Corrigendum
Oviz-Bio: a web-based platform for interactive cancer genomics data visualization
Jia, Wenlong; Li, Hechen; Li, Shiyi; Chen, Lingxi; Li, Shuai Cheng

Published in:
Nucleic Acids Research

Published: 20/08/2020

Document Version:
Final Published version, also known as Publisher’s PDF, Publisher’s Final version or Version of Record

License:
CC BY-NC

Publication record in CityU Scholars:
Go to record

Published version (DOI):
10.1093/nar/gkaa553

Publication details:

Citing this paper
Please note that where the full-text provided on CityU Scholars is the Post-print version (also known as Accepted Author Manuscript, Peer-reviewed or Author Final version), it may differ from the Final Published version. When citing, ensure that you check and use the publisher’s definitive version for pagination and other details.

General rights
Copyright for the publications made accessible via the CityU Scholars portal is retained by the author(s) and/or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights. Users may not further distribute the material or use it for any profit-making activity or commercial gain.

Publisher permission
Permission for previously published items are in accordance with publisher's copyright policies sourced from the SHERPA RoMEO database. Links to full text versions (either Published or Post-print) are only available if corresponding publishers allow open access.

Take down policy
Contact lbscholars@cityu.edu.hk if you believe that this document breaches copyright and provide us with details. We will remove access to the work immediately and investigate your claim.
Corrigendum

Oviz-Bio: a web-based platform for interactive cancer genomics data visualization

Wenlong Jia1,†, Hechen Li1,†, Shiyong Li1, Lingxi Chen1 and Shuai Cheng Li1,2,*

1Department of Computer Science, City University of Hong Kong, Kowloon Tong 999077, Hong Kong and
2Department of Biomedical Engineering, City University of Hong Kong, Kowloon Tong 999077, Hong Kong


In Figure 1, the protein layer of gene PIK3CA should start from the NO.2 exon. An updated figure is provided below, and the published article has been updated.

This correction does not affect the results and conclusions of the article.

REFERENCE

Figure 1. Demo representation of the ‘Mut On Genes’ visualization and features. Mutations on gene *PIK3CA* are displayed in three layers (genome, cDNA and protein), which can be switched by clicking layer tags. Mutations are denoted by different icons according to their types and function changes. Icons have tooltips containing related sample list. Exons and mutations are linked among the three layers to support synchronous highlights. Function domains are denoted by colored areas in the protein layer. The mutation list is downloaded from the TumorPortal database (40).