

Errata

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Sequencing and analysis of 10,967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis* reveals post-tetraploidization transcriptome remodeling

Ryan D. Morin, Elbert Chang, Anca Petrescu, Nancy Liao, Malachi Griffith, Robert Kirkpatrick, Yaron S. Butterfield, Alice C. Young, Jeffrey Stott, Sarah Barber, Ryan Babakaiff, Mark C. Dickson, Corey Matsuo, David Wong, George S. Yang, Duane E. Smailus, Keith D. Wetherby, Peggy N. Kwong, Jane Grimwood, Charles P. Brinkley III, Mabel Brown-John, Natalie D. Reddix-Dugue, Michael Mayo, Jeremy Schmutz, Jaclyn Beland, Morgan Park, Susan Gibson, Teika Olson, Gerard G. Bouffard, Miranda Tsai, Ruth Featherstone, Steve Chand, Asim S. Siddiqui, Wonhee Jang, Ed Lee, Steven L. Klein, Robert W. Blakesley, Barry R. Zeeberg, Sudarshan Narasimhan, John N. Weinstein, Christa Prange Pennacchio, Richard M. Myers, Eric D. Green, Lukas Wagner, Daniela S. Gerhard, Marco A. Marra, Steven J.M. Jones, and Robert A. Holt

One of the authors was inadvertently left off of this list. William Chow should be added after Malachi Griffith. His affiliation is British Columbia Genome Sciences Centre, BCCA, Vancouver, BC V5Z 1L3 Canada. The authors apologize for this omission.

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Evolutionary turnover of mammalian transcription start sites

Martin C. Frith, Jasmina Ponjavic, David Fredman, Chikatoshi Kai, Jun Kawai, Piero Carninci, Yoshihide Hayashizaki, and Albin Sandelin

One of the authors' names was inadvertently misspelled. Yoshihide Hayshizaki should be Yoshihide Hayashizaki.



Erratum

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