µL of Isopropanol and 250 µL of 3M Sodium Acetate (pH 5.2). Mix contents well by
164 pipetting. Incubate the microcentrifuge tube for 10 minutes at room temperature.
165
166 8| Centrifuge the microcentrifuge tube at 16,000g for 15 minutes at 4°C.
167 **▲ CRITICAL** A pellet of precipitated RNA should be visible after this centrifugation step.
168
169 9| Decant the liquid. Wash with 500 µL of 75% (vol/vol) ethanol.
170
171 10| Centrifuge the microcentrifuge tube at 7,500g for 5 minutes at 4°C. Decant the liquid.
172
173 11| Fast spin the microcentrifuge tube to collect any excess ethanol to the bottom of the tube.
174 Carefully remove the remaining liquid by pipetting without disturbing the pellet. Briefly air dry the
175 pellet.
176 **▲ CRITICAL** Avoid over drying the RNA pellet since this could make resolubilizing it difficult.
177
178 12| Resuspend the RNA pellet in 50-100 µL of RNase-free water. Aim at having a final RNA
179 concentration of ~ 1 µg µL⁻¹. The RNA concentration should be determined by
180 spectrophotometry (e.g. a Nanodrop) or by using a Qubit fluorometer, according to the
181 manufacturer's directions.
182
183 13| Treat the RNA with DNase to remove any residual genomic DNA contamination. We
184 recommend using Qiagen's RNase-free DNase I in association with Qiagen's RNeasy Mini Kit,
185 according to the manufacturer's direction.
186 **▲ CRITICAL** Do not exceed 100 µg of total RNA per RNeasy Mini Kit's spin column since this
187 is the maximum binding capacity of the column. As per the manufacturer's protocol, if a yield of
188 > 30 µg of DNase-treated RNA is expected, two rounds of elution with RNase-free water should
189 be done. We recommend incubating the column for 1 minute at room temperature after applying
190 RNase-free water for elution before centrifuging the tube according the manufacturer's protocol.
191 To achieve a higher concentration of eluted DNase-treated RNA, the manufacturer's protocol
192 suggests using the elute from the first round of elution and re-applying it to the column for the
193 second round of elution. We recommend adding a new volume of RNase-free water to the
194 column for the second elution step rather than re-using the elute from the first elution step since
195 we have found that this approach yields a higher amount of RNA.
196

197 14| Determine the concentration of DNase-treated RNA by spectrophotometry (e.g. a
198 Nanodrop) or by using a Qubit fluorometer, according to the manufacturer's directions.
199 ▲ **CRITICAL** For the upcoming biotinylation step, the concentration of DNase-treated RNA
200 should be $\geq 2.0 \mu\text{g } \mu\text{L}^{-1}$. If the Nanodrop and/or Qubit fluorometer's measurements show a
201 concentration of a lower value, we recommend concentration the RNA by using Qiagen's RNeasy
202 MinElute Cleanup kit, Qiagen's RNeasy Mini kit, or ThermoFisher's SpeedVac Concentrator, as
203 per the manufacturer's directions.

205 15| Determine the quality and integrity of RNA by using an Agilent Bioanalyzer's RNA Pico
206 Kit. Label sample and store RNA at -80°C .

207 ▲ **CRITICAL** Avoid repeated freezing and thawing of RNA samples.

208 ■ **PAUSE POINT (end of day 1)** RNA can be frozen and stored at -80°C overnight or until
209 ready to proceed.

211 RNA biotinylation

212 ▲ **CRITICAL** For the biotinylation step, there are two alternative approaches that we non-
213 preferentially use in our laboratory: the first is to use Invitrogen's Click-iT™ Nascent RNA
214 capture kit, as per the manufacturer's recommendations; and the second (explained below) is
215 dependent on reagents prepared in our laboratory. In our experience, both approaches show
216 very comparable results in terms of yield and quality of biotinylated RNA. For both approaches,
217 we recommend the following: (1) adding $30 \mu\text{g}$ of DNase-treated total RNA per a biotinylation
218 reaction for which the final reaction volume should be $50 \mu\text{L}$; (2) adding a spike-in control in the
219 form of 0.5 pg of 5-EU-tagged Fluc in each biotinylation reaction (i.e. 0.5 pg 5-EU-tagged Fluc /
220 $30 \mu\text{g}$ DNase-treated total RNA); and (3) incubating the biotinylation reaction in the dark at 25°C
221 for 30-45 minutes with gentle mixing at 600-700 rpm by using Eppendorf's Thermomixer and
222 ThermoTop.

224 16| In a clean RNase-free 1.5 mL microcentrifuge tube, combine $5 \mu\text{L}$ of 20 mg/mL THPTA, 1
225 μL of 100 mM CuSO_4 , $5 \mu\text{L}$ of 200 mM Sodium Ascorbate, $5 \mu\text{L}$ of 10 mM of Biotin Azide, $30 \mu\text{g}$
226 of DNase-treated RNA, and 0.5 pg of 5-EU-tagged Fluc. Add RNase-free water to achieve a final
227 volume of $50 \mu\text{L}$. Mix well by pipetting without introducing bubbles. Spin down the content using
228 a benchtop mini spin microcentrifuge. Incubate the biotinylation reaction in the dark at 25°C for
229 30-45 minutes with gentle mixing at 600-700 rpm by using Eppendorf's Thermomixer and
230 ThermoTop.

232 17| Terminate biotinylation reaction by adding $450 \mu\text{L}$ of 1X HEPES buffer to the
233 microcentrifuge tube for a final volume of $500 \mu\text{L}$. Transfer the contents of the microcentrifuge
234 tube to a 2 mL phase lock gel tube. Add an equal volume ($500 \mu\text{L}$) of chloroform. Mix well either
235 by vigorous shaking or vortexing for 15 s. Incubate the phase lock gel tube for 3 minutes at
236 room temperature.

237 ! **CAUTION** Wear gloves and use a fume hood when working with chloroform

238 ▲ **CRITICAL** Make sure to spin down the heavy gel to the bottom of the phase lock gel tube(s)
239 before transferring the sample to it.

240 ▲ **CRITICAL** The vigorous extended shaking after adding chloroform is important for high RNA
241 yield and quality.

243 18| Centrifuge the phase lock gel tube at $16,000g$ for 15 minutes at 4°C .

245 19| Transfer the upper aqueous phase to a new phase lock gel tube. Repeat steps 18 & 19.

246

247 20| Transfer the upper aqueous phase to a new RNase-free 1.5 mL microcentrifuge tube. Add
248 450 μL of Isopropanol and 50 μL of 5M NaCl. Mix contents well by pipetting. Incubate the
249 microcentrifuge tube for 10 minutes at room temperature.

250
251 21| Centrifuge the microcentrifuge tube at 16,000g for 15 minutes at 4°C.
252 ▲ **CRITICAL** A pellet of precipitated biotinylated RNA should be visible after this centrifugation
253 step.

254
255 22| Decant the liquid. Wash with 500 μL of 75% (vol/vol) ethanol.

256
257 23| Centrifuge the microcentrifuge tube at 7,500g for 5 minutes at 4°C. Decant the liquid.

258
259 24| Repeat 75% ethanol wash by repeated steps 23 & 24.

260
261 25| Fast spin the microcentrifuge tube to collect any excess ethanol to the bottom of the tube.
262 Carefully remove the remaining liquid by pipetting without disturbing the pellet. Briefly air dry the
263 pellet

264 ▲ **CRITICAL** Avoid over drying the RNA pellet since this could make resolubilizing it difficult.

265
266 26| Resuspend the RNA pellet in 10-15 μL of RNase-free water. Aim at having a final RNA
267 concentration of $\sim 2 \mu\text{g } \mu\text{L}^{-1}$. The RNA concentration should be determined by
268 spectrophotometry (e.g. a Nanodrop) or by using a Qubit fluorometer, according to the
269 manufacturer's directions

270
271 27| (*optional*) Determine the quality and integrity of RNA by using an Agilent Bioanalyzer's RNA
272 Pico Kit.. Label sample and store biotinylated RNA at -80°C.

273 ▲ **CRITICAL** Avoid repeated freezing and thawing of biotinylated RNA samples.

274 ■ **PAUSE POINT** Biotinylated RNA can be frozen and stored at -80°C overnight or until ready
275 to proceed.

276 277 **Isolation of biotinylated EU-tagged RNA (EU-RNA)**

278 ▲ **CRITICAL** For the biotinylated RNA isolation step, we recommend using Dynabeads MyOne
279 Streptavidin T1. We recommend incubating the Dynabeads in a blocking solution (as described
280 below) for ~ 24 hours before starting the isolation step since we have found that adding this step
281 significantly decreases the likelihood of non-specific RNA binding to the Dynabeads during the
282 isolation step. We recommend adding $\sim 20 \mu\text{g}$ of biotinylated RNA to 50 μL of blocked
283 Dynabeads per one isolation reaction. Accordingly, since biotinylated EU-RNA represents a tiny
284 fraction of the total RNA going into the isolation reaction, we recommend performing at least two
285 isolation reactions per each condition replicate.

286
287 28| Block Dynabeads MyOne Streptavidin T1 for 24 hours before isolation step

288 ▲ **CRITICAL** Before each washing incubation, vortex the Dynabeads after adding the
289 respective washing buffer. For washing incubations, we recommend using either a sample
290 mixer (e.g. HulaMixer® Sample Mixer) or a thermomixer (e.g. Eppendorf's Thermomixer) at
291 maximum speed with a heated top (e.g. Eppendorf's ThermoTop) for high temperature washes.
292 We strongly recommend applying a cap lock to each microcentrifuge tube during washing
293 incubations, especially for high-temperature, maximum-speed Thermomixer-based incubations,
294 to avoid accidental spilling. After each washing incubation, fast spin the microcentrifuge tube
295 using a benchtop mini spin microcentrifuge, apply the tube in a magnet (e.g. Dynamag-2
296 Magnet from Invitrogen) for 2-3 minutes to immobilize the beads, and discard the supernatant.

297
298 A. Resuspend the Dynabeads in the provided vial by vortexing for > 30 s.
299
300 B. Aliquot 50 μ L of Dynabeads (for each isolation reaction) in a new RNase-free 1.5 mL
301 microcentrifuge tube.
302
303 C. Wash with 1 mL of 1X Binding & Washing-Tween (B&W-T) buffer. Incubate for 2 minutes
304 using a sample mixer or a thermomixer at maximum speed, at room temperature.
305
306 D. Repeat step "C" twice, for a total of 3 washes with 1X Binding & Washing-Tween (B&W-T)
307 buffer.
308
309 E. Wash with 500 μ L of Solution "A". Incubate for 2 minutes using a sample mixer or a
310 thermomixer at maximum speed, at room temperature.
311
312 F. Repeat step "E" once, for a total of 2 washes with Solution "A".
313
314 G. Wash with 500 μ L of Solution "B". Incubate for 2 minutes using a sample mixer or a
315 thermomixer at maximum speed, at room temperature.
316
317 H. Wash with 1 mL of TNE2.0-T buffer. Incubate for 2 minutes using a sample mixer or a
318 thermomixer at maximum speed, at room temperature.
319
320 I. Wash with 1 mL of WASH65-T buffer. Incubate for 10 minutes using a thermomixer at
321 maximum speed, at 65°C.
322
323 J. Wash with 1 mL of TNE0.2-T buffer. Incubate for 2 minutes using a sample mixer or a
324 thermomixer at maximum speed, at room temperature.
325
326 K. After discarding the supernatant from the last washing step, add 500 μ L of 1X TNE Blocking
327 buffer. Mix the content by pipetting without introducing bubbles. Parafilm the microcentrifuge
328 tube. Incubate for 24 hours with mixing using a sample mixer, at 4°C.
329
330 L. After 24 hours of incubation with blocking buffer, fast spin the microcentrifuge tube using a
331 benchtop mini spin microcentrifuge. Put the tube in a magnet for 2-3 minutes to immobilize the
332 beads and discard the supernatant.
333
334 M. Wash with 1 mL of 1X Binding & Washing-Tween (1X B&W-T) buffer. Incubate for 2 minutes
335 using a sample mixer or a thermomixer at maximum speed, at room temperature.
336
337 N. Repeat step "M" once, for a total of 2 washes with 1X Binding & Washing-Tween (B&W-T)
338 buffer.
339
340 O. In a new RNase-free 5 mL centrifuge tube, resuspend the blocked Dynabeads in 2.5 mL of
341 **2X** Binding & Washing-Tween (**2X** B&W-T) buffer.
342
343 29| Bind biotinylated RNA to blocked Dynabeads to isolate EU-RNA
344
345 A. In a new RNase-free 1.5 mL microcentrifuge tube, add 21 μ g of biotinylated RNA to RNase-
346 free water for a final volume of 500 μ L. Mix well by pipetting. Denature biotinylated RNA by

347 incubating the microcentrifuge tube on a heat block for 10 minutes at 65-68°C. Immediately
348 place the microcentrifuge tube on ice for 5 minutes.

349
350 B. Add 2 µL of RNaseOUT. Mix well by pipetting.

351
352 C. (*optional*) Transfer 24 µL of the mixture to a new RNase-free 5 mL centrifuge tube. This
353 represents ~ 1 µg of the “input” biotinylated total RNA. Label as “INPUT” sample for the
354 condition replicate and store at -80°C.

355 ▲ **CRITICAL** This step is dependent on the experimental design (as discussed in the
356 “Experimental design” section). If a comparison to an “input” sample is not needed, then we
357 recommend starting with 20 µg of biotinylated RNA in step “30-A” instead of 20 µg.

358
359 D. Add denatured biotinylated RNA mixture to blocked Dynabeads mixture (from step 29-O).
360 Add nuclease-free water to bring the final volume to 5 mL. Mix well by pipetting.

361 ▲ **CRITICAL** Avoid introducing any bubbles during pipetting.

362
363 E. Incubate the blocked Dynabeads-biotinylated RNA mixture in the dark for 30 minutes with
364 rotation using a sample mixer (e.g. HulaMixer® Sample Mixer), at room temperature.

365
366 30| After incubation period in step “30-E”, Split the Dynabeads-biotinylated RNA mixture into 3
367 or 4 new RNase-free 1.5 mL microcentrifuge tubes. Fast spin the microcentrifuge tubes using a
368 benchtop mini spin microcentrifuge. Apply the tubes to a magnet for 2-3 minutes to immobilize
369 the beads.

370
371 31| (*optional*) Transfer the supernatant to new RNase-free 1.5 mL microcentrifuge tube(s). Label
372 as “Flow-through fraction 1 (FT1)” for the condition replicate and store at -80°C.

373 ▲ **CRITICAL** Following steps 18-28, RNA will need to be purified from the Flow-through fraction
374 1 (FT1) before it can be used for any downstream analyses.

375
376 32| Add 500 µL of TNE2.0-T buffer to each of the three microcentrifuge tubes. Mix well by
377 pipetting. Combine the total volume of 1.5 mL into a new RNase-free 1.5 mL microcentrifuge
378 tube. Fast spin the microcentrifuge tube using a benchtop mini spin microcentrifuge. Apply the
379 tube to a magnet for 2-3 minutes to immobilize the beads.

380
381 33| (*optional*) Transfer the supernatant to a new RNase-free 1.5 mL microcentrifuge tube. Label
382 as “Flow-through fraction 2 (FT2)” for the condition replicate and store at -80°C.

383 ▲ **CRITICAL** Following steps 18-28, RNA will need to be purified from the Flow-through fraction
384 2 (FT2) before it can be used for any downstream analyses.

385
386 34| Perform stringent washes of Dynabeads after biotinylated RNA binding step to get rid of any
387 non-specific RNA binding to Dynabeads

388 ▲ **CRITICAL** Before each washing incubation, vortex the Dynabeads after adding the
389 respective washing buffer. For washing incubations, we recommend using either a sample
390 mixer (e.g. HulaMixer® Sample Mixer) or a thermomixer (e.g. Eppendorf’s Thermomixer) at
391 maximum speed with a heated top (e.g. Eppendorf’s ThermoTop) for high temperature washes.
392 We strongly recommend applying a cap lock to each microcentrifuge tube during washing
393 incubations, especially for high-temperature, maximum-speed Thermomixer-based incubations,
394 to avoid accidental spilling. After each washing incubation, fast spin the microcentrifuge tube
395 using a benchtop mini spin microcentrifuge, apply the tube in a magnet (e.g. Dynamag-2

396 Magnet from Invitrogen) for 2-3 minutes to immobilize the beads, and discard the supernatant
397 unless otherwise specified.

398
399 A. Wash with 1 mL of TNE2.0-T buffer. Incubate for 2 minutes using a sample mixer or a
400 thermomixer at maximum speed, at room temperature.

401
402 B. Repeat step “A” three times, for a total of 4 washes with TNE2.0-T buffer.

403
404 C. Wash with 1 mL of 1X Binding & Washing-Tween (1X B&W-T) buffer. Incubate for 2 minutes
405 using a sample mixer or a thermomixer at maximum speed, at room temperature.

406
407 D. Repeat step “C” three times, for a total of 4 washes with 1X B&W-T buffer.

408
409 E. Wash with 1 mL of WASH65-T buffer. Incubate for 2 minutes using a thermomixer at
410 maximum speed, at 65°C.

411 ▲ **CRITICAL** We recommend prewarming WASH65-T buffer to 65°C before using it in washing
412 steps.

413
414 F. Repeat step “E” three times, for a total of 4 washes with WASH65-T buffer.

415
416 G. Wash with 1 mL of TNE0.2-T buffer. Incubate for 2 minutes using a thermomixer at
417 maximum speed, at 65°C.

418 ▲ **CRITICAL** We recommend prewarming TNE0.2-T buffer to 65°C before using it in washing
419 steps.

420
421 H. Repeat step “G” three times, for a total of 4 washes with TNE0.2-T buffer.

422
423 I. Wash with 1 mL of TNE0.2 buffer. Incubate for 2 minutes using a thermomixer at maximum
424 speed, at 65°C.

425 ▲ **CRITICAL** In this step, no Tween-20 is added to TNE0.2 buffer. We recommend prewarming
426 TNE0.2 buffer to 65°C before using it in this washing step.

427
428 J. Wash with 1 mL of RNase-free water. Incubate for 2 minutes using a sample mixer or a
429 thermomixer at maximum speed, at room temperature.

430
431 K. Repeat step “J” once, for a total of 2 washes with RNase-free water.

432 ▲ **CRITICAL (optional)** Instead of discarding the supernatant of this last wash, it can be
433 transferred to a new RNase-free 1.5 mL microcentrifuge tube and stored at -80°C as “Flow-
434 through fraction 3 (FT3)”. Following steps 18-28, RNA will need to be purified from the Flow-
435 through fraction 3 (FT3) before it can be used for any downstream analyses.

436 ▲ **CRITICAL STEP** At this point, we highly recommend that you **immediately** use the RNA
437 captured on the Dynabeads as a template for cDNA synthesis reaction or any other desired
438 downstream analyses. Do **not** store the RNA bound to the Dynabeads for future use.

439 440 **Illumina RNA-Seq library preparation**

441 ▲ **CRITICAL** While there are many workflows available to prepare RNA-Seq libraries
442 compatible with the Illumina platforms, we opted to use NuGen’s Ovation® Universal RNA-Seq
443 System since it provides a workflow suitable for whole transcriptome profiling with integrated
444 steps for efficient depletion of uninformative transcripts like rRNAs. The system is compatible
445 with input amounts of 10 – 100 ng of total or poly(A) selected RNA. For lower input amounts,

446 NuGen provides an alternative system named NuGen's Ovation® SoLo RNA-Seq System for
447 which the input amount needs to be in the range of 10 pg – 10 ng. Both systems provide
448 available workflows with rRNA depletion from a number of model organisms (e.g. human,
449 mouse, rat, Drosophila, and Arabidopsis).

450
451 35| Prepare first-strand cDNA using all the Dynabeads (with all the attached RNA) that are
452 recovered from step (35-K). Follow the manufacturer's protocol (NuGen Ovation® Universal
453 RNA-Seq System User Guide Doc No M01373v2, 2014) beginning with section V.A of the
454 protocol section (First Strand Primer Pre-mix Preparation), bypassing section V.B of the protocol
455 section (First Strand Synthesis with Integrated DNase Treatment) and finishing with section V.C
456 of the protocol section (First Strand cDNA synthesis Using DNase-treated RNA).

457 ▲ **CRITICAL** We highly recommend running the incubations for primer annealing and first-
458 strand cDNA synthesis with gentle mixing to prevent the beads from settling. This can be
459 achieved by using a thermomixer (e.g. Eppendorf's Thermomixer) with a heated top (e.g.
460 Eppendorf's ThermoTop) at the desired temperatures. Since we have recommended performing
461 at least two EU-RNA isolation reactions per each condition replicate, it is important to remember
462 that there are two first-strand cDNA synthesis reactions per each condition replicate.

463
464 36| Add 500 µL of 1X PBS to each reaction. Mix well by pipetting. Transfer the mixture into a
465 new RNase-free 1.5 mL microcentrifuge tube. Fast spin the microcentrifuge tube using a
466 benchtop mini spin microcentrifuge, apply the tube in a magnet for 2-3 minutes to immobilize the
467 beads, and discard the supernatant.

468 37| Repeat step 37 for a total of two washes with 1X PBS.

469 38| Resuspend the beads in 50 µL of RNaseA/T1/H elution mix (tabulated below, based on a
470 previous protocol) (52). Incubate the mixture at 37 °C for 30 min at 1,000 rpm in a Thermomixer
471 with a ThermoTop.

472

Component	Amount (µL)	Final Concentration
RNaseH buffer, 10X	5	1X
D-biotin, 50mM	12.5	12.5 mM
RNase cocktail enzyme	1	0.1 U/µL
RNaseH enzyme	1	0.1 U/µL
RNase-free water	30.5	
Total	50 (per reaction)	

473

474 39| Add 1 µL of 100% DMSO to each sample. Heat to 95 °C for 4 minutes with shaking using a
475 Thermomixer with a ThermoTop. Pulse-centrifuge the samples. Apply them to DynaMag2
476 magnet for 1-2 minutes. Transfer the supernatant with the eluted first-strand cDNA to a new
477 nuclease-free 1.5 mL microcentrifuge tube.

478

479 40| Purify the eluted first-strand cDNA using a Zymogen DNA Clean & Concentrator-5 column.
480 Add a 7X (350 µL) of DNA binding buffer. Mix by vortexing. Pulse-centrifuge the tubes. Add 1
481 volume (350 µL) of 96-100% ethanol and mix by vortexing. Wash the columns according to the
482 manufacturer's protocol. Elute the cDNA twice with 10 µL of nuclease-free water (for a final
483 volume of 20 µL).

484 ▲ **CRITICAL** Using of the Zymogen DNA Clean & Concentrator-5 columns under the conditions
485 detailed in step 40 will recover single-stranded cDNA as small as 20 nt. Standard binding

486 conditions, as detailed in the manufacturer's protocol, recover cDNA of 50 bp or larger, which
487 would result in a loss of short single-stranded cDNA molecules.

488 ■ **PAUSE POINT** cDNA samples can be stored at -80 °C for > 6 months.

489

490 41| Before proceeding to the second-strand cDNA synthesis step using NuGen's Ovation®
491 Universal RNA-Seq System, combine the purified eluted first-strand cDNA from each two (or
492 more) reactions of each condition replicate into one nuclease-free 1.5 mL microcentrifuge tube.
493 Concentrate the combined first-strand cDNA using a SpeedVac Concentrator until you reach a
494 final volume of 10 µL, which is the recommended volume for the second-strand cDNA synthesis
495 step as per the Ovation® Universal RNA-Seq System User Guide.

496 ▲ **CRITICAL** To avoid overdrying, we recommend setting the drying rate of the SpeedVac
497 Concentrator to "low" or "medium". If the sample gets overconcentrated to a volume less than 10
498 µL, bring up the volume to 10 µL using nuclease-free water. By the end of this step, each condition
499 replicate should have one single reaction since first-strand cDNA from all separate isolation
500 reactions should be pooled and concentrated into a final concentration of 10 µL.

501

502 42| Prepare second-strand cDNA using all the pooled, concentrated first-strand cDNA recovered
503 from step 42. Follow the directions of section V.D of the protocol section (Second Strand cDNA
504 Synthesis) in the manufacturer's protocol (NuGen Ovation® Universal RNA-Seq System User
505 Guide Doc No M01373v2, 2014).

506 ■ **PAUSE POINT** The double-stranded (ds)-cDNA produced at the end of this step can be
507 stored at -20 °C overnight or until you ready to proceed.

508

509 43| Treat ds-cDNA sample with Covaris M-series System according to the manufacturer's
510 directions to produce fragmented cDNA with a fragment size in the desired range. After
511 fragmentation, collect 100 µL from the Covaris tube. If the collected volume is lower than 100 µL,
512 add nuclease-free water to bring the total volume to 100 µL.

513 ▲ **CRITICAL** We recommend using the entire sample volume retrieved from step 43 (120 µL) for
514 the cDNA fragmentation step. Using the Covaris M220 System, we use the "snap-cap, 130 µL,
515 200 bp" DNA fragmentation protocol. Alternative fragmentation platforms and protocols may be
516 suitable for use with this RNA-Seq library preparation workflow; however, they have not been
517 validated by NuGEN.

518

519 44| Purify and concentrate the fragmented ds-cDNA using Agencourt RNAClean XP beads
520 following the directions in section V.F of the protocol section (cDNA Concentration After
521 Fragmentation) in the manufacturer's protocol (NuGen Ovation® Universal RNA-Seq System
522 User Guide Doc No M01373v2, 2014).

523 ■ **PAUSE POINT** The purified, concentrated double-stranded (ds)-cDNA produced at the end of
524 this step can be stored at -20 °C overnight or until you are ready to proceed.

525

526 45| Prepare the fragmented ds-cDNA sample for adaptor/barcode ligation by following the
527 manufacturer's directions in section V.G. (End Repair) of the protocol section.

528 46| Ligate the appropriate adaptor/barcode to end-repaired ds-cDNA from step 46. Following
529 the manufacturer's directions in section V.H. (Ligation) of the protocol section.

530 ▲ **CRITICAL** The ligation buffer mix in the NuGEN Ovation® Universal RNA-Seq System is very
531 viscous. Be sure to pipet this reagent slowly to achieve an accurate reaction volume. If you are
532 performing a 2 (or more)-plex multiplex sequencing, it is important to follow the manufacturer's
533 directions regarding their strict barcode pairing requirements.

534

535 47| Deplete rRNA content of the adapter-ligated ds-cDNA sample by following the manufacturer's
536 directions in sections V.I. (Strand Selection I), V.J. (Strand Selection I Purification), and V.K.
537 (Strand Selection II) of the protocol section.

538 ▲ **CRITICAL** Be sure to use the appropriate AnyDeplete rRNA primer mixture for your model
539 organism.

540

541 48| Prepare your library for amplification by cleaving the ligated adapter. Follow the
542 manufacturer's directions in section V.L. (Adaptor Cleavage) of the protocol section.

543

544 49| Amplify the ds-cDNA library sample by following the manufacturer's directions in section V.M.
545 (Library Amplification) of the protocol section.

546 ▲ **CRITICAL** We *highly* recommend determining the appropriate number of PCR cycles used
547 for library amplification via real-time qPCR by following the manufacturer's guidelines in Appendix
548 section VII.B. (Using qPCR to Determine the Number of PCR Cycles). To avoid excess library
549 amplification which could yield biases, the number of PCR cycles used for library amplification
550 should be within the exponential phase of the real-time qPCR amplification plot.

551

552 50| Purify the RNA-Seq library with Agencourt RNAClean XP beads following the directions in
553 section V.N of the protocol section (Bead Purification of the Amplified Material) in the
554 manufacturer's protocol.

555

556 51| Determine the quality of the RNA-Seq amplified library by using an Agilent Bioanalyzer DNA
557 high-sensitivity chip, according to the manufacturer's directions.

558

559 52| Quantify the concentration of the RNA-Seq library using a Qubit fluorometer, according to the
560 manufacturer's directions.

561 ■ **PAUSE POINT (end of day 2)** RNA-Seq libraries can be stored at -20°C until sequencing
562 run.

563

564 Pool equimolar amounts of each RNA-Seq library, for multiplex sequencing, into the final
565 concentration and volume recommended by the Illumina platform to be used. Sequence pooled
566 libraries on an Illumina-based machine using standard conditions.