



## Correction for Volume 13, p. 103

*Genome Res.* 2004 14: 786

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## Errata

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### **Genome Research 13:** 103–107 (2003)

#### **Human–Mouse Alignments With BLASTZ**

Scott Schwartz, W. James Kent, Arian Smit, Zheng Zhang, Robert Baertsch, Ross C. Hardison, David Haussler, and Webb Miller

In the second column on page 103, the Web address for axt-Best-processed BLASTZ alignments on the human and mouse genomes contains a typo. The correct Web address is:

<http://genome.cse.ucsc.edu/goldenPath/28jun2002/vsMm2>

The authors apologize for any confusion this may have caused.

### **Genome Research 14:** 414–425 (2004)

#### **Parallel Genotyping of Over 10,000 SNPs Using a One-Primer Assay on a High-Density Oligonucleotide Array**

Hajime Matsuzaki, Halina Loi, Shoulian Dong, Ya-Yu Tsai, Joy Fang, Jane Law, Xiaojun Di, Wei-Min Liu, Geoffrey Yang, Guoying Liu, Jing Huang, Giulia C. Kennedy, Thomas B. Ryder, Gregory A. Marcus, P. Sean Walsh, Mark D. Shriver, Jennifer M. Puck, Keith W. Jones, and Rui Mei

The Abstract for this article contained a typo. The sentence should have read:

“The selection of SNPs was primarily determined by computer-predicted lengths of restriction fragments containing the SNPs, and was further driven by strict empirical measurements of accuracy, reproducibility, and average call rate, which we estimate to be >99.5%, >99.9%, and >95%, respectively.”

The editors apologize for any confusion this may have caused.