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| --- | --- |
| Project title |  |

Database Study name:

*This will be assigned by the HTSF*

Principal Investigator

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

|  |
| --- |
| 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)*   |  |  | | --- | --- | | 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 Sample  Indicate # 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 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 | |  |  | |  |
|  |  |

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:**