RNA sequencing 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, RNAseq library preparation requires 0.5-1.0µg total RNA in nuclease free dH_2O (by NanoDrop or RiboGreen) with A260/A280 and A60/A230 ratios above 1.8. If a Bioanalyzer is available RNA with a RIN ≥8.0 is desirable.

Please provide two aliquots of each sample for processing

- Library preparation: 0.5-1.0µg total RNA at a minimum 50 ng/µL in nuclease free dH_2O.
- 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 library 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 handed in directly at the facility or can be shipped to us on dry ice at the following address.

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