

ASHG Contest Sample Entry

Sample Script for Video Version

Hi! My name is Abella and I am a post-doc in an AIDS Research Institute. This is my proposal for using the HIVE for single-cell analysis.

HIV infection occurs through four stages

First: Initial Infection

Second: there is an Asymptomatic stage

Third: Advanced HIV disease

And finally: AIDS

Each stage exhibits different characteristics including a progressively lower CD4+ cell count. I am studying the changes in expression profiles over time of both T-cells and B-cells as HIV goes through these stages of infection.

I have been using cryopreserved samples since it has been difficult to collect fresh samples remotely that would have yielded good data from my institute's droplet-based device. I would love to collect fresh HIV-infected blood and bone marrow samples from my collaborators in Brazil and process them as if they were still fresh for single cell sequencing.

I propose using the HIVE to capture fresh T-cell and B-cell samples over time, ship them to be processed in my lab all at once and then sequenced in our core facility to understand the transcriptome changes as the disease progresses.

I am also interested in understanding why Eosinophil cell numbers increase as infection progresses and the CD4+ T-cell population decreases. How do the expression profiles change in Eosinophils as they start to be infected? We aren't able to see these cell types at all in our cryopreserved samples, so it'll be interesting to learn more about them.

Thank you.