Genome **Biology**

Open Access

Erratum to: gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens

Fabian Schmich[1,2], Ewa Szczurek[1,2], Saskia Kreibich[3], Sabrina Dilling[3], Daniel Andritschke[3], Alain Casanova[4], Shyan Huey Low[4], Simone Eicher[4], Simone Muntwiler[4], Mario Emmenlauer[4], Pauli Rämo[4], Raquel Conde-Alvarez[5], Christian von Mering[2,6], Wolf-Dietrich Hardt[3], Christoph Dehio[4] and Niko Beerenwinkel[1,2]*

After the publication of this work [1], some content was missing from the Acknowledgements section. The corrected Acknowledgements section is given below:

Author details
[1]Department of Biosystems Science and Engineering, ETH, Zurich, Switzerland. [2]SIB Swiss Institute of Bioinformatics, Basel, Switzerland. [3]Department of Biology, ETH, Zurich, Switzerland. [4]Biozentrum, University of Basel, Basel, Switzerland. [5]Institute for Tropical Health and Departamento de Microbiología y Parasitología, Universidad de Navarra, Pamplona, Spain. [6]Institute of Molecular Life Sciences, University of Zurich, Zurich, Switzerland.

Reference
1. Schmich F, Szczurek E, Kreibich S, Dilling S, Andritschke D, Casanova A, et al. gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens. Genome Biol. 2015;16:220.

Submit your next manuscript to BioMed Central and take full advantage of:

- **Convenient online submission**
- **Thorough peer review**
- **No space constraints or color figure charges**
- **Immediate publication on acceptance**
- **Inclusion in PubMed, CAS, Scopus and Google Scholar**
- **Research which is freely available for redistribution**

Submit your manuscript at
www.biomedcentral.com/submit

BioMed Central

* Correspondence: niko.beerenwinkel@bsse.ethz.ch
[1]Department of Biosystems Science and Engineering, ETH, Zurich, Switzerland
[2]SIB Swiss Institute of Bioinformatics, Basel, Switzerland
Full list of author information is available at the end of the article