

AUTHOR'S CORRECTION

Analysis of Human Immunodeficiency Virus Type 1 *nef* Gene Sequences Present In Vivo

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Volume 67, no. 8, p. 4639–4650: It has come to our attention that on phylogenetic analysis some of the reported gene sequences do not group as would be expected for viral sequences from independent patient isolates.

There are two anomalous clusterings of sequences from different patient sources, and for this reason we have withdrawn these sequences from the GenBank database. In addition, three gene sequences show anomalous pairing with other well-defined patient sequence clusters; we are therefore withdrawing these entries also. The entries being withdrawn had accession numbers L15488, L15496 to L15499, L15503 to L15507, L15512 to L15514, L15516, and L15520 to L15529. We are in the process of validating the patient source of the sequence clusters involved.

The major conclusions of the article were based on patterns of sequence variability within *nef*, and we believe these conclusions remain valid. However, analysis of the remaining 30 sequences in our data set leads to the following revisions. There are five changes in the consensus Nef sequence (Ser-9 to Arg, Pro-14 to Ser, Lys-152 to Gln, Glu-155 to Lys, and Leu-198 to Lys). Also, the values of inpatient and interpatient variation given in Table 1 are incorrect, and there are no examples of a termination codon at position 124 in the revised data set. We regret any inconvenience or confusion caused by these entries.