

Product Application

Arabidopsis thaliana RNA Purification

Isolate high quality, amplifiable RNA from Arabidopsis thaliana using the ReliaPrep[™] RNA Tissue Miniprep System.

Kit:	ReliaPrep ™ RNA Tissue Miniprep System (Cat. #Z6111)	This protocol was developed by Promega Applications Scientists and is intended for research use only.
Analyses:	QuantiFluor [®] and NanoDrop-1000 quantitation, GoTaq [®] Probe 1-Step RT-qPCR System	The user is responsible for determining its suitability in the user's application. For further information, please contact
Sample Type(s):	Fresh Arabidopsis thaliana	techserv@promega.com
Input:	up to 20mg Arabidopsis thaliana stem and leaf tissue	
Materials Required:	 ReliaPrep[™] RNA Tissue Miniprep System (Cat. #Z6111) Liquid nitrogen Mortar and pestle Isopropanol 95% ethanol Tissue homogenizer (i.e. – Tissue-Tearor[™] homogenizer) 	

Microcentrifuge

Protocol (for non-fibrous tissue):

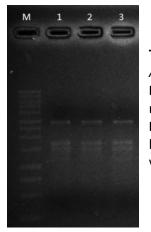
- 1. Prepare solutions as described in the technical manual (TM394).
- 2. Grind tissue sample material in liquid nitrogen using a mortar and pestle.
- 3. Add up to 20mg of ground *Arabidopsis* to a 2ml tube.
- 4. Add 500µl of LBA + TG Buffer to the tube.
- 5. Homogenize samples with a small tissue homogenizer for 30-60 seconds.
- 6. Clear homogenates by centrifugation for 3 minutes at 14,000 x g, then transfer to a clean tube.
- 7. Add 170µl of isopropanol. Mix by vortexing for 5 seconds.

Proceed with the protocol in the technical manual (TM394) to purify the RNA using the ReliaPrep[™] minicolumn.

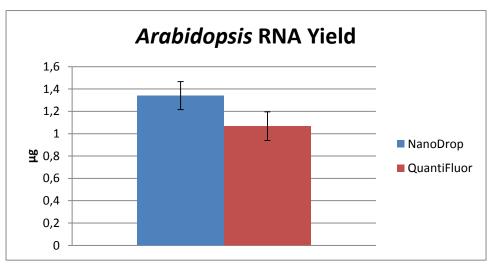
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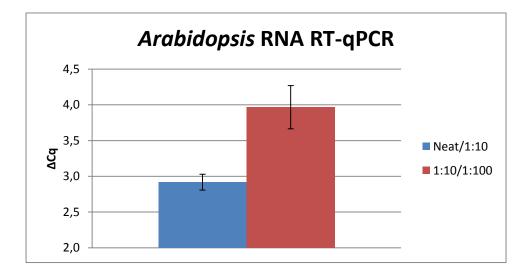


Results:



Top Panel: Gel electrophoresis analysis of RNA purified from 20mg fresh *Arabidopsis thaliana*. M = BenchTop 1kb DNA Ladder. **Middle Panel:** Yields of RNA purified from 20mg fresh *Arabidopsis thaliana* measured using the NanoDrop-1000 and the QuantiFluor® RNA System. **Bottom Panel:** RT-qPCR analysis of purified *Arabidopsis* RNA. ΔCq values between the neat and 1:10 samples were below the ideal value of 3.3 and ΔCq values between the 1:10 and 1:100 samples were above the ideal value of 3.3.





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