


# Hsp42 is the general small heat shock protein in the cytosol of *Saccharomyces cerevisiae*

Martin Haslbeck, Nathalie Braun, Thusnelda Stromer, Bettina Richter, Natascha Model, Sevil Weinkauff & Johannes Buchner\* 

**Correction to:** *The EMBO Journal* (2004) 23: 638–649. DOI 10.1038/sj.emboj.7600080 | Published online 29 January 2004

The authors of this report contacted *The EMBO Journal* to report a discrepancy in the assembly of Fig 9. The authors state that assembly of Fig 9B was mixed up in the process of resizing the images, with the microscopy image in the original Fig 9B representing a crop from the same micrograph also displayed in Fig 9F. In the corrected Fig 9, the phenotypic effects for  $\Delta$ Hsp26 at physiological conditions (30°C until early stationary phase) are much less significant than those observed for  $\Delta$ Hsp42, consistent with previous results by Susek and Lindquist (1989) as discussed in the original paragraph of the results section. Since the phenotypic differences between  $\Delta$ Hsp26 and  $\Delta$ Hsp42 at physiological temperatures had not been emphasized in the original result section, the following sentence on p. 645 of the article:

“At late logarithmic phase, consistent with the *in vivo* and *in vitro* results on the chaperone function of Hsp42 and Hsp26, both deletion strains showed a dramatic change in cell morphology when analyzed under heat shock conditions.”

is herewith being corrected to:

“Consistent with the *in vivo* and *in vitro* results on the chaperone function of Hsp42 and Hsp26, significant changes at late logarithmic phase were only visible for deletion of Hsp42. However, both deletion strains showed a dramatic change in cell morphology when analyzed under heat shock conditions.”

Despite these changes, the main conclusions of the article remain unchanged, and have since been verified and further refined by

multiple studies, e.g., in Specht *et al* (2011), Ungelenk *et al* (2016), Mackenzie *et al* (2016), and Grousl *et al* (2018). Additional replicates for panel 9B are included as Source Data with this corrigendum.

Per journal policy, *The EMBO Journal* conducted additional image screening of all other figures in this article. These analyses identified further duplications of two panels for experimental controls of gene deletion strains (top middle panel, bottom left panel) within Fig 5B and 5C, respectively. The Journal subsequently received scans of Western blots from the original laboratory books, confirming the absence of bands in the respective experimental settings, and stress induction of small heat shock proteins in other panels. The authors note that duplication of the “empty” panels appears to have been an oversight during figure assembly and does not affect the conclusions from Fig 5. The original scans from laboratory book pages are published as Source Data with this corrigendum.

Faint lines in Figs 3 and 4C were judged to be image scanning/processing artifacts based on available source data.

## References

Grousl T, Ungelenk S, Miller S, Ho CT, Khokhrina M, Mayer MP, Bukau B, Mogk A (2018) A prion-like domain in Hsp42 drives chaperone-facilitated aggregation of misfolded proteins. *J Cell Biol* 217: 1269–1285



Figure 9B. Original.

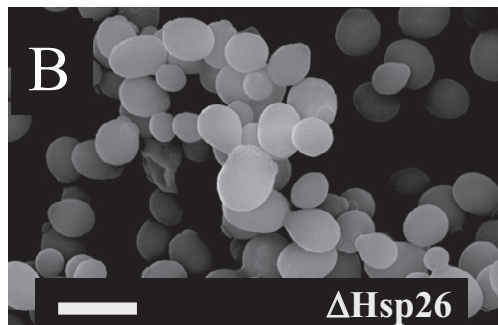


Figure 9B. Corrected.

Mackenzie RJ, Lawless C, Holman SW, Lanthaler K, Beynon RJ, Grant CM, Hubbard SJ, Evers CE (2016) Absolute protein quantification of the yeast chaperome under conditions of heat shock. *Proteomics* 16: 2128–2140

Specht S, Miller SB, Mogk A, Bukau B (2011) Hsp42 is required for sequestration of protein aggregates into deposition sites in *Saccharomyces cerevisiae*. *J Cell Biol* 195: 617–629

Susek RE, Lindquist SL (1989) hsp26 of *Saccharomyces cerevisiae* is related to the superfamily of small heat shock proteins but is

without a demonstrable function. *Mol Cell Biol* 9: 5265–5271

Ungelenk S, Moayed F, Ho CT, Grousl T, Scharf A, Mashaghi A, Tans S, Mayer MP, Mogk A, Bukau B (2016) Small heat shock proteins sequester misfolding proteins in near-native conformation for cellular protection and efficient refolding. *Nat Commun* 7: 13673