MARSHALL UNIVERSITY GENOMICS CORE REQUEST FORM

Complete one form for each separate experiment.

Date_____

P.I.Name_____ Email: _____

Institution_____ Phone: _____ FAX:_____

Payment Funding Source (e.g. NIH, NCI, or NIGMS grant)_____

US Mail Address_____ Invoice Address_____

_____ _____

_____ _____

_____ _____

We transfer HiSeq data via Illumina BaseSpace in most cases. Provide the name and address of the BaseSpace account owner. _____

Describe your experimental goals and design (one or two paragraphs):

Select check type of analysis from the following list and provide the requested information.

___ **Whole Genome Sequencing**

_____ organism (genus and species)
_____ cell or tissue (e.g. HeLa cells)
_____Sequencing Strategy (e.g. 2 x 250 paired end)
___ average read depth (e.g. 35X)
___number of samples **(attach sheet with sample names and DNA concentrations)**
_____ genomic DNA purification method

Data output (Choose all applicable):

____ Reads only (fastq)
____ Alignment to reference genome (bam)
____ Variant calls (vcf)

___ **Whole Exome Sequencing:**

_____ organism (genus and species)
_____ cell or tissue (e.g. HeLa cells)
_____ Sequencing Strategy (e.g. 2 x 50 or 2 x 100 paired end)
___ average read depth (e.g. 35X)
___ number of samples (**attach sheet with sample names and DNA concentrations**)
_____ genomic DNA purification method

Data output (Choose all applicable):

____ Reads only (fastq)
____ Alignment to reference genome (bam)
____ Variant calls (vcf)

___ **mRNA-Seq**

_____ organism (genus and species)
_____ cell or tissue (e.g. HeLa cells)
_____ Sequencing Strategy (2 x 100 paired end, 1 x 50 single read, 2 x 50 PE)
___ quality reads per sample (e.g. 50 million)
___ number of samples (**attach sheet with sample names, RIN values and RNA concentrations and indicate biological replicates**)
_____ RNA purification method

Data output (Choose all applicable):

____ Reads only (fastq)
____ Alignment to reference genome (bam)
____ Use known annotations in alignment
____ Gene-level counts
____ Exon-level counts
____ Statistical analysis (explain in experimental design)

___**miRNA-Seq**

_____ organism (genus and species)
___ quality reads per sample (e.g. 10 million)
_____ cell or tissue (e.g. HeLa cells)
___ number of samples (**attach sheet with sample names, RIN values and RNA concentrations**)
_____ RNA purification method
_____ data output

____**ChIP-Seq**

_____ organism (genus and species)
_____ cell or tissue (e.g. HeLa cells)
___ quality reads per sample (e.g. 50 million)
___ number of samples (**attach sheet with sample names, DNA concentrations**)
_____ DNA purification method

Data output (Choose all applicable):
____ Reads only (fastq)
____ Alignment to reference genome (bam)
____ Peak calls

Attach sheet with RNA sample ID's and amounts or Library quantities and bar codes.

Run Mode: Rapid Run Mode or High Output Mode?

Comparison: (Give cell line name and experimental treatment)
Cell line 1_____ vs Cell line 2 _____
Or
Tissue 1_____ vs Tissue 2_____

Define your fold change ratio (R) for your gene set: R = _____
For example R= (cells + drug)/(cells – drug) or R = tissue#1/tissue 2.

Number of Biological Replicates ____

RNA Extraction and Shipping to the Genomics Core Facility

(1) Use an RNA isolation method that is appropriate for the application (e.g. microarray expression profiling or RNA-Seq library construction).

For extraction of total RNA from WBC's, we recommend use of the Qiagen RNeasy product line. There are column-based protocols for increasing cell numbers. Qiagen has a Product Finder on its website (http://www.qiagen.com/products/productfinder/default.aspx)

(2) We request the RNA amounts for each sample as follows.

RNA Sample Quantities and Quality			
	total RNA per sample	260/280	RIN
Downstream Application			
microarray expression profiling	1-4 micrograms	>1.8	> 8
mRNA-Seq	1-4 micrograms	>1.8	> 8
microRNA-Seq	2-4 micrograms	>1.8	> 8

In most cases, we will not accept polyA+ RNA samples.

(3) Depending on the RNA extraction protocol, you may either (1) elute column-bound RNA with water and store appropriate aliquots at -80 degrees OR (2) precipitate RNA aliquots under either ethanol (isopropanol) and collect the pellet by centrifugation. If you precipitate the RNA, leave the ethanol/IPA in the tube during storage and shipping.

(4) Use screwcap tubes (or parafilm sealed snapcaps) for shipping RNA. Freeze the RNA samples at -80C for at least 1 hour before packaging for shipment.

(5) Pack the samples in a box filled with dry ice and ship by next day Fedex to

Donald A. Primerano, PhD
Robert C. Byrd Biotechnology Science Center
Room 336F
Marshall University
1700 3rd Avenue
Huntington WV 25755

(6) Please do not ship samples such that shipment will span a weekend. We recommend shipping on Monday, Tuesday or Wednesday.

DNA Extraction and Shipping to the Genomics Core Facility

(1) For whole genome sequencing, we need a minimum of 2 micrograms of genomic DNA. For Nextera Whole Exome sequence, we need at least 200 nanograms of genomic DNA. **We recommend using QIAamp DNA product line and ask that the investigator quantitate by fluorescence (preferably) or conventional A260 absorbance.**

(2) You may either (1) elute column-bound DNA with water and store appropriate aliquots at -80 degrees OR (2) precipitate DNA aliquots under either ethanol (isopropanol) and collect the pellet by centrifugation. If you precipitate the DNA, leave the ethanol/isopropanol in the tube during storage and shipping.

(3) Use screwcap tubes (or parafilm sealed snapcaps) for shipping DNA. Freeze the DNA samples at -80C for at least 1 hour before packaging for shipment.

(4) Pack the samples in a box filled with dry ice and ship by next day Fedex to

Donald A. Primerano PhD
Robert C. Byrd Biotechnology Science Center
Room 317
Marshall University
1700 3rd Avenue
Huntington WV 25755

(5) Please do not ship samples such that shipment will span a weekend. We recommend shipping on Monday, Tuesday or Wednesday.

Contacts:

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