UMass Medical School
Illumina Sequencing Library Construction Service
Molecular Biology Core Labs RRID: SCR_018263

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

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

Minimum Requirements:

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).

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