

CORRECTION

Correction: Reference Genes Selection and Normalization of Oxidative Stress Responsive Genes upon Different Temperature Stress Conditions in *Hypericum perforatum* L

The PLOS ONE Staff

There is an error in [Fig. 3](#), “Relative mRNA expression of target genes in cold-treated samples,” Panel B, as well as in the legend for [Fig 3](#). Please see the corrected [Fig. 3](#) and its legend here.



OPEN ACCESS

Citation: The PLOS ONE Staff (2015) Correction: Reference Genes Selection and Normalization of Oxidative Stress Responsive Genes upon Different Temperature Stress Conditions in *Hypericum perforatum* L. PLoS ONE 10(3): e0119982. doi:10.1371/journal.pone.0119982

Published: March 26, 2015

Copyright: © 2015 The PLOS ONE Staff. This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

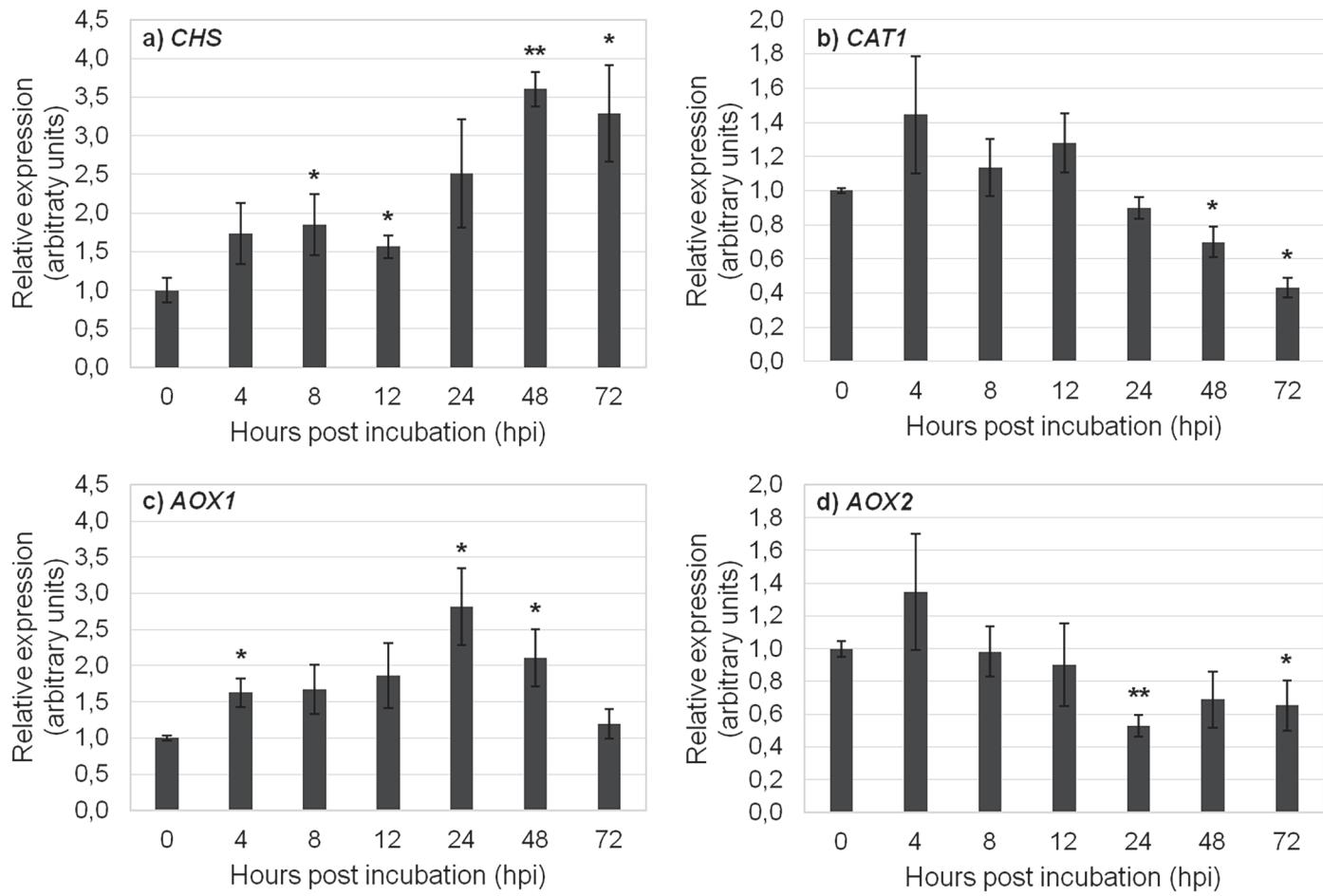


Fig 3. Relative mRNA expression of target genes in cold-treated samples. Expression of a) *CHS*, b) *CAT1*, c) *AOX1*, and d) *AOX2* in cold-treated samples using *TUB*, *GSA* and *GAPDH* as reference genes in data normalization. The relative expression values are depicted as the mean \pm standard deviation of three biological replicates and correspond to the ratio between treated and untreated samples for each time point. The bars represent the fold-change related to control group (0 hours) which was set to 1. Statistical significances (* $p \leq 0.05$ and ** $p \leq 0.01$) between the two means were determined by the t-test using IBM SPSS Statistics version 22.0 (SPSS Inc., USA).

doi:10.1371/journal.pone.0119982.g001

There is an error in Fig. 4, “Relative mRNA expression of target genes in heat-treated samples,” Panel B, as well as in the legend for Fig. 4. Please see the corrected Fig. 4 and its legend here.

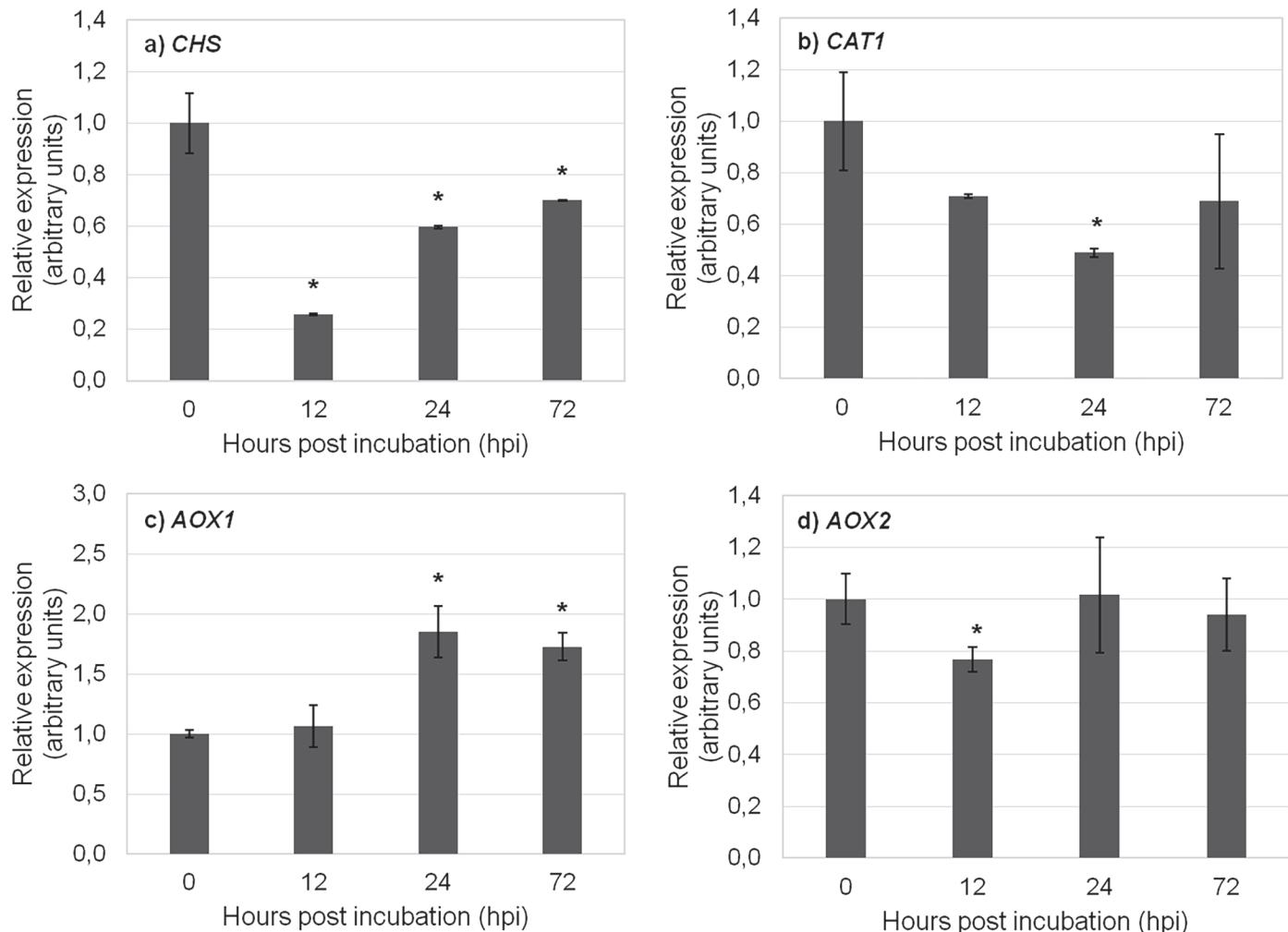


Fig 4. Relative mRNA expression of target genes in heat-treated samples. Expression of a) CHS, b) CAT1, c) AOX1, and d) AOX2 in heat-treated samples using TUB, 26S and H2A as reference genes in data normalization. The relative expression values are depicted as the mean \pm standard deviation of three biological replicates and correspond to the ratio between treated and untreated samples for each time point. The bars represent the fold-change related to control group (0 hours) which was set to 1. Statistical significances ($*p \leq 0.05$ and $**p \leq 0.01$) between the two means were determined by the t-test using IBM SPSS Statistics version 22.0 (SPSS Inc., USA).

doi:10.1371/journal.pone.0119982.g002

Reference

- Velada I, Ragonezi C, Arnholdt-Schmitt B, Cardoso H (2014) Reference Genes Selection and Normalization of Oxidative Stress Responsive Genes upon Different Temperature Stress Conditions in *Hypericum perforatum* L. PLoS ONE 9(12): e115206. doi: [10.1371/journal.pone.0115206](https://doi.org/10.1371/journal.pone.0115206) PMID: [25503716](https://pubmed.ncbi.nlm.nih.gov/25503716/)