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CORRECTION

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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 ri (i = 1, 10)" to " Reads ri (i = 1, 11)."

The original article [1] has been corrected.

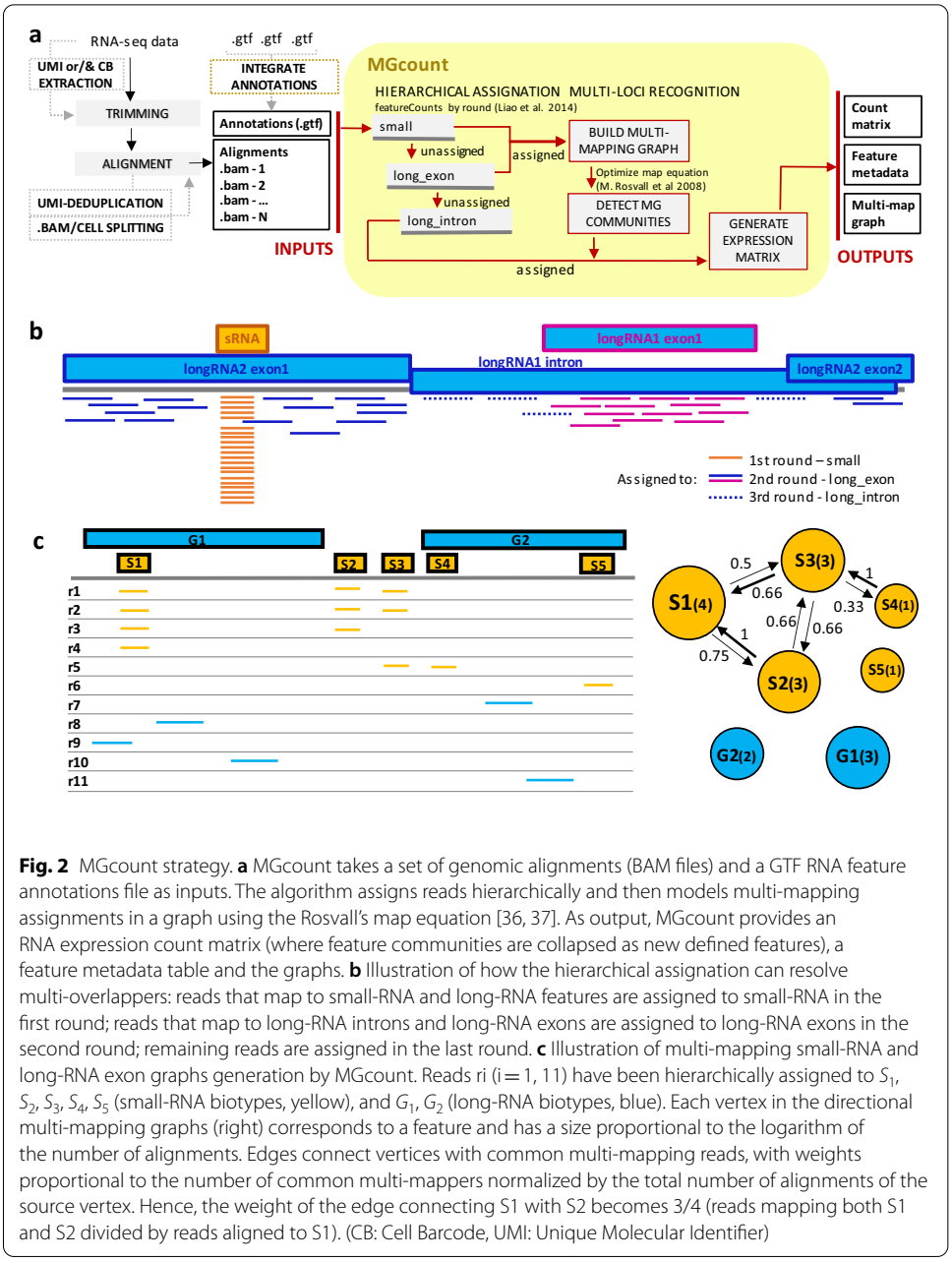

Fig. 2 MGcount strategy. **a** MGcount takes a set of genomic alignments (BAM files) and a GTF RNA feature annotations file as inputs. The algorithm assigns reads hierarchically and then models multi-mapping assignments in a graph using the Rosvall's map equation [36, 37]. As output, MGcount provides 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 ri (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 S1 with S2 becomes 3/4 (reads mapping both S1 and S2 divided by reads aligned to S1). (CB: Cell Barcode, UMI: Unique Molecular Identifier)

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