Toray miRNA Array Sample Requirements

Sample Preparation

We recommend preparing samples in an RNase free environment and DNase treating all RNA samples as part of a standard RNA isolation protocol to ensure accurate quantification prior to initial QC at CGS. DNA contamination may result in overestimation of RNA amounts.

Sample Requirements

Unless otherwise discussed, Toray miRNA expression arrays require 250ng of total RNA in no more than 2.2ul of nuclease free dH_2O (by Qubit, RiboGreen or Nanodrop) with A260/A280 > 1.8. If a Bioanalyzer is available RNA with a RIN ≥8.0 is desirable, however RNA with RINs as low as 2 can be used.

Please provide two aliquots of each sample for processing

- Sample preparation: 250 ng total RNA in ≤ 2.2ul dH_2O (≥115 ng/ul). If obtaining samples at this concentration is not possible, samples can be concentrated by vacuum desiccation either by the customer or by CGS.
- Quality control: 5 µl aliquot of above sample **in separate tube/plate** at the same concentration (providing a QC aliquot helps to avoid the freeze thawing of samples, helping to minimise RNA degradation and increase data quality).

For <24 samples please send samples and QC aliquots in 1.5mL tubes; for >24 samples please send in 96 well PCR plates and ensure the plates are adequately sealed to prevent sample loss and cross contamination.

Sample Labelling

Please make certain that the labels on both the sample preparation and quality control aliquots match each other and the sample sheet. For custom analysis, sample names should not include spaces and should reflect which (if any) experimental group the sample belongs to. For example in a case (C) control (CTRL) study with (T) and without treatment (NT) a suitable label would be assembled as follows, (patientID)_(C/CTRL)_(T/NT).

Shipping Requirements

RNA may be handled in directly at the facility or can be shipped to us on dry ice at the following address.

Cambridge Genomics Services
Department of Pathology,
Tennis Court Road,
Cambridge,
CB2 1QP, UK