Retraction

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Retraction

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Identification of programmed translational −1 frameshifting sites in the genome of *Saccharomyces cerevisiae*

Michaël Bekaert, Hugues Richard, Bernard Prum, and Jean-Pierre Rousset

Upon further analyses of some of the potential frameshifting sites reported in this study, the authors find that they are unable to reproduce several of the results reported in Tables 1 and 2. In particular, resequencing of all of the overlapping regions from the candidates presented in Table 2 fails to confirm that the sequence corresponding to candidates 12, 35 and 43 displays the expected frameshifted organization; rather, they are in-frame. They also find that the sequence corresponding to candidate 24 was cloned in-frame and contained an in-frame stop codon, contrary to being in the −1 frame, ruling out any possibility of detecting frameshifting from this sequence. The authors also prepared the correct construct for candidate 43 (YMR084w) and quantified its frameshifting activity in vivo, which occurred at a frequency of 0.05% instead of the previously published 5%. Therefore, the conclusions drawn from these data are not supported by the authors' subsequent experiments. The authors sincerely apologize for any inconvenience this may have caused other investigators in the field and also wish to thank Agnès Baudin-Baillieu and Céline Fabret who performed the experiments described here.

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