

Universal Patterns of Selection in Cancer and Somatic Tissues

Iñigo Martincorena,* Keiran M. Raine, Moritz Gerstung, Kevin J. Dawson, Kerstin Haase, Peter Van Loo, Helen Davies, Michael R. Stratton, and Peter J. Campbell*

*Correspondence: im3@sanger.ac.uk (I.M.), pc8@sanger.ac.uk (P.J.C.)
<https://doi.org/10.1016/j.cell.2018.06.001>

(Cell 171, 1029–1041.e1–e15; November 16, 2017)

It has come to our attention that in the Results and Discussion of the above article, we neglected to cite Davoli et al. (2013). This paper identified several of the cancer driver genes we mentioned in our paper and provided estimates of the number of genes under positive selection in cancer. The text and references in the online version of our paper have been corrected accordingly. We apologize for the omission and any inconvenience it may have caused to the scientific community.

REFERENCES

Davoli, T., Xu, A.W., Mengwasser, K.E., Sack, L.M., Yoon, J.C., Park, P.J., and Elledge, S.J. (2013). Cumulative haploinsufficiency and triplosensitivity drive aneuploidy patterns and shape the cancer genome. *Cell* 155, 948–962.

© 2018 The Author(s). Published by Elsevier Inc.

This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Mfd Dynamically Regulates Transcription via a Release and Catch-Up Mechanism

Tung T. Le, Yi Yang, Chuang Tan, Margaret M. Suhanovsky, Robert M. Fulbright, Jr., James T. Inman, Ming Li, Jaeyoon Lee, Sarah Perelman, Jeffrey W. Roberts, Alexandra M. Deaconescu, and Michelle D. Wang*

*Correspondence: mwang@physics.cornell.edu
<https://doi.org/10.1016/j.cell.2018.06.002>

(Cell 172, 344–357.e1–e7; January 11, 2018)

Our paper reported a mechanism where *E. coli* transcription-coupled repair factor Mfd utilizes DNA translocation to dynamically regulate transcription. We have identified three minor errors in the manuscript. The first error is located in the Results section, in the paragraph entitled “Mfd Translocates on Its Own.” The sentence originally read: “If the translocase moves *toward* the fork, dsDNA is unzipped, whereas if the translocase moves *away* from the fork, dsDNA is rezippped.” However, it should read: “If the translocase moves *away* from the fork, dsDNA is unzipped, whereas if the translocase moves *toward* the fork, dsDNA is rezippped.” The second text error is located in the legend of Figure 5A: “See also Figure S6.” should read “See also Figure S5.” Finally, an incorrect grant number is listed in the Acknowledgements; grant number MCB-0820293 should be MCB-1517764. These errors have now been corrected in the online version of the paper. We apologize for any inconvenience they may have caused to the readers.

© 2018 Elsevier Inc.

