

**Supplementary Table S2. Distribution of foamy viral and insulated FV vector integration sites in transduced human cord blood**

	n <sup>a</sup>	Total integrations (%)			Integrations in or near proto-oncogenes (%)	
		In genes	Within 50 kb of TSS	In DNase hypersensitivity sites	In proto-oncogenes	Within 50 kb of TSS
Random	10,000	44.74	44.40	1.01	8.59	6.51
Day 5						
FV-control	9,765	44.12	59.90	3.37	7.76	10.04
FV-cHS4-R	4,764	43.65 <sup>b</sup>	60.26 <sup>b</sup>	2.94 <sup>b</sup>	7.54 <sup>b</sup>	10.85 <sup>b</sup>
Day 10						
FV-control	13,120	44.34	59.49	2.80	7.64	9.96
FV-cHS4-R	5,976	43.41 <sup>b</sup>	59.11 <sup>b</sup>	2.76 <sup>b</sup>	7.65 <sup>b</sup>	10.11 <sup>b</sup>

<sup>a</sup>n, the total number of unique integrations captured.

<sup>b</sup> $\chi^2$  analysis showed no significant difference compared with uninsulated control.

FV, foamy virus; TSS, transcription start site.