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The authors regret that the printed version of the above article contained a number of errors. The correct and final version follows.
**Fig. 1.** Phylogenetic relationships of clade C T/F Envs used for SHIV construction. A maximum likelihood tree is shown that depicts the position of nine subtype C T/F env sequences (C2–C10; bold) in relation to each other and reference strains (made using PhyML version 3 with a TVM + I + G model chosen using Modeltest version 2.1.4). A tenth env sequence (C1-19912872) was identified as an A/C recombinant and is thus not included in the analysis. Reference sequences included subtype C [BR025 (accession U52953), ETH2220 (U46016), 98IN012 (AF286231), 04ZASK146 (AY772699), ZM246F (FJ496192), CH0131 (KC894107), CH0185 (KC156129), CH0067 (KC156125), CH0200 (KC149183), and CH0164 (KC894125)] and subtype B [HXB2 (K03455)] strains. C2–C7 env genes (indicated by arrows), along with C1-19912872 env (not shown), were cloned into the SHIV KB9 proviral backbone; SHIVs containing C3, C4 and C5 env genes (stars) were able to initiate a productive infection in monkeys. Bootstrap support values greater than 70% are shown at nodes in the tree. The scale bar represents 0.05 substitutions/site.

**Fig. 2.** In vivo selection of clade C T/F SHIVs. Seven clade C T/F env genes, C1 through C7, were cloned into the SHIV KB9 backbone to generate seven different clade C SHIVs. These seven clade C SHIVs were combined in equal ratios (100 TCID\textsubscript{50} of each of the viruses) to make a pool of viruses and were inoculated in two naive rhesus monkeys intravenously. Infecting clones of SHIVs were isolated from the monkeys at various timepoints during the course of infection as indicated by the arrows. Clones isolated from monkey AV032 are shown in “Red” letterings and the time point is indicated by “Red” arrow, whereas clones isolated from monkey AV056 are shown in “Black” letterings and timepoints are shown in “black” arrows. The number of clones present in the total number of isolated clones at each timepoint is noted in parentheses next to each of the clones. Among nineteen clones isolated from monkey AV032 at day 14 post-infection, four clones matched with SHIV KB9 C3, fourteen matched with SHIV KB9 C4 and one matched with SHIV KB9 C5 sequences. A total of seven clones of SHIV KB9 C3 were isolated from monkey AV056 at day 49 post-infection, four clones matched with SHIV KB9 C3, fourteen matched with SHIV KB9 C4, and one matched with SHIV KB9 C5 sequences. A total of seven clones of SHIV KB9 C3 were isolated from monkey AV056 at day 49 post-infection and, at day 98 post-infection, two SHIV KB9 C3 and eight SHIV KB9 C5 clones were detected in ten isolated clones. All five clones isolated from monkey AV032 at day 14 post-infection matched the sequence of SHIV KB9 C4.
Fig. 3. In vivo infectivity of the individual clones of SHIVs. Culture supernatants containing 1000 TCID50 of SHIV KB9 C3, SHIV KB9 C4 or SHIV KB9 C5 were used to infect two naïve rhesus monkeys each by the intravenous route. (A) Plasma viral RNA level in monkeys. The data associated with SHIV KB9 C3 are shown in red, SHIV KB9 C4 in blue and SHIV KB9 C5 in green symbols and lines. All three viruses were able to establish infection with high peak viremia of 10^6 – 10^7 RNA copies/ml, with sustained viremia up to 400 days post-infection. (B) CD4^+ T lymphocyte subsets were determined by multi-channel flow cytometry for CD3, CD4, CD8, CD28, CD95, CCR5 and CCR7. Total CD4^+ T lymphocyte counts were calculated by multiplying the total lymphocyte count by the percentage of CD3^+ CD4^+ T cells. CD4^+ T lymphocyte counts were monitored for all six monkeys post-infection and are shown using same color scheme as in (A). No significant decline in CD4^+ T lymphocyte counts was seen.

Fig. 4. Mucosal transmissibility of the SHIV KB9 C3, SHIV KB9 C4, and SHIV KB9 C5 challenge stocks. Undiluted stocks of SHIV KB9 C3 and SHIV KB9 C5 (A) SHIV KB9 C4 (B) were inoculated into naïve rhesus monkeys by the intrarectal route. Challenge stocks of all three clade C T/F SHIVs were able to establish infection in the monkeys by the mucosal route. Infections resulted in high peak viremia of 10^6 – 10^8 RNA copies/ml at 14–22 days post-infection. Persistent viremia of 10^3 RNA copies/ml was observed in the SHIV KB9 C3-infected monkey up to 130 days post-infection. For the SHIV KB9 C5-infected monkey, plasma viral RNA of 10^3 copies/ml was detected up to 330 days post-infection. For the SHIV KB9 C4-infected monkeys, viremia of 10^3 RNA copies/ml was observed up to 180 days post-infection.

Fig. 5. Determination of 50% monkey infectious doses (MID_{50}) of SHIV KB9 C3, and SHIV KB9 C5 challenge stocks. (A) Two different dilutions of SHIV KB9 C3 were inoculated into a total of five naïve rhesus monkeys by the intra-rectal route. Monkeys inoculated with a 1:10 dilution of the virus are shown in “Red” lines and symbols and those with a 1:5 dilution are shown in “Blue” lines and symbols. One of the three monkeys (monkey R552) receiving a 1:10 dilution of the virus remained uninfected. (B) Four different dilutions of SHIV KB9 C5 were inoculated into a total of eight naïve rhesus monkeys by the intra-rectal route. Monkeys inoculated with the undiluted virus stock or with, 1:2, 1:5 and 1:10 dilutions of the virus are shown in “Green”, “Magenta”, “Blue” and “Black” lines and symbols, respectively. One of the monkeys receiving 1:5 (monkey R550) and 1:10 (monkey R924) dilutions of the virus remained uninfected.
The authors would like to apologise for any inconvenience caused. (Figs. 1–6).

Fig. 6. Schematic diagram of T/F SHIVs constructs. T/F env genes were cloned into the SHIV KB9 backbone. A ClaI restriction site was introduced immediately upstream of the env ATG and an AgeI restriction site upstream of the 3’ gp41 HIV-SIV recombination junction of SHIV KB9. ClaI and AgeI restriction sites were introduced into the T/F env sequences as well to facilitate cloning of the T/F env in SHIV KB9. As a result of this cloning strategy, exon 2 of tat, rev and 3’ half of vpu of SHIV KB9 were replaced by those of the new T/F virus and exon 1 of tat, rev as well as the 5’ end of vpu, which lie outside env, remained from SHIV KB9. Genes from SHIV KB9 are shown in “Dotted” boxes and the cloned genes are shown in “White” boxes.