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 Editorial Policies and the Editorial Policy Checklist.

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	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐	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
☒	☐	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. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	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
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	QuantaSoft software (Bio-Rad, v.1.6) was used for ddPCR data collection R-script (codes already published) were used for the ddPCR analyses.
Data analysis	QX manager software (Bio-Rad, version 2.1.0.25) was used for the ddPCR analysis FlowJo (BD Biosciences, v10.8.1 and v10.10.0)was used for the flow cytometry analyses. Graphpad Prism v10.4.2 and Biorender was used to create figures. Extreme limiting dilution analysis (https://bioinf.wehi.edu.au/software/elda/) was used to calculate infection frequencies and confidence intervals for quantitative viral outgrowth assay (qVOA). Co-receptor tropism was determined by analyzing the V3 sequence using the online bioinformatics tool geno2pheno[coreceptor] (https://coreceptor.geno2pheno.org/). The confidence interval for total HIV DNA was calculated using aggregated data from all droplet digital PCR (ddPCR) replicates, applying the Clopper-Pearson method to obtain the exact binomial proportion confidence interval, and subsequently normalized to copies per million cells.

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

Data sharing is possible upon reasonable request, except data related to the protection of the participant's privacy.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	The study focused on a HIV-1 positive male individual (n=1) who received CCR5Δ32/Δ32 hematopoietic stem cells from his brother. Due to the nature of this case report, the analysis did not allow for the assessment of sex bias.
Reporting on race, ethnicity, or other socially relevant groupings	Socially relevant categorization variables were not considered in this study because it is a case report.
Population characteristics	The case report describes a 62-year-old male individual who was previously HIV-1 positive and is now in remission four years after receiving CCR5Δ32/Δ32 hematopoietic stem cell transplantation (HSCT). Due to the nature of this case report, broader demographic trends and characteristics typically associated with larger populations cannot be assessed.
Recruitment	The subject was enrolled at the Department of Haematology, Oslo University Hospital, and was included in both the IciStem cohort (IciS2-56) and the EU2Cure cohort (#1-10-72-38-23).
Ethics oversight	The patient has provided written informed consent.The study was approved by the Norwegian Regional Committee for Medical and Health Research Ethics (REK#469419).

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 nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

Sample size	Sample size calculation was not applicable for this case study (n=1). Controls were utilized to provide a reference for data comparison.
Data exclusions	All data were included without any exclusions.
Replication	Standard Operating Procedures (SOPs) were followed. Number of technical replicate wells were the same for CS-IPDA and Total HIV ddPCR runs. Longitudinal timepoint samples: CD4, PBMC, 3 months post HSCT : HIV : 6 replicates; RPP30: 2 replicates CD4, PBMC, 9 months post HSCT: HIV : 6 replicates; RPP30: 2 replicates CD4, PBMC, 27 months post HSCT : HIV : 12 replicates; RPP30: 2 replicates CD4, leukapheresis sample: HIV : 88 replicates RPP30: 3 replicates CD45, Terminal Ileum, : HIV : 6 replicates; RPP30: replicates CD45, Sigmoid Colon : HIV : 6 replicates; RPP30: 2 replicates
Randomization	Randomization was not applicable as this study focused on a single patient case.

Blinding | Blinding was not applicable, given that this study involved a single patient case.

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

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

ELISpot:
1. Anti-Human mAb 1-D1K, Mabtech, catalog #3420-3-1000
2. Anti-Human IFN-g mAb 7-B6-1-Biotin, Mabtech, catalog #3420-6-250
3. Streptavidin-ALP, Mabtech, catalog #3310-10-1000

Proliferation:
1. CD3: PE/Dazzle 594, clone OKT3, Biolegend, catalog #317345
2. CD4: PE/Fire 700, clone SK3, Biolegend, catalog #344665
3. CD8: APC, clone SK1, Biolegend, catalog #344721

Flow cytometry cell sorting (FACS) of gut CD45+ cells for reservoir analyses:
1.CD45: FITC, clone HI30, Becton Dickinson, catalog #555482
2.CD3 : APC, clone UCHT1, Becton Dickinson, catalog#555335
3.CD8: PercP, clone OX-8,Becton Dickinson, catalog #345774

Sorting of CD34+ cells for chimerism analyses: CD34 MicroBeads, Miltenyi Biotec, Cat #1130-046-702

Sorting of CD45+ cells for chimerism analyses:
1. CD45: PerCP-Cy5.5, clone 2D1, Becton Dickinson, catalog #332784
2. CD3: Amcyan (PB), clone SK7, Becton Dickinson, catalog # 339186
3. CD4: PE, clone SK3, Becton Dickinson, catalog # 566910
4. CD8: APC clone RPA-T8 , Becton Dickinson, catalog # 555369

Validation

Negative control samples were included for all the experiments.
Proliferation:
1. CD3 PE/Dazzle 594; Verified reativity: Human (Biolegend); Application: Flow cytometry (Quality tested, Biolegend)
2. CD4 PE/Fire 700; Verified reativity: Human (Biolegend); Application: Flow cytometry (Quality tested, Biolegend)
3. CD8 APC, SK1; Verified reativity: Human, Cynomolgus, Rhesus (Biolegend); Application: Flow cytometry (Quality tested, Biolegend)

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s) | ACH-2 cells (Cat No. 349), TZM-bl cells (Cat No. 8129), MOLT-4/CCR5 cell lines (Cat No 4984) were both obtained from the NIH HIV Reagent Program (https://www.beiresources.org/HIV.aspx).

Authentication | Authentication was determined by evaluating growth characteristics, morphological features, expected behavior, and functionality.

Mycoplasma contamination | TZM-bl cells and MOLT-4/CCR5 cell lines were tested negative for mycoplasma.

Commonly misidentified lines (See ICLAC register) | No commonly misidentified cell lines were used in this study.

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	This study involves a single individual and is not registered as a clinical trial.
Study protocol	A trial protocol is not available since this study is a case report.
Data collection	All clincial data were collected at Oslo University Hospital from 2010 to 2025.
Outcomes	Absence of viral rebound was observed 24 months after the analytical treatment interruption.

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

Flow Cytometry

Plots

Confirm that:

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

☒ 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.

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

Methodology

Sample preparation	Cryopreserved peripheral blood mononuclear cells (PBMCs) were thawed and washed in RPMI supplemented with fetal bovine serum (FBS) and penicillin/streptomycin (P/S). How the samples were treated beyond this timepoint depends on the experimental conditions employed and is described in Materials and Methods.
Instrument	MACSQuant16 (Miltenyi Biotec)
Software	FlowJo 10.10.0
Cell population abundance	200.000 PBMCs were seeded in each well for stimulation in the lymphocyte proliferation assay.
Gating strategy	In the lymphocyte proliferation assay, cells were gated as follows: Live cells were gated as the negative population in a dead cell stain. Single cells were gated in a SSC-A/SSC-H plot. Lymphocytes were gated in a SSC-A/FSC-A plot. CD3 positive cells were gated in a SSC-A/CD3-A plot. Single positive CD4 and CD8 cells were gated in a CD8-A/CD4-A plot. Percentage proliferating cells was gated in a SSC-A/CTV-A plot for both CD4 and CD8 single positive cells as populations were dimmer than the undivided peak.

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