

Published in final edited form as: *Cell.* 2018 June 14; 173(7): 1823. doi:10.1016/j.cell.2018.06.002.

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, Peter J. Campbell*

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 AW, Mengwasser KE, Sack LM, Yoon JC, Park PJ, Elledge SJ. 2013; Cumulative haploinsufficiency and triplosensitivity drive aneuploidy patterns and shape the cancer genome. Cell. 155:948–962. [PubMed: 24183448]

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

^{*}Correspondence: im3@sanger.ac.uk (I.M.), pc8@sanger.ac.uk (P.J.C.).