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**Sequencing Sample Submission Form**

**University of Colorado Anschutz Medical Campus**

## Contact Information

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| --- | --- | --- | --- |
| PI Name | Gregg Randolph | PI Email | Grandoll1@uwyo.edu |
| Post Doc/Student/Tech | Shannon Harris | Email | Sharri48@uwyo.edu |
| Institution | University of Wyoming | Phone | 307-766-4290 |
| Address | 16th and Gibbon Streets |
| City | Laramie | State | WY | Zip Code | 82071 |

## Experiment and Sample Information

* 1. **If you are submitting DNA/RNA samples for sequencing library preparation, please indicate sequencing type.** The optimal quantity of starting material is listed below. Please provide extra for QC. If sufficient RNA/DNA quantity and concentration is not available, please consult the Core personnel before submitting.

**Note:** All material submitted will be quality tested and quantitated. Any remaining material can be retrieved from the core by the customer after they receive their sequencing data.  Any material not retrieved by the customer after 60 days will be discarded.

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| --- | --- | --- |
|  | **Genomic DNA Lib** | 10-100ng Genomic DNA in 50µl or less water/TE /EB buffer  |
|  | **PCR Free WGS Lib** | 1ug Genomic DNA in 50ul or less water/TE/EB buffer |
|  | **Small RNA Lib** | 100ng -1µg Total RNA in 5µl or less water/TE buffer  |
|  | **Exome Lib** | 10ng, 200ng, or 1ug Prep Genomic DNA in 50µl water/TE buffer |
|  | **ChIP Lib** | 1ng-10ng ChIP DNA in 10µl or less water/TE buffer  |
|  | **ATAC Lib** | 50,000 Live Cells in PBS (no more than 50ul volume) |
|  | **Poly A Selected Total RNA Lib** | 10ng -500ng Total RNA in 50µl or less water/TE buffer  |
|  | **Low Input Ribo Depleted Total RNA**  | 500pg to 10ng Total RNA in 10ul or less water/TE buffer |
|  | **Ribo Depleted Total RNA Lib** | 100ng-1µg Total RNA (1µg to 4µg) in 10µl or less water/TE buffer  |
|  | **Other / Custom** |  |

Please attach / list below sample QA/QC data if any (Nano Drop, Pico Green, QPCR, Qubit, Bioanalyzer, etc)

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* 1. **Submission of Ready to Sequence Libraries:**
1. **Type of Library and kit used for construction: \_\_\_Custom Restriction Fragment Sequencing\_\_\_\_\_\_\_\_\_\_\_**
2. **Size of Library: \_\_\_300-500 bp\_\_ Attached Tape Station Trace or Gel Image \_\_\_ Yes \_X\_No (core will do)**
3. **Concentration of Library Pool (nM): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ (Is this determined by Qubit?\_\_\_\_ qPCR? \_\_X\_\_)**
4. **Please Indicate Length and Location of Tag**:

Tag Sequence Length: (example 6 base pairs) \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Dual Index: \_\_\_\_\_X\_\_\_\_\_Yes \_\_\_\_\_\_\_\_\_\_\_\_\_\_ NO

Location of Tag: \_\_\_\_\_\_\_\_\_ Read 1 \_\_\_\_\_\_\_\_\_\_\_ Index Read \_\_\_\_\_\_\_\_\_\_\_\_Read 2

Other Tag Information we need to know: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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Are Custom Primers Required: \_\_\_\_\_\_\_\_\_\_\_YES (Provide Protocol) \_\_\_\_\_\_X\_\_\_\_ NO

1. **Provide Excel Spread Sheet that includes Sample ID and Index Tag Sequence via email in addition to this form.**
2. Please provide entire primer sequence so that we can determine correct orientation of your sequencing primer.

**IMPORTANT DISCLOSURE:** It is customer’s responsibility to ensure your library is Illumina sequencing compatible. We will do our best to get you the target read number per sample, however there is no read number guarantee for customer made sequencing libraries. Please note if you fail to submit a sample and index sequence or you submit the wrong index sequence with a sample, and it causes a barcode collision, you will be charged for re-sequencing your pool in addition to the initial sequencing run fee. The NovaSEQ requires a large number of samples to be pooled together. One barcode error on your submission cannot only affect your sample set but also has the potential to destroy additional customer’s samples.

* 1. **Sample information**

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| **1** | Species of samples submitting  | BigHorn Sheep  |
| **2** | Sample names and concentration (if available) in the box below.(Add more rows if needed) |

|  |  |  |
| --- | --- | --- |
| Sample Name | Concentration | Tag Sequence (if any) |
| 5CM\* |  |  |
| 18-143N |  |  |
| SB33N |  |  |
| 18-143T |  |  |
| 51N |  |  |
| excontrol |  |  |
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* 1. **Choose a sequencing run option below.**

**NovaSEQ 6000 (Library Insert Size 200bp to 800bp – ideal range 200-500bp)**

 \_\_\_\_\_\_ Paired End 150 cycle 2x150

 **NovaSEQ 6000 Full Flow Cell Purchase Other Options**

 **\_\_\_\_\_ SP Flow Cell \_\_\_100 Cycle \_\_\_\_300 Cycle \_\_\_\_500 Cycle XP Split of Flow Cell Yes No**

 **\_\_\_\_\_\_ S1 Flow Cell \_\_\_\_100 Cycle \_\_\_\_200 Cycle \_\_\_\_300 Cycle Add PhiX Yes No \_\_\_\_\_\_%**

 **\_\_\_\_\_\_ S2 Flow Cell \_\_\_\_100 Cycle \_\_\_\_200 Cycle \_\_\_\_300 Cycle**

 **\_\_\_\_\_\_ S4 Flow Cell \_\_\_\_100 Cycle \_\_\_\_200 Cycle \_\_\_\_300 Cycle**

**MiSEQ Add PhiX Yes\_\_\_No ­­­­­\_X\_\_ \_0\_\_%**

\_\_\_\_\_ Single Read 50 cycles (1x50) V2 Chemistry

\_\_\_\_\_ Single Read 150 cycles (1x150) V3 Chemistry

\_\_\_\_\_ Paired End Read 150 cycles (2x150) V2 Chemistry

\_\_X\_\_\_ Paired End Read 250 cycles (2x250) V2 Chemistry

\_\_\_\_\_Paired End Read 300 cycles (2x300) V3 Chemistry

**CUSTOM RUN: State Machine: NovaSEQ6000, Next SEQ, or MiSEQ, and Run Length Desired**

**\_\_\_MiSeq 2x250, No Index reads, we just want the fastq. Please only sequence 5CM. Please wait to sequence until after we get a chance to review tape station output for all samples submitted\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

* 1. **How many reads per sample do you want or X Coverage per sample for WGS and Exome SEQ?**

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* 1. **Data analysis/bioinformatics options**

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| --- | --- |
|  |  Email of person who will receive data via Server or FTP Account \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_  |
|  | USB Drive (Charge applicable and will be based on size of drive) |
|  |  |

## Payment Information

**3.1 University of Colorado Faculty**

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| --- | --- |
| Speed Type |  |
| Sequencing Pilot AwardRBI Pilot Award | \_\_\_Yes \_\_\_No\_\_\_Yes \_\_\_No |

**3.2 Not Affiliated with the University of Colorado**

 \_\_\_\_\_\_\_ Payment by Check

 \_\_\_\_\_\_\_ Payment by Credit Card

 \_\_\_\_\_\_\_ Payment by Wire Transfer

## Sample Drop off or by Shipping

Email or call to schedule a time for sample drop off.

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| --- | --- | --- |
| Contact | Katrina Diener | Katrina.diener@CUAnschutz.edu; Microarray.core@CUAnschutz.edu (303) 724- 6050 |
| Contact | Todd Woessner | Brian.Woessner@CUAnschutz.edu(303) 724-6047 |
| Hours of operation for sample drop off | 9:00am to 3:00pm Monday – Friday, excluding University Holidays. |
| Location/ Shipping Address | Genomics and Microarray CoreUniversity of Colorado Anschutz Medical Campus12700 E. 19th Ave Bldg.: RC-2, Room 9400 Aurora, CO 80045 |

## Required Signatures

Please have both the Principle Investigator (PI) that will be paying for the Sequencing Services and the Research/Technician/Student/ Post-Doc preparing the samples sign below acknowledging that all of the information provided on the form is correct. Signature of this form acknowledges that the PI and Technician/Student/Post-Doc have agreed to all sample submission, quality, quantity, project scheduling, and researcher financial responsibility requirements. Signature of this form authorizes the UC Genomics and Microarray Core to order all consumables necessary for the researcher’s sequencing project and confirms that the PI is financially responsible for items ordered for their project and all labor cost associated with the project.

|  |  |  |  |
| --- | --- | --- | --- |
| Principle Investigator Signature |  | Date |  |

|  |  |  |  |
| --- | --- | --- | --- |
| Technician/Student/Post-Doc Signature |  | Date |  |

##  Data and Sample Retrieval

All data from sequencing run will be deleted from our servers 31 days after you receive notification that your data is ready to be downloaded from our server via email.

Please pick up original DNA / RNA submitted along with constructed libraries no later than 60 days after data has been downloaded from our server. If you do not pick up your samples and libraries they will be destroyed.