UNIVERSITY OF LIVERPOOL | CENTRE FOR GENOMIC RESEARCH

Sample requirements for NimbleGen RNA sequence capture libraries

- **RNA quantity:** Please submit ≥150 ng total RNA in a volume of maximally 10 ul nuclease-free water (free of DNA, contaminating salts, metal ions, ethanol, and phenol).
- **DNA Removal:** DNA contamination of the RNA sample is likely to adversely affect the data quality. We recommend treating the RNA sample with DNase and remove the enzyme prior to library preparation.
- **Accurate quantification** of nucleic acids in the sample(s) is necessary. Use a dye based method such as Qubit (Life Technologies).
- **Sample purity:** Purification should be confirmed by values of ≥1.80 for both NanoDrop 260/230 and 260/280 ratios. If the samples need further purification after submission, the additional expenses will be added to the formal quote.
- **Quality of the RNA:** Please provide a gel image of all samples to confirm sample integrity. We recommend working with intact total RNA with RIN values ≥ 8 as starting material for the library preparation workflow. This value is calculated by the Agilent Bioanalyser software for most types of RNA. However, for some species the software cannot compute the RIN value. In those cases, RNA integrity can be estimated by the sharpness of the rRNA bands and a baseline value close to zero in the 200-1000 bp range.
- If possible, please label the samples and tubes 1, 2, 3 etc. in order to ease our sample identification. Please remember to underscore numbers that can be read upside-down such as 6, 9, 16, 91, 69, 96 etc.