Brown University Genomics Core Facility
Next Generation Sequencing Sample Submission Form

Customer Information:

User Name: PI Name:

Institution: Department:

Email: Phone:

Please choose one:

Oscar Account:

or

Illumina Basespace account:

Requested Experiments:

Single sample   Multiplexed samples

Choose one of the following:

Medium Output Flowcell   Reagent Kit: 300 cycles

                                                      150 cycles

or

High Output Flowcell   Reagent Kit: 300 cycles

                                                      150 cycles

                                                      75 cycles

Run Configuration:

Read 1:   cycles

Index Read 1   cycles

Index Read 2   cycles

Read2   cycles

(Please indicate above the number of cycles for each read. Please note that the **sum** of cycles for **read 1** and **read 2** cannot be higher than the number of cycles of the chosen reagent kit)

Sample Information:

gDNA   small RNA   mRNA   cDNA   CHiP   Other (specify below)

Species:

Reference Genome:

Concentration Measured By:

Nanodrop   Qubit   Bioanalyzer   Pico Green   qPCR

Other (please specify)

Sample Information

	Sample Name	Concentration (ng/uL)	Volume (uL)	Multiplex set	library name, manufacturer
Sample 1					
Sample 2					
Sample 3					
Sample 4					
Sample 5					
Sample 6					
Sample 7					
Sample 8					
Sample 9					
Sample 10					
Sample 11					
Sample 12					
Sample 13					
Sample 14					
Sample 15					

	Sample Name	Concentration (ng/uL)	Volume (uL)	Multiplex set	library name, manufacturer
Sample 16					
Sample 17					
Sample 18					
Sample 19					
Sample 20					
Sample 21					
Sample 22					
Sample 23					
Sample 24					
Sample 25					
Sample 26					
Sample 27					
Sample 28					
Sample 29					
Sample 30					

Other comments:

[Genomics Core Use ONLY]:

Date Received: _____ By: _____

Sequencing Start Date: _____ Sequencing Completion Data: _____

Additional Notes/Comments: _____