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| Project title  |       |

Database Study name:

*This will be assigned by the HTSF*

Principal Investigator

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

Co-investigator(s) and Other Personnel Involved in Project

|  |  |  |  |
| --- | --- | --- | --- |
| Name | *Email* | *UNC ONYEN* | *Telephone* |
|       |  |       |       |
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Project Information *(check all that apply; this information may help you qualify for extra support from the cores and the biostatistics/informatics group)*

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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 |
| [ ]  Lineburger Cancer Center |
| [ ]  nonUNC- Academic Institution |
| [ ]  Industry |

*Please list the ACCOUNANT for the funding source(s) you plan to use for this project.* ***We do not need the funding account number (CFS) at this time.*** *You may list more than one account if necessary when you submit your samples to the HTSF.*

|  |  |  |  |
| --- | --- | --- | --- |
| Accountant Name | *Department* | *E-mail* | *Telephone* |
|       |       |       |       |

Sample Details:

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

Estimated RNA/DNA (per sample):       units: [ ] µg [ ] ng [ ] pg

**Sample type to submit**

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

[ ]  Whole Genomic DNA

[ ]  Amplicon

[ ]  Total RNA

[ ]  mRNA

[ ]  Study prepared libraries

 Specify Library Type:

[ ]  POOLS: Study made libraries which are pooled

 Specify Library Type:

 Specify number of libraries in pool:

[ ]  Other (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 (may require 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 (may require consult)       [ ]  R&D[ ]  CHiPSeq/ FAIREseq[ ]  Amplicon / 16s metagenomics [ ]  Other Illumina Library services Please indicate what is required (may require consult)      ***If HTG services are required, please use the HTSF Project Initiation for HTG services instead of this form.***Sequencing Services Requested *(check all that apply and circle or highlight desired format)*Sequencing Platform(s) *(check all that apply)*

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| [ ]  Illumina HiSeq2500 sequencing – V4 chemistry – High Output[ ]  Illumina HiSeq2500 sequencing – Rapid Run[ ]  Illumina HiSeq4000 sequencing[ ]  Illumina MiSeq sequencing[ ]  Illumina MiSeq NANO sequencing[ ]  Illumina NOVAseq6000 sequencing (this system currently requires a consult with HTSF) [ ]  SP [ ]  S1 [ ]  S1\_XP [ ]  S2 [ ]  S1\_XP [ ]  S4 [ ]  S4\_XP Sequencing Services Requested *(check all that apply and circle or highlight desired format)*[ ]  Single End[ ]  Paired End[ ]  Multiplex Sequencing (pooled libraries – aka more than one library in a lane) Number of samples in pool:       Number of seq cycles: Indicate # of cycles:      Number of lane to run for each pool or SampleIndicate # of lanes:       **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 CUTOM PRIMER WILL BE REQUESTED AT SUBMISSION )*Project Size and TimetableOverall 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 KURE

 Study folder data path (if known):

 [ ]  Do you require a folder to be set up?

[ ]  Data analysis Assistance – assistance requested for analysis. This can include suggesting software, basic training to analyze your data and suggestions of possible UNC faculty/ staff to assist

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

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

*Please insert brief statements below each of the following headings.*

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

Analysis*(required)*

*What analyses are of interest? (e.g., compare Group A to Group B, determine the effects of the transgene, and analyze the interaction between the transgene and the treatment)*

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