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

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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

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