

Life Sciences Reporting Summary

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For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

Non-Human Primate: These are observational studies based largely on archival tissue samples from other experiments.
Human: These tissues are from an observational study of volunteers initiating ART in Kampala, Uganda. No formal sample-size calculations were made.

2. Data exclusions

Describe any data exclusions.

None

3. Replication

Describe whether the experimental findings were reliably reproduced.

Yes, we have a rigorous process for verifying QIA results including 2 different individuals completing analysis on randomly selected images to maintain quality control.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

not applicable

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

None

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or the Methods section if additional space is needed).

n/a Confirmed

- ☒ ☐ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
- ☒ ☐ A statement indicating how many times each experiment was replicated
- ☐ ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☐ ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☐ ☒ The test results (e.g. p values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

Photoshop, Prism, Microsoft Excel

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* [guidance for providing algorithms and software for publication](#) may be useful for any submission.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

No restriction

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

not applicable

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

not applicable

b. Describe the method of cell line authentication used.

not applicable

c. Report whether the cell lines were tested for mycoplasma contamination.

not applicable

d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

Provide a rationale for the use of commonly misidentified cell lines OR state that no commonly misidentified cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

Rhesus macaques of Indian origin (*Macaca mulatta*; RMs) used for SIV infection in these studies were mature male and female animals ranging in age from approximately 3–12 years, and were negative for MHC alleles associated with SIV control (Mamu A*01, B*08, and B*17). Eight RMs were housed at Advanced Bioscience Laboratories (ABL) in accordance with the Association for the Assessment and Accreditation of Laboratory Animal Care (AAALAC) standards and all procedures were performed according to protocols approved by the ABL Institutional Animal Care and Use Committee (IACUC) (Protocol # AUP504, OLAW Assurance #A3467-01). Animals at ABL were intravenously (i.v.) inoculated with either 1.9×10^4 TCID₅₀ SIVmac251 (generated in the laboratory of Dr. Ron Desrosiers during 2006) or 100 TCID₅₀ SIVmac251 (generated in 2010 in the laboratory of Dr. Ron Desrosiers). Three RMs (P568, P096, and P533) were infected with SIVmac251 (no ART) and sacrificed at 14, 43, and 90 days post infection. Five additional RMs (R365, R366, R367, R406 and R410) were infected with SIVmac251 and placed on ART at 8 wpi started on an ART regimen that consisted of the NRTIs tenofovir (PMPA; 20 mg/kg; Gilead Biosciences) and emtricitabine (FTC; 50 mg/kg; Gilead Biosciences) administered subcutaneously, and the integrase strand transfer inhibitor raltegravir (RAL; 150mg BID) plus the protease inhibitors darunavir (DRV; 400 mg; BID) and ritonavir (RTV; 100 mg; BID) given orally; and treated for 20–22 weeks prior to being sacrificed. These 8 RMs were utilized to perform a comprehensive tissue analysis of where SIV persisted in untreated and ART treated infection.

The experimental conditions and ART regimens employed for the 11 rhesus macaques housed at the National Cancer Institute were previously described for 5 RM (DCCN, DCHV, DCT3, DCEG, and DCJB) which received 26–32 weeks of ART beginning at 4 weeks post-infection and 6 RM (DCLJ, DCT2, DCEA, DC1G, DCCP and DCEW) which received a different regimen and also begun at 4 weeks post-infection, for 31–32 weeks. 22, 24, 25 Lymph nodes were collected by surgical extraction before (4 wpi) and 26–32 weeks after the initiation of ART (30–40 wpi) and immediately fixed in freshly prepared neutral buffered 4% paraformaldehyde (PFA) for 24 h at room temperature. After fixation for 24 h, fixative was replaced with 80% ethanol and tissues were paraffin embedded as previously described.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

HIV-infected people in Kampala, Uganda who were eligible to start ART were recruited into a longitudinal protocol that was conducted at the Joint Clinical Research Center (JCRC). All subjects gave written informed consent and the Institutional Review Boards (IRB) of the University of Minnesota and JCRC and the Uganda National Council of Science and Technology (UNCST) approved the study. This was a longitudinal pathogenesis based study with no pre-determined comparators, as such we did not have a pre-determined sample size for recruitment.