# nature portfolio

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# **Reporting Summary**

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

#### **Statistics**

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.				
n/a	Cor	firmed		
	X	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement		
	X	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly		
	×	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.		
×		A description of all covariates tested		
	X	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons		
	×	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)		
	×	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.		
X		For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings		
×		For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes		
X		Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated		
		Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.		

### Software and code

Policy information about availability of computer code				
Data collection	Data collection was performed using Microsoft Excel and imported into SAS for analysis. Excel sheets can be provided upon request.			
Data analysis	The analysis for this manuscript was performed using SAS software version 9.4 (proc import, proc means and proc npar1way). Code can be provided upon request.			

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

#### Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

All data supporting the findings of this study are available within the paper and its Supplementary Information. Source data are also provided with this paper. Any additional requests for information can be directed to the corresponding author. The antibodies used for flow cytometry analysis are provided in Supplementary Table 2.

### Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data where this information has been collected, and consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.
Population characteristics	Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."
Recruitment	Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.
Ethics oversight	Identify the organization(s) that approved the study protocol.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

### Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>

## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	This is an observational study that includes three groups of 4 macaques each: i) 4 macaques treated with emtricitabine (FTC), tenofovir alafenamide (TAF), cabotegravir long-acting (CAB LA) and rilpivirine long-acting (RPV LA), ii) 4 macaques treated with FTC/TAF/CAB LA/RPV LA and vesatolimod, and iii) 4 untreated controls
Data exclusions	All data are included
Replication	We used groups of 4 macaques for the in vivo studies to account for animal to animal variability in acute infection kinetics and drug metabolism. For clarity and reproduction purposes, we include in the manuscript all the individual SHIV RNA and antibody levels. Drug concentrations are provided as median and ranges.
Randomization	The study was not randomized. When possible, we selected animals that responded to positive reinforcement training for optimal drug delivery with foods.
Blinding	Blinding was not done given the need to prepare individual drug doses according to weight

### Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems	Methods	
n/a Involved in the study	n/a Involved in the study	
Antibodies	ChIP-seq	
Eukaryotic cell lines	Flow cytometry	
Palaeontology and archaeology	X MRI-based neuroimaging	
Animals and other organisms		
🗶 🗌 Clinical data		
Dual use research of concern		

### Antibodies

Antibodies used	Antibody MT807R1 for in vivo CD8+ T cell depletion
Validation	The rhesus IgG1 recombinant Anti-CD8 alpha [MT807R1] monoclonal antibody was engineered and produced by the Nonhuman Primate Reagent Resource (Cat# PR-0817, RRID:AB_2716320).

### Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Indian Rhesus macaques	
Wild animals	Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.	
Reporting on sex	We did not considered sex in the study design because of limited animal availability. We included one female in the eART+VES group and 1 female in the control group. The terminal PK study with CAB LA and RPV LA was done in a female macaque. The Source data file specifies which animals were females	
Field-collected samples	For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.	
Ethics oversight	CDC Institutional Animal Care and Use Committee	

Note that full information on the approval of the study protocol must also be provided in the manuscript.

### Flow Cytometry

#### Plots

Confirm that:

**X** The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

**X** The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

All plots are contour plots with outliers or pseudocolor plots.

**X** A numerical value for number of cells or percentage (with statistics) is provided.

#### Methodology

Sample preparation	Blood was collected in CPT tubes and enriched for mononuclear cells using density centrifugation
Instrument	LSRII flow cytometer
Software	FlowJo software (TreeStar, Inc.)
Cell population abundance	A minimum of 20,000 PBMC were collected
Gating strategy	Viable singlet CD45+ cells were discriminated for lymphocytes using forward and side scatter characteristics. From this population CD3 expressing cells were discriminated for CD4 and CD8 cell surface expression.

**x** Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.