

S1 Table. The number of CD4⁺ T cells used for PCR amplification of proviral *gag* cDNA fragments for sequencing

Macaques	CD4 ⁺ T-cell numbers ^a		
	2 months pi	1 year pi	2 years pi
R06-037	8.6 x 10 ⁴	1.8 x 10 ⁵	*6.6 x 10 ⁴
R05-005	6.2 x 10 ⁴	2.0 x 10 ⁵	*9.4 x 10 ⁴
R07-002	6.2 x 10 ⁴	1.3 x 10 ⁵	5.5 x 10 ⁴
R03-018	5.0 x 10 ⁴	1.1 x 10 ⁵	4.4 x 10 ⁴
R07-001	1.3 x 10 ⁵	2.2 x 10 ⁵	*1.0 x 10 ⁵
R07-006	5.5 x 10 ⁴	2.0 x 10 ⁵	*1.0 x 10 ⁵
R07-003	7.2 x 10 ⁴	1.8 x 10 ⁵	8.6 x 10 ⁴
R07-008	5.5 x 10 ⁴	4.4 x 10 ⁵	8.1 x 10 ⁴
R09-009	5.5 x 10 ⁴	1.1 x 10 ⁵	1.1 x 10 ⁵
R09-010	6.6 x 10 ⁴	1.7 x 10 ⁵	6.1 x 10 ⁴

^aPBMCs obtained from macaques at 2 months, 1 year, and 2 years post-infection (pi) were used. Cellular DNAs were extracted from CD4⁺ T cells isolated from PBMCs and were used as the template for nested PCR amplification of proviral *gag* cDNA fragments for sequencing. The amount of DNA used as the template for the first PCR amplification is corresponding to that derived from the indicated number of CD4⁺ T cells. In macaques R06-037, R05-005, R07-001, and R07-006 at 2 years indicated by the asterisk (*), cellular DNAs were extracted after 8 days of culture. The cell numbers are different among samples because of difference in available cell numbers.