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Authors: Ulrike C. Lange, Julia K. Bialek, Thomas Walther, Joachim Hauber

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Pinpointing recurrent proviral integration sites in new models for latent HIV-1 infection

Ulrike C. Lange[1,2,3,*], Julia K. Bialek[1,2,§], Thomas Walther[1,§], Joachim Hauber[1,3]

[1]Heinrich Pette Institute – Leibniz Institute for Experimental Virology, 20251 Hamburg, Germany; [2]Department of Anesthesiology, University Medical Center Hamburg-Eppendorf, Hamburg, Germany; [3]Center for Infection Research (DZIF), partner site Hamburg, Germany.

§ contributed equally

* corresponding author

contact information for corresponding author:

Ulrike C. Lange
Heinrich Pette Institute
Martinistrasse 52
20251 Hamburg
Germany
e-mail: ulrike.lange@leibniz-hpi.de

Highlights

- Description of a practical workflow to generate T-cell based models for HIV infection using CRISPR/Cas9-based genome engineering.
- The method enables selection of the proviral integration site to mimic clinically relevant integration sites observed in HIV-infected patients.
- Two BACH2-HIV reporter models are presented providing unique tools to analyze locus-specific effects of HIV-integration and/or activity.

Abstract

HIV infection is characterized by accumulation of proviral sequences within the human host genome. Integration of viral-derived DNA occurs at preferential loci, suggesting a site-specific crosstalk between viral sequences and human genes. We here describe a genome engineering workflow to generate models for HIV-1 infection that for the first time recapitulate proviral