How It Works:
Total RNA is assayed for overall quality. The RNA is then used to synthesize ds-cDNA followed by generation of labeled cRNA, which is fragmented and hybridized to an Illumina BeadChip. Hybridized fragments are detected by laser excitation and scanning. Results are returned as relative expression levels for each transcript interrogated.

What We Need:
We ask users to submit 1.5 µg of RNA at a concentration of 150 ng/µL for each sample to ensure high quality. Processing requires 150 ng of RNA, and we request additional material for quality controls or in case repeat runs are needed.

What We Offer:
HumanHT-12 BeadChips accommodate up to 12 samples/chip and target over 47K probes. Mouse- and rat-specific BeadChips are also available. Standard processing allows us to analyze intact RNA samples, while DASL® (cDNA-mediated Annealing, Selection, Extension, Ligation) assays enable analysis of difficult or degraded RNA samples, such as FFPE tissues. Users can contact the Core Director and bioinformatics staff to discuss proper experimental design and data interpretation. To submit samples for expression, users can submit their forms through NUcore.

Pricing:
Full-service processing for expression analysis begins at $85/sample plus the cost of the BeadChips. DASL preparation can also be performed for an additional fee. Contact the Genomics Core at genomics-core@cgm.northwestern.edu to discuss your project and obtain a quote.