

MICROBIOLOGY. For the article “Symmetrical base preferences surrounding HIV-1 and avian sarcoma/leukosis virus but not murine leukemia virus integration sites,” by Alexander G. Holman and John M. Coffin, which appeared in issue 17, April 26, 2005, of *Proc. Natl. Acad. Sci. USA* (102, 6103–6107; first published March 31, 2005; 10.1073/pnas.0501646102), the authors note the following: “After our report appeared in the PNAS Early Edition, we observed that the simultaneously published paper by Wu *et al.* (1) reported similar base preferences for all integration sites; however, the placement of the integration site in the analysis of the murine leukemia virus (MLV) data set differed by one base. Further analysis revealed a small initial error that propagated through our analysis, ultimately leading us to misplace the location of the MLV integration site by one base. As a consequence, the MLV integration site preferences incorrectly appeared to be asymmetric. We now conclude that HIV-1, avian sarcoma/leukosis virus (ASLV), and MLV all show symmetrical base preferences surrounding their integration sites. Accordingly, the title of the article should be corrected to read ‘Symmetrical base preferences surrounding HIV-1, avian sarcoma/leukosis virus, and murine leukemia virus integration sites,’ and it has been corrected in the online version. Fig. 2 and Figs. 11 and 12, which are published as supporting information on the PNAS web site, can be corrected by placing the integration site between offset 0 and 1 instead of –1 and 0. A corrected version of Fig. 4 and its legend appear below. The remainder of the analysis was unaffected by this error, and with the described correction, we remain confident in our overall conclusions.”

1. Wu, X., Li, Y., Crise, B., Burgess, S. M. & Munroe, D. J. (2005) *J. Virol.* 79, 5211–5214.

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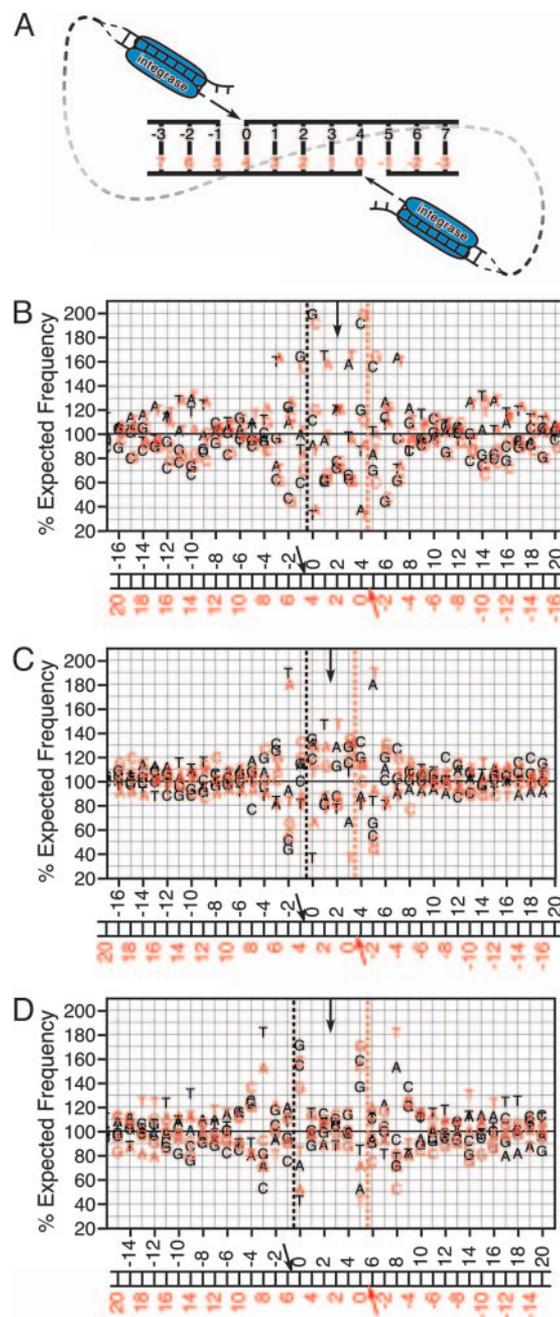


Fig. 4. Comparison of the observed integration preferences to the inferred preferences for the opposite LTR. (A) Schematic of the topology of HIV-1 integration. HIV-1 integration complexes join the viral LTRs to opposite strands of the DNA separated by five bases. MLV joins with an offset of four bases, whereas ASLV uses a six-base offset (not pictured). (B) Symmetry observed in HIV-1 with five-base offset. Black lettering represents the base preference seen from the top LTR (Fig. 1). The integration site is indicated by the black dashed vertical line in the graph and the black arrow in the numbering schematic. The vertical arrow indicates the expected axis of symmetry based on the characteristic five-base spacing between the sites of HIV-1 DNA integration. The red lettering represents the same base preferences; however, they are reversed and shifted five bases to represent the preferences as observed from the bottom LTR. The inferred integration site is indicated by the red vertical line in the graph and the red arrow in the numbering schematic. (C) Symmetry observed in MLV with four-base offset. (D) Symmetry observed in ALV with six-base offset.