

GENOMICS RESEARCH CORE

Microarray Services**Sample Submission Guidelines**

- 500 ng of total RNA for standard processing
 - If this is a prohibitive amount, please contact the Genomics Research Core. There are lower input options available.
- RNA good quality
 - OD260/280 ratio 1.8 or higher
 - Bioanalyzer RIN >6 (to be assessed by Genomics Research Core)
- Tubes must be labeled with simple sample ID on top. Investigator initials and a number work well. USE NO TAPE. Keep IDs short so that they can be written legibly on the tube lid.
- Submit only the amount of material needed for analysis. Unused material that is not retrieved by your laboratory within 6 months of project completion will be discarded.
- Samples can be brought to the Core Lab facility at 3343 Forbes Ave, 3rd floor, or to our sample drop off room S534 in Scaife Hall.
- Samples must be accompanied by a gene expression array drop off form indicating the Principal Investigator, contact for this study, array platform and type to be used, service requested and sample specific information.