

- alleles, their defective regulation by p107, and altered phosphorylation of the c-Myc transactivation domain. *Mol. Cell. Biol.* **15**, 4031–4042 (1995).
24. Eilers, M., Schirm, S. & Bishop, J. M. The MYC protein activates transcription of the α -prothymosin gene. *EMBO J.* **10**, 133–141 (1991).
25. Geiduschek, E. P. & Kassavetis, G. A. The RNA polymerase III transcription apparatus. *J. Mol. Biol.* **310**, 1–26 (2001).
26. Hateboer, G. *et al.* TATA-binding protein and the retinoblastoma gene product bind to overlapping epitopes on c-Myc and adenovirus E1A protein. *Proc. Natl Acad. Sci. USA* **90**, 8489–8493 (1993).
27. Cole, M. D. & McMahon, S. B. The Myc oncoprotein: a critical evaluation of transactivation and target gene regulation. *Oncogene* **18**, 2916–2924 (1999).
28. Eisenman, R. N. Deconstructing Myc. *Genes Dev.* **15**, 2023–2030 (2001).
29. Schübeler, D. *et al.* Nuclear localization and histone acetylation: a pathway for chromatin opening and transcriptional activation of the human β -globin locus. *Genes Dev.* **14**, 940–950 (2000).
30. White, R. J., Gottlieb, T. M., Downes, C. S. & Jackson, S. P. Mitotic regulation of a TATA-binding-protein-containing complex. *Mol. Cell. Biol.* **15**, 1983–1992 (1995).

Acknowledgements We thank C. Ngouenet and Z. Felton-Edkins for technical assistance, and R. Reeder, S. Cowley and C. Yost for critique of this manuscript. This work was funded by grants from CONACYT-Mexico (N.G.), the National Institutes of Health/National Cancer Institute (C.G. and R.N.E.), and from Cancer Research UK (R.J.W.).

Competing interests statement The authors declare that they have no competing financial interests.

Correspondence and requests for materials should be addressed to R.N.E. (e-mail: eisenman@fhcrc.org) or R.J.W. (e-mail: rwhite@udcf.gla.ac.uk).

errata

The role of parasites in sympatric and allopatric host diversification

Angus Buckling & Paul B. Rainey

Nature **420**, 496–499 (2002).

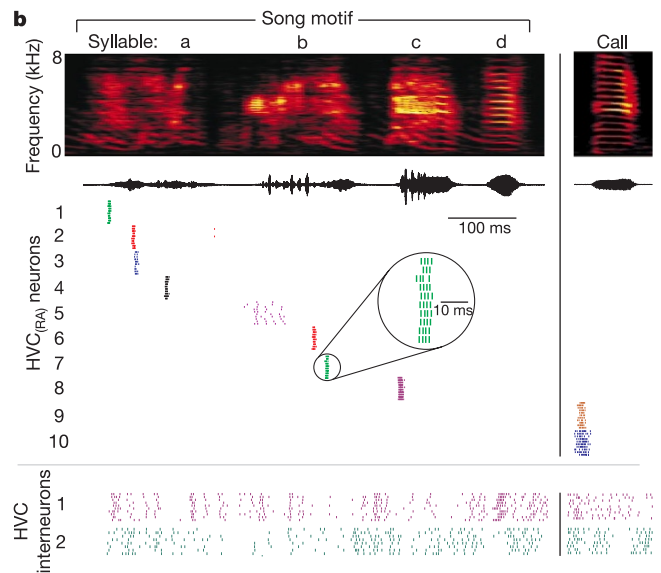
In Fig. 2b of this Letter, the third bar (dark grey) from the left was incorrectly shown. Its allopatric diversity value should have been 0.007 not 0.19. This error does not alter the conclusions of the paper.

An ultra-sparse code underlies the generation of neural sequences in a songbird

Richard H. R. Hahnloser, Alexay A. Kozhevnikov & Michale S. Fee

Nature **419**, 65–70 (2002).

In this Letter, the numbering on the middle panel of Fig. 2b was misaligned. The figure should have appeared as shown.



In the Acknowledgements, F. Nottebohm’s surname was misspelled.