## **ERRATUM**

**Open Access** 



# Erratum to: How can functional annotations be derived from profiles of phenotypic annotations?

Beatriz Serrano-Solano<sup>1</sup>, Antonio Díaz Ramos<sup>2</sup>, Jean-Karim Hériché<sup>3</sup> and Juan A. G. Ranea<sup>1,4\*</sup>

### **Erratum**

Upon publication of this article [1], it was brought to our attention that Table 1 was incorrectly presented. The correct Table 1 is shown below and has been updated in the original article.

#### Author details

<sup>1</sup>Department of Molecular Biology and Biochemistry, University of Málaga, Boulevard Louis Pasteur, 29071 Málaga, Spain. <sup>2</sup>Department of Algebra, Geometry and Topology, University of Málaga, Boulevard Louis Pasteur, 29071 Málaga, Spain. <sup>3</sup>European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany. <sup>4</sup>CIBER de Enfermedades raras (CIBERER), Madrid, Spain.

#### Received: 15 March 2017 Accepted: 15 March 2017 Published online: 27 March 2017

#### Reference

Serrano-Solano B, et al. How can functional annotations be derived from 1 profiles of phenotypic annotations? BMC Bioinformatics. 2017;18:96. doi:10. 1186/s12859-017-1503-5.

\* Correspondence: ranea@uma.es

<sup>1</sup>Department of Molecular Biology and Biochemistry, University of Málaga, Boulevard Louis Pasteur, 29071 Málaga, Spain

<sup>4</sup>CIBER de Enfermedades raras (CIBERER), Madrid, Spain



© The Author(s), 2017 Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.

Experiment	Description	Phenotypes	IDs in CMPO
CellMorph [3]	Genome-wide RNAi screen that examines changes in the morphology of individual HeLa cells within cell populations.	<ul> <li>Decreased cell number</li> <li>Cell with projections</li> <li>Elongated cell</li> <li>More lamellipodia cells</li> <li>Increased number of actin filament</li> <li>Round cell</li> <li>Increased cell size</li> <li>Decreased cell size</li> <li>Bright nuclei</li> <li>Metaphase arrested</li> <li>Increased cell size in population</li> </ul>	CMPO:0000052 CMPO:0000071 CMPO:0000077 CMPO:0000105 CMPO:0000105 CMPO:00001128 CMPO:0000128 CMPO:0000129 CMPO:0000154 CMPO:0000305 CMPO:0000340
MitoCheck [2]	Genome-wide RNAi screen for genes required for chromosome segregation in HeLa cells. The screen also reports genes involved in other processes such as cell movement.	<ul> <li>Cell death</li> <li>Increased nucleus size</li> <li>Graped micronucleus</li> <li>Abnormal nucleus shape</li> <li>Mitosis delayed</li> <li>Binuclear cell</li> <li>Absence of mitotic chromosome decondensation</li> <li>Increased cell movement speed</li> <li>Increased cell movement distance</li> <li>Proliferating cells</li> <li>Metaphase delayed</li> <li>Abnormal chromosome segregation</li> <li>Prometaphase delayed</li> <li>Increased variability of nuclear shape in population</li> <li>Mitotic metaphase plate congression</li> </ul>	CMPO:0000030 CMPO:0000140 CMPO:0000157 CMPO:0000202 CMPO:0000213 CMPO:0000236 CMPO:0000237 CMPO:0000237 CMPO:0000344 CMPO:0000345 CMPO:0000348
EMBL secretion [4]	Genome-wide RNAi screen for interference with ER-to-plasma membrane transport of the secretory cargo protein tsO45G in HeLa cells.	<ul> <li>Increased rate of protein secretion</li> <li>Mild decrease in rate of protein secretion</li> <li>Strong decrease in rate of protein secretion</li> <li>Decreased rate of intracellular protein transport</li> </ul>	CMPO:0000246 CMPO:0000318 CMPO:0000319 CMPO:0000346
GR00053 [10]	Genome-wide RNAi screen for genes involved in DNA damage responses in HeLa cells.	- Increased number of site of double-strand break	CMPO:0000182
GR00290 [9]	Genome-wide RNAi screen for genes regulating centriole formation in HeLa cells.	- Increased centriole replication - Decreased centriole replication	CMPO:0000361 CMPO:0000362
Copenhagen DNA damage Ubiquitin [8]	RNAi screen of >1300 genes involved in the ubiquitin-proteasome system or encoding zinc-finger proteins looking for modulators of cellular responses to ionizing radiation in HeLa and U2OS cells.	- Decreased number of site of double-strand brea	CMPO:0000181
EMBL chromosome condensation [7]	RNAi screen of 100 bioinformatically- selected genes for changes in mitotic prophase duration in HeLa cells.	- Increased duration of mitotic prophase - Decreased duration of mitotic prophase	CMPO:0000328 CMPO:0000329

Table 1 Set of 36 phenotypes obtained from the listed siRNA experiments sorted by its CMPO identifier