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## **CORRIGENDUM**

## Nutrients drive transcriptional changes that maintain metabolic homeostasis but alter genome architecture in *Microcystis*

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**Correction to:** *The ISME Journal* (2014) **8,** 2080–2092; doi:10.1038/ismej.2014.78; published online 23 May 2014

Since the publication of this article, the authors have noticed an incorrect axis label in one of the figures. In Figure 2b, the *x* axis should read 'N-Reduced (Nitrate) Mean Normalized RPKM (log10)'.

The correct figure is shown here.

The errors have now been rectified, and the correct article appears in this issue. The html and online pdf versions have also been rectified, and now carry the correct paper.

The authors would like to apologize for any inconvenience this may have caused.

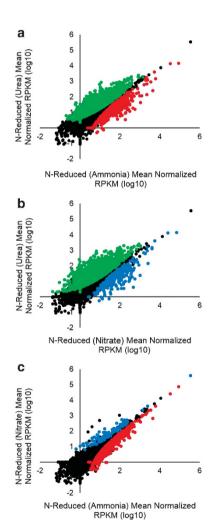


Figure 2 Comparison of global genomic expression between reduced nitrogen treatments. Black points represent expression values of the 6364 genes of M. aeruginosa NIES 843. Colored points represent significant up-regulation of expression in the specified low nitrogen treatment compared with the second at P < 0.05. (a) Expression values of N-reduced (urea) (green) vs N-reduced (ammonium) (red) treatments; (b) expression values of N-reduced (urea) (green) vs N-reduced (nitrate) (blue) treatments; (c) expression values of N-reduced (ammonium) (red) vs N-reduced (nitrate) (blue) treatments.