Errata

Genome Research 13: 2717–2724 (2003)

Clone-Based Systematic Haplotyping (CSH): A Procedure for Physical Haplotyping of Whole Genomes

Carola Burgtorf, Pamela Kepper, Margret Hoehe, Carsten Schmitt, Richard Reinhardt, Hans Lehrach, and Sascha Sauer

In the first line of the first column on page 2721, additional text was erroneously inserted by the printer. That portion of the article should instead read:

based on the following equation:

$$p = \sum_{i=2}^{n} f^{n}/2$$

where f is the fraction of the genome per pool, and p is the probability of two or more clones of different alleles in one pool.

The editors apologize for any confusion this may have caused.

Genome Research 13: 1787–1799 (2003)

Integrated Mapping, Chromosomal Sequencing and Sequence Analysis of *Cryptosporidium parvum*

Alan T. Bankier, Helen F. Spriggs, Berthold Fartmann, Bernard A. Konfortov, Martin Madera, Christine Vogel, Sarah A. Teichmann, Al Ivens, and Paul H. Dear

The authors inadvertently failed to give proper attribution for the gene-finding software used in the analysis. Their use of GeneID should have cited Glöckner et al. (2002), "Sequence and analysis of chromosome 2 of *Dictyostelium discoideum*," *Nature* **418:** 79–85. The training on *D. discoideum* gene sets of HMMgene was done by Rolf Olsen and Anders Krogh, and of Genefinder by Marie-Adele Rajandream; neither of these training sets has been published. In addition, they acknowledge Neil Hall for making available unpublished sequences of *Theileria annulata* (http://www.sanger.ac.uk/Projects/Protozoa/) for comparison with *C. parvum*. The authors apologize to those concerned for these omissions.