NUSeq Core: RNA-seq Service Request Form



Email: nuseq@northwestern.edu Phone: (312) 503-3702

I. CONTACT INFORMATION PI Name:_____ PI E-mail: _____ Department:____ Chart String or PO Number: **Contact Name:** Contact E-mail: II. PROJECT INFORMATION **Short Description of the Project:** Alterations to genome (knock-outs, knock-ins, etc, if any): **Special Notes or Instructions:**

III. EXPERIMENTAL DESIGN

Control and experimental groups:				
Pairwise comparisons to be performed:				

Sample Number	Sample ID	Sample Name	Sample Group
1			
2			
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
13			
14			
15			
16			
17			
18			

For Sample ID, please provide a simple ID, such as your initials followed by an integer. For example, MS-1, MS-2, ... etc.

^{**} if more than 18 samples, please provide the required information on a separate spreadsheet.

IV. ESTIMATED COSTS

This section will be filled in by the NUSeq Core.

Library Construction *	Per Sample Cost	Number of Samples	Total Cost
mRNA-seq (Poly-A enrichment)			
RNA-seq (RiboZero rRNA depletion)			
Small RNA -seq			
Ultra low input mRNA-seq			
Ultra low input total RNA-seq			
Custom Library			
Illumina NextSeq 500	Per Flowcell Cost	Number of Flowcells	Total Cost
42PE			
75SE			
75PE			
150SE			
150PE			
Bioinformatics Analysis **	Per Hour	Number of Hours	Total Cost
Basic			
Custom			
Total Estimated Cost			

^{*} Library construction cost includes sample QC. However, if some samples don't pass QC, they will not be processed for library construction and QC cost will be assessed separately on these samples.

V. NOTES

This section will be filled in by the NUSeq Core.

Date	Description

^{**} Basic analysis includes data QC, alignment, gene quantification, differential expression, and pathway analysis. Any additional request will be considered custom and billed at a higher rate.