DEVELOPMENTAL BIOLOGY

Correction for "Progressive lengthening of 3′ untranslated regions of mRNAs by alternative polyadenylation during mouse embryonic development," by Zhe Ji, Ju Youn Lee, Zhenhua Pan, Bingjun Jiang, and Bin Tian, which appeared in issue 17, April 28, 2009, of *Proc Natl Acad Sci USA* (106:7028–7033; first published April 16, 2009; 10.1073/pnas.0900028106).

The authors note that due to a printer's error, Fig. 1*B* appeared incorrectly on page 7028. The corrected figure and its legend appear below.

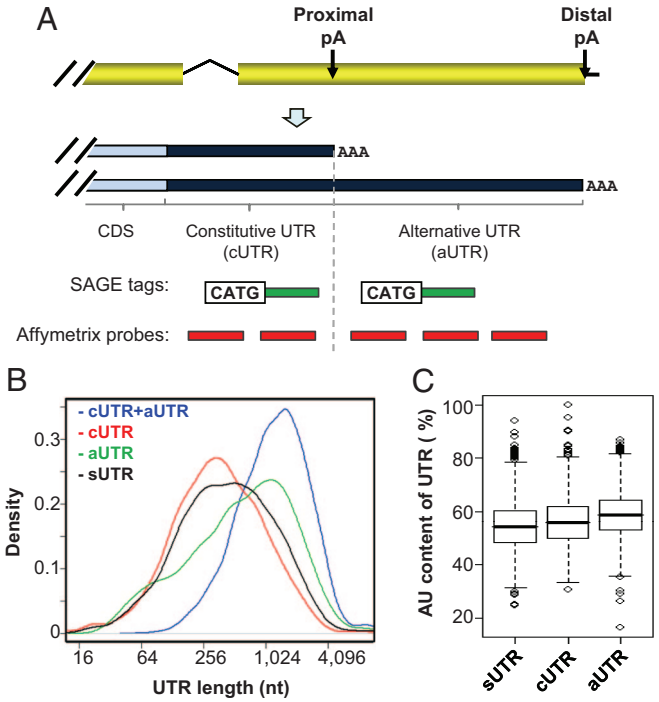

Fig. 1. Alternative polyadenylation (APA) leading to alternative 3′ UTRs. (*A*) Schematics of APA in the 3′-most exon and using SAGE tags and Affymetrix GeneChip probes to examine APA. Two transcript variants resulting from proximal and distal poly(A) sites are shown. The dotted vertical line separates 2 UTR regions, i.e., constitutive UTR (cUTR) and alternative UTR (aUTR). CDS, coding sequence; pA, poly(A) site; AAA, poly(A) tail. (*B*) Distribution of length for different UTR groups. The full 3′ UTRs for genes with APA are shown by cUTR + aUTR [4,139 genes, median = 1,288 nucleotide (nt)]. Constitutive and alternative regions are represented by cUTR (median = 358 nt) and aUTR (median = 685 nt), respectively. sUTRs are 3′ UTRs not affected by APA (7,242 genes, median = 439 nt). (*C*) AU content for different UTR sequences.

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CELL BIOLOGY, COMPUTER SCIENCE

Correction for "Stochastic hybrid modeling of DNA replication across a complete genome," by J. Lygeros, K. Koutroumpas, S. Dimopoulos, I. Legouras, P. Kouretas, C. Heichinger, P. Nurse, and Z. Lygerou, which appeared in issue 34, August 26, 2008, of *Proc Natl Acad Sci USA* (105:12295–12300; first published August 19, 2008; 10.1073/pnas.0805549105).

The authors wish to note the following: "We wish to add direct references to a stochastic model of DNA replication previously applied to the *Xenopus laevis* early embryonic divisions. That model was applied to molecular combing experiments on cell-free extracts from *Xenopus laevis* embryos." The additional references appear below.

39. Herrick J, Jun S, Bechhoefer J, Bensimon A (2002) Kinetic model of DNA replication in eukaryotic organisms. *J Mol Biol* 320:741–750.
40. Jun S, Bechhoefer J (2005) Nucleation and growth in one dimension. II. Application to DNA replication kinetics. *Phys Rev E Stat Nonlin Soft Matter Phys* 71:011909.
41. Bechhoefer J, Marshall B (2007) How *Xenopus laevis* replicates DNA reliably even though its origins of replication are located and initiated stochastically. *Phys Rev Lett* 98:098105.

www.pnas.org/cgi/doi/10.1073/pnas.0905246106

MICROBIOLOGY

Correction for "Electrically conductive bacterial nanowires produced by *Shewanella oneidensis* strain MR-1 and other microorganisms," by Yuri A. Gorby, Svetlana Yanina, Jeffrey S. McLean, Kevin M. Rosso, Dianne Moyles, Alice Dohnalkova, Terry J. Beveridge, In Seop Chang, Byung Hong Kim, Kyung Shik Kim, David E. Culley, Samantha B. Reed, Margaret F. Romine, Daad A. Saffarini, Eric A. Hill, Liang Shi, Dwayne A. Elias, David W. Kennedy, Grigoriy Pinchuk, Kazuya Watanabe, Shun'ichi Ishii, Bruce Logan, Kenneth H. Nealson, and Jim K. Fredrickson, which appeared in issue 30, July 25, 2006, of *Proc Natl Acad Sci USA* (103:11358–11363; first published July 18, 2006; 10.1073/pnas.0604517103).

The authors note that in Table 1 on page 11360, the units for "Electrochemical activity," designated as mA, should have been designated as **μA**. This error does not affect the conclusions of the article. The corrected table appears below.

Table 1. Metal-reduction and electrochemical properties of *S. oneidensis* MR-1, GSPD and ΔMTRC/OMCA

Strain	Ferrihydrite-reduction-extractable Fe(II),* mM	Electrochemical activity, μA
MR-1	2.17 ± 0.19	68.0 ± 7.8
ΔMTRC/OMCA	0.67 ± 0.13	14.3 ± 2.08
GSPD	0.42 ± 0.02	12.3 ± 0.58

*HFO (20 mM) reduction sampled at 24 h and extracted with 0.5 N HCl overnight. Fe(II) was determined by using the ferrozine assay (30).

www.pnas.org/cgi/doi/10.1073/pnas.0903426106