RNA Submission Guidelines

The success of an RNA project is primarily dependent upon the **quality** of the RNA received.

The Genomics Core does not recommend one specific procedure for isolating RNA per se, but rather suggests that if the lab is already working successfully with RNA in other molecular biological applications that they continue to use the same method. If purity and/or quality issues should arise, Genomics Core staff will be happy to make alternate suggestions.

RNA sample requirements

We prefer to start with total RNA. Most Illumina RNA-based assays recommend a 100ng- 1ug total RNA input. We would like 3-4 µL extra for QC purposes. The concentration of your RNA ideally should be 50-500ng/ µL. If your RNA is >500ng/ µL, please dilute before sending as we prefer not to have to do this in-house.

RNA samples should meet the following requirements:

1. It is **strongly** recommended that all samples be treated with RNase-free DNase prior to submission to ensure samples are free of gDNA contamination. DNase treated samples must also be clean-up post treatment.
2. The A_{260}/A_{280} should be 1.8-2.1. A ratio <1.8 is often indicative of protein/DNA contamination. A ratio >2.1 may also indicate residual guanidine thiocyanate or beta-mercaptoethanol. Protein contamination should be removed by re-extraction using phenol:chloroform:isoamyl alcohol or another pass over a commercially available column. Other contaminants can be cleaned up by EtOH precipitation.
3. Samples may be quantified on a spectrophotometer or NanoDrop. Please provide a copy of the results if samples quantified on a NanoDrop. Quantification of RNA by RiboGreen is also appropriate.
4. Samples should be in nuclease-free water. If your sample(s) is not in water, note the type of buffer on the submission form.
5. If pooled RNA samples are to be submitted, please discuss with us before sending RNA.
6. Samples <24 should be submitted in either a 0.5 mL or 1.5 mL nuclease-free microfuge tube with the sample name **clearly** written on the cap—no more than 6-8 letters/numbers—**and the PI's name on the side**. If >24 samples submitted, the samples must be in a nuclease-free PCR plate sealed appropriately with the PI name on the side of the plate skirt (spreadsheet with plate layout should be e-mailed to genomics@vai.org and should also accompany plate), otherwise additional sample handling charges may apply.

Shipping

1. A filled out submission form must accompany all shipments.
2. All items shipped should be sealed in a plastic bag.
3. Sample should be shipped on dry ice overnight to:

   Van Andel Institute
   Attention: Marie Adams
   333 Bostwick Avenue, room 2011
   Grand Rapids, MI 49503