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):

General version (November 2013)
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)

General version (November 2013)
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 _____

General version (November 2013)
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.

<table>
<thead>
<tr>
<th>Downstream Application</th>
<th>total RNA per sample</th>
<th>260/280</th>
<th>RIN</th>
</tr>
</thead>
<tbody>
<tr>
<td>microarray expression profiling</td>
<td>1-4 micrograms</td>
<td>&gt;1.8</td>
<td>&gt; 8</td>
</tr>
<tr>
<td>mRNA-Seq</td>
<td>1-4 micrograms</td>
<td>&gt;1.8</td>
<td>&gt; 8</td>
</tr>
<tr>
<td>microRNA-Seq</td>
<td>2-4 micrograms</td>
<td>&gt;1.8</td>
<td>&gt; 8</td>
</tr>
</tbody>
</table>

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.

General version (November 2013)
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

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**Contacts:**  
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General version (November 2013)