



Corrigendum: Transcriptional Time Course After Rotator Cuff Tear

Laura S. Vasquez-Bolanos ^{1,2}, Michael C. Gibbons ^{1,2}, Severin Ruoss ², Isabella T. Wu², Mario Vargas-Vila ², Sydnee A. Hyman ^{1,2}, Mary C. Esparza ², Donald C. Fithian ², John G. Lane ², Anshuman Singh ^{2,3}, Chanond A. Nasamran ⁴, Kathleen M. Fisch ⁴ and Samuel R. Ward ^{1,2,5*}

¹ Department of Bioengineering, University of California, San Diego, San Diego, CA, United States, ² Department of Orthopaedic Surgery, University of California, San Diego, San Diego, CA, United States, ³ Department of Orthopaedic Surgery, Kaiser Permanente, San Diego, CA, United States, ⁴ Center for Computational Biology and Bioinformatics, Department of Medicine, University of California, San Diego, San Diego, CA, United States, ⁵ Department of Radiology, University of California, San Diego, CA, United States

Keywords: rotator cuff, rotator cuff muscle dysfunction, transcriptome (RNA-seq), time series data analysis, muscle biology, tenotomy, muscle atrophy

OPEN ACCESS

Edited and reviewed by:

Anselmo Sigari Moriscot, University of São Paulo, Brazil

*Correspondence:

Samuel R. Ward s1ward@ucsd.edu

Specialty section:

This article was submitted to Striated Muscle Physiology, a section of the journal Frontiers in Physiology

Received: 13 September 2021 Accepted: 07 October 2021 Published: 29 October 2021

Citation:

Vasquez-Bolanos LS, Gibbons MC, Ruoss S, Wu IT, Vargas-Vila M, Hyman SA, Esparza MC, Fithian DC, Lane JG, Singh A, Nasamran CA, Fisch KM and Ward SR (2021) Corrigendum: Transcriptional Time Course After Rotator Cuff Tear. Front. Physiol. 12:775297. doi: 10.3389/fphys.2021.775297

A Corrigendum on

Transcriptional Time Course After Rotator Cuff Tear

1

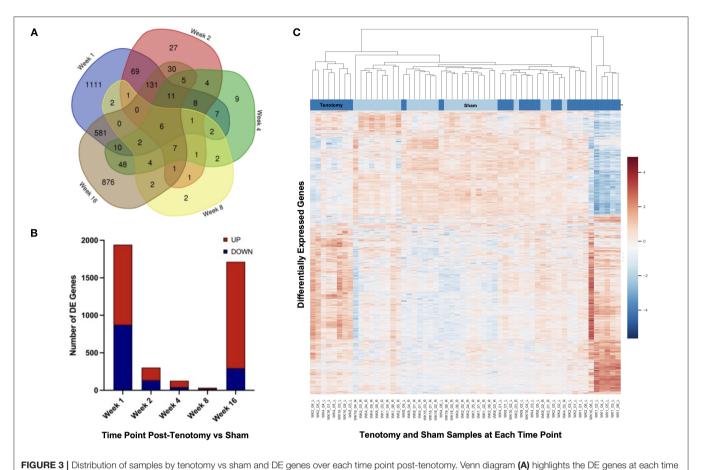
by Vasquez-Bolanos, L. S., Gibbons, M. C., Ruoss, S., Wu, I. T., Vargas-Vila, M., Hyman, S. A., Esparza, M. C., Fithian, D. C., Lane, J. G., Singh, A., Nasamran, C. A., Fisch, K. M., and Ward, S. R. (2021). Front. Physiol. 12:707116. doi: 10.3389/fphys.2021.707116

In the original article, there was a mistake in **Figure 3** as published. **An older version of the figure was published by mistake.** The corrected **Figure 3** 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.

Publisher's Note: All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

Copyright © 2021 Vasquez-Bolanos, Gibbons, Ruoss, Wu, Vargas-Vila, Hyman, Esparza, Fithian, Lane, Singh, Nasamran, Fisch and Ward. 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.



point and the overlap with other time points. The bar chart (B) displays the number of DE genes which are up or down regulated at each timepoint. Data in the heatmap (C) is presented as normalized expression for each tenotomy and sham sample at each time point post-tenotomy with a z-score scale by rows and an average hierarchical clustering by columns.