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| **HTSF Account title** |  |

**Principal Investigator**

|  |  |
| --- | --- |
| *Name:* |  |

**Other LAB Personnel** (including coPI)

|  |  |  |  |
| --- | --- | --- | --- |
| Name | *Email* | *UNC ONYEN* | *Telephone* |
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(Add lines as needed, non UNC Personnel will not have an ONYEN)

**Project Information** *(check all that apply)*

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| --- | --- |
| This is clinical research (as defined by the NIH) | This is translational research |

***The UNC Genomics Core Laboratories are not HIPAA compliant and cannot accept samples with identifying patient information*.**

**Sample Details:**

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| --- |
| Species:  Human  Mouse  Other (please specify:     )  RNA/DNA source(s) (tissue/ cell type/ FFPE/ Frozen): |

**Sample type to submit**

**RAW MATERIAL**

ChIP DNA/ FAIRE seq DNA (specify antibody used):

Whole Genomic DNA

Amplicon

Total RNA

mRNA

**LIBRARIES**:

Study prepared libraries

Specify Library Type made by study:

**POOLS:**

Study made libraries which are pooled

Specify Library Type made by study:

Specify number of libraries in pool:

**Other**

There is a limited number of other material types that UNC HTSF will accept. Please confirm with the HTSF prior to submitting. **HTSF DOES NOT ISOLATE RNA or DNA**

(Specify):

**Library Services Requested** *(check all that apply and circle or highlight desired format)*

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| --- | --- |
| **QA/QC Service ONLY***: (specific QAQC method will be indicated upon submission)*  DNA QC  RNA QC |  |
| **Library Preparation Services:**  Illumina Library preparation  DNA  Final Library type:  DNA SEQ  Exome Capture  Custom Service request: Please indicate what is required (*requires consult)*    R&D  RNA Tru Seq  Final Library type:  Total RNA  mRNA  Low conc. RNA  small RNA ( miRNA/ micro RNA)  Custom Service request: Please indicate what is required *(requires consult)*    R&D  CHiPSeq/ FAIREseq  Amplicon / 16s metagenomics  Other Illumina Library services Please indicate what is required (*requires consult)*    **Sequencing Services Requested** *(check all that apply and circle or highlight desired format)*  **Sequencing Platform(s)** *(check all that apply)*   |  |  | | --- | --- | | * Please reach out to the HTSF if you are unsure which Platform best fits your seq needs. * Each platform version yields different amounts of data and number of lanes * Cluster or read #/ platform and # of lane/ platform is available on request   Illumina MiSeq sequencing  Illumina MiSeq NANO sequencing  Illumina NOVAseq6000 sequencing  SP  S1  S2  S4  Illumina NEXTseq 2000 sequencing  P1  P2  P3  **Sequencing Services Requested** *(check all that apply and circle or highlight desired format)*  **Read Format:**  Single End  Paired End  **Number of seq cycles:**  Indicate # of cycles:  **Number of lane to run for each pool**  Indicate # of lanes:  **Number of samples in a pool ( estimate)**  *A pool is a single volume created form equal molar amounts of a series of libraries combined into that single volume. An aliquot from the pool is removed to prepare to run on the sequencer.*  Indicate # libraries/ pool:  **Additional Required Sequence Information** (check all that may apply)  Libraries have/ require Dual Barcodes?  Custom Primer required.  Old Nextera (HTSF supplied)  Study Custom Primer  Custom Primer name:  *(note: SEQUENCE OF CUSTOM PRIMER WILL BE REQUESTED AT SUBMISSION )*  **Project Size and Timetable**  Overall estimate number of project samples  Samples are already available and we are ready to start as soon as possible.  We expect to be ready to start on       *(specify estimated date)*  Comment: | S1 | |  |  | |  |
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**Data Delivery and Analysis:**

**Data Delivery** –

LCCC pipeline

Study Data folder on ITS Research Computing

Study folder data path (if known):

Do you require a folder to be set up? HTSF can request a folder to be created for your needs.

PLEASE NOTE: All non UNC studies will have data delivered via Google Cloud at this time. There is a small fee/Gb for this service. You will receive an email with the link to access the data with 5 days of delivery.

**DATA Analysis --**

Study requires Data analysis Assistance –

# The HTSF will request BARC (**Bioinformatics and Analytics Research Collaborative**) to reach out to arrange a consult to determine your needs and the cost for the service

Data analysis – Project will do it’s own analysis, Please list people responsible for analysis

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| --- | --- | --- | --- |
| Name | *Email* | *ONYEN* | *Telephone* |
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**PROJECT DESCRIPTION**

*Please insert brief statements*

**Hypothesis/Specific Aims Background and Significance** *(One paragraph maximum please.)*

**Comments, Special Considerations and/or Additional Instructions:**