HIV-1 lentivirus tethering to the genome is associated with transcription factor binding sites found in genes that favour virus survival

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Lentiviral vectors are attractive for permanent and effective gene delivery as they can integrate into the host genome. However, this can cause insertional mutagenesis highlighting the importance to further understand the integration process. Insertion site tethering is believed to involve cellular proteins such as PSIP1/LEDGF/p75, which binds to virus pre-integration complexes to target the virus genome to that of the host. Transcription factors that bind both the vector LTR and host genome are also suspected influential to this. To determine the role of TF in the tethering process, we mapped predicted transcription factor binding sites near to IS chosen by HIV-1 LV in infected human induced pluripotent stem cells and their hepatocyte-like cell derivatives. These sites were also found in both the native and self-inactivated LTR configurations and significant enriched in transcription factors essential to HIV-1 life cycle and virus survival. These sites also reside in HIV-1 patient IS and in mice infected with SIN LTR configuration HIV-1 based recombinant LV. Our *in silco* data analysis suggests pTFBS present in the virus LTR and IS sites selected by HIV-1 LV are important to virus survival and propagation.