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| **HTSF Account title**  |       |

**Principal Investigator**

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| *Name:* |       |

**Other LAB Personnel** (including coPI)

|  |  |  |  |
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| 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)*

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| * 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:**