Correction

Correction: Release of extraction-resistant mRNA in stationary phase *Saccharomyces cerevisiae* produces a massive increase in transcript abundance in response to stress

Anthony D Aragon*, Gabriel A Quiñones[†], Edward V Thomas[‡], Sushmita Roy[§] and Margaret Werner-Washburne*

Addresses: *Department of Biology, University of New Mexico, Albuquerque, NM 87131, USA. [†]Cancer Biology Program, Stanford University, Stanford, CA 94305, USA. [‡]Sandia National Laboratories, Albuquerque, NM 87185, USA. [§]Department of Computer Science, University of New Mexico, Albuquerque, NM 87131, USA.

Correspondence: Margaret Werner-Washburne. Email: maggieww@unm.edu

We wish to report a correction to our study [1]. This does not alter the interpretation of the data. The strain S288c that was used in the study was reported incorrectly as having the genotype: MATα *his3 leu2-3,112 lys2 trp1 ura3-52*. In fact the S288c strain we used, stored in our laboratory as MW481, is MATα *gal2mal2*.

References

1. Aragon AD, Quiñones GA, Thomas EV, Roy S, Werner-Washburne M: **Release of extraction-resistant mRNA in stationary phase *Saccharomyces cerevisiae* produces a massive increase in transcript abundance in response to stress.** *Genome Biol* 2006, **7**:R9.