

Correction

Correction: Gan, L.; Denecke, B. Profiling Pre-MicroRNA and Mature MicroRNA Expressions Using a Single Microarray and Avoiding Separate Sample Preparation. *Microarrays* 2013, *2*, 24–33.

Lin Gan and Bernd Denecke *

Interdisciplinary Centre for Clinical Research Aachen, RWTH Aachen University, Pauwelstr. 30, 52074 Aachen, Germany; E-Mail: lgan@ukaachen.de

* Author to whom correspondence should be addressed; E-Mail: bernd.denecke@rwth-aachen.de; Tel.: +49-241-80-89918; Fax: +49-241-80-82124.

Received: 30 May 2013 / Accepted: 3 June 2013 / Published: 24 June 2013

It came to our attention that a paper has recently been published concerning one of the GEO datasets (GSE34413) we cited in our published paper [1]. The original reference (reference 27) cited for this dataset leads to a paper about a similar study from the same research group [2]. In order to provide readers with exact citation information, we would like to update reference 27 in our previous paper to the new published paper concerning GSE34413 [3]. The authors apologize for this inconvenience.

References

1. Gan, L.; Denecke, B. Profiling pre-microrna and mature microrna expressions using a single microarray and avoiding separate sample preparation. *Microarrays* **2013**, *2*, 24–33.
2. Kleiber, M.L.; Laufer, B.I.; Wright, E.; Diehl, E.J.; Singh, S.M. Long-term alterations to the brain transcriptome in a maternal voluntary consumption model of fetal alcohol spectrum disorders. *Brain Res.* **2012**, *1458*, 18–33.
3. Laufer, B.I.; Mantha, K.; Kleiber, M.L.; Diehl, E.J.; Addison, S.M.; Singh, S.M. Long-lasting alterations to DNA methylation and ncRNAs could underlie the effects of fetal alcohol exposure in mice. *Dis. Model. Mech.* **2013**, doi: 10.1242/dmm.010975.

© 2013 by the authors; licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution license (<http://creativecommons.org/licenses/by/3.0/>).