Errata

'Sequence Analysis of the Washington/1964 strain of Human Parainfluenza Virus Type 1 (HPIV1) and Recovery and Characterization of Wild Type Recombinant HPIV1 Produced by Reverse Genetics' by J.T. Newman, S.R. Surman, J.M. Riggs, C.T. Hansen, P.L. Collins, B.R. Murphy, and M.H. Skiadopoulos published in *Virus Genes* 24:1, 77–92, 2002.

Recently, the authors found errors in Tables 1 and 4 of this article.

1. In Table 1 of our manuscript, we made a comparison between HPIV1 and Sendai virus (MPIV1) in the nucleotide lengths of each of the gene units. Upon further analysis of the data, we have uncovered three errors in the numbers presented in this table.

- a. The 5' UTR length for the N gene should be 43 nt, not 39 nt for both HPIV1 and MPIV1.
 - b. The 3' UTR for the F gene of MPIV1 should be 53 nt, not 52 nt. There is a reference to this value in the text on page 83, line 26.
 - c. The 5' UTR for the L gene of MPIV1 should be 104 nt, not 105 nt.
2. In Table 4, there is an error in footnote 'b' which should read as '^br_AHPIV1 and r_BHPIV1 are independent preparations of rHPIV1 that were recovered with pTM(N₁), pTM(P₁), and pTM(L₃) support plasmids or pTM(N₃), pTM(P₃), and pTM(L₃) support plasmids, respectively (see text).'

Finally, the name of one of the contributing authors was misspelled. Chris T. Hansen should be spelled as Chris T. Hanson.