UMass Medical School
Illumina Sequencing Library Construction Service
Molecular Biology Core Labs

Client Information: Name: _____ Phone: _____

Email: _____ Date: _____

PI/Lab: _____ Account #: _____

PI signature: _____

Library Construction Information (Please submit one ticket for each set of libraries to be mixed):

Illumina Library	**Minimum Requirements:**
Indicate starting material: ☐ Genomic DNA ☐ Amplicon(s) ☐ cDNA (double stranded) ☐ Total RNA for cDNA library* ☐ Small RNA* ☐ NanoString collection‡, # of samples: _____ ☐ Cells for 10X Chromium single-cell library ☐ Other cells ☐ Other _____ (describe) What is the preferred insert size? _____ (Optimal library inserts are ≤ 500 bases) Instrument: _____ Desired read length: _____ ** Must be stored in water* *‡ Include the _SeqCodeIndices.csv file from the NanoString instrument*	genomic DNA: 2-3 µg amplicon: 1 µg (2 µg if shearing required) cDNA: 1 µg (2 µg if shearing required) total RNA: 2-5 µg small RNA: 50-100 ng NanoString: dried + Seq Code plates and enzyme Master Mix cells for Chromium: 10,000 viable cells other cells: ask before submission

Species: _____ Source: _____

How was the material prepared? _____

What buffer is the material in? _____

List the name and part # of any kits used in preparation: _____

How was the material quantified? _____

Is the material from a human pathogen, or does it contain any restricted, potentially hazardous, or infectious material? If yes, please detail: _____

Your signature confirming this statement: _____

Sample Name	Concentration	Volume (µl)

(If additional samples, list on supplemental sheet.)

Please attach any available information about the sample material (*e.g.* gel photos, Fragment Analyzer/Bioanalyzer traces, etc).