

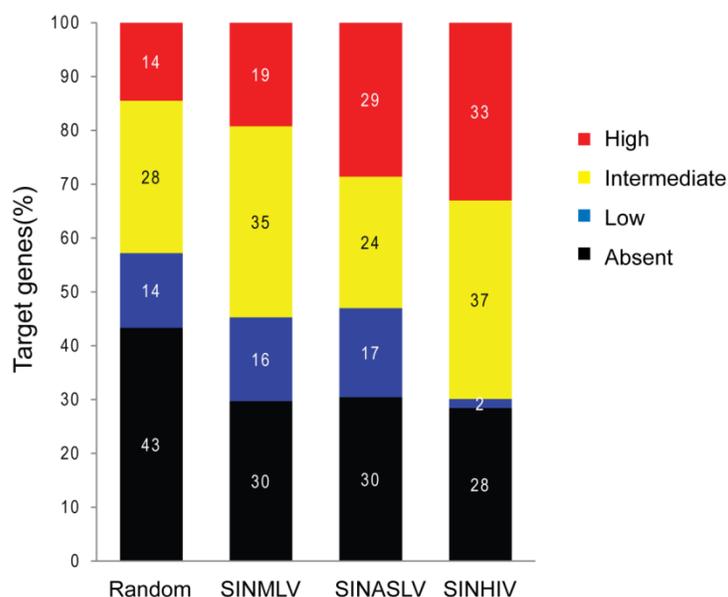
Supplementary Information

Table S1. Integration distribution around DNase I hypersensitive sites in the genome of human HPSCs.

Vector	DNase I hypersensitive sites (%)
SIN-ASLV (8250)	18.26
SIN-MLV (13,097)	77.75
SIN-HIV (32,827)	12.21
Random (40,000)	9.00

Percentage of SIN-MLV, SIN-ASLV and SIN-HIV integrations and random sequences harboring a DNase I hypersensitive site in a ± 1 kb interval.

Figure S1. Association of vector integration sites with CD34+ HSPCs gene expression.



Histogram distribution of expression values from an Affymetrix microarray (HG-U133 + 2.0) analysis of RNA obtained from cytokine-stimulated CD34⁺ cells. Expression levels were divided into four classes: absent, low (below the 25th percentile of the normalized distribution), intermediate (between the 25th and the 75th percentile) and high (above the 75th percentile). The percentage distribution of the expression values of genes targeted by SIN-MLV, SIN-ASLV and SIN-HIV integration sites and random sequences.