

Correction

Improving Estimates of Compensatory
cis–trans Regulatory Divergence

Hunter B. Fraser*

*Correspondence: hbfraser@stanford.edu (H.B. Fraser).
DOI of original article: <https://doi.org/10.1016/j.tig.2018.09.003>
(Trends in Genetics 35, 3–5; 2019)

In this article, I regretfully neglected to cite a paper [1] in which the authors proposed separating RNA-seq technical replicates (the same library sequenced on different lanes) to estimate *cis* and *trans* components of gene expression divergence. While similar in spirit to the approach that I proposed, it should be noted that separating technical but not biological replicates will still lead to an artifactual negative *cis–trans* correlation if there is any error in allele-specific expression estimates driven either by biological variation among samples or by variation in library construction (e.g., due to PCR ‘jackpots’).

Reference

1. Emerson, J.J. *et al.* (2010) Natural selection on *cis* and *trans* regulation in yeasts. *Genome Res.* 20, 826–836