



# Corrigendum: Functional Urate-Associated Genetic Variants Influence Expression of lincRNAs *LINC01229* and *MAFTRR*

Megan Leask <sup>1,2</sup>, Amy Dowdle <sup>1</sup>, Hamish Salvesen <sup>1</sup>, Ruth Topless <sup>3</sup>, Tayaza Fadason <sup>4</sup>, Wenhua Wei <sup>5</sup>, William Schierding <sup>2,4</sup>, Judith Marsman <sup>1,2</sup>, Jisha Antony <sup>1</sup>, Justin M. O'Sullivan <sup>2,4</sup>, Tony R. Merriman <sup>2,3\*</sup> and Julia A. Horsfield <sup>1,2\*</sup>

<sup>1</sup> Department of Pathology, Dunedin School of Medicine, University of Otago, Dunedin, New Zealand, <sup>2</sup> Maurice Wilkins Centre for Molecular Biodiscovery, The University of Auckland, Auckland, New Zealand, <sup>3</sup> Department of Biochemistry, School of Biomedical Sciences, University of Otago, Dunedin, New Zealand, <sup>4</sup> Liggins Institute, The University of Auckland, Auckland, New Zealand, <sup>5</sup> Department of Women's and Children's Health, Dunedin School of Medicine, University of Otago, Dunedin, New Zealand

Keywords: enhancer, eQTL, gout, HNF4A, lincRNA, MAF, non-coding, serum urate

### **OPEN ACCESS**

### Approved by:

Frontiers in Genetics Editorial Office, Frontiers Media SA, Switzerland

### \*Correspondence:

Tony R. Merriman tony.merriman@otago.ac.nz Julia A. Horsfield julia.horsfield@otago.ac.nz

### Specialty section:

This article was submitted to Epigenomics and Epigenetics, a section of the journal Frontiers in Genetics

> Received: 01 April 2019 Accepted: 09 April 2019 Published: 24 April 2019

### Citation:

Leask M, Dowdle A, Salvesen H, Topless R, Fadason T, Wei W, Schierding W, Marsman J, Antony J, O'Sullivan JM, Merriman TR and Horsfield JA (2019) Corrigendum: Functional Urate-Associated Genetic Variants Influence Expression of lincRNAs LINC01229 and MAFTRR. Front. Genet. 10:382. doi: 10.3389/fgene.2019.00382

# A Corrigendum on

# Functional Urate-Associated Genetic Variants Influence Expression of lincRNAs LINC01229 and MAFTRR

by Leask, M., Dowdle, A., Salvesen, H., Topless, R., Fadason, T., Wei, W., et al. (2019). Front. Genet. 9:733. doi: 10.3389/fgene.2018.00733

### Addition of an Author

"Jisha Antony" was not included as an author in the published article. The corrected Author Contributions Statement appears below. The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

## **AUTHOR CONTRIBUTIONS**

ML, JH, JO, and TM designed the study. ML performed the functional annotations, the eQTL analyses, the enhancer assays, the *in situ* hybridization and the siRNA assays. HS isolated and cloned the rs4077450\_rs4077451 minor and major allele fragments into the plasmid constructs and was supervised by JM. AD carried out the luciferase assay and was supervised by JA. RT carried out the conditional analysis. WS and TF carried out the CoDeS3D analyses. ML, JH, and TM wrote the manuscript with input from JO and WW.

Copyright © 2019 Leask, Dowdle, Salvesen, Topless, Fadason, Wei, Schierding, Marsman, Antony, O'Sullivan, Merriman and Horsfield. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

1