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APPENDICES

Appendix A. Conversion Criteria for Risk of Bias Assessment

Question	Definitely Low Risk of Bias (++)	Probably Low Risk of Bias (+)	Probably High Risk of Bias (-/NR)	Definitely High Risk of Bias (--)
Was the administered dose or exposure level adequately randomized?	There is direct evidence that animals were allocated to any study group (including control) using random consistent method **AND** there is direct concurrent control group is used as indication that randomization covered to all study groups	There is indirect evidence that animals were allocated to any study group (including control) using random consistent method **AND** there is direct/indirect evidence that concurrent control is used as indication that randomization covered all study groups **OR** It is deemed that allocation without clear random component would not appreciably bias the result	There is indirect evidence that animals were allocated to any study group (including controls) using the non-random method **OR** There is indirect evidence that there was a lack of concurrent control group **OR** There is insufficient information provided about how subjects were allocated to study groups (NR)	There is direct evidence that animals were allocated to any study group (including controls) using the non-random method **OR** There is direct evidence that there was a lack of concurrent control group
Was allocation to study groups adequately concealed?	There is direct evidence at the time of assigning study groups that the research personnel did not know what group of animals were allocated to **AND** it is unlikely that they could broke the blinding of allocation until the assignment was completed	There is indirect evidence at the time of assigning study groups that the research personnel did not know what group of animals were allocated to **AND** it is unlikely that they could broke the blinding of allocation until the assignment was completed **OR** It is deemed that allocation that lack of adequate allocation concealment would not appreciably bias the result	There is indirect evidence at the time of assigning study groups which the research personnel did not know what group of animals were allocated to **AND** It is likely that they could break the blinding of allocation until the assignment was completed **OR** There is insufficient information provided about allocation to study groups (NR)	There is direct evidence at the time of assigning study groups which the research personnel did not know what group of animals were allocated to **AND** It is likely that they could have broken the blinding of allocation until the assignment was completed
Were experimental conditions identical across study groups?	There is direct evidence that same vehicle was used in control and experimental animals	There is indirect evidence that same vehicle was used in control and experimental animals	There is indirect evidence that difference vehicle was used in control and experimental animals	There is direct evidence that difference vehicle was used in control and experimental animals

	AND evidence that non-treatment-related experimental conditions were identical across study groups (Study reports in detail explicitly)	**AND** Identical non-treatment related experimental conditions are assumed if authors did not report differences in housing or husbandry **OR** It is deemed that vehicle used would not appreciably bias the result **AND** Identical non-treatment related experimental conditions are assumed if authors did not report differences in housing or husbandry	**OR** Author did not report the vehicle used (NR) **OR** There is indirect evidence that non-treatment-related experimental conditions were not comparable between study group	or the control is untreated **OR** There is direct evidence that non-treatment-related experimental conditions were not comparable between study groups
Were the research personnel and human subjects blinded to the study group during the study?	There is direct evidence that the research personnel were adequately blinded to study group and it is unlikely that they broke the blinding during the study	There is direct evidence that the research personnel were adequately blinded to the study groups **AND** it is unlikely they broke the blinding during the study **OR** It is deemed that lack of adequate blinding during the study would not appreciably bias the results	There is indirect evidence that the research personnel were not adequately blinded to study group **OR** There is insufficient information provided about blinding to study group (NR)	There is direct evidence that the research personnel were not adequately blinded to study group
Were outcome data complete without attrition or exclusion from analysis?	There is direct evidence that loss of animals was adequately addressed **AND** reasons were documented when animal was removed from the study **OR** Missing data have been imputed using appropriate methods (Ensure that characteristics of animals are not significantly different	There is indirect evidence that loss of animals was adequately addressed and reasons were documented when animal were removed from the study **OR** It is deemed that the proportion lost would not appreciably bias the results	There is indirect evidence that loss of animal was not adequately addressed and loss of animals was unacceptably large **OR** There is insufficient information provided about loss of animals (NR)	There is direct evidence that loss of animals was not adequately addressed **AND** loss of animal was unacceptably large

	from animals retained from the analysis)			
Can we be confident in the exposure characterization?	There is direct evidence that the exposure was independently characterized by the researcher and purity confirmed as ≥99% for single substance or non-mixture evaluations **AND** The exposure was consistently administered across treatment groups (The same method and time-frame)	There is indirect evidence that the exposure was independently characterized by the researcher and purity confirmed as ≥99% for single substance or non-mixture evaluations **AND** there is indirect evidence that exposure was consistently administered across treatment groups (The same method and time-frame) **OR** There is a direct evidence that purity was independently confirmed as ≥98% AND it is deemed that impurity up to 2% would not appreciably bias the results **AND** there is indirect evidence that exposure was consistently administered across treatment groups (The same method and time-frame)	There is indirect evidence that the exposure was assessed using poorly validated methods **OR** There is insufficient information provided about the validity of the exposure assessment method but no evidence for concern (NR)	There is direct evidence that the exposure was assessed using poorly validated methods
Can we be confident in the outcome assessment?	There is direct evidence that the outcome was assessed using well-established or gold standards method **AND** the assessment conducted at the same length of time in all study groups **AND** there is direct evidence that the outcome assessors were adequately	There is direct evidence that the outcome was assessed using well-established or gold standards method **AND** the assessment conducted at the same length of time in all study groups **AND** there is indirect evidence that the outcome assessors were adequately	There is indirect evidence that the outcome assessment method is an insensitive instrument **OR** The length of time after initial exposure differed by study group **OR** There is indirect evidence that it was possible for outcome	There is direct evidence that the outcome assessment method is an insensitive instrument **OR** The length of time after initial exposure differed by study group **OR** There is direct evidence that it was possible for outcome

	blinded to the study group and it is unlikely that they broke the blinding prior to reporting outcomes	blinded to the study group and it is unlikely that they broke the blinding prior to reporting outcomes **OR** It is deemed that the outcome assessment method used would not appreciably bias the results **AND** there is indirect evidence that the outcome assessors were adequately blinded to the study group and it is unlikely that they broke the blinding prior to reporting outcomes **OR** It is deemed that lack of adequate blinding of outcome assessors would not appreciably bias the results	assessors to infer the study group prior to reporting outcomes without sufficient quality control measures **OR** There is insufficient information provided about blinding of outcome assessors (NR)	assessors to infer the study group prior to reporting outcomes without sufficient quality control measures
Were all measured outcomes reported?	There is direct evidence that all of the study measured outcomes outline in the protocol, methods, abstract, and/or introduction (data that relevant for evaluation) have been reported	There is indirect evidence that all of the study measured outcomes outline in the protocol, methods, abstract, and/or introduction (data that relevant for evaluation) have been reported **OR** Analyses that had not been planned in advance are clearly indicated as such **AND** it is deemed that the additional analyses were appropriate and selective reporting would not appreciably bias the results	There is indirect evidence that all of the study measured outcomes outline in the protocol, methods, abstract, and/or introduction have been reported **OR** There is indirect evidence that unplanned analyses were included that may appreciably bias results **OR** There is insufficient information provided about selective outcome reporting (NR)	There is direct evidence that all of the study measured outcomes outline in the protocol, methods, abstract, and/or introduction have been reported
Were there no other potential threats to internal validity (statistical	There is direct evidence that the statistical method selected is appropriate	There is indirect evidence that the statistical method selected is appropriate	There is insufficient information provided about selective outcome reporting	There is direct evidence that the statistical method selected is not

methods were appropriate and researchers adhered to study protocol)?	(rationale on the selection of statistical method) **AND** there is indirect evidence that the researcher adhere to the study protocol **AND** there is direct evidence on limitation of the study or potential confounding and modifying variables	(rationale on the selection of statistical method) **AND** there is indirect evidence that the researcher adhere to study protocol **AND** there is indirect evidence on limitation of the study or potential confounding and modifying variables	(NR)	appropriate (rationale on the selection of statistical method) **AND/OR** There is direct evidence that the researcher adhere to study protocol **AND/OR** there is direct evidence that the confounding and modifying variables cause bias in the study

Appendix B. Criteria for Determining Initial Confidence in the Body of Evidence Quality Assessment

Study Design Features	Description
Controlled Exposure	The exposure of the substance should be experimentally controlled
Exposure Conducted before Outcome	The exposure assessment showed that the exposure occurred before the development of the outcome or concurrent with aggravation/amplification of an existing condition
Individual Outcome Data	The outcomes should be assessed on individual level
Comparison Group Used	Appropriate comparison group should be used in the study

Appendix C. Criteria for Determining Final Confidence in the Body of Evidence Quality Assessment

Domains	Description
Risk of Bias Across Studies	Confidence was downgraded if most of the information was derived from tier 3 risk of bias

	study.
Unexplained Consistency	Confidence was downgraded if there is an unexplained consistency that not linked to the variation in the characteristic of the animal model used, exposure or treatment settings, and timing of outcome measurement
Indirectness	Confidence was downgraded if the study using non-vertebrate mammalian model or genetically modified rodents, bird, reptile, amphibian, and fish
Imprecision	Confidence was downgraded if the study has a large standard deviations and improper statistical analysis was used
Publication Bias	Confidence was downgraded if the studies were published in abstracts or type of grey literature or the conflict of interests present, or preliminary study
Large Magnitude Effect	Confidence was increased if statistically significant association or causation relationship observed
Dose Response	Confidence was increased if non-monotonic dose-response observed within studies
All Plausible Confounding	Confidence was increased if the study address the possible confounding that might affect the interpretation
Consistency Across Animal Study	Confidence was increased if there is a consistency across different strain of animals or species

Appendix D. Risk of Bias Across Studies Tiering Criteria

	Risk of Bias Domains and Ratings								
	Key Criteria			**Other Risk of Bias Criteria**					
Tier 1 : A Study must be rated as “definitely low” or “probably low” risk of bias for key criteria **AND** have most other risk of bias criteria answered “definitely low” or “ probably low” risk of bias Tier 2 : A Study meets neither criteria for tier 1 or tier 3 Tier 3 : A study must be rated as “definitely high” or “probably high” risk of bias for key criteria **AND** have most other risk of bias criteria answered “definitely high” or “probably high” risk of bias	Can we be confident in the exposure characterization?	Can we be confident in the outcome assessment ?	Were there no other potential threats to internal validity (statistical methods were appropriate and researchers adhered to study protocol)?	Was the administered dose or exposure level adequately randomized?	Was allocation to study groups adequately concealed?	Were experimental conditions identical across study groups?	Were the research personnel and human subjects blinded to the study group during the study?	Were outcome data complete without attrition or exclusion from analysis?	Were all measured outcomes reported?

Appendix F. Prisma-P 2020 Checklist

Section and Topic	Item #	Checklist item	Location where item is reported
TITLE			
Title	1	Identify the report as a systematic review.	Cover Page
ABSTRACT			
Abstract	2	See the PRISMA 2020 for Abstracts checklist.	Page IV
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of existing knowledge.	Page 1-5
Objectives	4	Provide an explicit statement of the objective(s) or question(s) the review addresses.	Page 5
METHODS			
Eligibility criteria	5	Specify the inclusion and exclusion criteria for the review and how studies were grouped for the syntheses.	Page 41-42
Information sources	6	Specify all databases, registers, websites, organisations, reference lists and other sources searched or consulted to identify studies. Specify the date when each source was last searched or consulted.	Page 42-43

Search strategy	7	Present the full search strategies for all databases, registers and websites, including any filters and limits used.	Page 42-43
Selection process	8	Specify the methods used to decide whether a study met the inclusion criteria of the review, including how many reviewers screened each record and each report retrieved, whether they worked independently, and if applicable, details of automation tools used in the process.	Page 44
Data collection process	9	Specify the methods used to collect data from reports, including how many reviewers collected data from each report, whether they worked independently, any processes for obtaining or confirming data from study investigators, and if applicable, details of automation tools used in the process.	Page 44
Data items	10a	List and define all outcomes for which data were sought. Specify whether all results that were compatible with each outcome domain in each study were sought (e.g. for all measures, time points, analyses), and if not, the methods used to decide which results to collect.	Page 45-47
	10b	List and define all other variables for which data were sought (e.g. participant and intervention characteristics, funding sources). Describe any assumptions made about any missing or unclear information.	-
Study risk of bias assessment	11	Specify the methods used to assess risk of bias in the included studies, including details of the tool(s) used, how many reviewers assessed each study and whether they worked independently, and if applicable, details of automation tools used in the process.	Page 47
Effect measures	12	Specify for each outcome the effect measure(s) (e.g. risk ratio, mean difference) used in the synthesis or presentation of results.	-
Synthesis methods	13a	Describe the processes used to decide which studies were eligible for each synthesis (e.g. tabulating the study intervention characteristics and comparing against the planned groups for each synthesis (item #5)).	Page 45-47
	13b	Describe any methods required to prepare the data for presentation or synthesis, such as handling of missing summary statistics, or data conversions.	-

	13c	Describe any methods used to tabulate or visually display results of individual studies and syntheses.	-
	13d	Describe any methods used to synthesize results and provide a rationale for the choice(s). If meta-analysis was performed, describe the model(s), method(s) to identify the presence and extent of statistical heterogeneity, and software package(s) used.	-
	13e	Describe any methods used to explore possible causes of heterogeneity among study results (e.g. subgroup analysis, meta-regression).	-
	13f	Describe any sensitivity analyses conducted to assess robustness of the synthesized results.	-
Reporting bias assessment	14	Describe any methods used to assess risk of bias due to missing results in a synthesis (arising from reporting biases).	Page 47
Certainty assessment	15	Describe any methods used to assess certainty (or confidence) in the body of evidence for an outcome.	Page 48
RESULTS			
Study selection	16a	Describe the results of the search and selection process, from the number of records identified in the search to the number of studies included in the review, ideally using a flow diagram.	Page 57
	16b	Cite studies that might appear to meet the inclusion criteria, but which were excluded, and explain why they were excluded.	-
Study characteristics	17	Cite each included study and present its characteristics.	Page 58

Risk of bias in studies	18	Present assessments of risk of bias for each included study.	Page 59
Results of individual studies	19	For all outcomes, present, for each study: (a) summary statistics for each group (where appropriate) and (b) an effect estimate and its precision (e.g. confidence/credible interval), ideally using structured tables or plots.	Page 69, Page 77, Page 81
Results of syntheses	20a	For each synthesis, briefly summarise the characteristics and risk of bias among contributing studies.	Page 57
	20b	Present results of all statistical syntheses conducted. If meta-analysis was done, present for each the summary estimate and its precision (e.g. confidence/credible interval) and measures of statistical heterogeneity. If comparing groups, describe the direction of the effect.	-
	20c	Present results of all investigations of possible causes of heterogeneity among study results.	-
	20d	Present results of all sensitivity analyses conducted to assess the robustness of the synthesized results.	-
Reporting biases	21	Present assessments of risk of bias due to missing results (arising from reporting biases) for each synthesis assessed.	Page 58
Certainty of evidence	22	Present assessments of certainty (or confidence) in the body of evidence for each outcome assessed.	Page 58
DISCUSSION			
Discussion	23a	Provide a general interpretation of the results in the context of other evidence.	Page 86-Page 97

	23b	Discuss any limitations of the evidence included in the review.	Page 98
	23c	Discuss any limitations of the review processes used.	Page 105
	23d	Discuss implications of the results for practice, policy, and future research.	Page 109
OTHER INFORMATION			
Registration and protocol	24a	Provide registration information for the review, including register name and registration number, or state that the review was not registered.	-
	24b	Indicate where the review protocol can be accessed, or state that a protocol was not prepared.	-
	24c	Describe and explain any amendments to information provided at registration or in the protocol.	-
Support	25	Describe sources of financial or non-financial support for the review, and the role of the funders or sponsors in the review.	-
Competing interests	26	Declare any competing interests of review authors.	-
Availability of data, code and other materials	27	Report which of the following are publicly available and where they can be found: template data collection forms; data extracted from included studies; data used for all analyses; analytic code; any other materials used in the review.	-

Appendix F. GENEzol™ Reagent (Geneaid) RNA extraction Protocol

RNA Extraction Protocol Procedure

Please read the entire instruction manual prior to starting the Protocol Procedure.

1. Sample Homogenization

Sample preparation should be performed at room temperature. Please follow the table below for specific sample preparation. To avoid DNA contamination of extracted RNA, be sure and use the indicated volume of GENEzol™ Reagent.

Sample	Procedure
Adherent Cultured Cells	1. Remove the culture medium from culture dish. 2. **Directly add 100 µl of GENEzol™ Reagent per cm^2 of culture dish surface area.** 3. Lyse the cells directly in the culture dish by pipetting several times. 4. Incubate the sample mixture for 5 minutes at room temperature. 5. Transfer the sample to a new 1.5 ml of microcentrifuge tube (RNase-free).
Suspension Cultured Cells	1. **Transfer cells (up to 5 x 10^6)** to a 1.5 ml microcentrifuge tube (RNase-free). 2. Harvest cells by centrifugation at 300 x g for 5 minutes to form a cell pellet. 3. Remove the culture medium completely. 4. **Add 1 ml of GENEzol™ Reagent** to the cell pellet and lyse the cells by pipetting several times. 5. Incubate the sample mixture for 5 minutes at room temperature.
Tissue	1. **Add 1 ml of GENEzol™ Reagent to 50–100 mg of tissue** sample. 2. Homogenize tissue samples using a glass-Teflon or Polytron homogenizer. 3. Incubate the homogenized sample for 5 minutes at room temperature. 4. Transfer the sample to a new 1.5 ml of microcentrifuge tube (RNase-free).
Body Fluids (blood, buffy coat, plasma, serum)	1. **Transfer up to 300 µl of liquid sample** to a 1.5 ml of microcentrifuge tube (RNase-free). 2. **Add 3 volumes of GENEzol™ Reagent to each volume of liquid sample (3:1)** 3. Mix well by vortex. 4. Incubate the sample mixture for 5 minutes at room temperature.
NOTE: For samples which contain high levels of fat, proteins, polysaccharides, or extracellular material, perform this optional step following sample homogenization. However, if DNA extraction is required, DO NOT perform this additional step. 1. Centrifuge the sample at 12-16,000 x g for 10 minutes to remove insoluble particles. NOTE: Following centrifugation of high fat content samples, a layer a fat will float on the supernatant. Remove and discard the fatty layer. 2. Transfer the clear supernatant to a new 1.5 ml microcentrifuge tube (RNase-free). 3. Proceed to Step 2 Phase Separation.	

2. Phase Separation

1. **Add 200 µl of chloroform to the sample per 1 ml of GENEzol™ Reagent used in sample homogenization.**
2. Shake the microcentrifuge tube vigorously for 10 seconds.
3. Centrifuge the sample at 12–16,000 x g for 15 minutes at 4ºC to separate the phases.

NOTE: RNA is in the colorless upper aqueous phase which is approximately 50% of the total volume.

4. Transfer the upper aqueous phase to a new 1.5 ml microcentrifuge tube (RNase-free).

NOTE: Be careful not to draw any of the interphase layer (white) or organic phase layer (red) when transferring the aqueous layer. If DNA isolation is required, save the interphase and organic phase then proceed with the DNA Extraction protocol on page 3.

3. RNA Precipitation

1. **Add 1 volume of isopropanol to the aqueous phase** then mix by inverting the tube several times.
2. Incubate the sample mixture for 10 minutes at room temperature.
3. Centrifuge the sample at 12–16,000 x g for 10 minutes at 4ºC to form a tight RNA pellet.
4. Carefully remove and discard the supernatant.

4. RNA Wash

1. **Add 1 ml of 70% ethanol** to wash the RNA pellet then vortex briefly.
2. Centrifuge the sample at 12–16,000 x g for 5 minutes at 4ºC.
3. Being careful not to contact the RNA pellet, remove the supernatant with a pipette.
4. Air-dry the RNA pellet for 5-10 minutes at room temperature.

NOTE: DO NOT dry the RNA pellet by vacuum centrifuge and avoid over drying the RNA pellet.

5. RNA Resuspension

1. **Add 20-50 µl of RNase-free Water** to resuspend the RNA pellet.
2. Incubate at 55-60ºC for 10-15 minutes to dissolve the RNA pellet.

NOTE: Occasionaly tapping the bottom of the tube during incubation will promote RNA rehydration.

The RNA is ready for downstream applications or storage at -70ºC.

Appendix G. GENEzol™ TriRNA Pure Kit (Geneaid) Protocol

RNA Purification Protocol Procedure

Please read the entire instruction manual prior to starting the Protocol Procedure.

Additional Requirements

absolute ethanol, lysozyme and bacteria lysis buffer (bacteria only), 1.5 ml microcentrifuge tubes (RNase-free)

Optional Requirements

1 µL of 20 mM EGTA (pH=8.0) for Optional Step 2: DNA Digestion in Solution

1. Sample Homogenization and Lysis

Sample preparation should be performed at room temperature. Please follow the table below for specific sample preparation. To avoid DNA contamination of extracted RNA, be sure and use the indicated volume of GENEzol™ Reagent. Lysozyme (LY420) and Bacteria Lysis Buffer (BLB00030) can be purchased directly from Geneaid.

Sample	Procedure
Adherent Cultured Cells	1. Remove the culture medium from the culture dish. 2. **Directly add 100 µl of GENEzol™ Reagent per cm^2 of culture dish surface area.** 3. Lyse the cells directly in the culture dish by pipetting several times. 4. Incubate the sample mixture for 5 minutes at room temperature. 5. Transfer the sample to a 1.5 ml microcentrifuge tube (RNase-free).
Suspension Cultured Cells	1. **Transfer cells (up to 5 x 10^6)** to a 1.5 ml microcentrifuge tube (RNase-free). 2. Harvest by centrifugation at 300 x g for 5 minutes then remove the culture medium completely. 3. **700 µl of GENEzol™ Reagent** should be added to the cell pellet then mixed several times by pipette. 4. Incubate the sample mixture for 5 minutes at room temperature.
Tissue	1. **Excise 10-50 mg of tissue** directly from the animal or remove the tissue sample from storage. Do not use more than 50 mg of tissue per reaction. 2. **Homogenize tissue samples using one of the following methods: A.** Transfer the tissue and 700 µl of GENEzol™ Reagent to a 2 ml centrifuge tube containing ceramic beads or stainless steel beads then homogenize the sample with a TissueLyser, Disruptor Genie or similar. **B.** Transfer the tissue and 700 µl of GENEzol™ Reagent to a 1.5 ml centrifuge tube and grind the tissue with a micropestle a few times then shear the tissue by passing the lysate through a 20-G needle syringe 10 times. **C.** Transfer the tissue and 700 µl of GENEzol™ Reagent to a glass-Teflon or Polytron homogenizer. Transfer the homogenized sample to a 1.5 ml microcentrifuge tube (RNase-free). 3. Incubate the homogenized sample for 5 minutes at room temperature.
Body Fluids (blood, buffy coat, plasma, serum)	1. **Transfer up to 200 µl of liquid sample** to a 1.5 ml of microcentrifuge tube (RNase-free). 2. **Add 3 volumes of GENEzol™ Reagent per 1 volume of sample (3:1)** then mix well by vortex. 3. Incubate the sample mixture for 5 minutes at room temperature.
Bacteria	1. **Transfer bacteria cells (up to 1 x 10^9)** to a 1.5 ml microcentrifuge tube (RNase-free). 2. Centrifuge at 12-16,000 x g for 2 minutes then remove the supernatant completely. 3. **Weigh and transfer 10 mg of lysozyme powder** to a new 1.5 ml microcentrifuge tube (RNase-free). 4. **Add 1 ml of bacteria lysis buffer** to the microcentrifuge tube containing **10 mg of lysozyme**. 5. Vortex the tube until the lysozyme powder is completely dissolved. 6. **Add 100 µl of bacteria lysis buffer containing lysozyme** to the bacteria cell pellet. 7. Resuspend the cell pellet by vortex or pipetting. NOTE: Residual bacteria lysis buffer containing lysozyme should be stored at 4°C for 2 weeks. 8. Incubate the sample for 5 minutes at room temperature. 9. Add **700 µl of GENEzol™ Reagent,** mix well by pipette then incubate at room temperature for 5 minutes.
Plant	1. **Cut off 20-50 mg of fresh or frozen plant tissue**. Do not use more than 50 mg of plant tissue per rxn. 2. **Homogenize plant tissue samples using one of the following methods: A.** Transfer the plant tissue and 700 µl GENEzol™ Reagent to a 2 ml centrifuge tube containing ceramic beads or stainless steel beads then homogenize the sample with a TissueLyser, Disruptor Genie or similar. **B.** Add liquid nitrogen to a mortar (RNase-free) and grind the plant tissue thoroughly using a pestle (RNase-free). Transfer the plant tissue powder and 700 µl of GENEzol™ Reagent to a 1.5 ml centrifuge tube then vortex briefly. 3. Incubate the homogenized sample for 5 minutes at room temperature.

2. RNA Binding

1. Centrifuge the sample at 12-16,000 x g for 1 minute to remove cell debris then transfer the clear supernatant to a new 1.5 ml microcentrifuge tube (RNase-free).

NOTE: When extracting RNA from cultured cell samples, cell debris will not commonly collect on the bottom of the microcentrifuge tube. In this case, proceed without transferring the supernatant.

2. **Add 1 volume of absolute ethanol directly to 1 volume of sample mixture (1:1) in GENEzol™ Reagent**.

3. Mix well by vortex then place a **RB Column in a 2 ml Collection Tube**.

4. **Transfer 700 µl of the sample mixture to the RB Column**. Centrifuge at 14-16,000 x g for 1 minute then discard the flow-through.

5. Repeat the RNA Binding Step by transferring the remaining sample mixture to the **RB Column**.

6. Centrifuge at 14-16,000 x g for 1 minute then discard the flow-through. Place the **RB Column** in a new **2 ml Collection Tube**.

Optional Step 1: In Column DNase I Digestion

IMPORTANT

DNA contamination is significantly reduced following In Column DNase I Digestion. However, traces of residual DNA may be detected in very sensitive applications. In this situation, please perform Optional Step 2: DNA Digestion In Solution instead to efficiently remove trace amounts of DNA. Standard DNase buffers are incompatible with In Column DNase I Digestion and may affect RNA integrity and reduce yield.

1. Add **400 µl of Wash Buffer (make sure ethanol was added) to the RB Column** then centrifuge at 14-16,000 x g for 30 seconds.
2. Discard the flow-through and place the **RB Column** back in the **2 ml Collection Tube**.
3. Prepare DNase I solution in a 1.5 ml microcentrifuge tube (RNase-free) as follows:

DNase I	5 µl (2 U/µl)
DNase I Reaction Buffer	45 µl
Total volume	50 µl

4. Gently pipette the DNase I solution to mix (DO NOT vortex) then add **DNase I solution (50 µl)** into the **CENTER** of the **RB column** matrix.
5. Incubate the column for 15 minutes at room temperature (20-30ºC) then proceed with RNA Wash.

3. RNA Wash

1. **Add 400 µl of Pre-Wash Buffer (make sure ethanol was added)** to the **RB Column** then centrifuge at 14-16,000 x g for 30 seconds.
2. Discard the flow-through then place the **RB Column** back in the **2 ml Collection Tube**.
3. **Add 600 µl of Wash Buffer (make sure ethanol was added)** to the **RB Column**.
4. Centrifuge at 14-16,000 x g for 30 seconds then discard the flow-through. Place the **RB Column** back in the **2 ml Collection Tube**.
5. **Add 600 µl of Wash Buffer (make sure ethanol was added)** to the **RB Column**.
6. Centrifuge at 14-16,000 x g for 30 seconds then discard the flow-through.
7. Place the **RB Column** back in the **2 ml Collection Tube**.

NOTE: For blood samples only, wash the RB Column again with 600 µl of Wash Buffer.

8. Centrifuge at 14-16,000 x g for 3 minutes to dry the column matrix.

4. RNA Elution

1. Place the dry **RB Column** in a clean 1.5 ml microcentrifuge tube (RNase-free).
2. **Add 25-50 µl of RNase-free Water** into the **CENTER** of the column matrix.
3. Let stand for at least 3 minutes to ensure the **RNase-free Water** is completely absorbed by the matrix.
4. Centrifuge at 14-16,000 x g for 1 minute to elute the purified RNA.

Optional Step 2: DNA Digestion In Solution

1. Prepare DNase I reaction in a 1.5 ml microcentrifuge tube (RNase-free) as follows:

RNA in RNase-free water	1-40 µl
DNase I	0.5 µl/µg RNA
DNase I Reaction Buffer	5 µl
RNase-free water	add to final volume = 50 µl
Total volume	50 µl

2. Gently pipette the DNase I reaction solution to mix (DO NOT vortex) then incubate the microcentrifuge tube at 37ºC for 15-30 minutes.
3. Stop the reaction by adding 1 µl of 20 mM EGTA (pH=8.0) then incubate the microcentrifuge tube at 65°C for 10 minutes.

NOTE: DNase I Reaction Buffer may cause aberrant migration or smearing of RNA on gels. If analyzing RNA by gel electrophoresis, repurify the RNA sample by using the Geneaid™ RNA Cleanup Kit instead of stopping the reaction with EGTA.

Appendix H. RevertAid First Strand cDNA Synthesis Kit (THermo Scientific™) Protocol

PROTOCOLS

I. First Strand cDNA Synthesis

After thawing, mix and briefly centrifuge the components of the kit. Store on ice.

1. Add the following reagents into a sterile, nuclease-free tube on ice in the indicated order:

Template RNA	total RNA *or* poly(A) mRNA *or* specific RNA	0.1 ng - 5 µg 10 pg - 0.5 µg 0.01 pg - 0.5 µg
Primer	Oligo $(dT)_{18}$ primer *or* Random Hexamer primer *or* gene-specific primer	1 µL 1 µL 15-20 pmol
Water, nuclease-free		to 12 µL
	Total volume	12 µL

2. *Optional.* If the RNA template is GC-rich or contains secondary structures, mix gently, centrifuge briefly and incubate at 65°C for 5 min. Chill on ice, spin down and place the vial back on ice.
3. Add the following components in the indicated order:

5X Reaction Buffer	4 µL
RiboLock RNase Inhibitor (20 U/µL)	1 µL
10 mM dNTP Mix	2 µL
RevertAid M-MuLV RT (200 U/µL)	1 µL
Total volume	20 µL

4. Mix gently and centrifuge briefly.
5. For oligo$(dT)_{18}$ or gene-specific primed cDNA synthesis, incubate for 60 min at 42°C.
   For random hexamer primed synthesis, incubate for 5 min at 25°C followed by 60 min at 42°C.
   Note. For GC-rich RNA templates the reaction temperature can be increased up to 45°C.
6. Terminate the reaction by heating at 70°C for 5 min.

The reverse transcription reaction product can be directly used in PCR applications or stored at -20°C for less than one week. For longer storage, -70°C is recommended

Appendix I. QuantiNova SYBR Green RT-PCR Kit (Qiagen) Protocol

1. Thaw QuantiNova SYBR Green RT-PCR Master Mix, QuantiNova Yellow Template Dilution Buffer, template RNA, QuantiNova Internal Control RNA (optional), primers, QN ROX Reference Dye (if required) and RNase-free water. Mix the individual solutions.
2. Prepare a reaction mix according to Table 1. Due to the 2-phase hot start of both the RT and the PCR reactions, it is not necessary to keep samples on ice during reaction setup or while programming the real-time cycler.

Table1. Reaction mix setup

Component	96-well block, Rotor-Gene	384-well block	Final concentration
2x SYBR Green RT-PCR Master Mix	10 µl	5 µl	1x
QN ROX Reference Dye (AB instruments only)	1 µl/0.1 µl*	0.5 µl/0.05 µl*	1x
QN SYBR Green RT-Mix	0.2 µl	0.1 µl	1x
20x primer mix (or Ctrl_QNIC_1_SG QuantiTect Primer Assay†)	1 µl†	0.5 µl†	0.5 µM forward primer 0.5 µM reverse primer
QN IC RNA (optional)	1 µl	1 µl	1x
RNase-free water	Variable	Variable	–
Template RNA (added at step 4)	Variable	Variable	≤200 ng/reaction
Total reaction volume	**20 µl**	**10 µl**	**–**

*Results in a 1:20 dilution for high ROX dye cyclers (i.e., ABI PRISM 7000, Applied Biosystems 7300, 7900 and StepOne Real-Time PCR Systems) and a 1:200 dilution for low-ROX dye cyclers (i.e., Applied Biosystems 7500 and ViiA7 Real-Time PCR Systems) in the final 1x reaction.

† If using the QN IC RNA to monitor RT-PCR amplification, add 2 µl (for 96-well) or 1 µl (for 384-well) of the 10x Ctrl_QNIC_1_SG QuantiTect Primer Assay.

3. Mix the reaction thoroughly and dispense appropriate volumes into PCR tubes, PCR capillaries or wells of a PCR plate.
4. Add template RNA (200 ng – 100 fg per reaction, depending on target transcript abundance) to the individual PCR tubes, capillaries or wells containing the reaction mix.
5. Program the real-time cycler according to Table 2.

   Note: Data acquisition should be performed during the combined annealing/extension step.
6. Place the PCR tubes or plates in the real-time cycler and start the cycling program.

Table 2. Cycling conditions

Step	Time	Temperature	Ramp rate
RT-step	10 min	50°C	Maximal/fast mode
PCR initial heat activation	2 min	95°C	Maximal/fast mode
2-step cycling			
Denaturation	5 s	95°C	Maximal/fast mode
Combined annealing/extension	10 s*	60°C	Maximal/fast mode
Number of cycles	40†		

*If your cycler does not accept this short time for data acquisition, choose the shortest acceptable time.

† The number of cycles depends on the amount of template RNA.

Appendix J. Normalized RT-PCR Amplification Curve for Primer Efficiency Determination

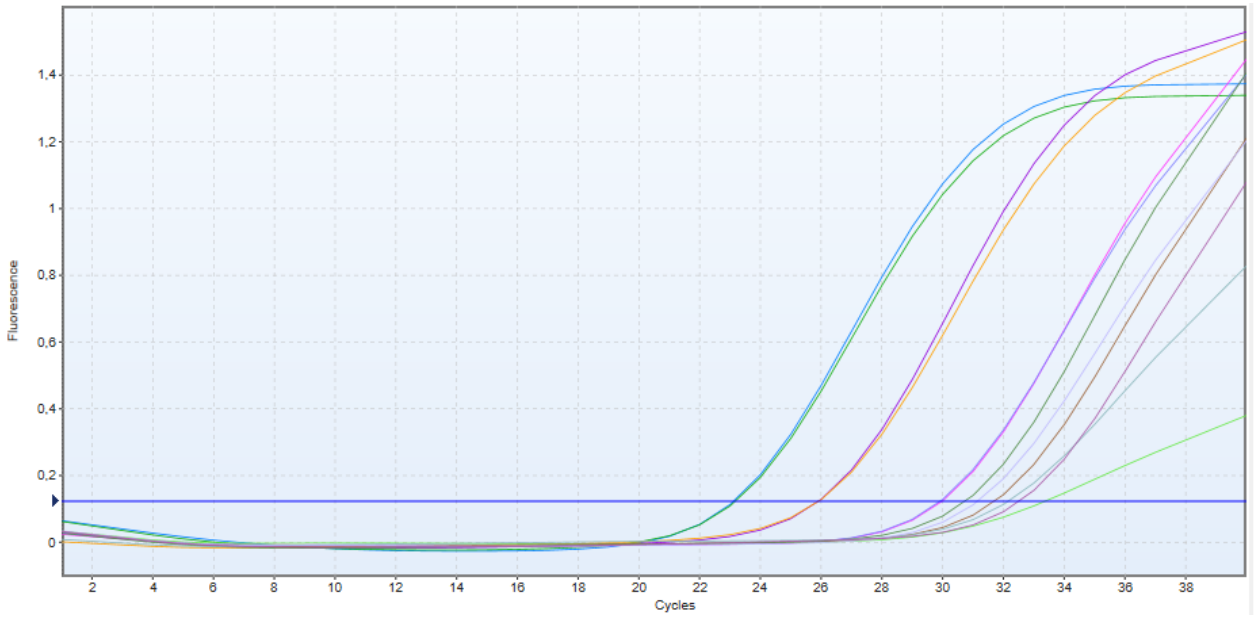

Figure J.1. Normalized RT-PCR Amplification Curve for GAPDH. Each dilution of the cDNA was analyzed for GAPDH expression in duplicates. Each line represents a single reaction and the Ct-value obtained from the replicates were averaged and plotted against the log concentration of the reaction

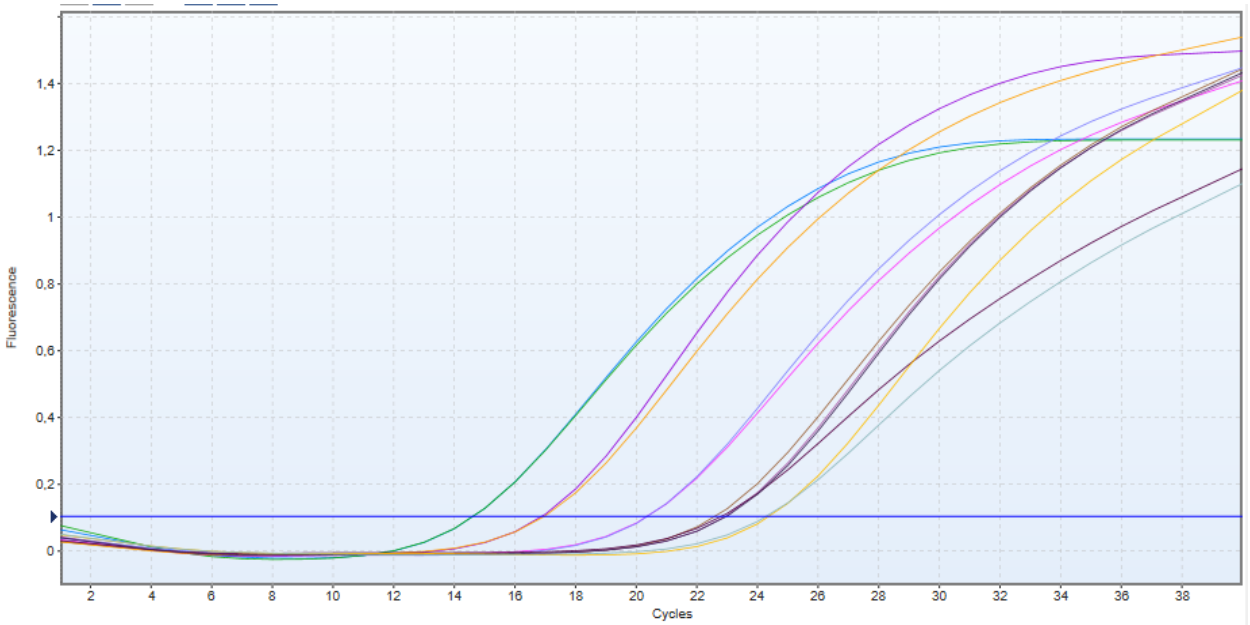

Figure J.2. Normalized RT-PCR Amplification Curve for THRα.. Each dilution of the cDNA was analyzed for THRα expression in duplicates. Each line represents a single reaction and the Ct-value obtained from the replicates were averaged and plotted against the log concentration of the reaction.

Appendix K. Ct-value Data Obtained from RT-PCR Analysis for Primer Efficiency Determination

Table K.1. Ct-values from RT-PCR Analysis of GAPDH for Primer Efficiency Determination

Sample Name	Line Color	Ct-Value	Average Ct-value
GAPDH Non-diluted A		13.86	13.95
GAPDH Non-diluted B		14.04	
GAPDH 1:10 A		16.89	16.925
GAPDH 1:10 B		16.96	
GAPDH 1:100 A		20.38	20.365
GAPDH 1:100 B		20.39	
GAPDH 1:500 A		22.62	22.72
GAPDH 1:500 B		22.82	
GAPDH 1:1000 A		22.94	22.96
GAPDH 1:1000 B		22.98	
NTC A		24.4	24,35
NTC B		24.3	

Table K.2. Ct-values from RT-PCR Analysis of *THRα* for Primer Efficiency Determination

Sample Name	Line Colour	Ct-Value	Average Ct-value
THRα Non-diluted A		23.13	23.16
THRα Non-diluted B		23.19	
THRα 1:10 A		25.92	25.92
THRα 1:10 B		25.92	
THRα 1:100 A		29.98	29.95
THRα 1:100 B		29.92	
THRα 1:500 A		30.76	31.24

THRα 1:500 B		31.72	
THRα 1:1000 A		32.54	32.96
THRα 1:1000 B		33.38	
NTC A		34.17	34.165
NTC B		34.16	

Appendix L. Normalized RT-PCR Amplification Curve for Gene Expression Analysis

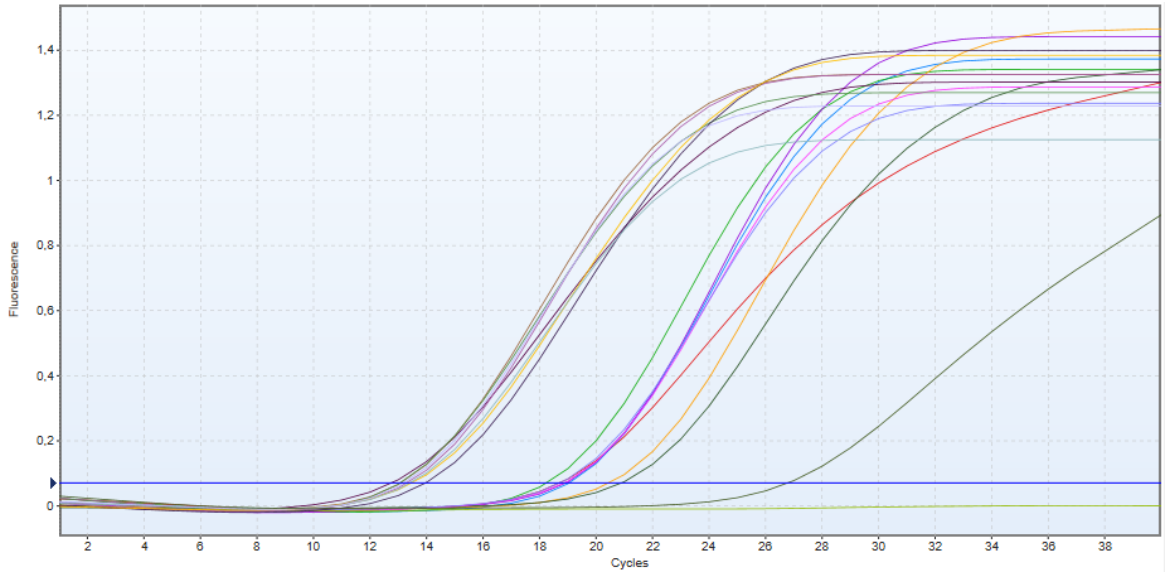

Figure L.1. Normalized RT-PCR Amplification Curve for THRα expression analysis in embryonic day 16 mice brain (1st technical replication). Each line represents a single reaction of either BPS or control samples. There are 4 samples analyzed from both treatment groups. The Ct-value obtained from this

technical replication were averaged with the Ct-value obtained from other technical replicates.

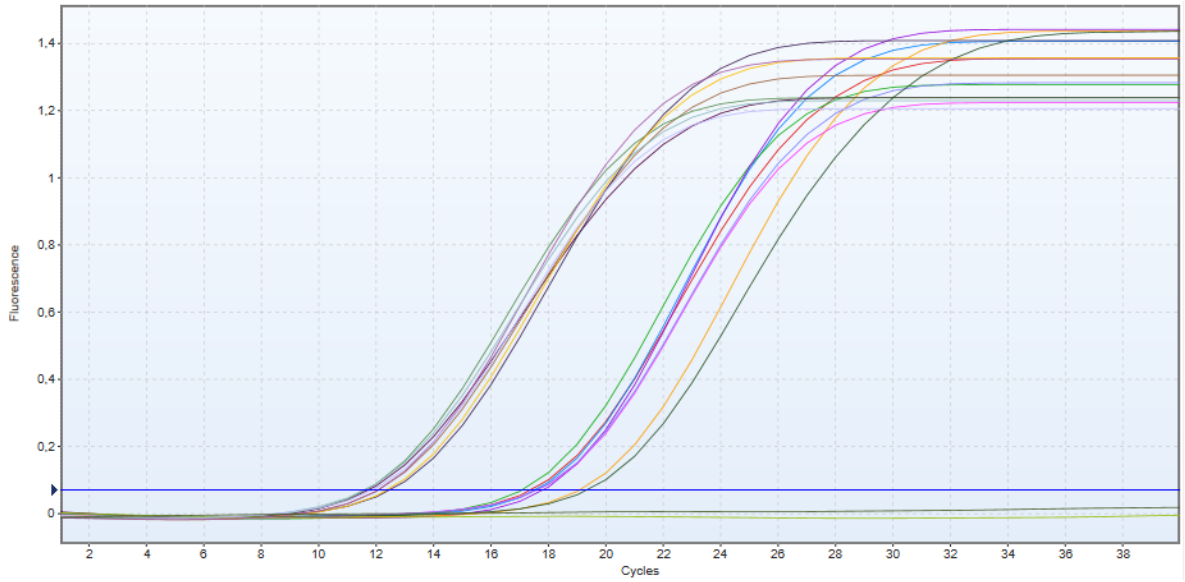

Figure L.2. Normalized RT-PCR Amplification Curve for THRα expression analysis in embryonic day 16 mice brain (2nd technical replication). Each line represents a single reaction of either BPS or control samples. There are 4 samples analyzed from both treatment groups. The Ct-value obtained from this technical replication were averaged with the Ct-value obtained from other technical replicates.

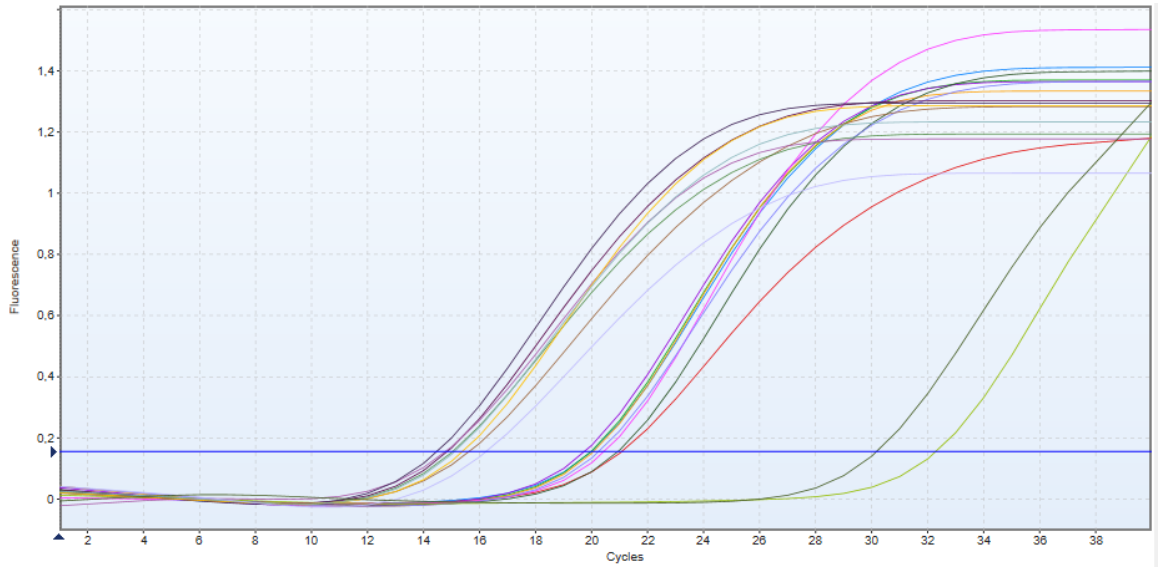

Figure L.3. Normalized RT-PCR Amplification Curve for THRα expression analysis in postnatal day 1 mice brain (1st technical replication). Each line represents a single reaction of either BPS or control

samples. There are 4 samples analyzed from both treatment groups. The Ct-value obtained from this technical replication were averaged with the Ct-value obtained from other technical replicates.

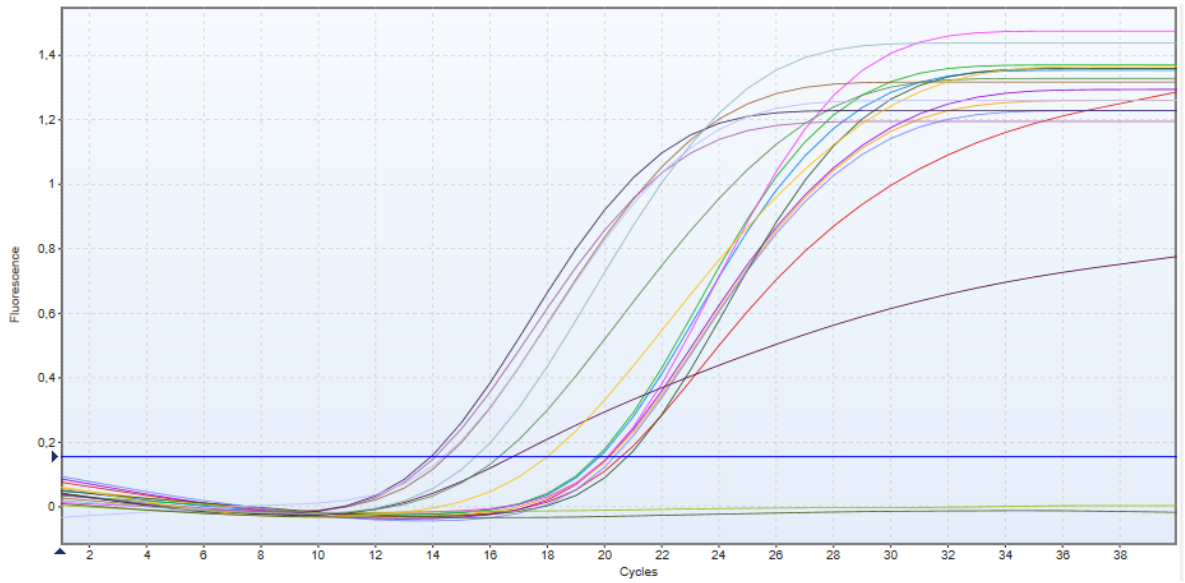

Figure L.3. Normalized RT-PCR Amplification Curve for THRα expression analysis in postnatal day 1 mice brain (2nd technical replication). Each line represents a single reaction of either BPS or control samples. There are 4 samples analyzed from both treatment groups. The Ct-value obtained from this technical replication were averaged with the Ct-value obtained from other technical replicates.

Appendix M. Ct-value Data Obtained from RT-PCR for Gene Expression Analysis

Table K.2. Ct-values from RT-PCR Analysis of *THRα* for Primer Efficiency Determination

Time point	Gene	Sample Name	Line Color	Ct-value		Average Ct-value
Embryonic day 16 Brain	*GAPDH*	Control 1		11.76	12.78	12.27
		Control 2		12.09	13.09	12.59
		Control 3		11.65	13.07	12.36
		Control 4		12.08	13.33	12.705
		BPS 1		12.51	13.97	13.24
		BPS 2		12.41	13.5	12.955
		BPS 3		11.62	13.44	12.53
		BPS 4		11.89	13.22	12.555
		NTC		-	26.8	-
	THRα	Control 1		17.41	18.73	18.07
		Control 2		17.57	19.05	18.31
		Control 3		17.09	18.27	17.68
		Control 4		17.83	18.94	18.385
		BPS 1		19.1	20.49	19.795
		BPS 2		19.38	20.91	20.145
		BPS 3		17.64	18.88	18.26
		BPS 4		17.62	18.74	18.18
		NTC		-	-	-
Postnatal day 1 brain	*GAPDH*	Control 1		16.79	14.85	15.82
		Control 2		14.51	15.64	15.075
		Control 3		16.34	15.04	15.69
		Control 4		14.1	14.79	14.445
		BPS 1		13.94	14.5	14.22
		BPS 2		18	15.41	16.705

	BPS 3		15.52	15.11	15.315
	BPS 4		14.4	16.24	15.32
	NTC		-	30.19	15.82
THRα	Control 1		20.6	21.08	20.84
	Control 2		19.84	20	19.92
	Control 3		19.76	19.98	19.87
	Control 4		20.15	19.77	19.96
	BPS 1		20.2	20.07	20.135
	BPS 2		20.81	20.94	20.875
	BPS 3		20.13	20.47	20.3
	BPS 4		20.36	20.27	20.315
	NTC		-	32.31	-

Appendix N. Melting Curve of RT-PCR for Gene Expression Analysis

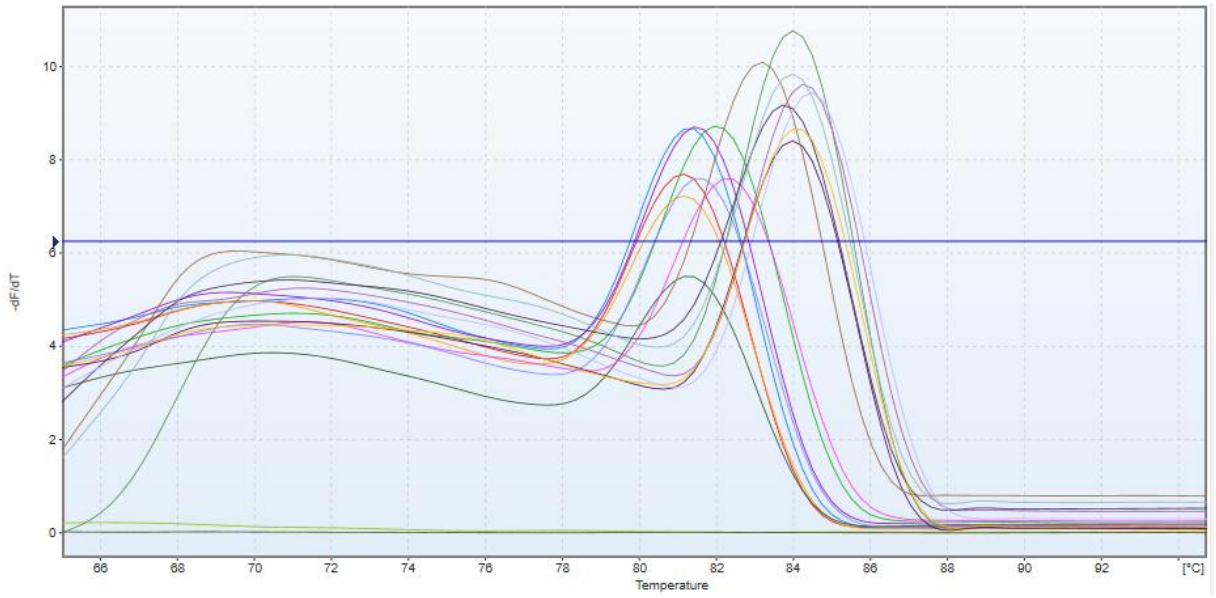

Figure N.1. Melting Curve Analysis of 1st technical replication of THRα expression analysis in embryonic day 16 mice brain. Each line represents a single reaction of either BPS or control samples.

There is only a single peak observed in each sample indicating no contamination or primer dimer formation.

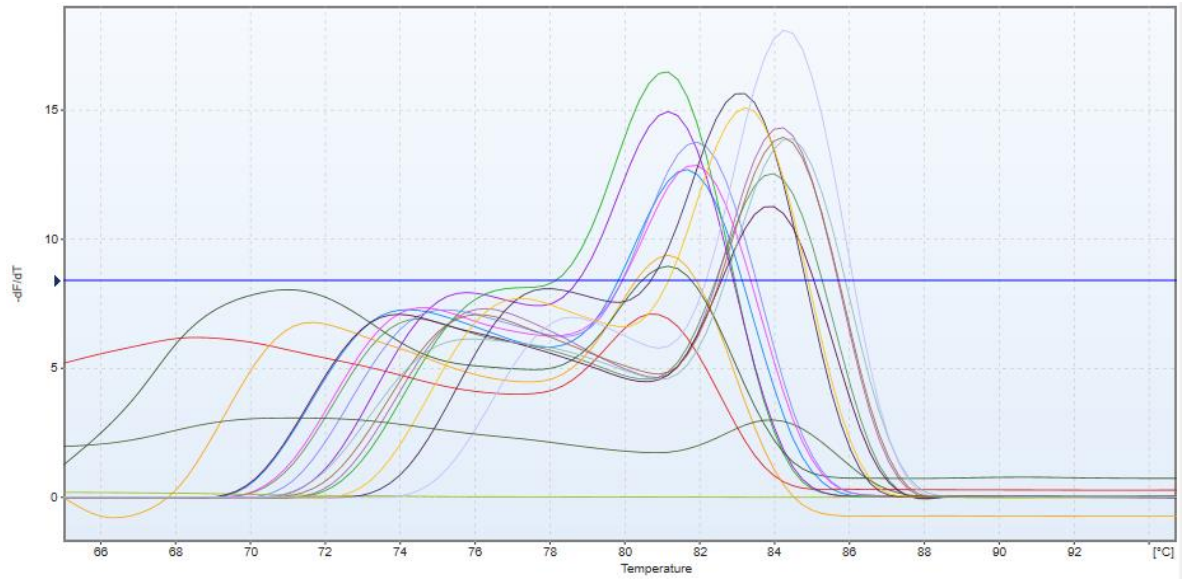

Figure N.2. Melting Curve Analysis of 2^{nt} technical replication of THRα expression analysis in embryonic day 16 mice brain. Each line represents a single reaction of either BPS or control samples. There is only a single peak observed in each sample indicating no contamination or primer dimer formation.

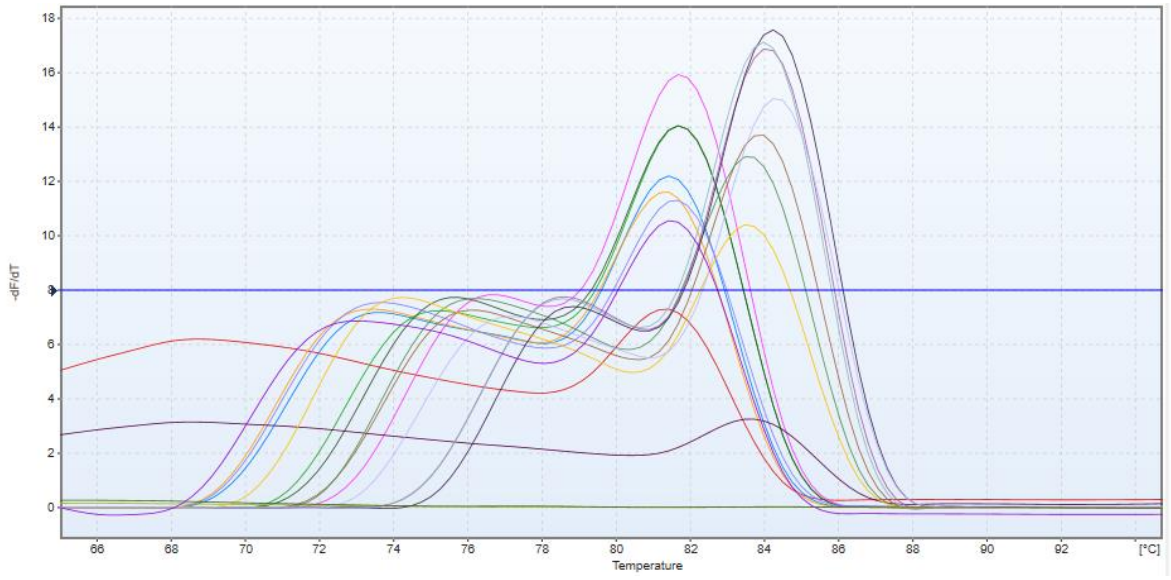

Figure N.3. Melting Curve Analysis of 1^{nt} technical replication of THRα expression analysis in postnatal day 1 mice brain. Each line represents a single reaction of either BPS or control samples. There is only a single peak observed in each sample indicating no contamination or primer dimer formation.

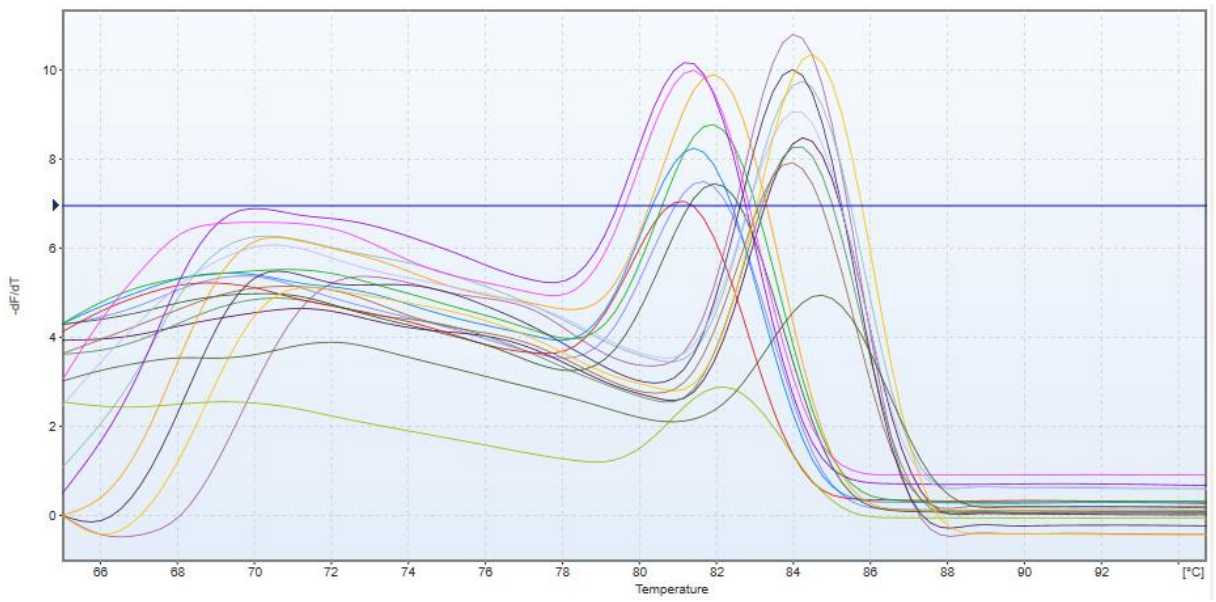

Figure N.4. Melting Curve Analysis of 2nd technical replication of THRα expression analysis in postnatal day 1 mice brain. Each line represents a single reaction of either BPS or control samples. There is only a single peak observed in each sample indicating no contamination or primer dimer formation.

Appendix O. Details on Technical Issues due to Nanodrop Imprecision

Inconsistencies were found on the nanodrop measurement as demonstrated by the measurement for sample 3 & 4 from BPS treated group on embryonic day 16. As seen on figure O.1. below, the measurement of RNA purity and concentration for sample E16 BPS 3 & 4 showed a good result with A260/A280 ratio of 1.95 and concentration of 581.0 ng/µl for sample 3 and A260/A280 ratio of 1.95 and concentration of 578.7 ng/µl for sample 4. This measurement was taken on 29th April 2021. The same samples then measured on 11th May 2021, following the claims that the nanodrop cannot be used and showed a negative result. Surprisingly, the measurement of the same samples showed a negative result with no A260/A280 ratio (See figure 0.2). Furthermore, the measurement of nucleus free water (blank) showed a positive result with A260/A280 ratio of 48.67 and concentration of 0.5 ng/µl. Another measurement showed no A260/A280 ratio value and concentration of -35.9 ng/ µl, indicating imprecision results generated by Nanodrop used.

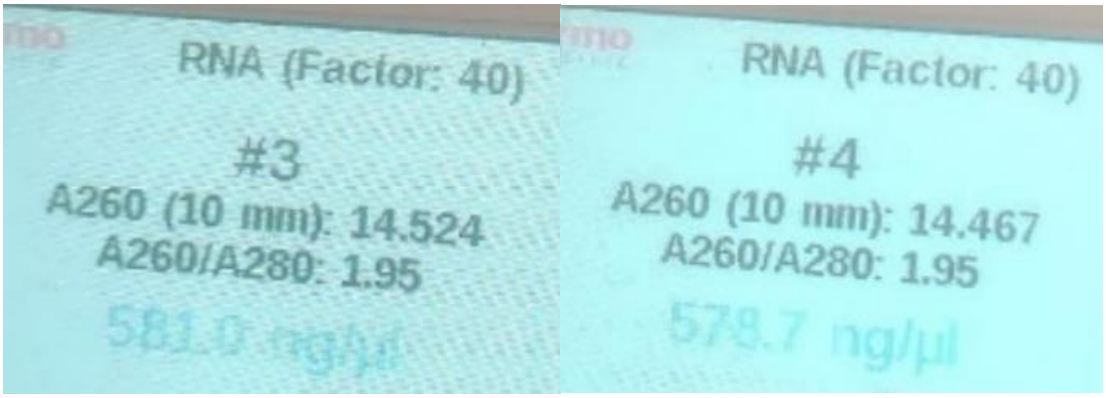

Figure O.1. Result of Nanodrop Reading of Sample 3 (left) & 4 (right) BPS E16. This measurement was taken on 29th April 2021 right after the extraction.

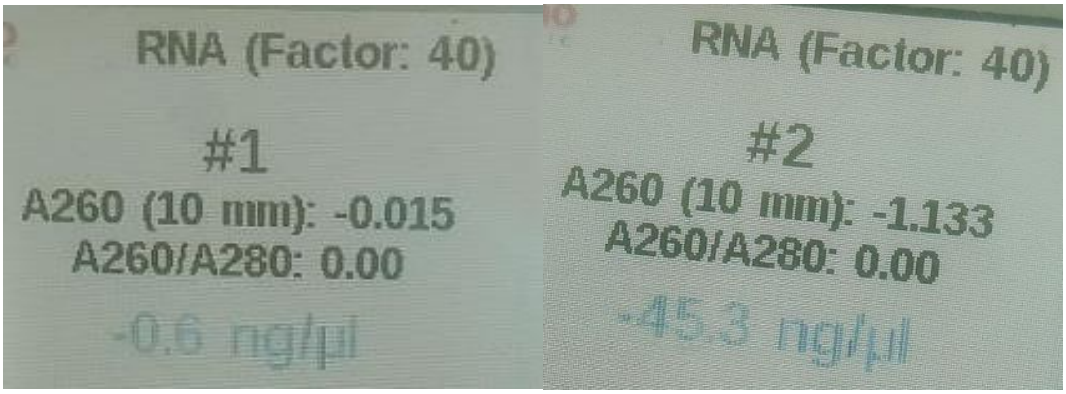

Figure O.2. Result of Nanodrop Reading of Sample 3 (left) & 4 (right) BPS E16. This measurement was taken on 11th May 2021.

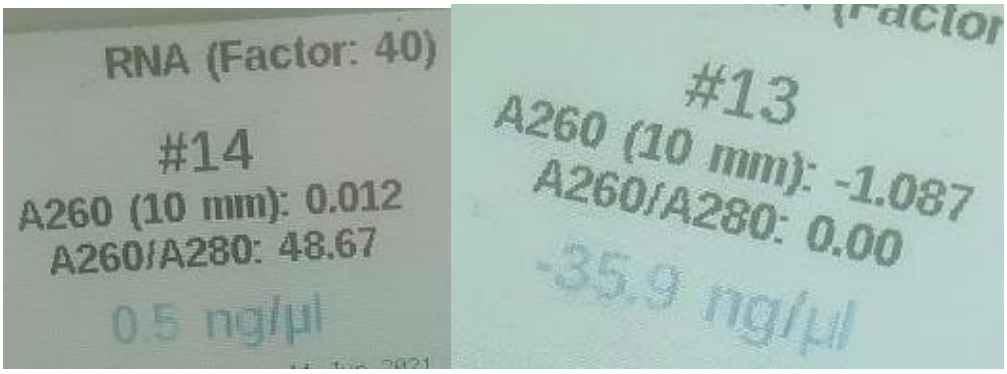

Figure O.3. Result of Nanodrop Reading of Nucleus free water (blank). Two measurement was made and the results were inconsistent. This measurement was taken on 11th May 2021