**DNA sequencing request form**

|  |  |
| --- | --- |
| Date:Click or tap here to enter text.Contact person: Click or tap here to enter text.Contact email: Click or tap here to enter text. | Contact phone #: Click or tap here to enter text.Primary DLMP Investigator: Click or tap here to enter text.Primary DLMP Investigator email:Click or tap here to enter text. |

To facilitate efficient DNA sequencing of your NGS libraries, we will need the following information:

**Platform**

 [ ]  NovaSeq

**Sequencing recipe**

Specify single end or paired end, desired read lengths, and index reads. For example: Paired-end 2x151 unique dual index.

Click or tap here to enter text.

**Data analysis pipeline**

[ ]  None (Only raw fastq files will be returned)

[ ]  Whole genome/exome variant calling

[ ]  Bulk RNA-Seq

[ ]  scRNA-Seq (10X Genomics only)

[ ]  Duplex Sequencing (Contact Scott Kennedy prior to submitting samples, scottrk@uw.edu )

[ ]  Digital Spatial Profiling (Nanostring GeoMx only)

[ ]  Other (Contact Scott Kennedy prior to submitting samples, scottrk@uw.edu )

**Reference genome**

Organism: Click or tap here to enter text.

Reference Genome: Click or tap here to enter text.

**Desired Illumina kit**

Please provide sequencing reagents on dry ice and appropriate flow cell

 [ ]  NovaSeq 6000 S1 Reagent Kit v1.5 (100 cycles) 20028319

 [ ]  NovaSeq 6000 S1 Reagent Kit v1.5 (200 cycles) 20028318

 [ ]  NovaSeq 6000 S1 Reagent Kit v1.5 (300 cycles) 20028317

 [ ]  NovaSeq 6000 S2 Reagent Kit v1.5 (100 cycles) 20028316

 [ ]  NovaSeq 6000 S2 Reagent Kit v1.5 (200 cycles) 20028315

 [ ]  NovaSeq 6000 S2 Reagent Kit v1.5 (300 cycles) 20028314

 [ ]  NovaSeq 6000 S4 Reagent Kit v1.5 (200 cycles) 20028313

 [ ]  NovaSeq 6000 S4 Reagent Kit v1.5 (300 cycles) 20028312

 [ ]  NovaSeq 6000 SP Reagent Kit v1.5 (100 cycles) 20028401

 [ ]  NovaSeq 6000 SP Reagent Kit v1.5 (200 cycles) 20040719

 [ ]  NovaSeq 6000 SP Reagent Kit v1.5 (300 cycles) 20028400

 [ ]  NovaSeq 6000 SP Reagent Kit v1.5 (500 cycles) 20028402

**Pool concentration** **provided**\_\_\_\_\_\_\_ nM (>6nM is required). Your run quality and yield will be adversely impacted by an inaccurate concentration. NGS libraries must be pooled and provided in a single tube.

**Attach formatted sample sheet**

Please ensure your sample sheet is properly formatted. Our staff will not be able to load the instrument if your sample sheet cannot be uploaded to the Sequencing Control Software and your reagents may be wasted. Formatting questions can be directed to Scott Kennedy ( scottrk@uw.edu )

**Data format**

Transfer will be raw bcl files for the run. Note that demultiplexing will not be performed by UW Virology.

[ ]  Option 1: AWS bucket: we will provide access to an s3 path.

List UW Net IDs requiring access: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

[ ]  Option 2: External hard drive: requestor will need to bring a USB drive with sufficient storage space, to be dropped off along with sequencing reagents and libraries.

[ ]  Option 3: BaseSpace transfer: Run will be transferred to requestor’s basespace account and any storage charges (icredits) billed by Illumina are your responsibility. Provide the email address associated with your basespace account \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_.

**Provide a brief description of samples in the NGS library:**

**Sequencing run approved** \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ **Date** \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

 Virology Sequencing Manager

**Run QC summary**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Flow Cell ID** | **Illumina Run ID** | **Pool Qubit (ng/ul)** | **Pool Size (TS Peak)** | **Final Loading Qubit (ng/ul)** | **Final Loading Conc. (nM)** | **Q30** | **PF** | **Tech Initials** | **Date loaded** |
|  |  |  |  |  |  |  |  |  |  |