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| **Project title**  |       |

**Principal Investigator**

|  |  |
| --- | --- |
| *Name:* |       |
| *Title:* |       |
| *Department:* |       |
| *Institution:* | [ ]  UNC [ ]  Other       |
| *Address:* |       |
| *E-mail:* |       | *Telephone:* |       |
| *UNC ONYEN* |       |

**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*.**

**Funding Sources**

Is one or more members of the study part of:

|  |
| --- |
| [ ]  UNC |
| List department: |
| [ ]  Lineburger Cancer Center |
| [ ]  nonUNC- Academic Institution |
| List Institution: |
| [ ]  Industry |
| List company :  |

*Please list the ACCOUNANT for the funding source(s) you plan to use for this project. You may list more than one account if necessary when you submit your samples to the HTSF.*

**UNC billing via Chartfield String**

**We do not need the funding account number (CFS) at this time.**

|  |  |  |  |
| --- | --- | --- | --- |
| Accountant Name | *Department* | *E-mail* | *Telephone* |
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**non UNC Billing**

|  |  |  |
| --- | --- | --- |
| Accountant Name | *E-mail* | *Telephone* |
|  |  |  |
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Payment will be via

Payment instructions will be sent at time of invoicing

[ ]  Electronic check

[ ]  Credit card

[ ]  Purchase Order (HTSF will require a copy of the PO# at time of submission)

**Sample Details:**

|  |
| --- |
| 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)*

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