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CORRECTION

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# Correction: MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts

Andrea Hita<sup>1,2</sup>, Gilles Brocart<sup>1</sup>, Ana Fernandez<sup>1,2</sup>, Marc Rehmsmeier<sup>2</sup>, Anna Alemany<sup>3†</sup> and Sol Schwartzman<sup>1\*†</sup> 

The original article can be found online at <https://doi.org/10.1186/s12859-021-04544-3>.

<sup>†</sup>Anna Alemany and Sol Schwartzman contributed equally to this work

\*Correspondence: [sol.schwartzman@diagenode.com](mailto:sol.schwartzman@diagenode.com)

<sup>1</sup> Epigenetics Unit, Diagenode s.a., Liège, Belgium  
Full list of author information is available at the end of the article

## Correction to: BMC Bioinformatics (2022) 23:39

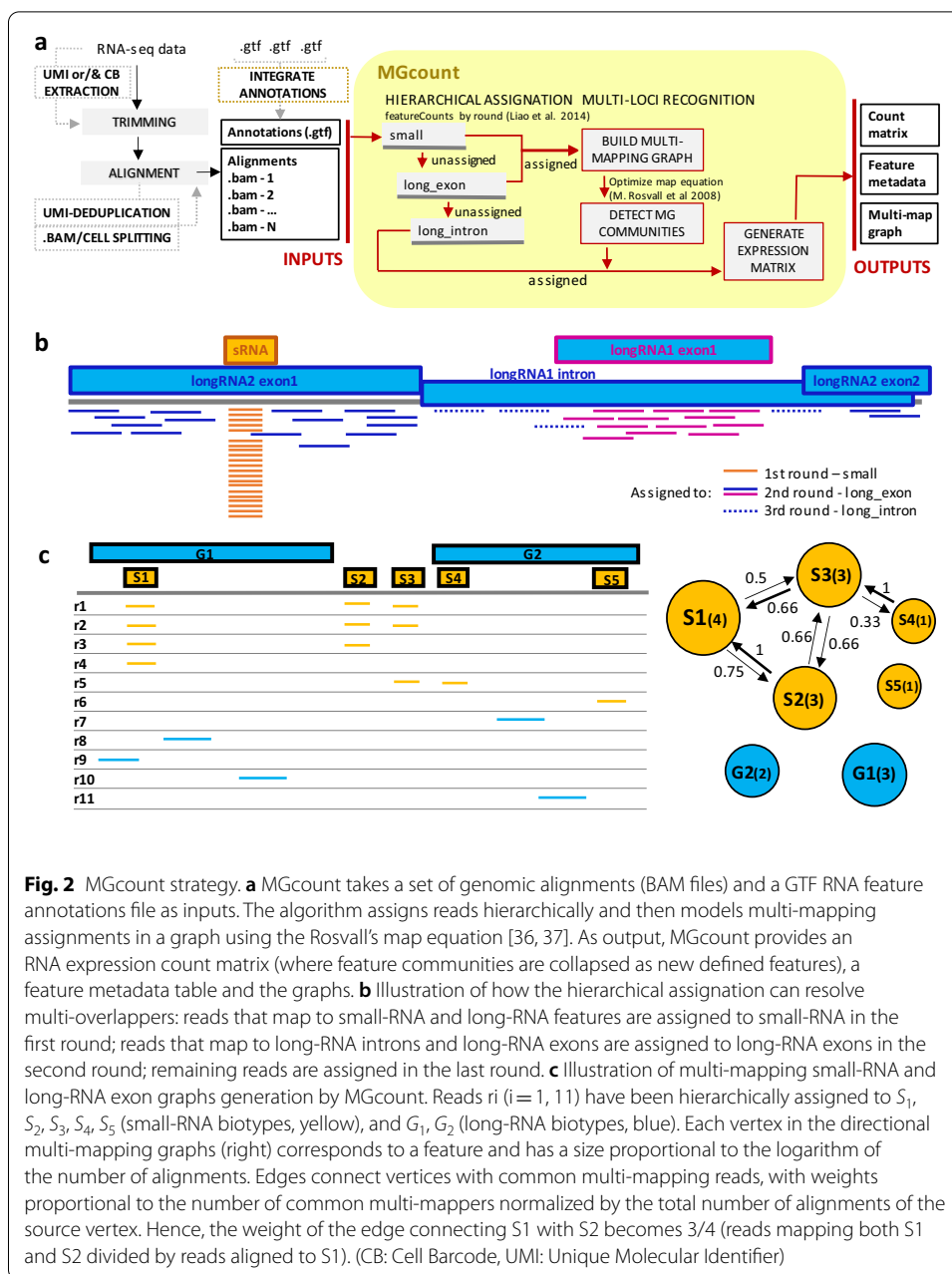
<https://doi.org/10.1186/s12859-021-04544-3>

Following the publication of the original article [1], the authors identified an error in Fig. 2 and caption 2c. The correct figure is given below, and the caption has been updated from “Reads  $r_i$  ( $i = 1, 10$ )” to “Reads  $r_i$  ( $i = 1, 11$ ).”

The original article [1] has been corrected.



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**Fig. 2** MGcount strategy. **a** MGcount takes a set of genomic alignments (BAM files) and a GTF RNA feature annotations file as inputs. The algorithm assigns reads hierarchically and then models multi-mapping assignments in a graph using the Rosvall’s map equation [36, 37]. As output, MGcount provides an RNA expression count matrix (where feature communities are collapsed as new defined features), a feature metadata table and the graphs. **b** Illustration of how the hierarchical assignation can resolve multi-overlappers: reads that map to small-RNA and long-RNA features are assigned to small-RNA in the first round; reads that map to long-RNA introns and long-RNA exons are assigned to long-RNA exons in the second round; remaining reads are assigned in the last round. **c** Illustration of multi-mapping small-RNA and long-RNA exon graphs generation by MGcount. Reads  $r_i$  ( $i = 1, 11$ ) have been hierarchically assigned to  $S_1, S_2, S_3, S_4, S_5$  (small-RNA biotypes, yellow), and  $G_1, G_2$  (long-RNA biotypes, blue). Each vertex in the directional multi-mapping graphs (right) corresponds to a feature and has a size proportional to the logarithm of the number of alignments. Edges connect vertices with common multi-mapping reads, with weights proportional to the number of common multi-mappers normalized by the total number of alignments of the source vertex. Hence, the weight of the edge connecting  $S_1$  with  $S_2$  becomes  $3/4$  (reads mapping both  $S_1$  and  $S_2$  divided by reads aligned to  $S_1$ ). (CB: Cell Barcode, UMI: Unique Molecular Identifier)

**Author details**

<sup>1</sup>Epigenetics Unit, Diagenode s.a., Liège, Belgium. <sup>2</sup>Department of Biology, Humboldt-Universität Zu Berlin, Berlin, Germany. <sup>3</sup>Department of Anatomy and Embryology, Leiden University Medical Centre, Leiden, The Netherlands.

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