



## Correction for Volume 14, p. 2279

*Genome Res.* 2004 14: 2510

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Cold Spring Harbor Laboratory Press

**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
<i>H. sapiens</i>	98	975	78%	65%	11%
<i>C. elegans</i>	86	516	74%	58%	11%
<i>D. melanogaster</i>	85	484	50%	30%	12%
<i>A. thaliana</i>	79	318	60%	43%	11%
<i>S. cerevisiae</i>	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  $ENC_{diff}$ . The formula should read:

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

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

The authors apologize for any confusion this may have caused.