

Corrigendum: Spontaneous DNA breakage in single living *Escherichia coli* cells

Jeanine M Pennington & Susan M Rosenberg

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In the version of this article initially published, our estimate of the rate of formation of spontaneous DNA double-strand breaks (DSBs) in *E. coli* proportional to DNA content in humans should read that it differs from that of Vilenchik and Knudson (*Proc. Natl. Acad. Sci. USA* 100, 12871–12876; 2003) by fourfold, not “approximately tenfold” (page 800, line 3, and page 800, line 59). We estimated that there are 0.01 DSBs per *E. coli* genome replication. Because *E. coli* has approximately 4.7×10^6 bp per genome (Blattner, F.R. *et al.*, *Science* 277, 1453–1474; 1997), we estimate that approximately 2×10^{-9} DSBs per bp are replicated, or about fourfold fewer than the estimate of about 0.8×10^{-8} DSBs per bp replicated in human somatic cells (or 50 DSBs per diploid human genome replication) from Vilenchik and Knudson (*Proc. Natl. Acad. Sci. USA* 100, 12871–12876; 2003). This would bring the number of DSBs per human genome replication down to approximately 13, if it were proportional to that in *E. coli*. Our error arose from calculating the human equivalent based on haploid, not diploid, human genome size. This error has been corrected in the HTML and PDF versions of the article.

Corrigendum: Genome-wide analysis of mammalian promoter architecture and evolution

Piero Carninci, Albin Sandelin, Boris Lenhard, Shintaro Katayama, Kazuro Shimokawa, Jasmina Ponjavic, Colin A M Semple, Martin S Taylor, Pär G Engström, Martin C Frith, Alistair R R Forrest, Wynand B Alkema, Sin Lam Tan, Charles Plessy, Rimantas Kodzius, Timothy Ravasi, Takeya Kasukawa, Shiro Fukuda, Mutsumi Kanamori-Katayama, Yayoi Kitazume, Hideya Kawaji, Chikatoshi Kai, Mari Nakamura, Hideaki Konno, Kenji Nakano, Salim Mottagui-Tabar, Peter Arner, Alessandra Chesì, Stefano Gustincich, Francesca Persichetti, Harukazu Suzuki, Sean M Grimmond, Christine A Wells, Valerio Orlando, Claes Wahlestedt, Edison T Liu, Matthias Harbers, Jun Kawai, Vladimir B Bajic, David A Hume & Yoshihide Hayashizaki

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In the version of this article initially published, two of the smaller bar plots in Figure 1e were mistakenly duplicated. Specifically, the *Zfp385* plot is an erroneous copy of the *137774* plot, and the *Txndc7* plot is an erroneous copy of the *Pik3r5* plot. See below for the corrected version of the figure. This error does not change the conclusions of the study in any way, as the bar plots are just a few visual examples of more than 5,000 tag clusters, and the correct plots follow the same distribution patterns as the erroneous ones. This error has been corrected in the HTML and PDF versions of the article.

