

	MLV (n=432)	SIV (n=328)	MLV (n=459)	SIV (n=362)
Identity to the human genome	at least 90%		at least 80%	
Inside RefSeq genes	49.1%	73.5%	49.7%	72.9%

Table S1. Comparison of retroviral integration sites distribution within transcription units with and without the rhesus sequences that were less than 90% orthologous to the human genome.