 **UNIVERSITY OF CAPE TOWN COMPUTATIONAL BIOLOGY DIVISION**

**Bioinformatics Support Request**

Please provide us with more information on your request for support. Complete the form as comprehensively as possible, and please indicate where there is still uncertainty.

**Please note, the earlier we are involved the better – for example, it would be better for us to be involved during the study design and even grant application stage**.

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| **CONTACT DETAILS** | |
| Date of request | **10 February 2023** |
| Name | **Nyaradzo TL Chigorimbo-Tsikiwa** |
| Email address | **Nyaradzo.chigorimbo-tsikiwa@uct.ac.za** |
| Research Group/Department | **Chigorimbo-Tsikiwa research group, Medical Virology, Pathology Dept** |
| Faculty | **Health sciences** |
| IF student, name & email of supervisor |  |

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| **PROJECT DETAILS** |
| 1. What is the scientific question? |
| To assess the impact of aSTI on the foreskin special transcriptome and ex vivo HIV-1 infection |
| 2. Who are the partners on the project? |
| Sophia Liu and Fei Chen Broad Institute of Harvard and MIT,  Cambridge, USA |
| 3. What type of collaboration with CBIO is expected? For a project that is done as collaboration or for a fee, we will put the agreement in writing. |
| As a research collaboration with our research group or for a fee basis. |
| 4. Are there any ethical issues we should be aware of? |
| None. We have ethics for the collection of samples |
| 5. How much work is expected from CBIO and when? |
| Currently we are producing proof of concept data from limited samples which will be used in a grant application to expand the work |
| 6. What type of data will be generated (e.g. sequencing, genotyping, expression, etc.) and what technology platform will be used? |
| Sequencing data |
| 7. When do you expect the data? Does it need to be transferred from somewhere else? |
| Prelim Data is available now, need to be transferred from the BROAD. |
| 8. How large will the data be? How long does it need to stored for, and have you made arrangements for storage? |
| Not sure yet |
| 9. What bioinformatics analysis needs to be done? Which tools are required? |
| Currently BAM files |
| 10. If a collaborative model is being used, what papers are envisaged and who will the authors be? |
| We envision 1. A grant application and a paper detailing the impact of aSTI on HIV-1 susceptibility in the Male genital tract using gene expression at a fine scale. Possibly we will be able to collate it to foreskin metaproteomics data as well if funds allow. |

**PLEASE FORWARD THE COMPLETED FORM TO:**

[Nicola.mulder@uct.ac.za](mailto:Nicola.mulder@uct.ac.za)