

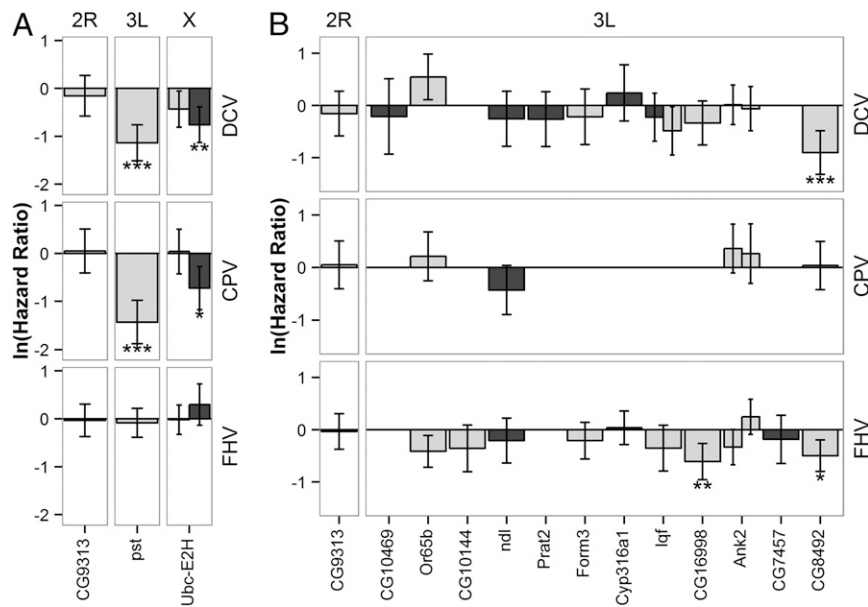
# Corrections

## EVOLUTION

Correction for “Host adaptation to viruses relies on few genes with different cross-resistance properties,” by Nelson E. Martins, Vítor G. Faria, Viola Nolte, Christian Schlötterer, Luis Teixeira, Élio Sucena, and Sara Magalhães, which appeared in issue 16,

April 22, 2014, of *Proc Natl Acad Sci USA* (111:5938–5943; first published April 7, 2014; 10.1073/pnas.1400378111).

The authors note that Fig. 4 appeared incorrectly. The corrected figure and its legend appear below.



**Fig. 4.** RNAi knockdown of candidate genes. Natural logarithm of hazard ratios between survival of flies with knocked-down candidate genes and their controls upon infection with DCV (*Top*), CrPV (*Middle*), and FHV (*Bottom*), using as genetic background KK (gray bars), GD (black bars) or both, whenever a construct was available in both backgrounds. (*A*) RNA interference against the candidate genes identified by the peaks in Fig. 3, *pst* and *Ubc-E2H*. (*B*) Tests to other genes in the large 3L peak. Vertical bars correspond to the 95% confidence intervals of the estimated hazard ratios. \**P* < 0.05; \*\**P* < 0.01; \*\*\**P* < 0.001.

[www.pnas.org/cgi/doi/10.1073/pnas.1418561111](http://www.pnas.org/cgi/doi/10.1073/pnas.1418561111)

**MEDICAL SCIENCES, APPLIED MATHEMATICS**

Correction for “Predicting the outcomes of treatment to eradicate the latent reservoir for HIV-1,” by Alison L. Hill, Daniel I. S. Rosenbloom, Feng Fu, Martin A. Nowak, and Robert F. Siliciano, which appeared in issue 37, September 16, 2014, of *Proc Natl Acad Sci USA* (111:13475–13480; first published August 5, 2014; 10.1073/pnas.1406663111).

The authors note that, due to a printer’s error, Table 1 appeared incorrectly. The corrected table appears below. The online version has been corrected.

**Table 1. Estimated values for the key parameters of the stochastic viral dynamics model**

Parameter	Symbol	Estimation method	Ref(s).	Best estimate	Distribution*
LR decay rate	$\delta$	Long-term ART, $\delta = \ln(2)/\tau_{1/2}$	(3, 4)	$5.2 \times 10^{-4} \text{ d}^{-1}$	$\delta \sim \mathcal{N}(5.2, 1.6) \times 10^{-4} \text{ d}^{-1}$
LR exit rate	$A$	Viral rebound after ART interruption	(5, 58)	57 cells $\text{d}^{-1}$	$\log_{10}(A) \sim \mathcal{N}(1.76, 1.0)$
Growth rate	$r$			0.4 $\text{d}^{-1}$	$\log_{10}(r) \sim \mathcal{N}(-0.40, 0.19)$
Establishment probability	$P_{Est}$	Population genetic modeling	(59, 60)	0.069	Composite distribution (Materials and Methods)

\*Notation  $X \sim \mathcal{N}(\mu, \sigma)$  means that  $X$  is a random variable drawn from a normal distribution with mean  $\mu$  and SD  $\sigma$ .

[www.pnas.org/cgi/doi/10.1073/pnas.1418638111](http://www.pnas.org/cgi/doi/10.1073/pnas.1418638111)