Correction for Volume 13, p. 875

Genome Res. 2004 14: 2510

Errata

Genome Research 14: 2221–2234 (2004)

Genome sequence of *Haloarcula marismortui:* A halophilic archaeon from the Dead Sea

Nitin S. Baliga, Richard Bonneau, Marc T. Facciotti, Min Pan, Gustavo Glusman, Eric W. Deutsch, Paul Shannon, Yulun Chiu, Rueyhung Sting Weng, Rueichi Richie Gan, Pingliang Hung, Shailesh V. Date, Edward Marcotte, Leroy Hood, and Wailap Victor Ng

The sequence data from this study were submitted to GenBank under accession nos. AY596290–AY596298, not AY59290–AY59298. The authors apologize for any confusion these typos may have caused.

Genome Research 14: 1786–1796 (2004)

De novo repeat classification and fragment assembly

Paul A. Pevzner, Haixu Tang, and Glenn Tesler

Pavel A. Pevzner's name was inadvertently misspelled in the above article. We apologize for any confusion this may have caused.

Genome Research 13: 875–882 (2003)

Genomic gene clustering analysis of pathways in eukaryotes

Jennifer M. Lee and Erik L.L. Sonnhammer

The authors have discovered an error in part of the analysis of pathways in *S. cerevisiae* described in Table 1 and wish to correct the data. The corrected table is reprinted below. The authors apologize for any inconvenience this error may have caused other investigators in the field.

Table 1. Pathways Analyzed and Percentage Showing Significant Clustering in Unmerged and Merged Data Sets

Organism	# Pathways analyzed	# Genes	% Significant unmerged data	% Significant merged data	% in random data
H. sapiens	98	975	78%	65%	11%
C. elegans	86	516	74%	58%	11%
D. melanogaster	85	484	50%	30%	12%
A. thaliana	79	318	60%	43%	11%
S. cerevisiae	89	682	35%	20%	10%

The percent significant refers to pathways in which the score is more than 3* (3rd quartile − median) + median. The same analysis was carried out on randomized pathways where genes were picked randomly from all genes, using the merged data.

Genome Research 14: 2279–2286 (2004)

Codon usage bias from tRNA's point of view: Redundancy, specialization, and efficient decoding for translation optimization

Eduardo P.C. Rocha

In the first paragraph of the first column on page 2281 and in Figure 1, there is a typo in the definition of ENC_{dif}. The formula should read:

$$ENC_{dif} = -(ENC'_{RP} - ENC'_{All})/ENC'_{All}$$

Thus, positive values of ENC_{dif} indicate codon usage bias in ribosomal proteins as mentioned throughout the text.

The authors apologize for any confusion this may have caused.

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