SUPPLEMENTS:

Table S1. Microsatellite locus informations.

We used Cervus (Kalinovski et al, 2007) and Genecap (Wilberg et al, 2004) to assess for each locus: the number of different alleles (a), the number of samples genotyped at each locus (b), observed and expected heterozygoty (c and d, respectively), polymorphic information content (e), and probabilities of individuals within the population sharing the same genotype using two different assumptions: Hardy-Wainberg (HW) equilibrium (f) and sibling (Sib) identity (g).

Locus	Number of alleles [a]	Number of samples [b]	Hobs [c]	Hexp [d]	PIC [e]	HW P(ID) [f]	Sib P(ID) [g]
D18S536	8	230	0,652	0,644	0,589	0,146	0,441
D4S243	7	209	0,785	0,788	0,755	0,076	0,375
D10S676	8	224	0,871	0,723	0,671	0,127	0,421
D9S922	8	191	0,796	0,765	0,734	0,092	0,396
D2S1326	9	193	0,902	0,817	0,789	0,057	0,354
D2S1333	13	176	0,795	0,839	0,818	0,042	0,339
D4S1627	9	178	0,770	0,780	0,747	0,083	0,384

Kalinowski, S. T., M. L. Taper, and T. C. Marshall. 2007. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Mol Ecol **16:**1099-106.

Wilberg, M. J., and B. P. Dreher. 2004. GENECAP: a program for analysis of multilocus genotype data for non-invasive sampling and capture-recapture population estimation. Molecular Ecology Notes **4:**783-785.

Figure S1. Phylogenetic analysis of partial *pol* nucleotide sequences (202 bp without gaps) of SIVgor strains.

The tree was inferred by maximum likelihood phylogeny (PhyML) with previously characterized SIVcpz*Ptt*/SIVgor/HIV-1 strains. Stars represent the support values above 850 from 1,000 maximum likelihood bootstraps. The scale bar represents 0.05 substitutions per site. Sample number and collection date, individual identification (IDs), clusters (11, 20, and 39) and social groups (A, C, G, E, and F1/2/3) are noted and refer to Table 1. The color code is conserved through Figures 2 to 4 and S1. A plain bracket highlights individuals from the same group infected with similar strains (very low genetic distance).