**Corrigendum**

Proteolytic refolding of the HIV-1 capsid protein amino-terminus facilitates viral core assembly

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In Figure 9 of the above paper, we presented an alignment of 12 retroviral CA proteins. In this figure, the Moloney murine leukemia virus (MMLV) alignment was incorrect. MMLV Pro45 in Figure 9 is actually the first amino acid of the CA protein, and Asp54 of MMLV aligns with Asp51 of HIV-1 CA. Correct alignments have appeared elsewhere [Momany et al. (1996) *Nature Struct. Biol.*, 3, 763; McClure (1991) *Mol. Biol. Evol.*, 8, 835]. We are grateful to Jonathan Stoye for pointing out the error.

In order to test the functional importance of the putative Pro1–Asp54 salt bridge in MMLV CA, we mutated CA Asp54 to Ala in the MMLV vector pCLeco, as described in the paper. As expected, this mutation abolished infectivity (>10<sup>6</sup>-fold reduced) with a moderate reduction in particle formation and slightly aberrant Gag processing. Thus, our conclusion on the importance of the conserved CA salt bridge is not changed.

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**Corrigendum**

On how a transcription factor can avoid its proteolytic activation in the absence of signal transduction

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